



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 10:16 PM UTC

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:

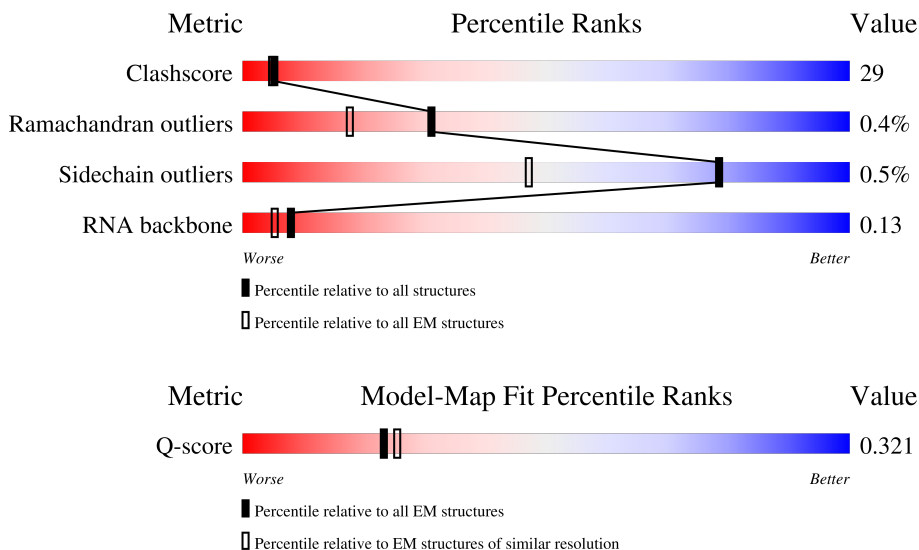
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	18998	 94%
1	2	18998	 97%
2	h	166	 16% 43% 51% 5%

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Mol	Chain	Length	Quality of chain
3	aw	139	24% 60% 40%
4	m	325	24% 52% 36% 11%
5	f	371	15% 21% 19% 60%
6	s	179	25% 47% 45% 8%
7	au	247	32% 48% 49%
8	am	313	30% 45% 42% 13%
9	n	171	27% 39% 44% 17%
10	ae	655	20% 52% 37% 11%
11	ay	169	21% 46% 37% 17%
12	ag	564	34% 54% 44%
13	aj	397	10% 42% 38% 20%
14	e	822	26% 60% 38%
15	d	351	19% 59% 39%
16	az	163	14% 51% 44% 6%
17	ax	184	26% 52% 36% 12%
18	r	467	17% 54% 42%
19	af	835	16% 38% 32% 30%
20	u	890	26% 47% 32% 21%
21	aa	1813	24% 48% 36% 16%
22	ab	1177	34% 56% 42%
23	ak	325	36% 39% 43% 18%
24	ac	1267	32% 47% 40% 12%
25	ad	811	31% 45% 40% 14%
26	an	302	21% 56% 44%
27	ao	291	17% 33% 32% 34%

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Mol	Chain	Length	Quality of chain
28	ap	245	17% 54% 44%
29	aq	295	48% 34% 38% 28%
30	as	270	47% 49% 42% 9%
31	at	397	42% 30% 21% 49%
32	y	485	15% 33% 25% 42%
33	w	190	54% 45% 36% 18%
34	v	214	9% 15% 14% 71%
35	t	267	41% 42% 42% 15%
36	p	321	11% 40% 33% 26%
37	j	189	42% 47% 48% 5%
38	l	677	32% 39% 41% 19%
39	ar	282	32% 45% 44% 11%
40	av	236	35% 34% 29% 36%
41	ai	379	23% 62% 38%
42	x	268	19% 59% 35% 5%
43	i	429	18% 32% 30% 38%
44	g	192	31% 30% 21% 48%
45	o	604	35% 43% 29% 27%
46	c	311	32% 44% 37% 19%
47	k	312	12% 21% 16% 63%
48	q	425	9% 23% 23% 54%
49	b	159	25% 45% 52%
50	a	431	35% 50% 44% 5%
51	ba	94	27% 21% 6% 72%
52	z	1169	19% 50% 32% 17%

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Mol	Chain	Length	Quality of chain
53	bd	89	13% 10% 36% 54%
54	A	466	35% 49% 29% 21%
55	B	435	31% 55% 43%
56	C	261	15% 43% 38% 19%
57	D	204	41% 34% 28% 37%
58	E	345	38% 52% 43% 6%
59	F	171	51% 50% 48%
60	G	373	28% 51% 45%
61	H	167	31% 49% 47%
62	I	304	30% 43% 41% 15%
63	J	143	46% 49% 48%
64	K	193	44% 45% 48% 7%
65	L	185	50% 56% 40%
66	M	278	25% 46% 45% 7%
67	N	251	12% 49% 27% 25%
68	O	475	31% 36% 27% 35%
69	P	184	17% 44% 45% 10%
70	Q	233	20% 51% 42% 7%
71	R	479	29% 59% 40%
72	S	408	14% 21% 16% 63%
73	T	82	18% 33% 34% 33%
74	U	117	21% 38% 33% 7% 21%
75	V	150	23% 45% 49% 6%
76	W	185	11% 18% 10% 71%
77	X	512	32% 54% 36% 9%

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Mol	Chain	Length	Quality of chain
78	Y	292	
79	Z	197	
80	BA	167	
81	UA	203	
82	BB	156	
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	
95	Aa	195	
96	Ao	284	
97	BM	457	
98	Ar	205	
99	Aj	503	
100	BH	229	
101	Am	340	
102	Aq	341	

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Mol	Chain	Length	Quality of chain
103	BE	118	
104	Ak	323	
105	BP	254	
106	Ad	237	
107	BF	109	
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	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
124	ZN	BG	1401	-	-	X	-
124	ZN	T	101	-	-	X	-

2 Entry composition

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
			Total	C	N	O	P		
1	2	604	12723	5725	2119	4275	604	0	0
1	1	1084	22858	10292	3832	7650	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
			Total	C	N	O	S		
2	h	157	1311	831	248	224	8	0	0

- Molecule 3 is a protein called mS69.

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

- Molecule 4 is a protein called bS18m.

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

- Molecule 5 is a protein called uS11m.

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

- Molecule 6 is a protein called mS33.

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

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

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

- Molecule 8 is a protein called mS59.

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

- Molecule 9 is a protein called uS19m.

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

- Molecule 10 is a protein called mS53.

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

- Molecule 11 is a protein called mS71.

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

- 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
			Total	C	N	O	S		
19	af	585	4698	2963	853	857	25	0	0

- Molecule 20 is a protein called mS35.

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

- Molecule 21 is a protein called mS48.

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

- Molecule 22 is a protein called mS49.

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

- Molecule 23 is a protein called mS58.

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

- Molecule 24 is a protein called mS50.

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

- Molecule 25 is a protein called mS51.

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

- 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
			Total	C	N	O	S		
54	A	368	2996	1929	496	556	15	0	0

- Molecule 55 is a protein called uL4m.

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

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

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

- Molecule 57 is a protein called uL10m.

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
89	At	165	1346	824	260	254	8	0	0

- Molecule 90 is a protein called mL96.

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

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

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

- Molecule 92 is a protein called mL69.

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

- Molecule 93 is a protein called mL80.

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

- Molecule 94 is a protein called mL87.

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

- Molecule 95 is a protein called mL42.

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

- Molecule 96 is a protein called mL79.

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

- Molecule 97 is a protein called mL70.

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

- Molecule 98 is a protein called mL84.

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

- Molecule 99 is a protein called mL72.

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

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

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

- Molecule 101 is a protein called mL75.

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

- Molecule 102 is a protein called mL82.

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

- 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
			Total	C	N	O	S		
117	Ax	167	1388	876	268	233	11	0	0

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

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

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

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

- Molecule 120 is a protein called mL100.

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

- Molecule 121 is a protein called UB.

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

- Molecule 122 is a protein called UC.

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

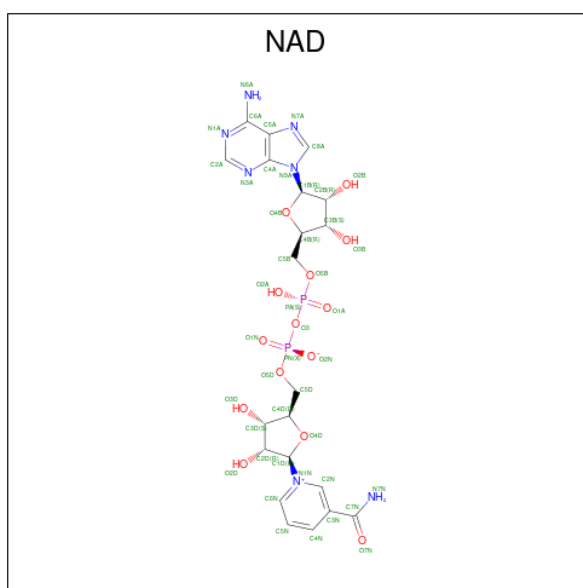
- Molecule 123 is a protein called UD.

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

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

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

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



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

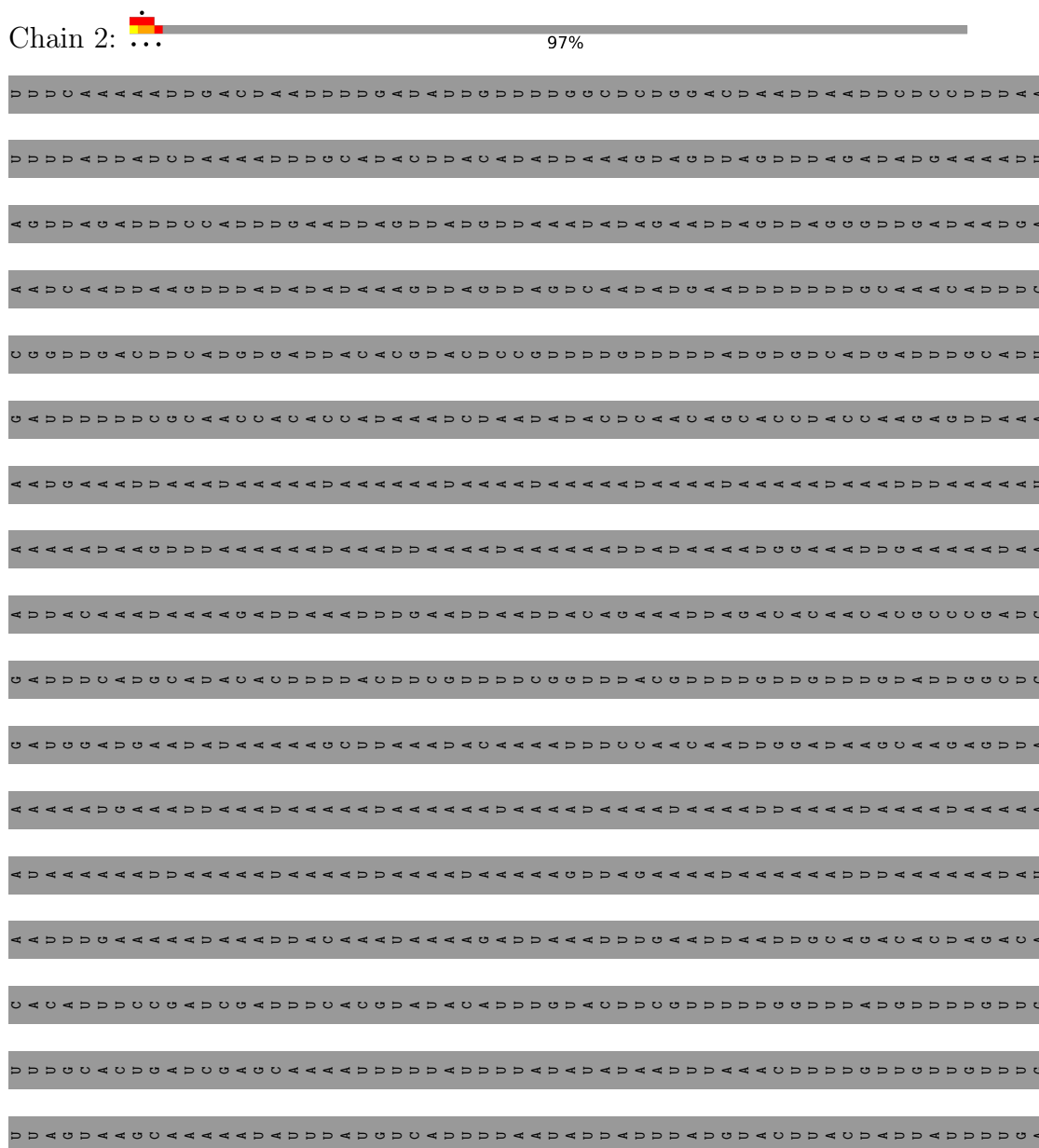
- Molecule 126 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

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



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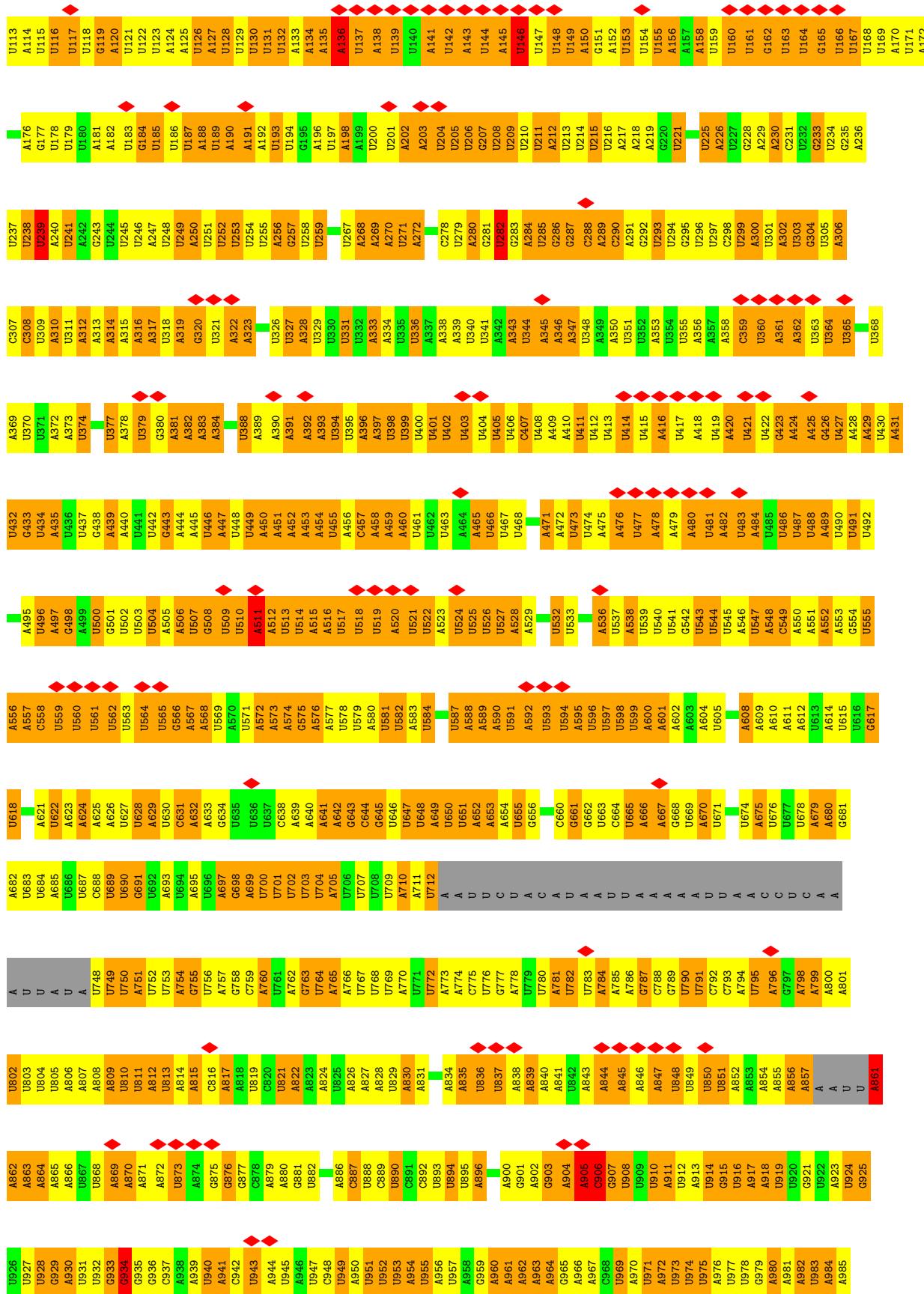
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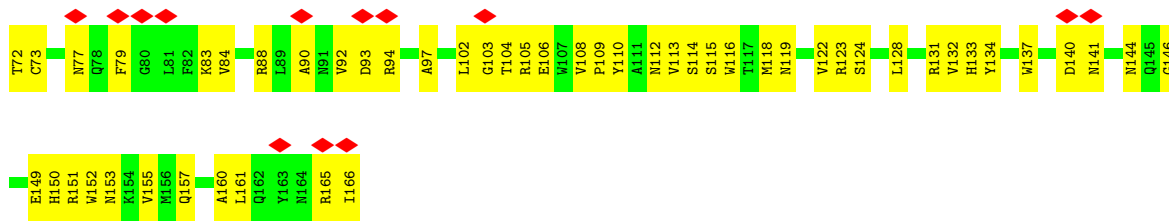
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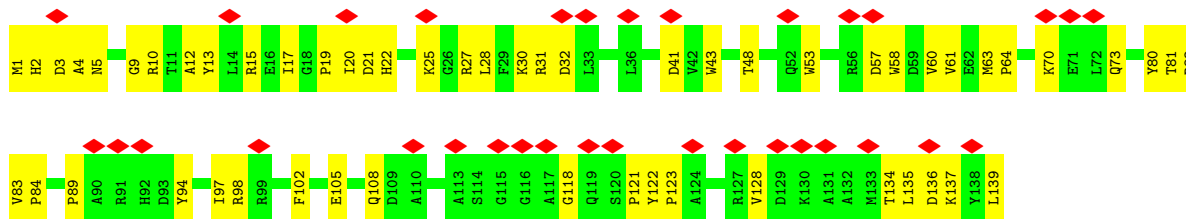
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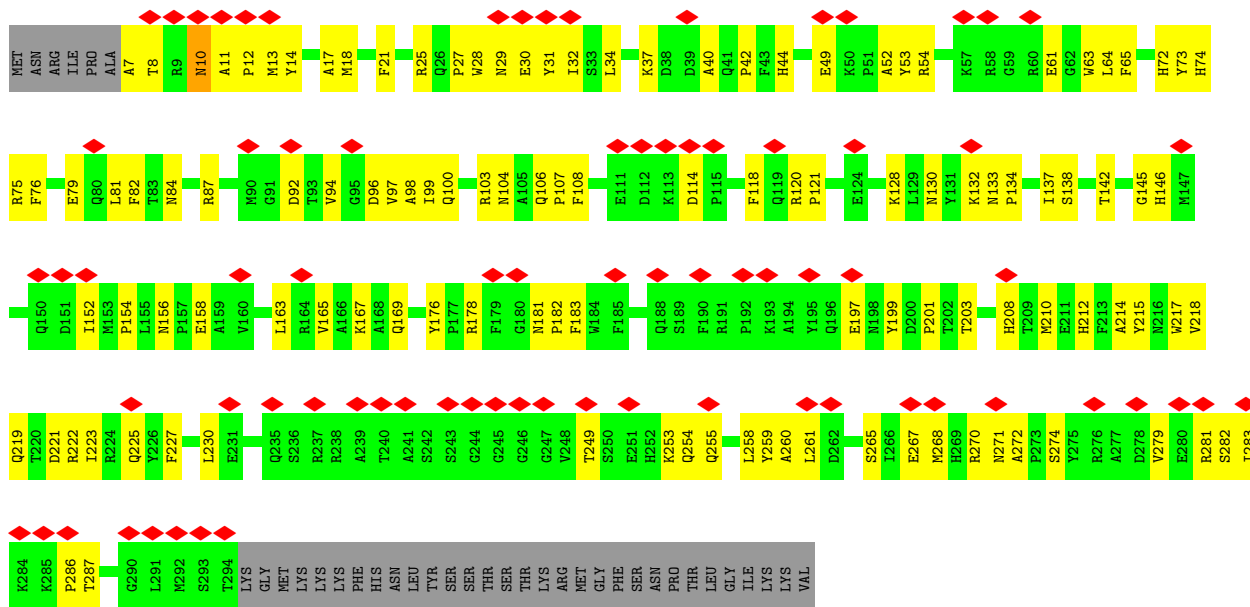
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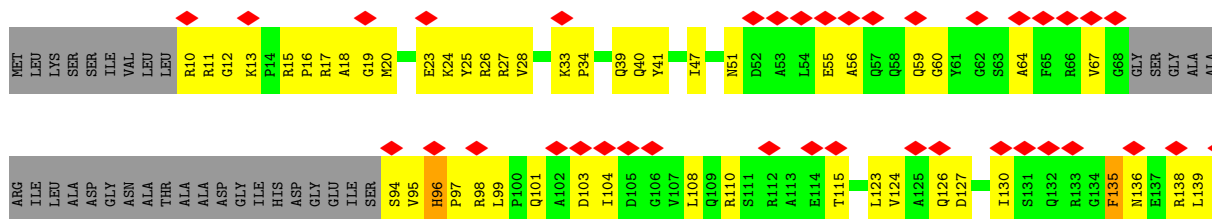
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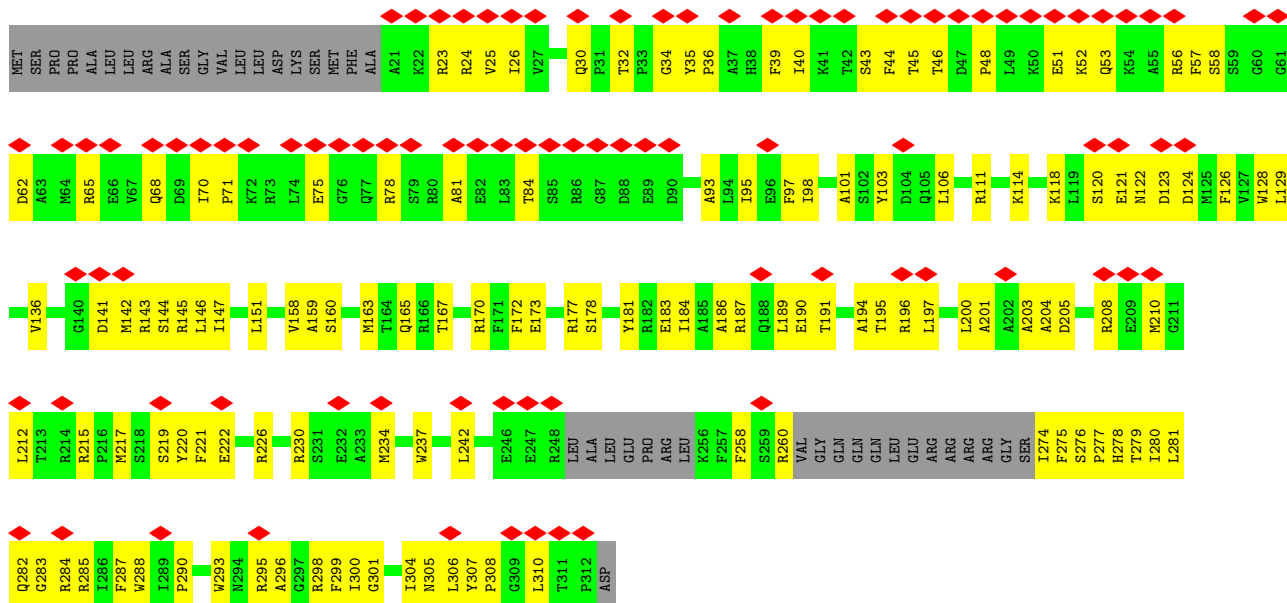


• Molecule 4: bS18m

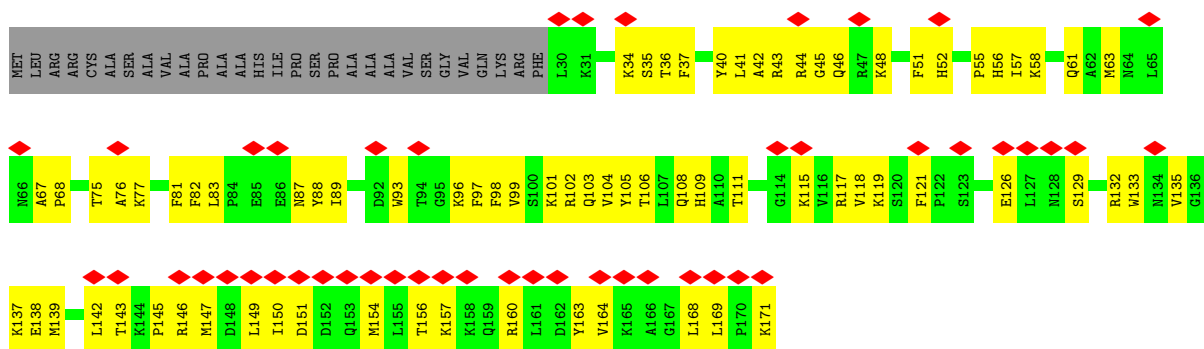


• Molecule 5: uS11m

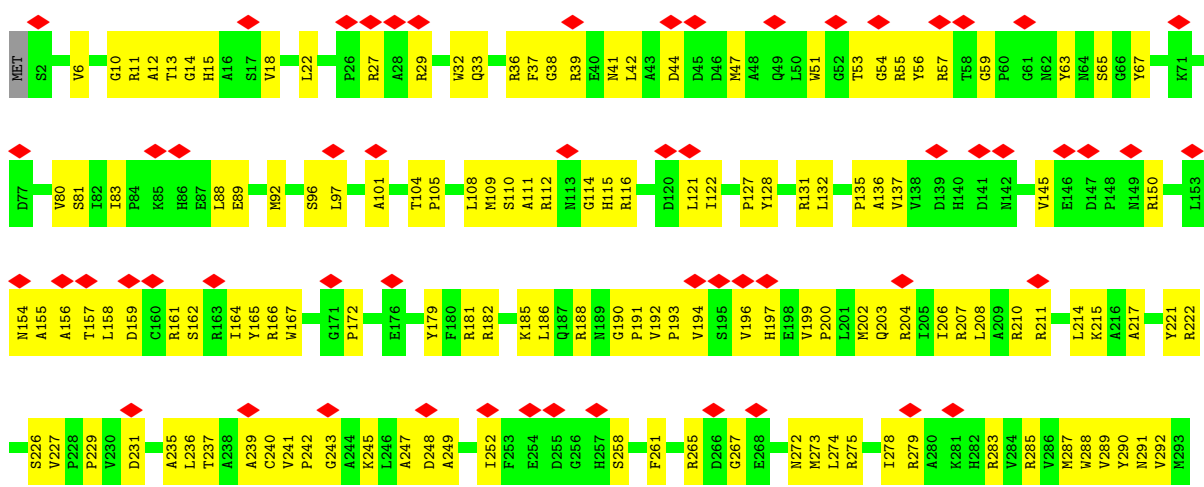


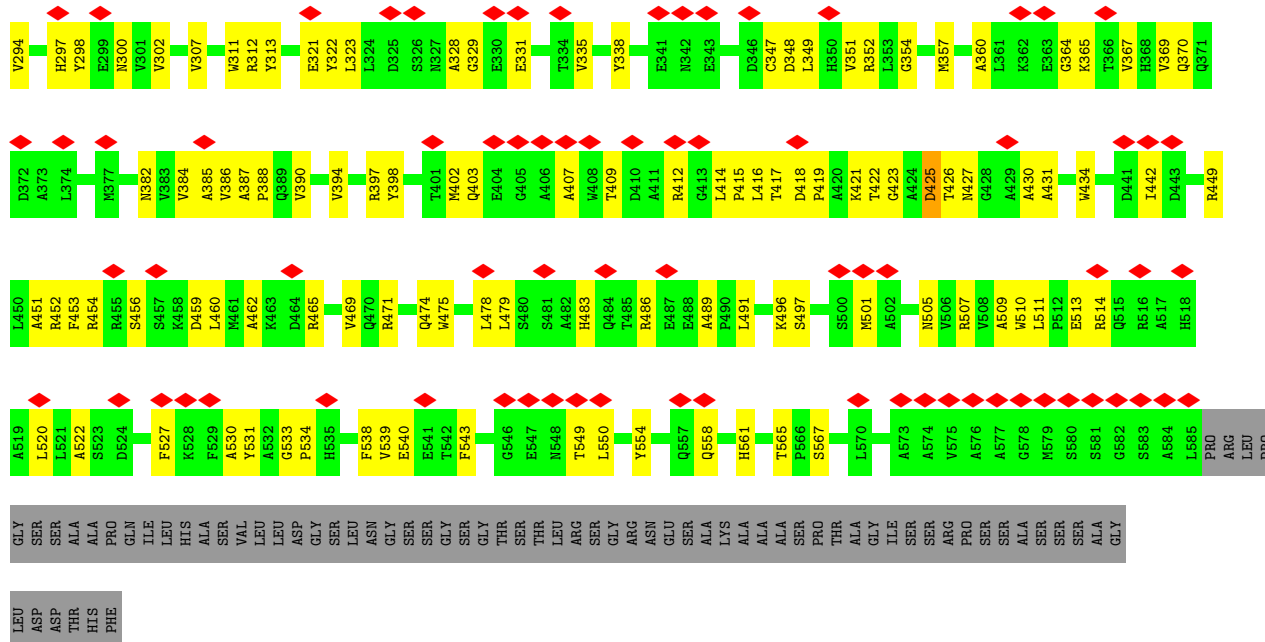


• Molecule 9: uS19m

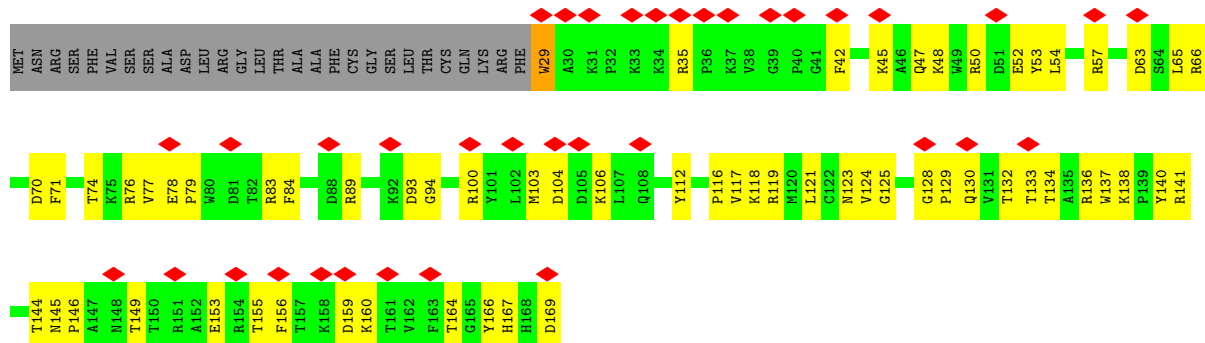


• Molecule 10: mS53

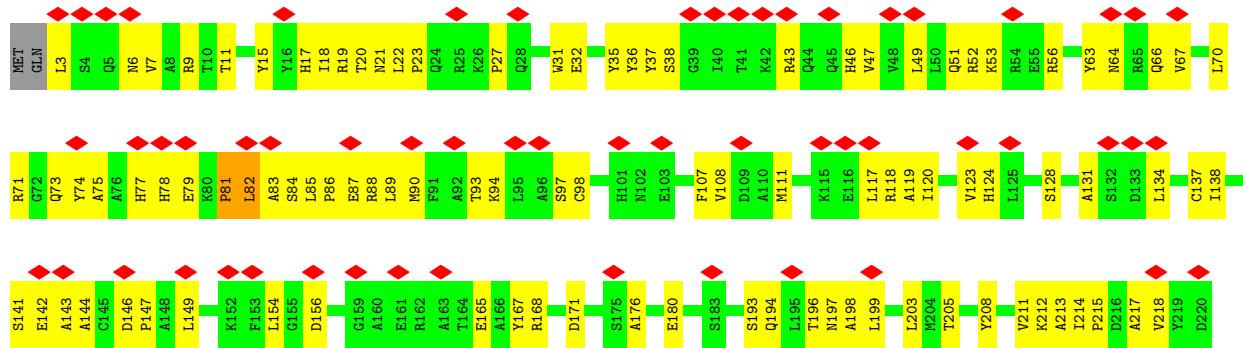


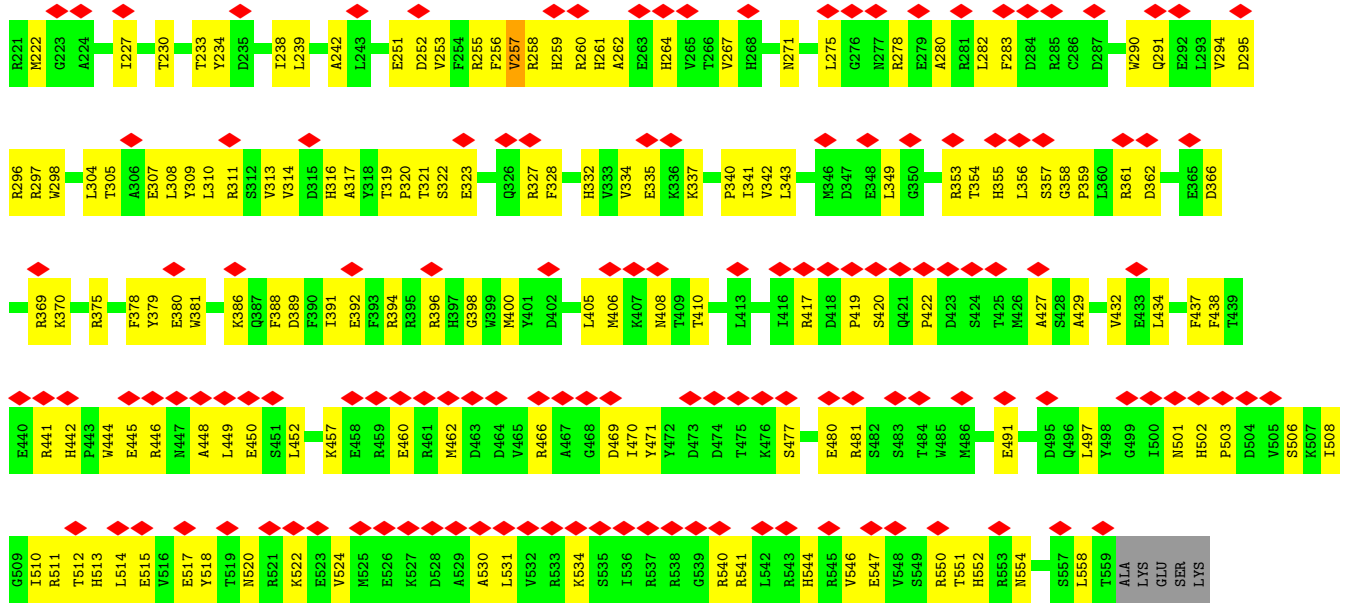


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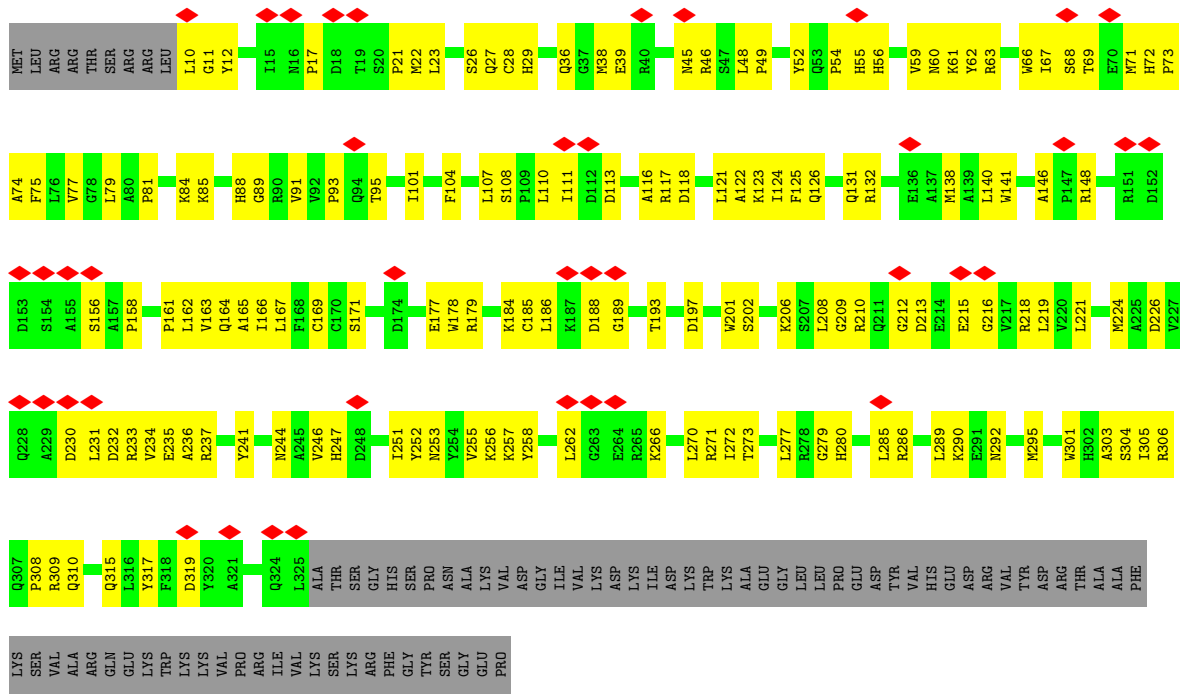


● Molecule 12: mS55

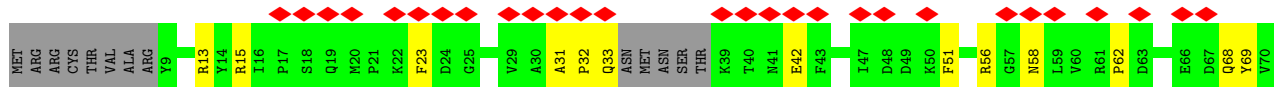


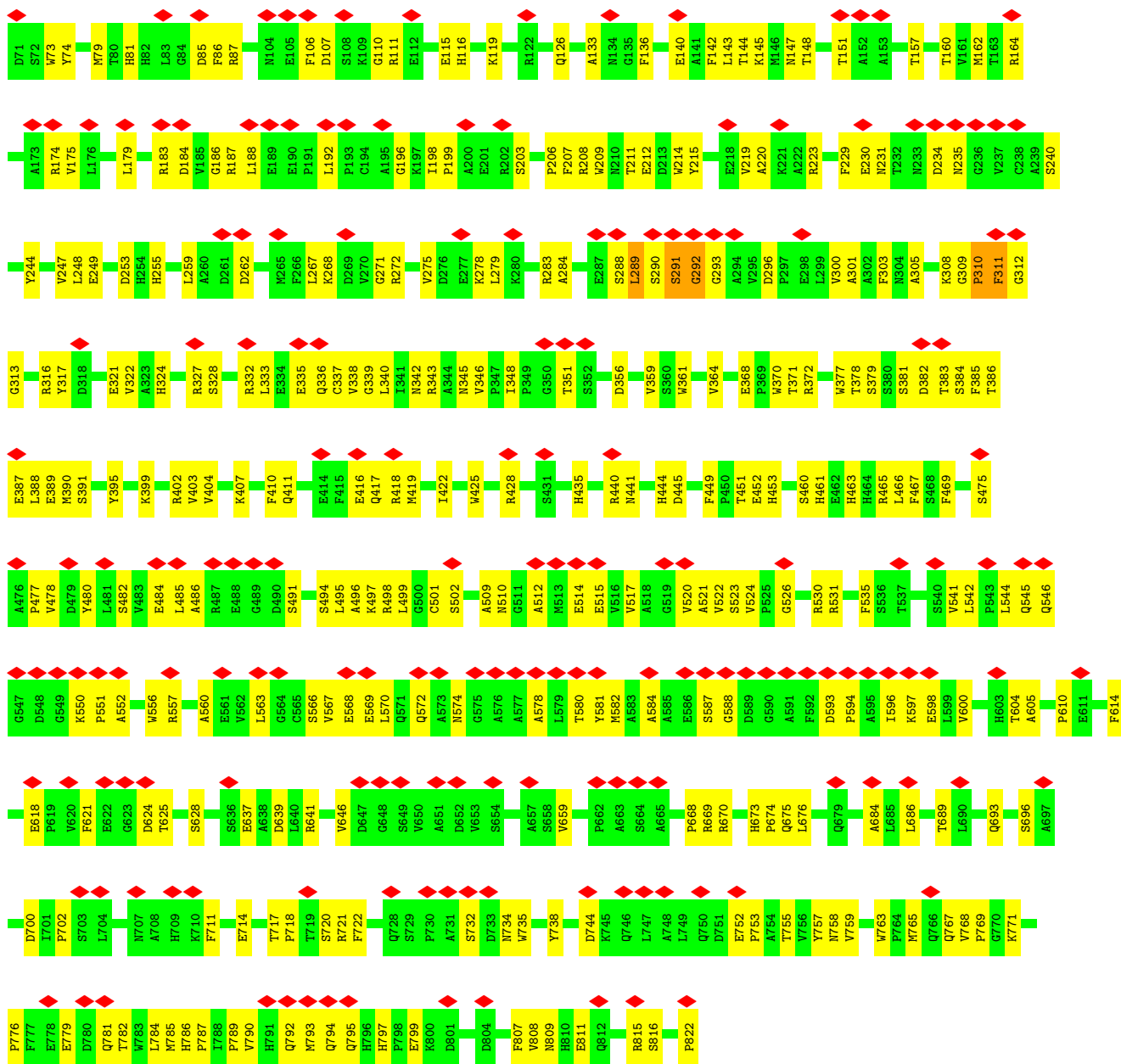


• Molecule 13: mS57

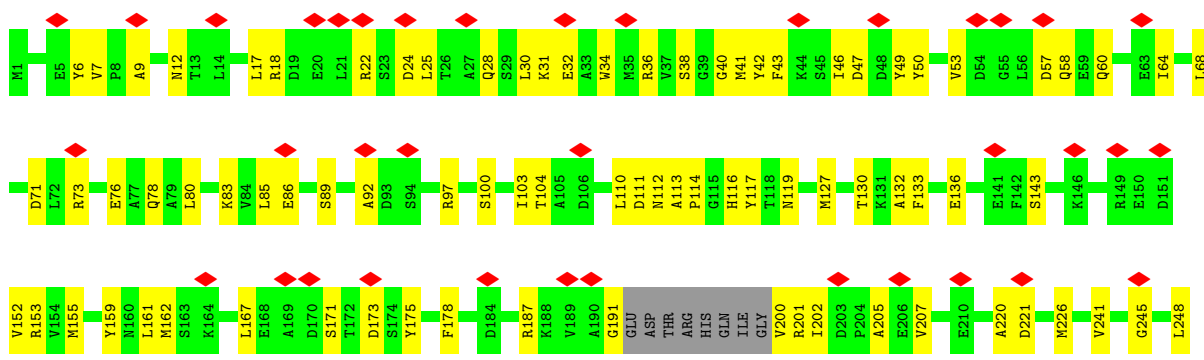


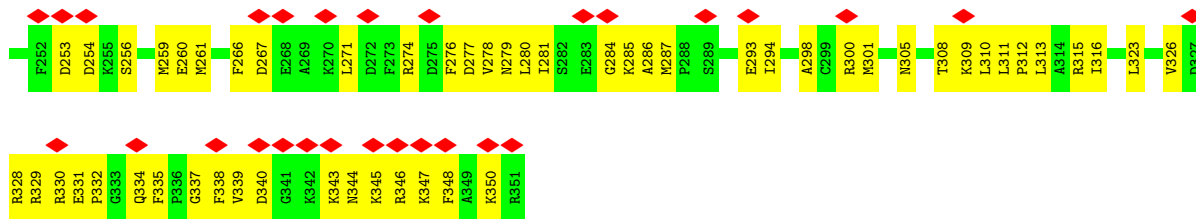
• Molecule 14: uS10m



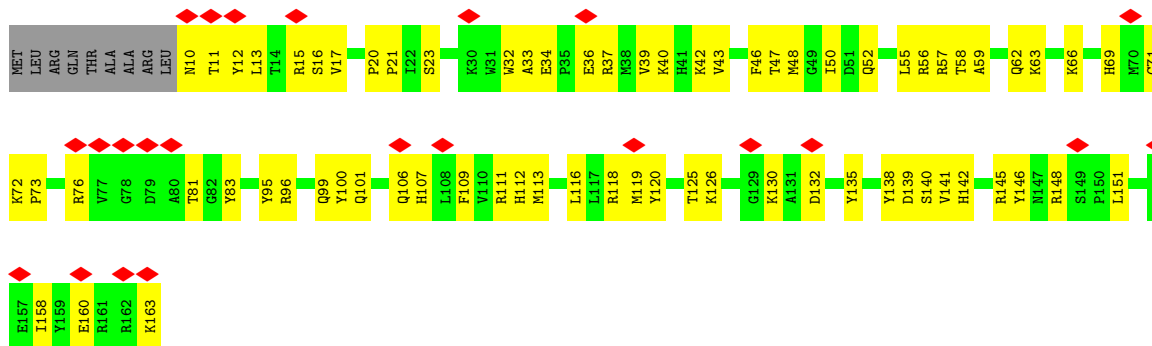


• Molecule 15: uS9m

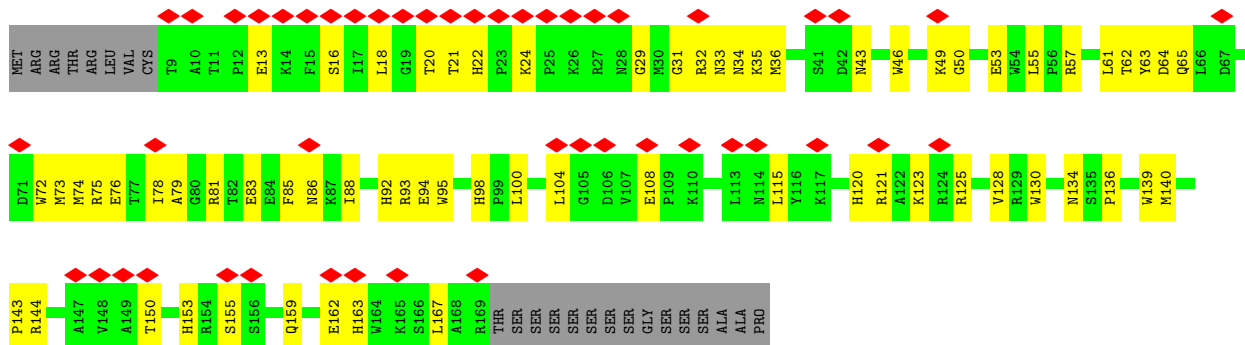




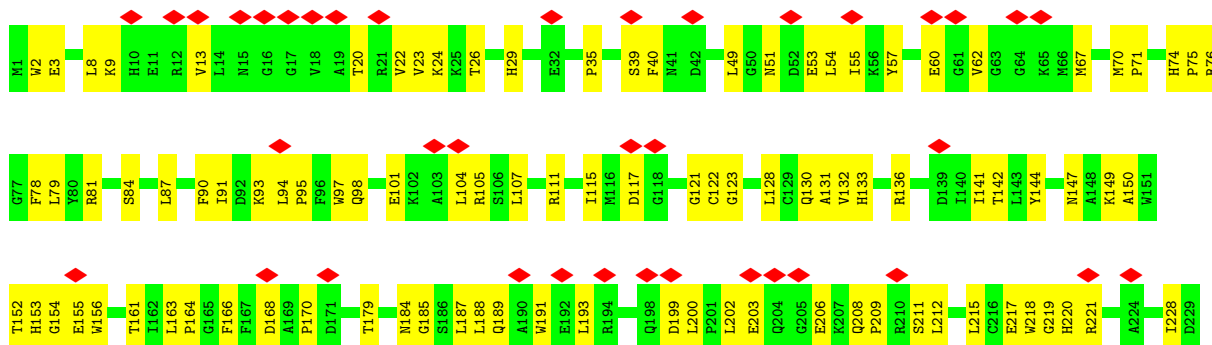
• Molecule 16: mS72

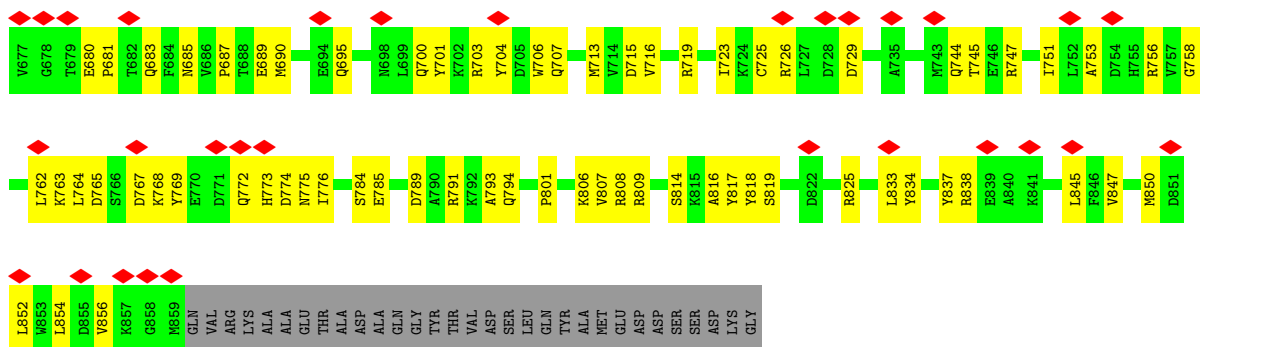


• Molecule 17: mS70

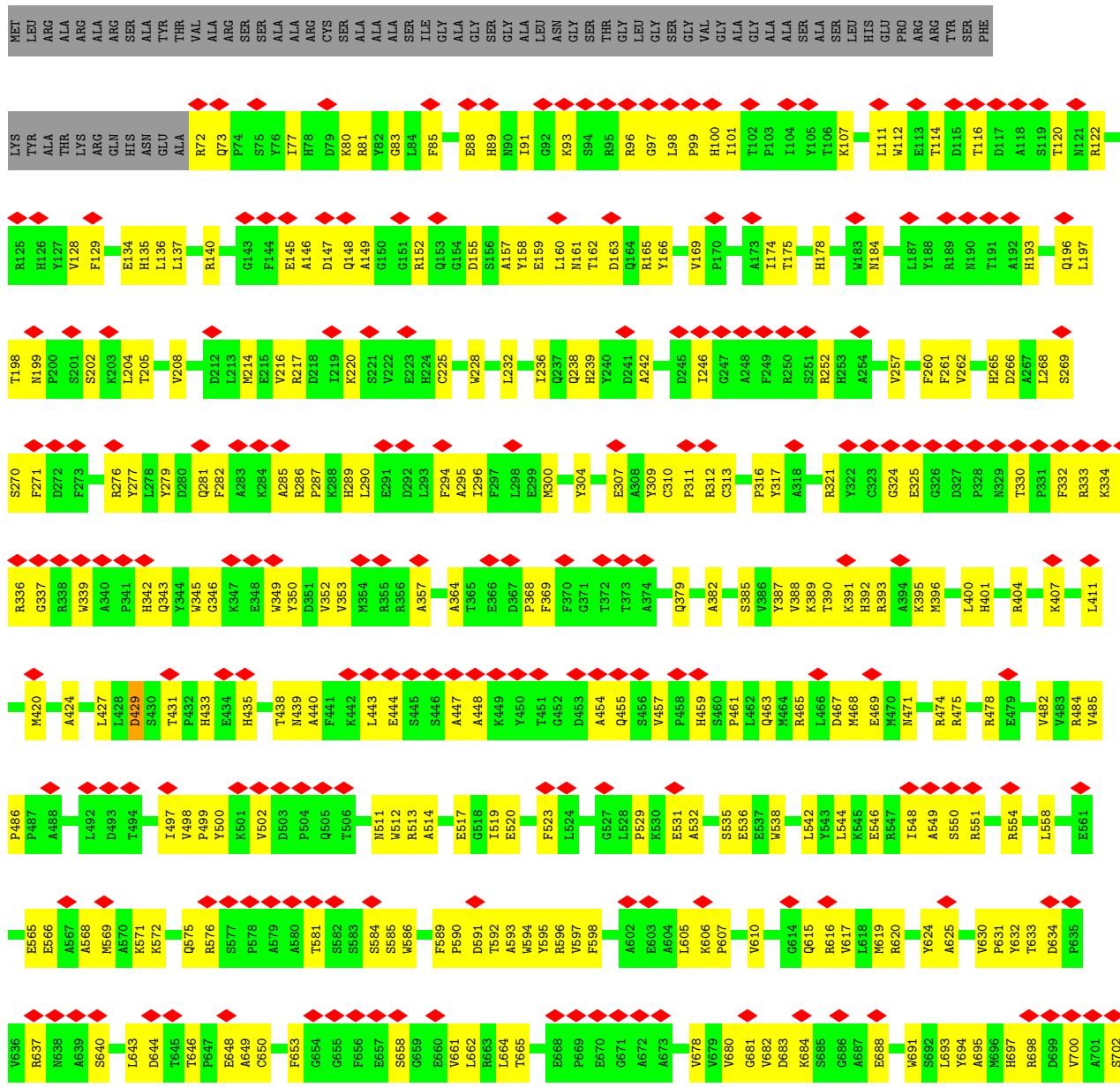


• Molecule 18: mS29

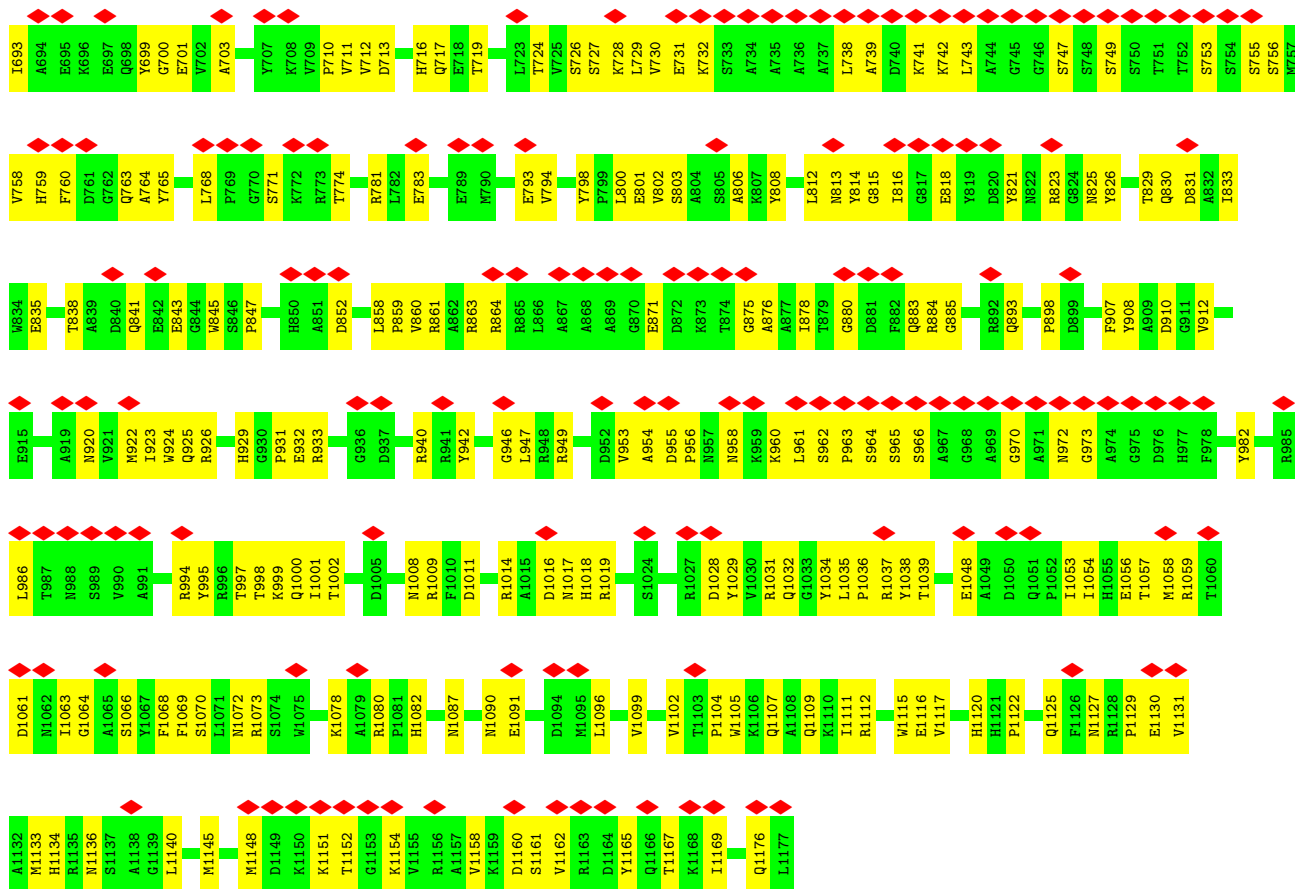




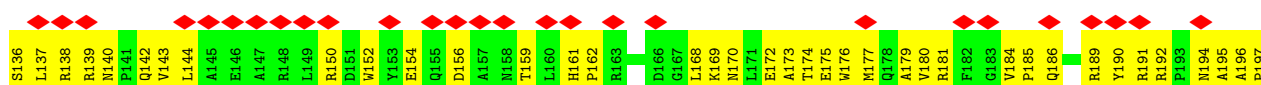
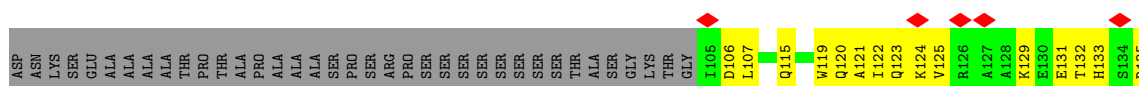
• Molecule 21: mS48



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Y1486	V1489	R1490	L1491	L1492	P1493	P1494	E1495	I1496	G1497	F1498	F1499	E1502	L1505	L1506	E1507	R1516	R1517	Y1518	G1519	I1520	L1521	A1522	G1523	P1524	A1525	R1526	V1527	P1528	A1529	S1530	G1531	F1532	I1533	A1534	A1535	M1536	C1537	K1538	S1539	L1540	T1541	Y1542	M1543	R1546	E1549	Y1550	V1551	T1555	E1556	Q1559						
M1280	R1281	V1282	T1283	P1284	T1287	S1288	M1289	R1292	Q1296	C1297	P1298	E1299	K1300	E1301	L1302	L1303	L1304	G1305	G1306	F1307	F1308	L1309	V1310	P1311	L1314	I1315	F1316	S1317	TRP	ASN	GLY	PRO	GLN	SER	ASN	VAL	SER	ALA	ALA	THR	ASN	SER	SER	SER	SER	ASN	ALA	ALA	ASN	ASN	ALA	GLY	ALA	ARG	SER	GLY
ALA	GLY	SER	ILE	ALA	VAL	GLN	GLN	MET	LEU	GLU	ARC	THR	ARG	HIS	GLY	SER	PRD	GLY	SER	SER	GLY	SER	SER	SER	SER	GLY	D1370	K1373	M1374	V1375	G1376	K1377	V1378	L1379	E1380	E1381	A1383	W1384	D1387	G1388	V1389	A1390	V1393	L1394	M1400	P1404	T1405	L1406	E1407	Q1408	E1409	M1412	M1420			
L1139	P1142	C1143	ALA	ASP	ALA	SER	ALA	ALA	ASP	SER	ILE	G1153	G1158	C1159	D1163	V1164	D1165	A1168	F1169	A1170	L1171	E1172	H1173	A1174	S1176	Q1177	F1178	R1179	G1180	D1181	SER	ASP	GLU	PRO	Y1186	Q1192	R1193	GLY	MET	SER	SER	GLY	GLY	ASN	ALA	LEU	G1131	L1132	SER	PRO						
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S771	E772	R775	S776	V777	L781	T786	Q789	L790	Y791	K792	L793	Q794	T795	L796	T797	D798	A799	D800	G801	E802	P803	R804	L805	L806	Q807	E808	P809	W812	R813	T814	R817	N818	D819	F820	V821	D822	E823	R824	L825	K826	E827	L828	E829	F833	K834	R835	E836	L837	W838	A839	S840	L841				



• Molecule 23: mS58

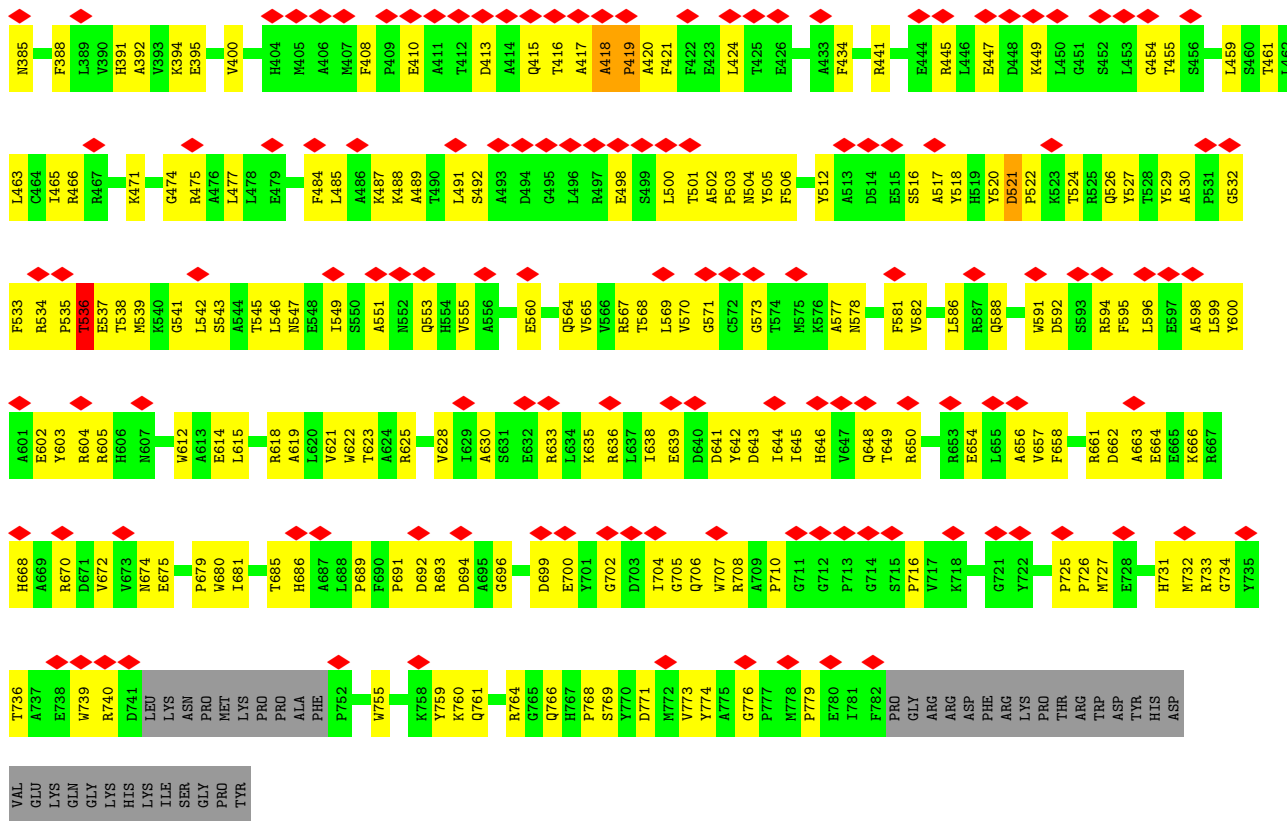


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 PHE
 THR
 GLN

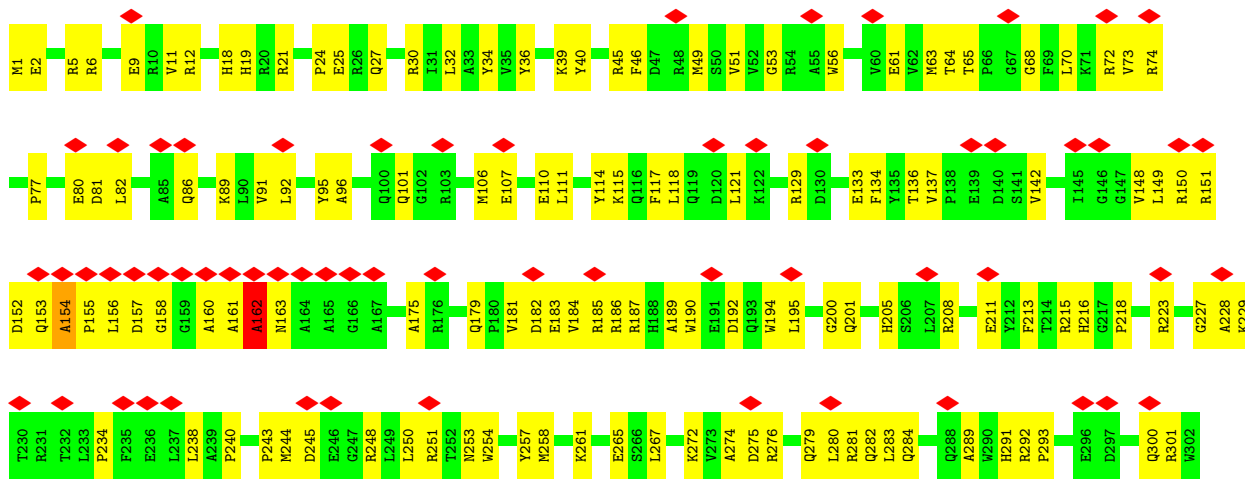
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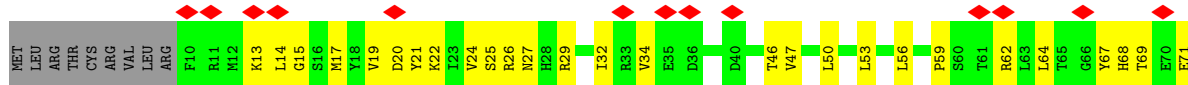
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SER	CYS	VAL	VAL	VAL	ALA	ALA	SER	ALA	ALA	ALA	PRO	ARG	VAL	ARG	THR	THR	LEU	LEU	ASP	MET	VAL	VAL	Y85	T86	P87	I88	Y89	A90	P91	D92	P93	A94	H97	L98	L101	R102	S103	A104	D105	E106	C107	R108	T109	L110	W111	A112	Q113	H114	I115	P116	V117	P118	S119	L120	T121	R122		
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F190	E191	T192	V195	R196	R199	Q200	R203	T204	S205	K206	F337	R207	Y208	T209	K341	Q210	V211	LEU	GLY	ALA	ALA	ALA	GLY	ARG	GLY	ARG	K285	P286	D287	A288	P289	V290	Q291	F292	F293	E294	A295	F296	Q297	Q298	T300	R303	I304	P305	L306	P309	S310	T311	W312	V313	H314	T175	E249	A250	D251	T252	F253	F254
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G391	A392	A393	A394	A396	T397	E398	W401	M404	E405	K408	E409	Q410	R411	R412	M413	D414	E415	G416	V417	D419	P420	E421	D422	L423	L424	D425	T426	T427	A428	E429	W430	K436	I437	Q438	A439	I440	L441	E442	Q443	P444	L445	T446	S447	S448	C449	M451	G452	E453	K454	S455	Y456	G457						
F458	S459	L460	Q461	D462	F463	W464	L465	H466	R469	A472	V476	H477	E480	S481	E482	S483	L484	A485	R486	A490	R494	E498	L501	P502	D503	F505	A506	G507	L508	E509	E510	S511	V512	A513	K514	A515	R516	L517	D518	L519	R520	L524	K525	F526	H527	F528	N529	S530	V531									
R534	M535	H536	K539	F540	A543	S544	Q547	H548	T549	H550	A552	S553	H554	Q555	L556	L557	F558	H559	Y560	A561	A562	S563	T564	Q565	V566	V567	A571	E572	M573	Y574	Y575	A576	T577	K578	P579	L580	Q583	L584	D585	Y586	A587	S588	P589	Y590	T591	F592	R593	H598	H599	R602								
V605	E606	H609	Q612	L615	L616	L617	S618	A619	A620	P621	L622	A623	K624	A625	V628	I629	G630	R631	R634	Q635	F640	R643	R644	Y648	Q652	Q656	R657	L658	L659	M660	P661	V662	K663	S664	V665	Q666	V667	T668	A669	P670	A671	P672	E673	L674	L675	A676	A677	G678										
A679	D680	L681	L682	T683	I684	L685	R686	E687	E688	R689	T690	P691	K692	A693	K694	A695	A696	T697	G697	E698	A699	W703	F704	G706	S707	R708	Q709	T710	V711	S712	Y713	D714	W715	T716	D721	K722	L723	R724	D727	S728	S729	A732	E733	Q734	A735	R738	L741	R742	G745	R746	L747	E748						
T749	S750	L751	W752	R753	R754	W755	T756	E758	E759	R760	Q761	K762	W763	R764	E766	K769	E770	A771	V772	D773	V774	T781	F782	V783	E786	Y790	H793	L794	Y795	R796	K797	L798	T799	R800	GLU	GLN	GLN	GLN	GLU	GLN	TYR	SER	ASP	THR	VAL	VAL	PRO	THR	PRO	PRO	ALA	TRP						
ASP	GLU	ALA	SER	G823	E824	H825	V826	F827	M830	L831	D832	D833	D834	L837	S838	E839	T840	Q841	S842	T843	E844	Y845	F846	Y849	D850	R851	A852	A853	G854	R855	R856	L857	P858	Y862	R863	V864	A865	V866	R867	D870	R871	E872	L873	H874	P875	T876	E877	H878	L881	M882	S883	A884	A885					

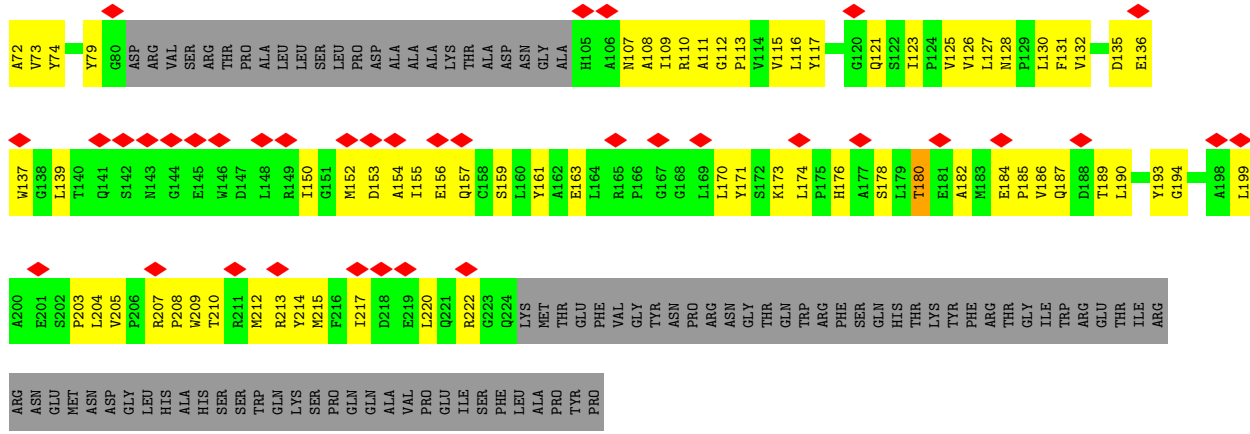


• Molecule 26: mS60

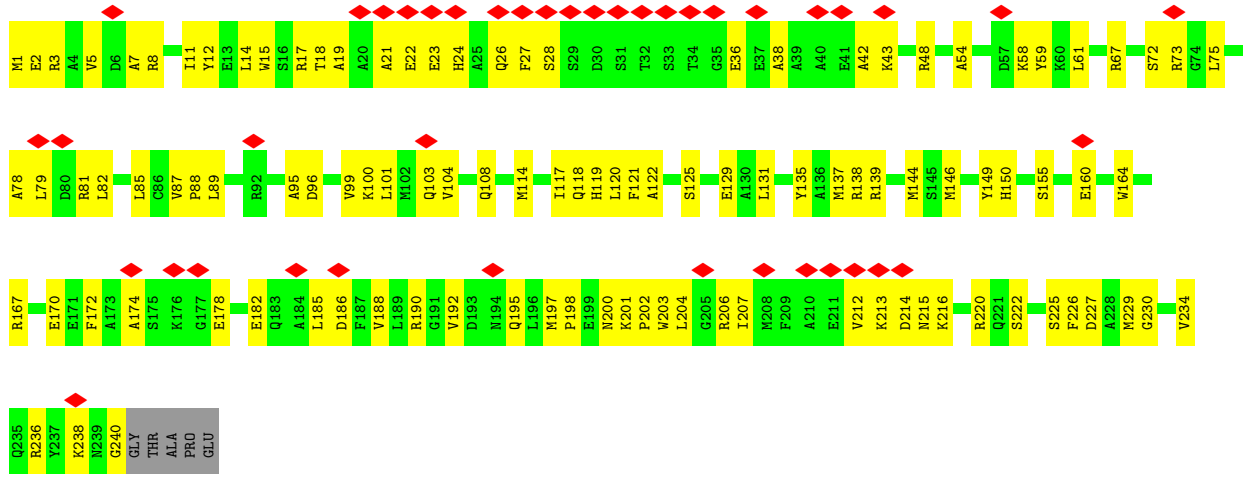


• Molecule 27: mS61

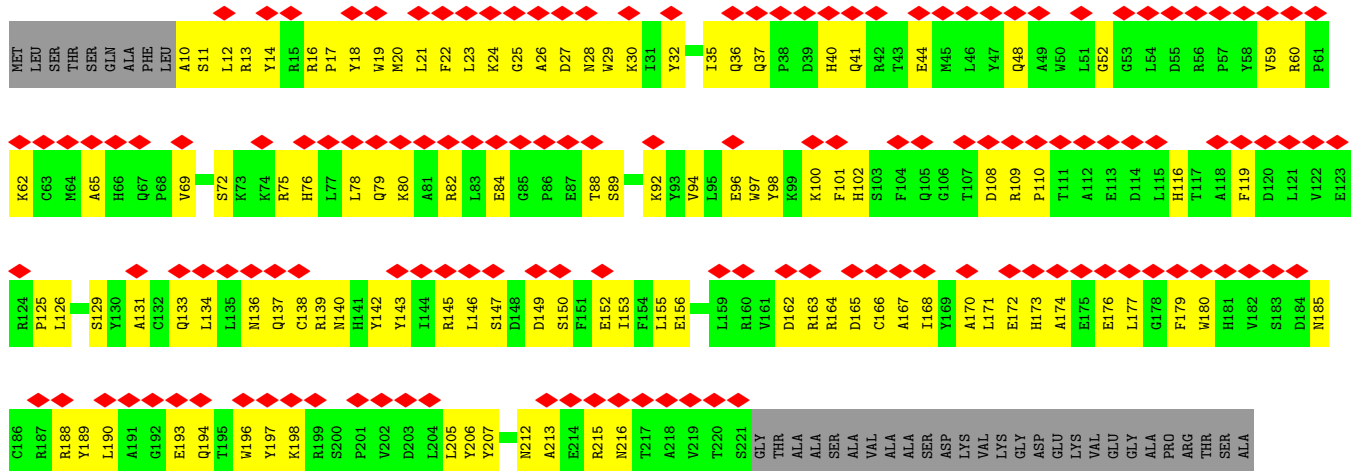


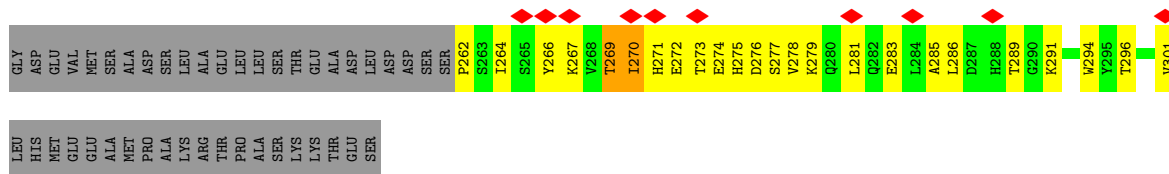


• Molecule 28: mS62

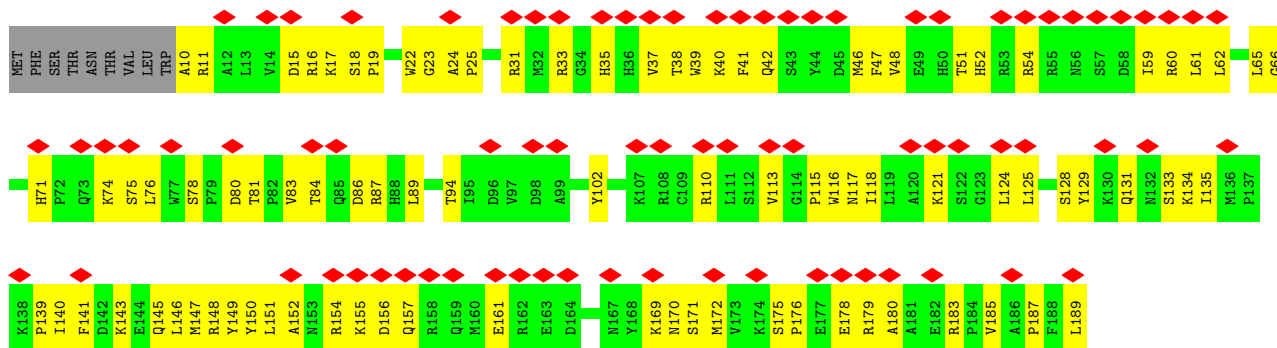
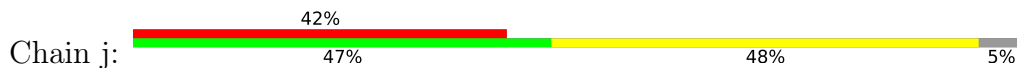


• Molecule 29: mS63

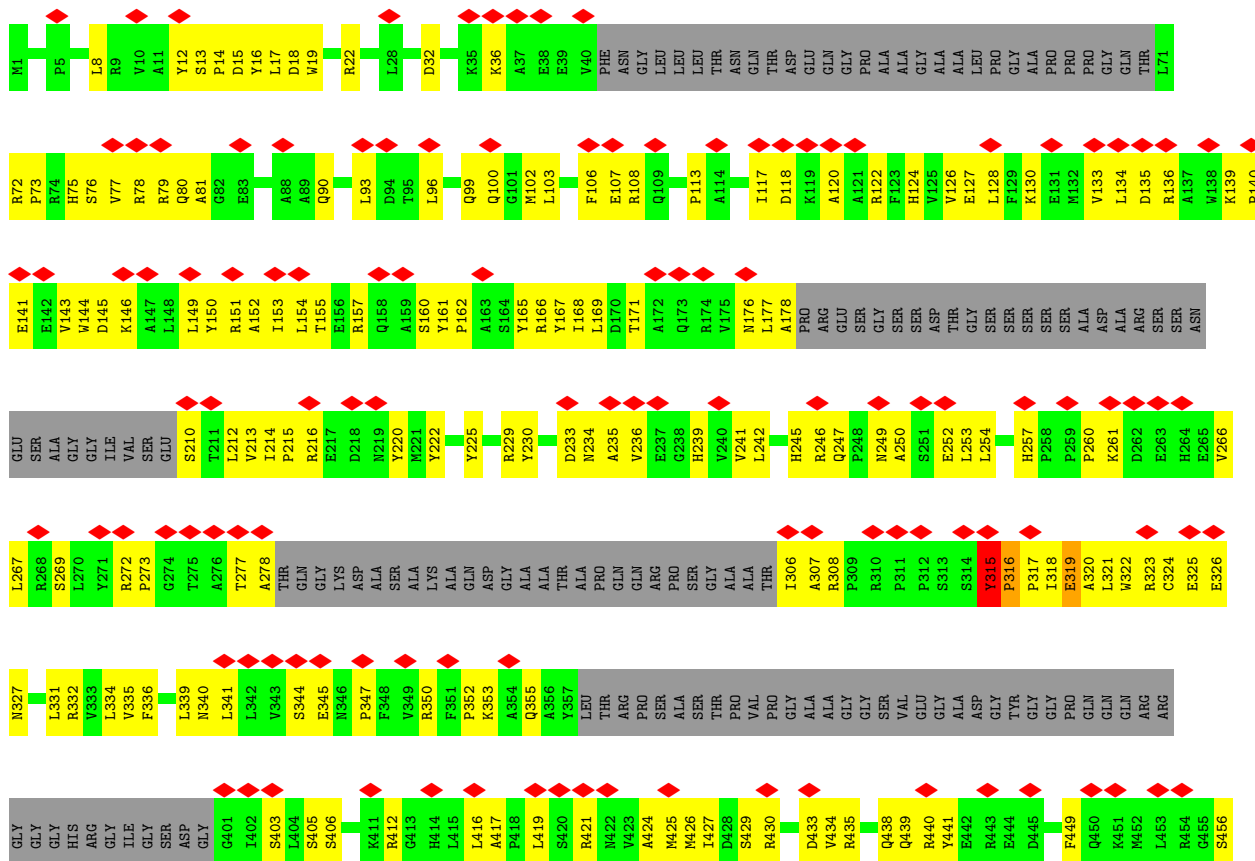


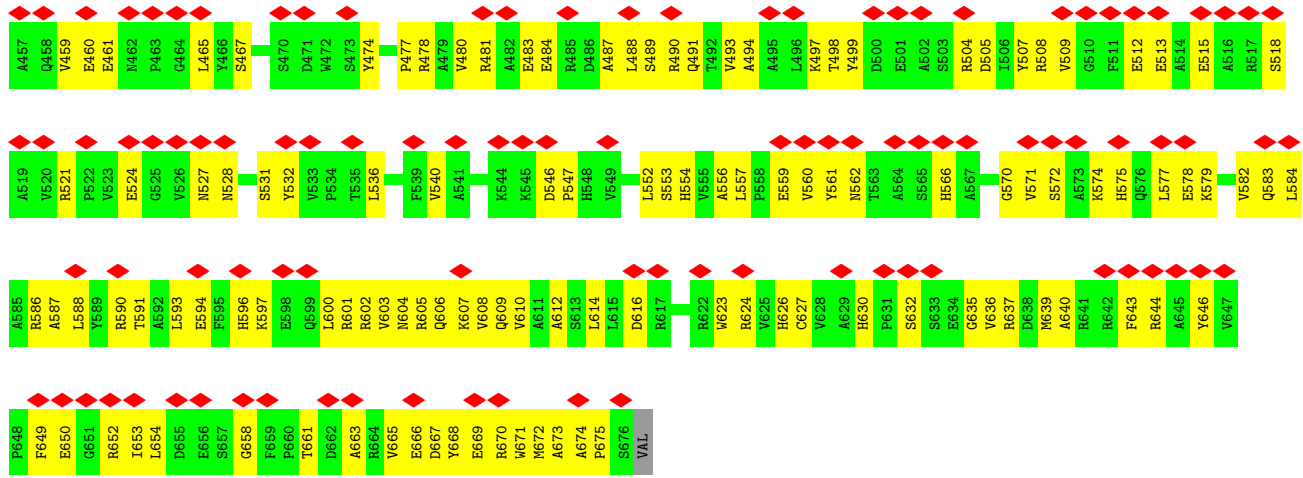


• Molecule 37: bS16m

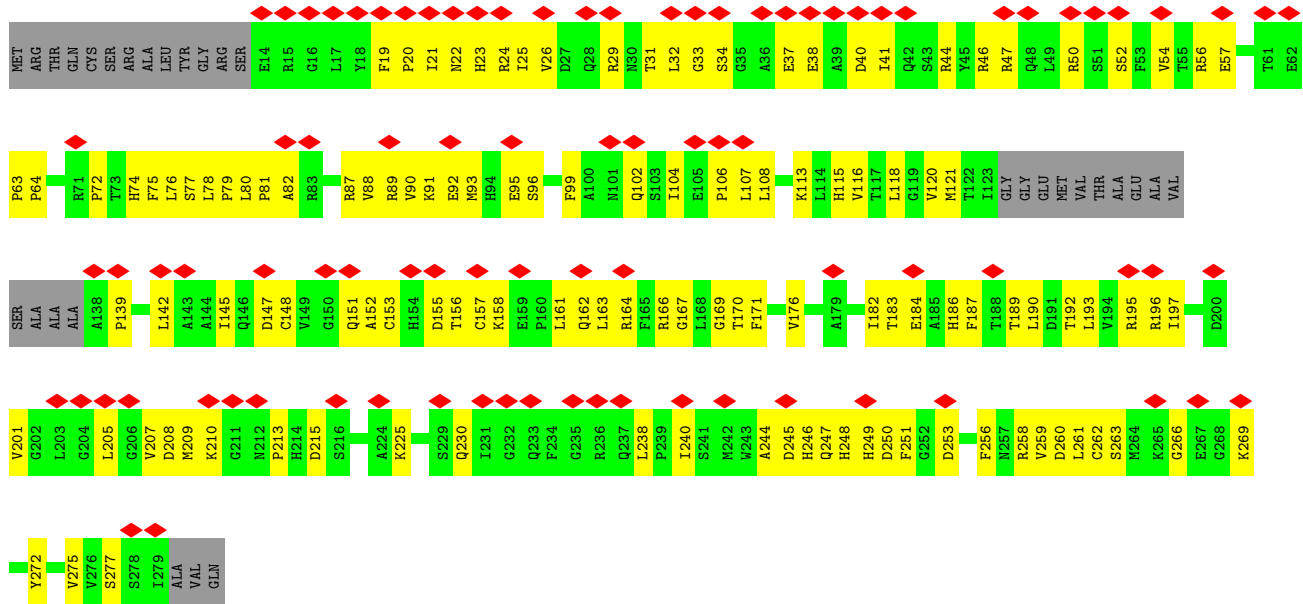


• Molecule 38: mS52

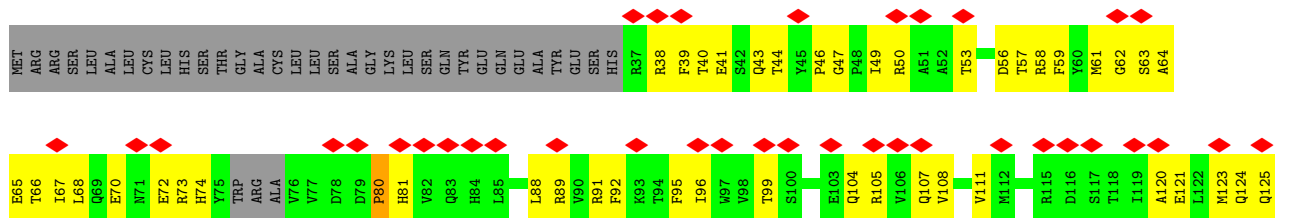


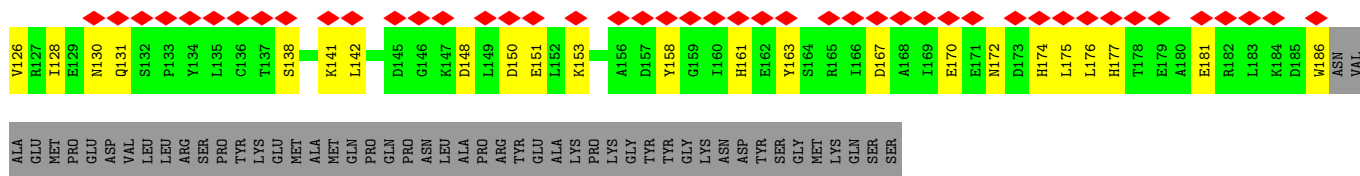


• Molecule 39: AKAP7_NLS domain-containing protein

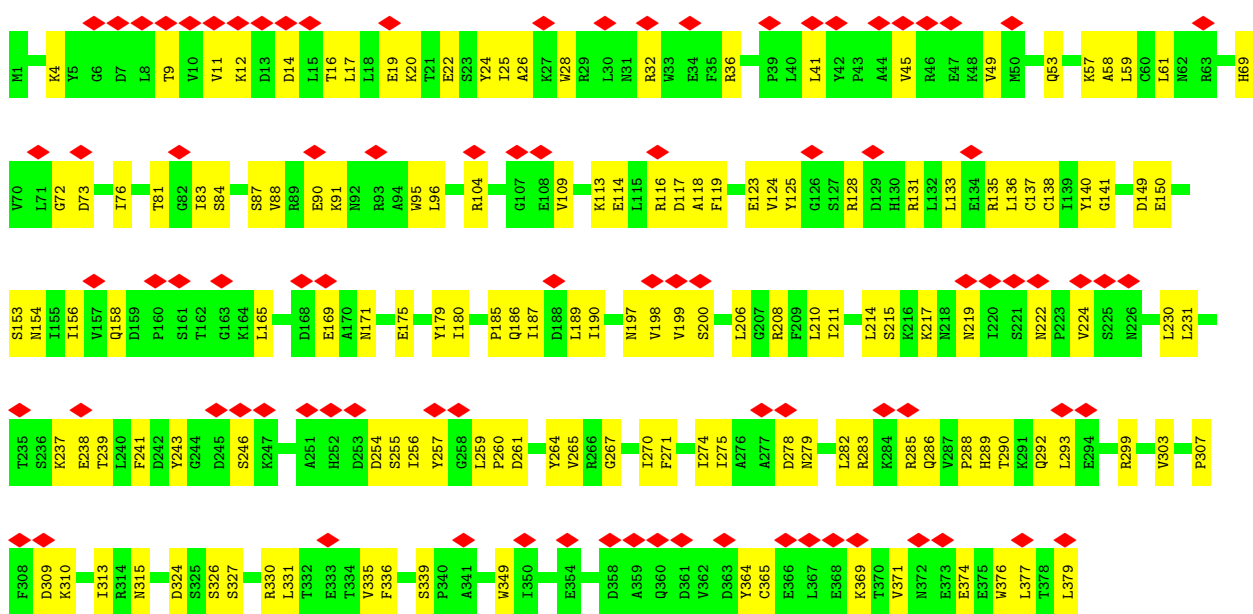


• Molecule 40: Ubiquitin-like domain-containing protein

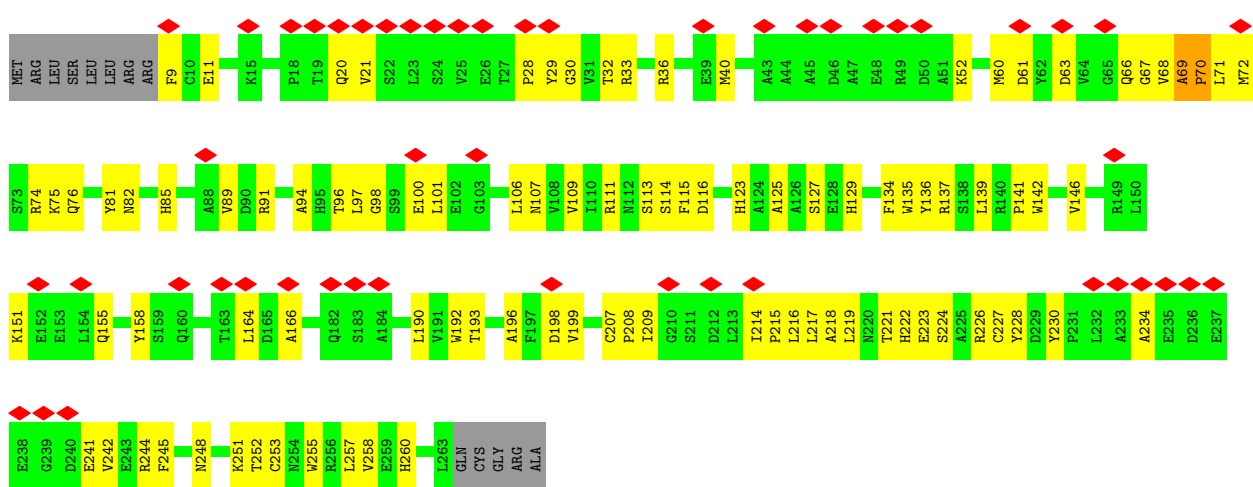




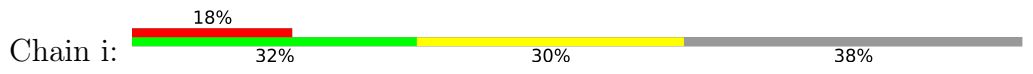
• Molecule 41: mS56

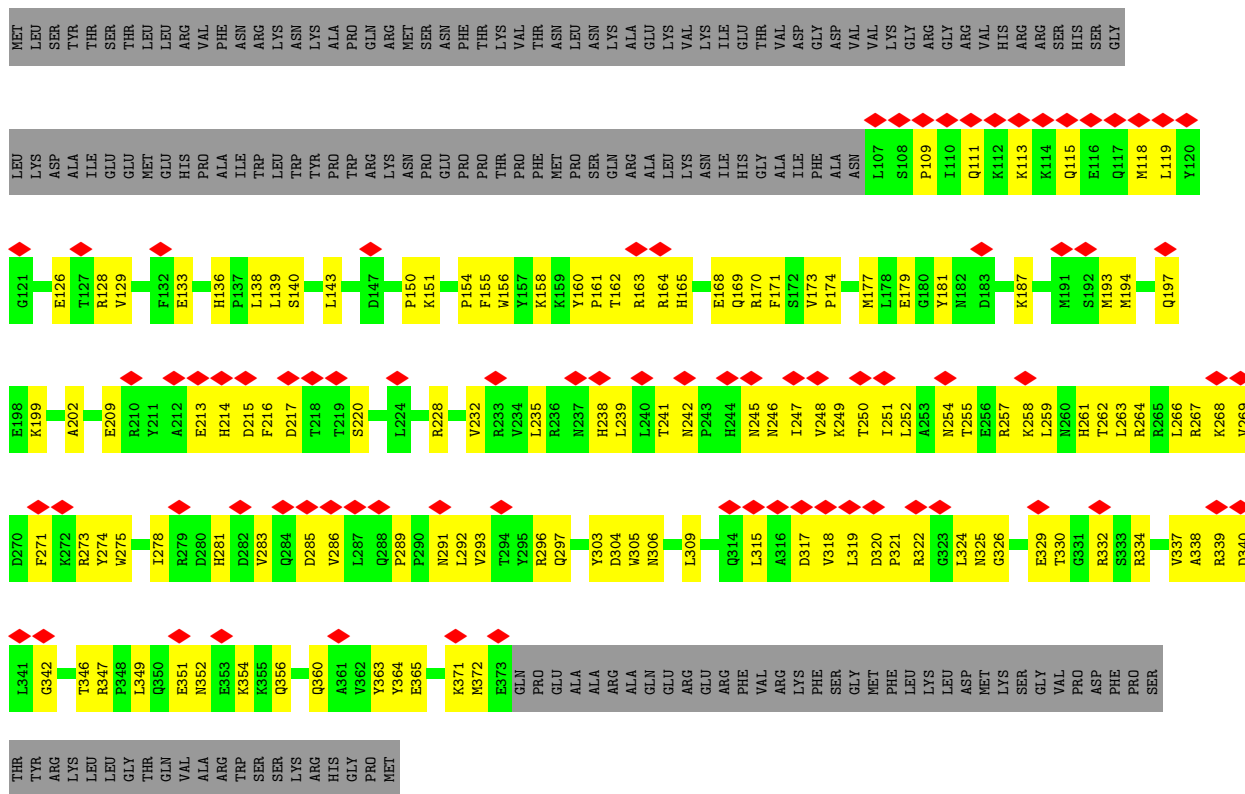


• Molecule 42: Putative superoxide dismutase

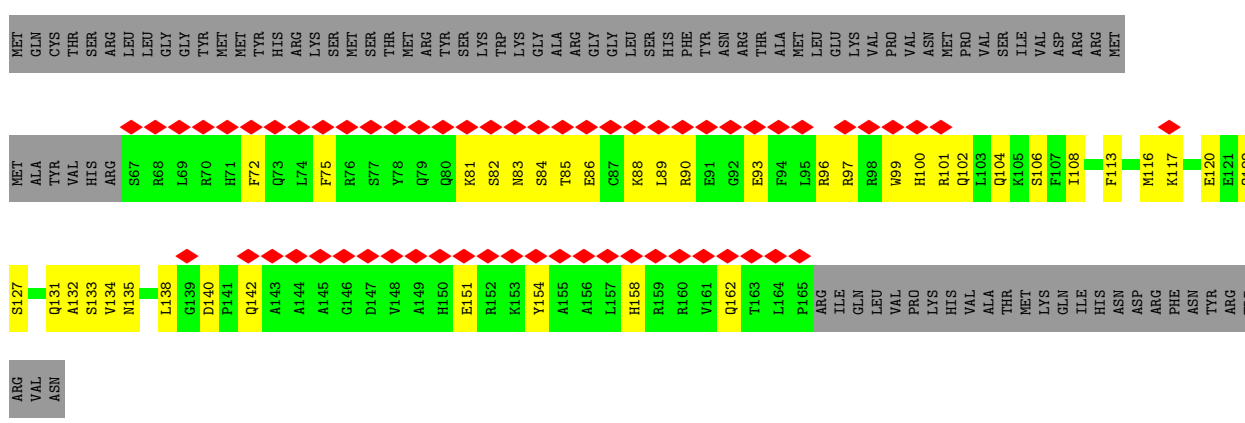
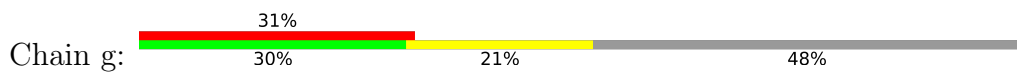


• Molecule 43: uS15m

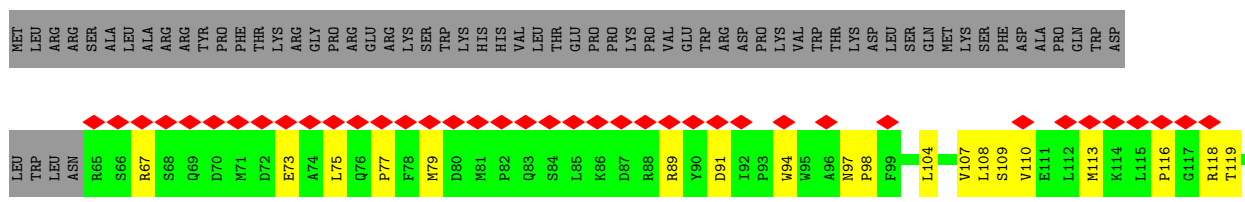


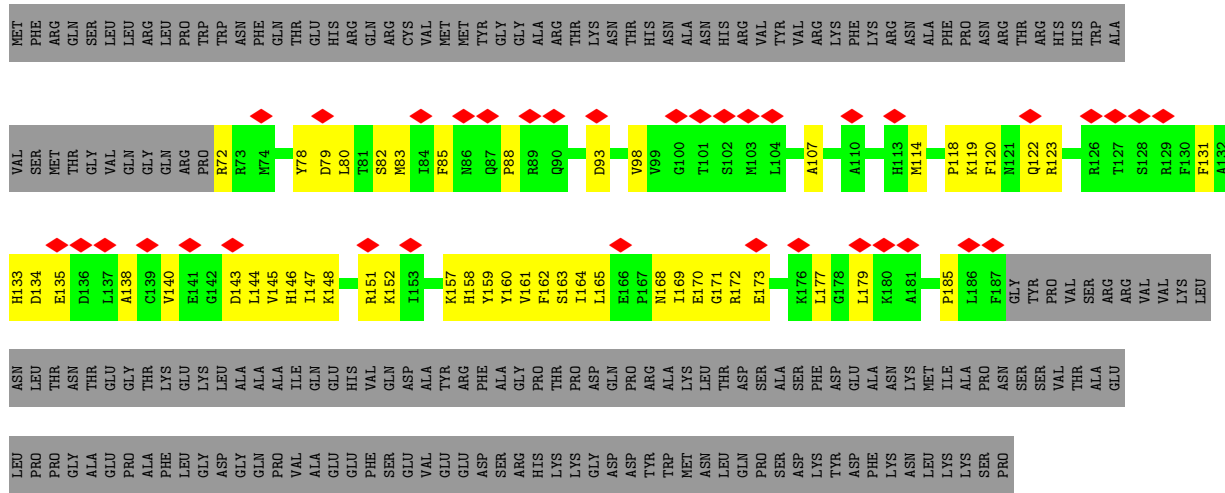


• Molecule 44: bS21m

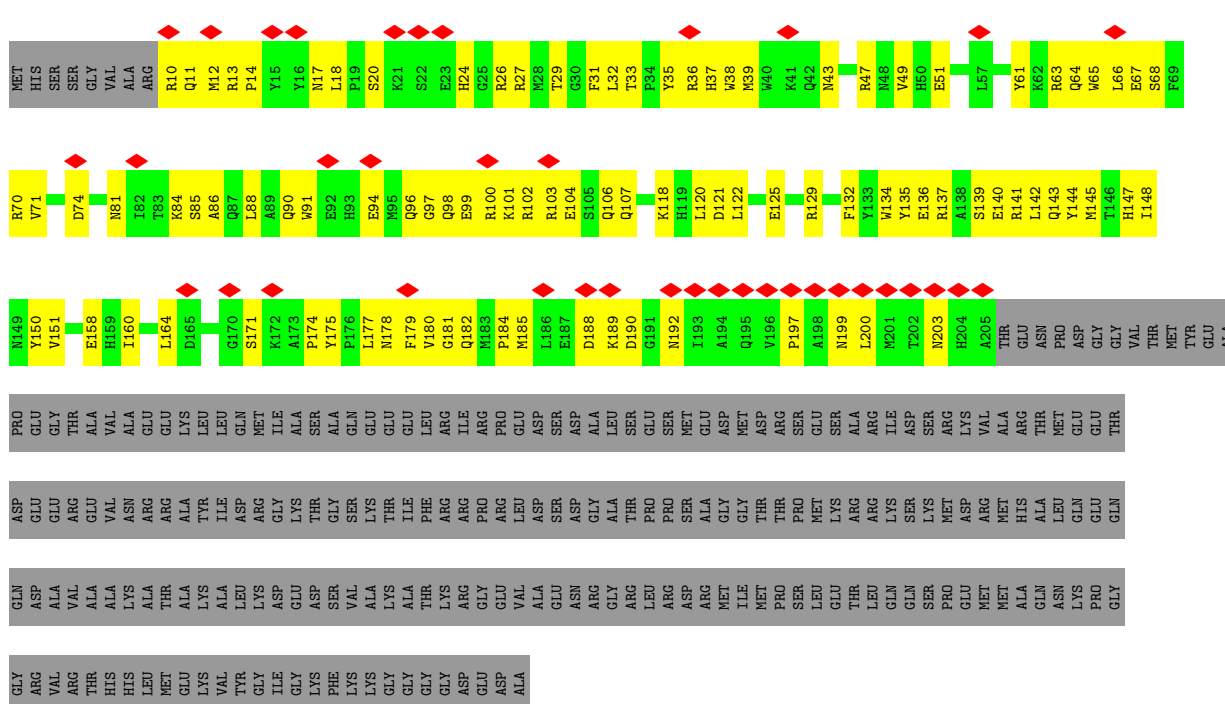


• Molecule 45: mS22

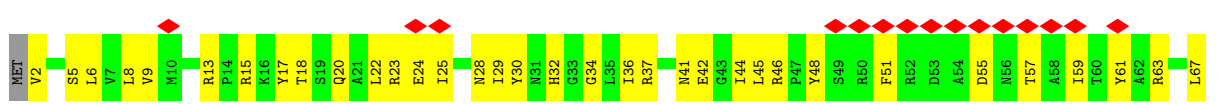
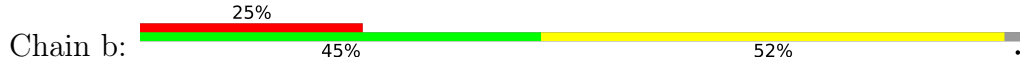


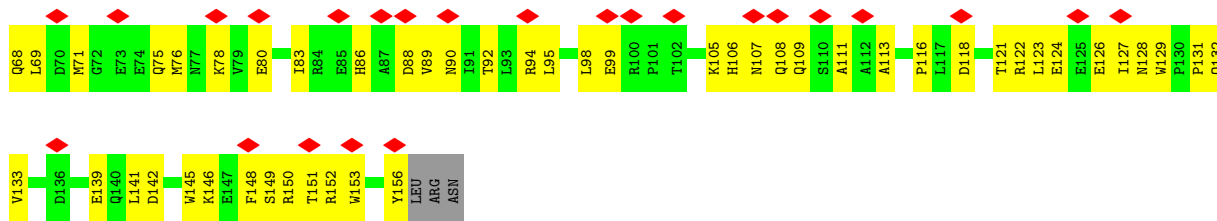


• Molecule 48: mS26

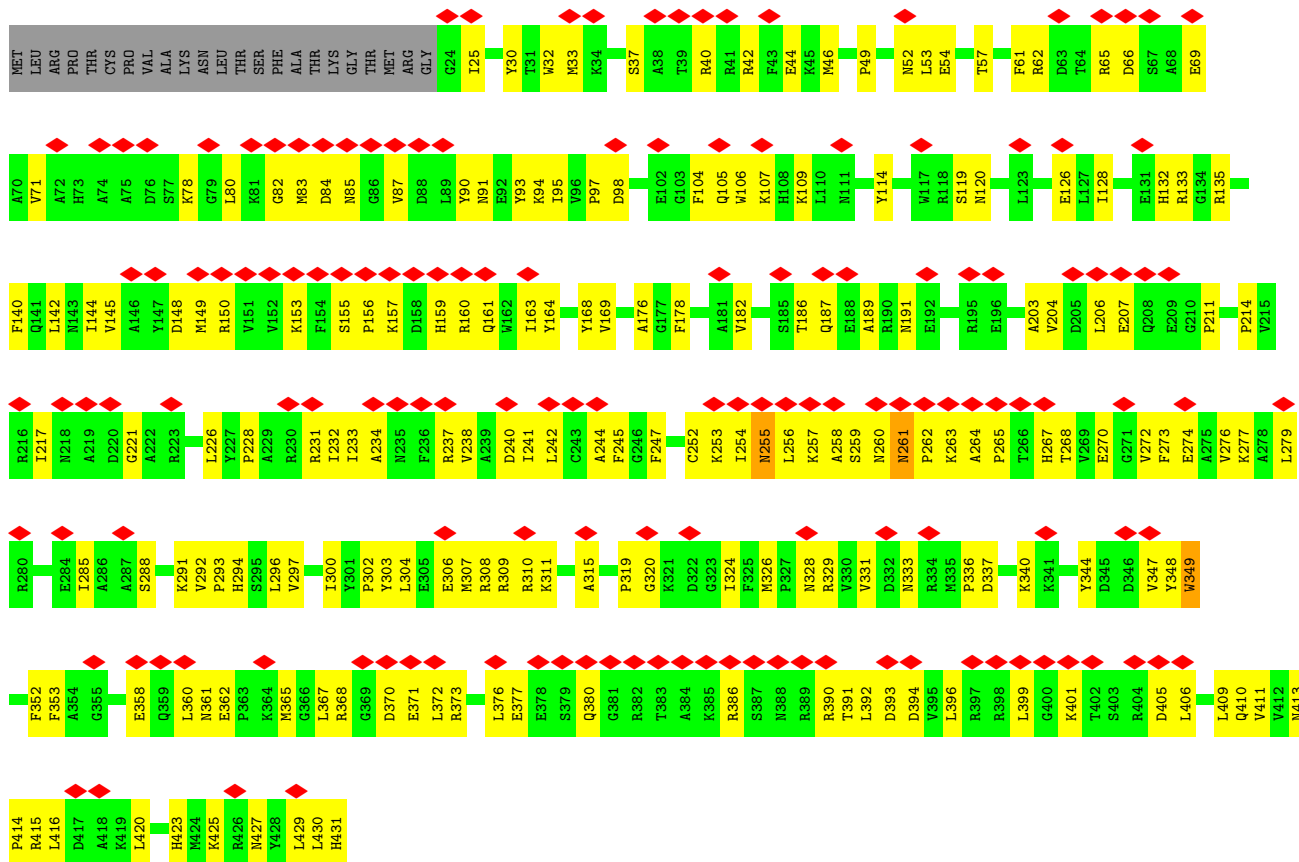


• Molecule 49: bS6m

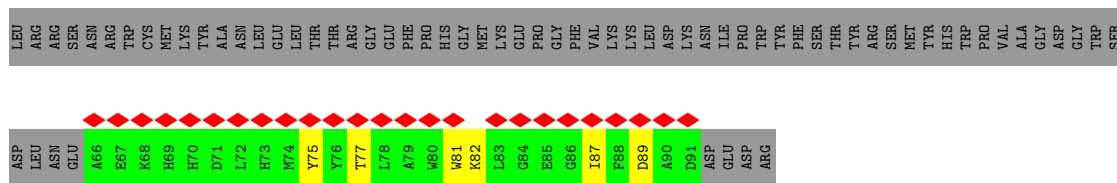




• Molecule 50: Ribosomal_S5_C domain-containing protein

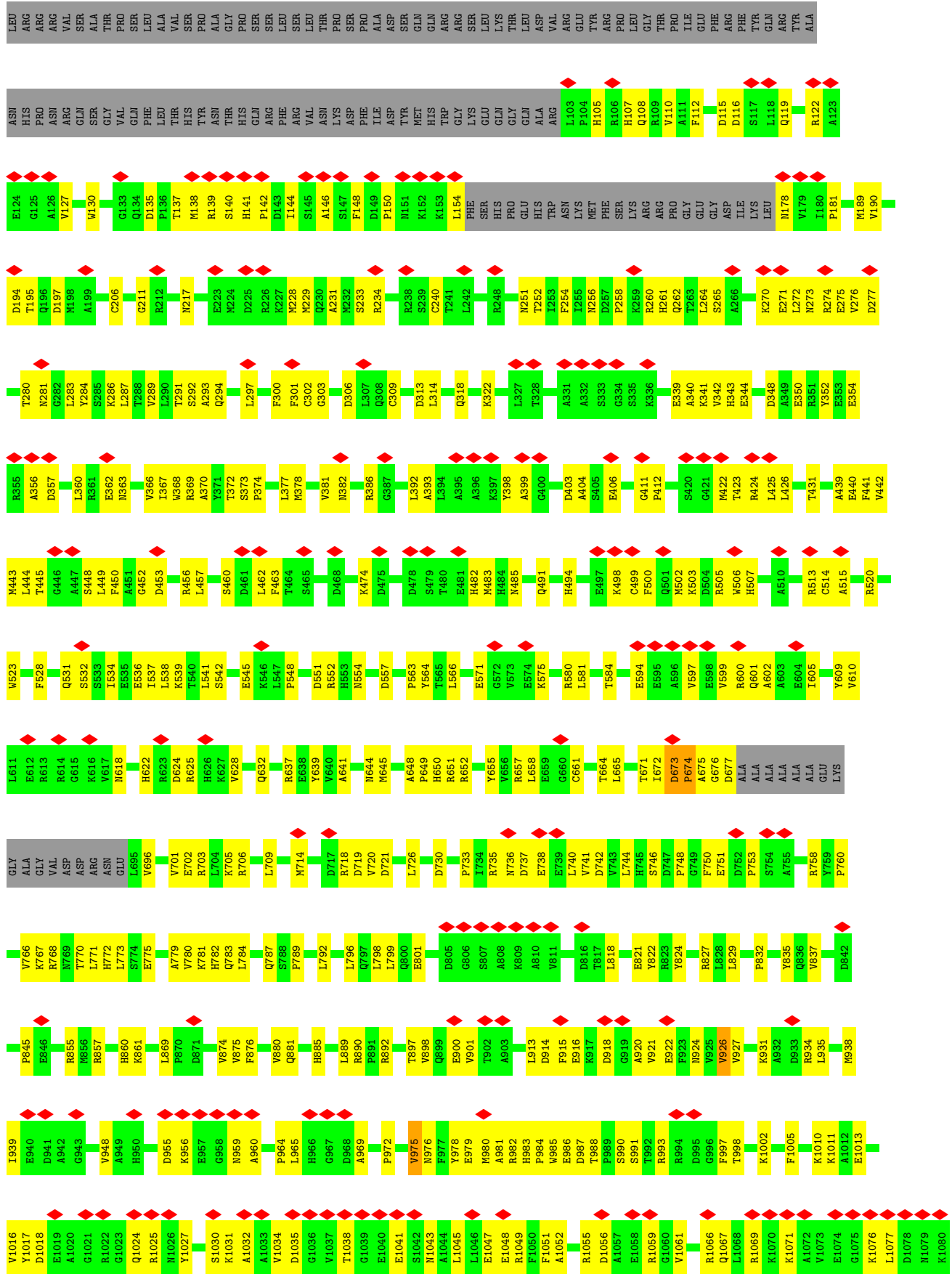


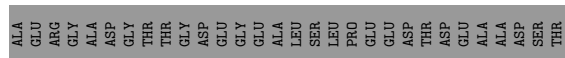
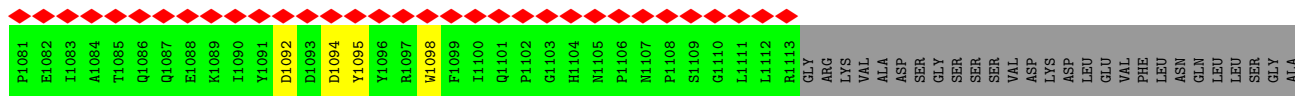
• Molecule 51: mS73



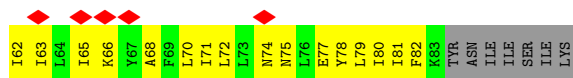
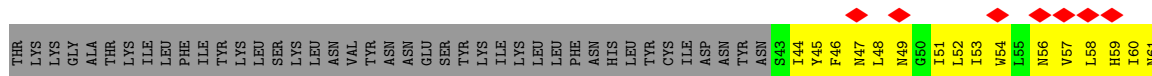
• Molecule 52: mS47



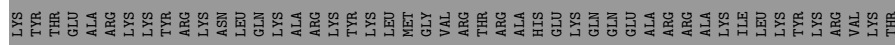
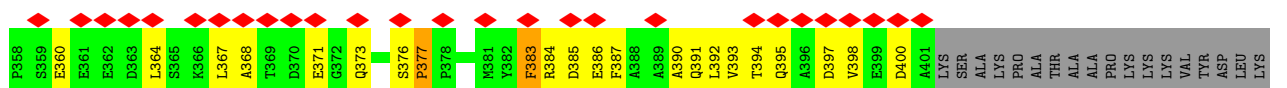
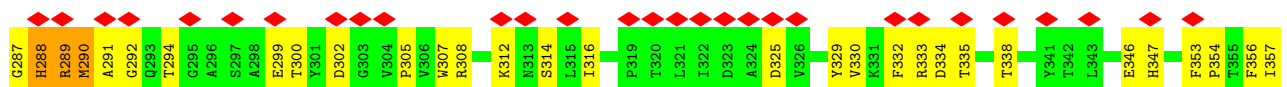
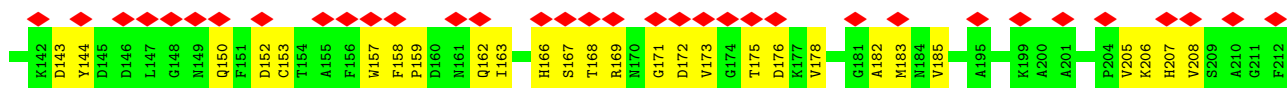
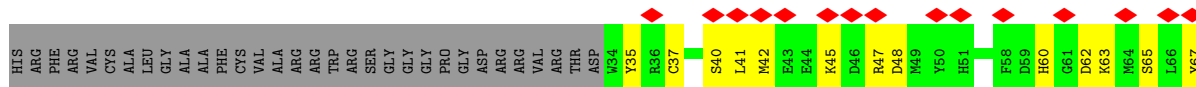




• Molecule 53: uS3m

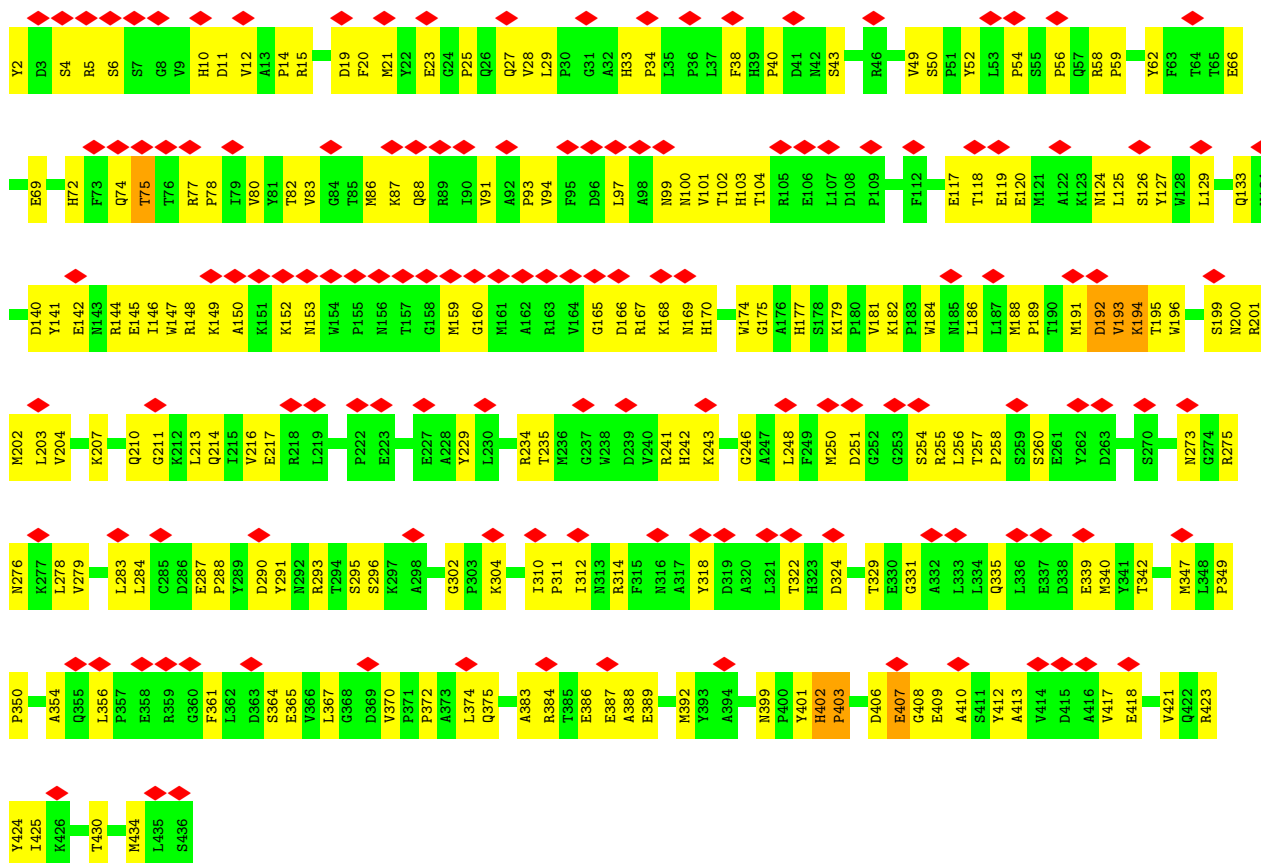


• Molecule 54: Ribosomal protein L3-like protein

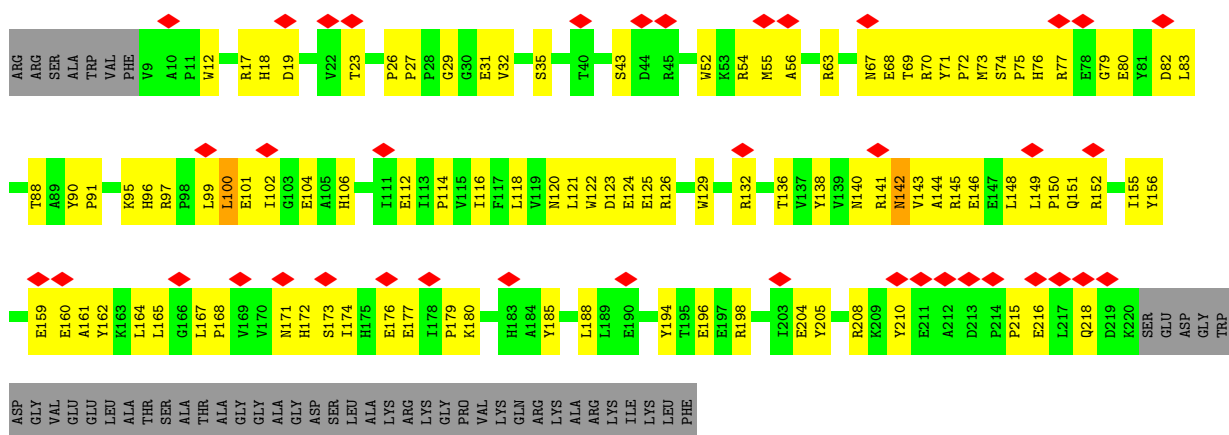
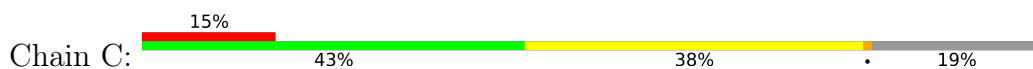


• Molecule 55: uL4m



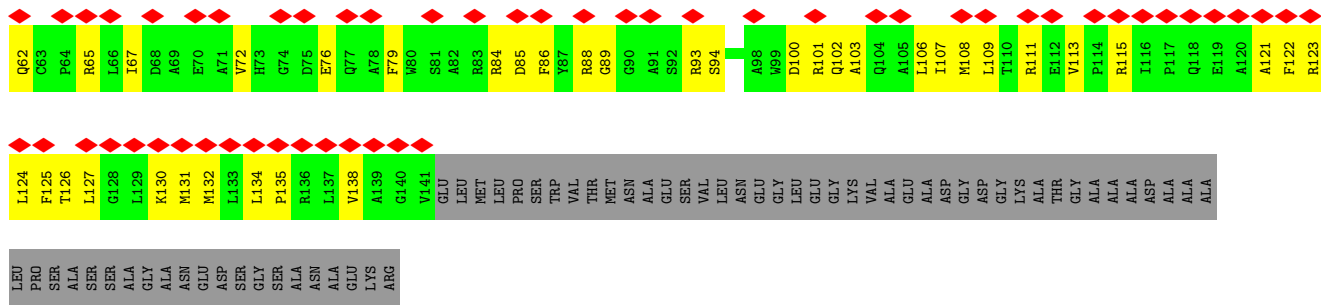


• Molecule 56: RIBOSOMAL_L9 domain-containing protein

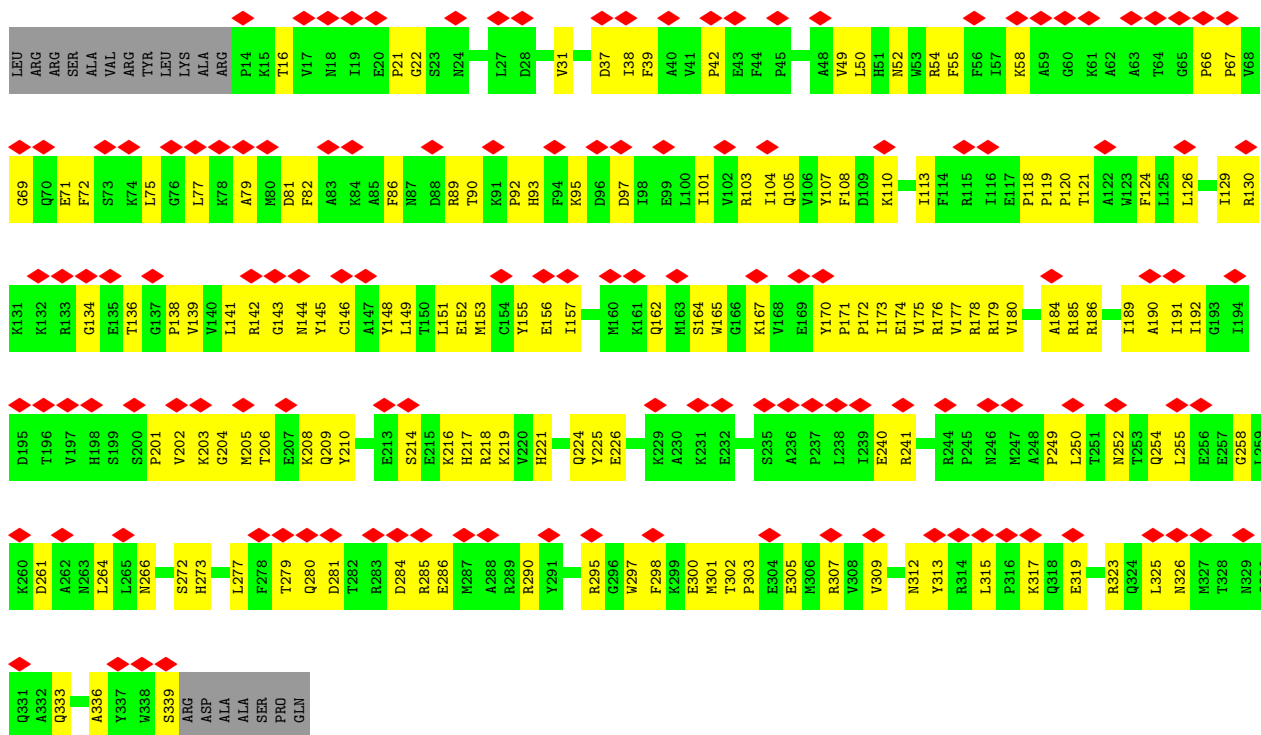


• Molecule 57: uL10m

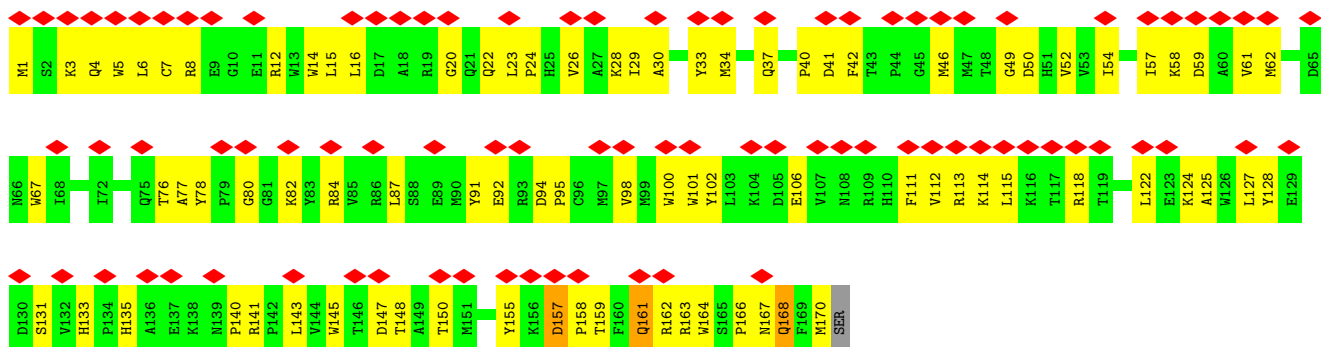




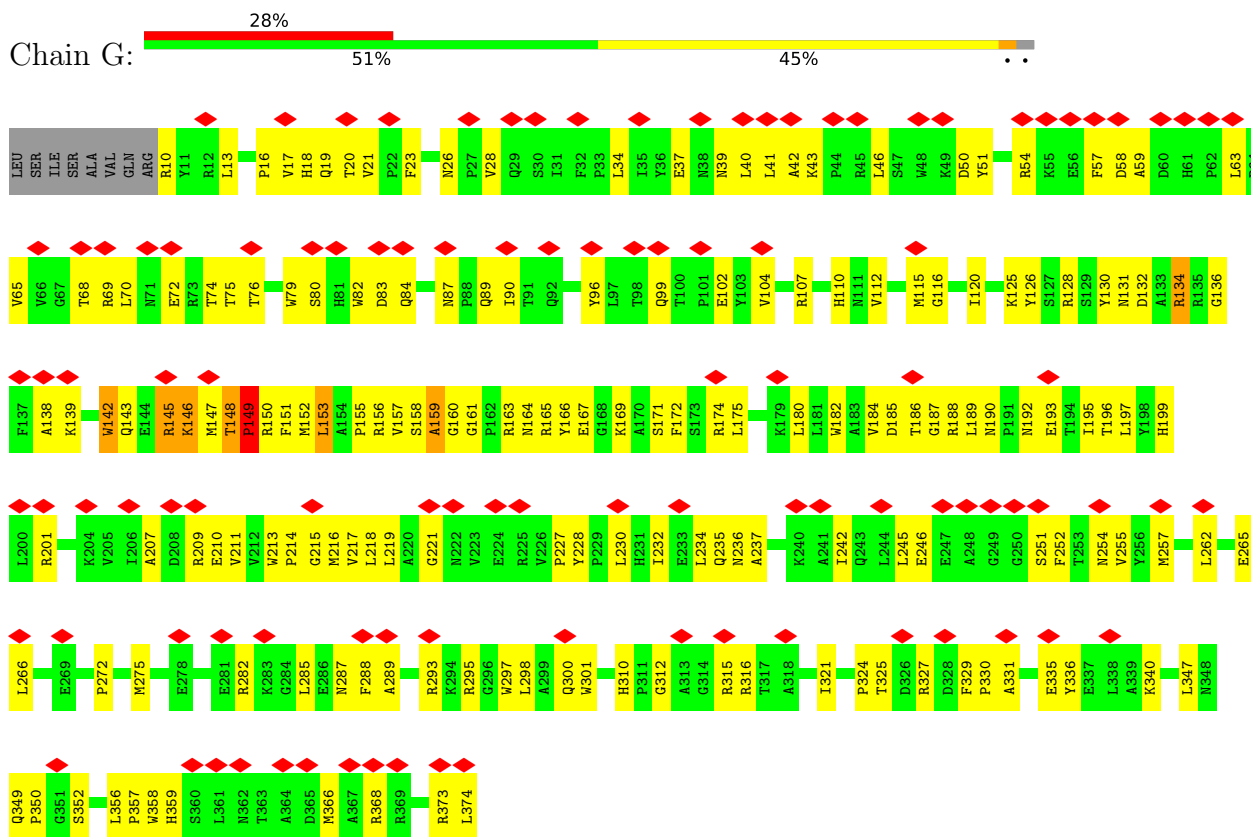
• Molecule 58: Putative ribosomal protein L11



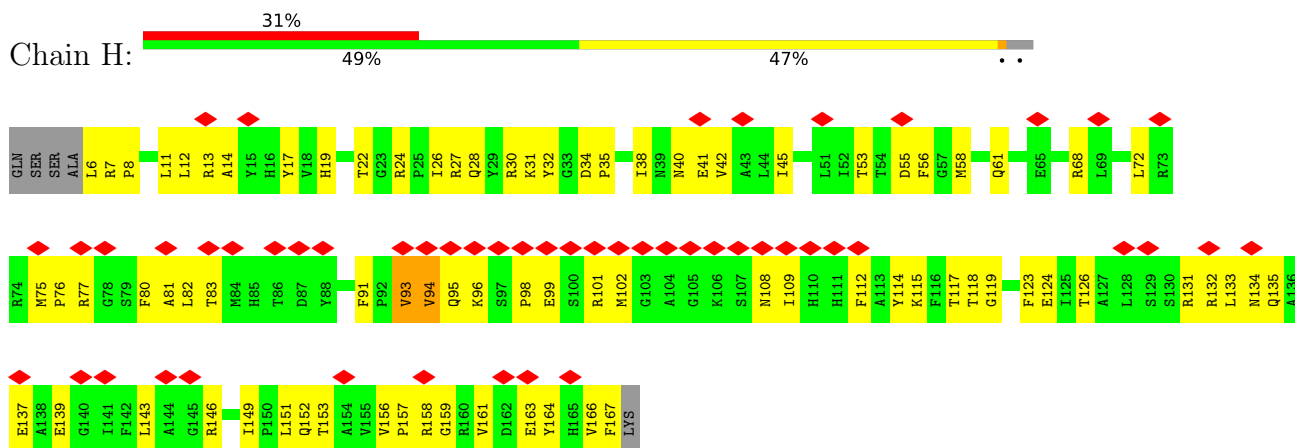
• Molecule 59: 50S ribosomal protein L13-like protein



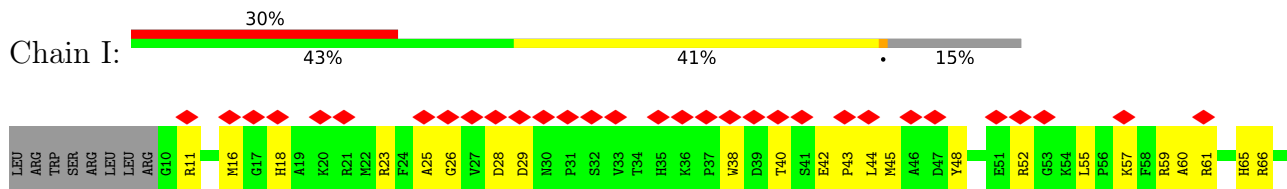
• Molecule 60: Ribosomal_L18e/L15P domain-containing protein

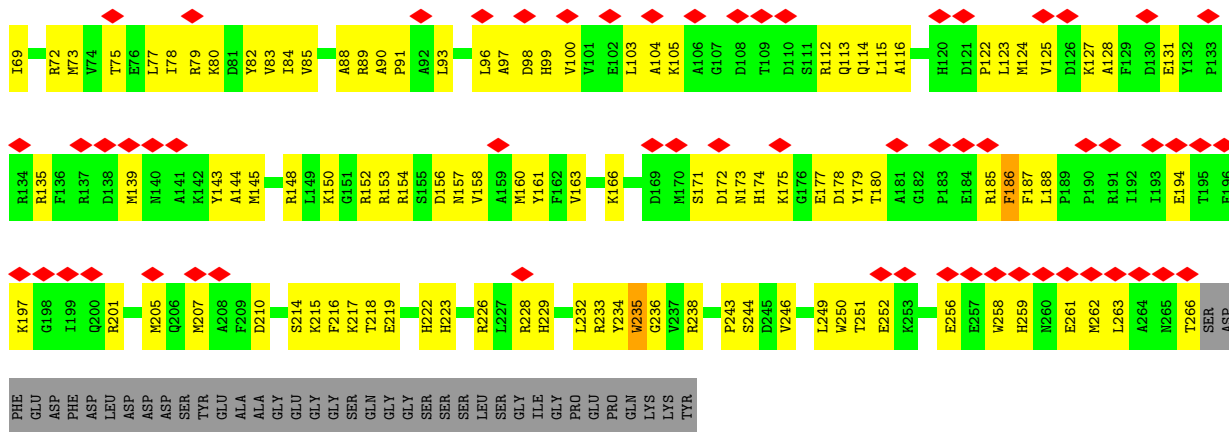


• Molecule 61: Ribosomal_L16 domain-containing protein

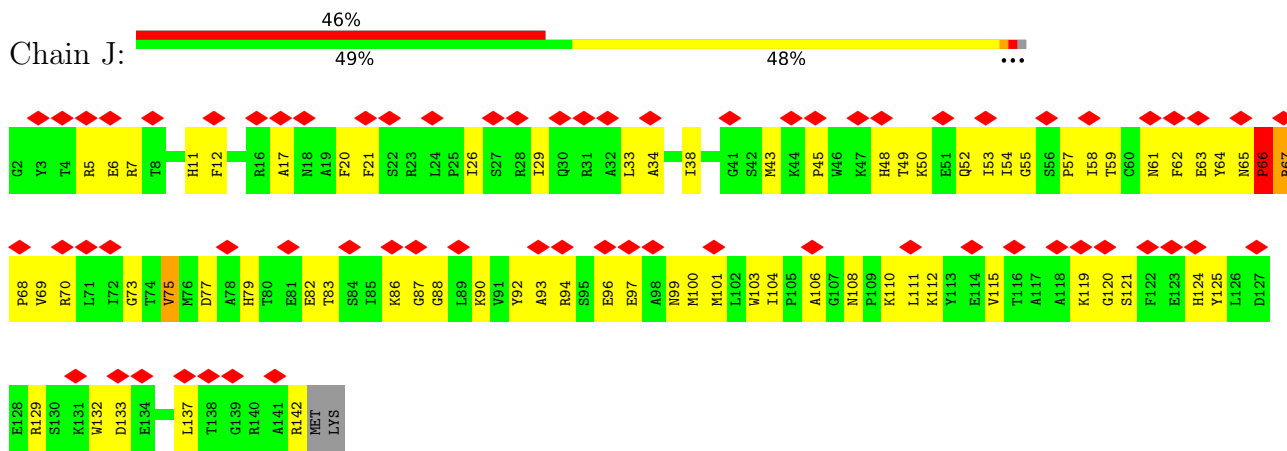


• Molecule 62: Putative 50S ribosomal protein L17

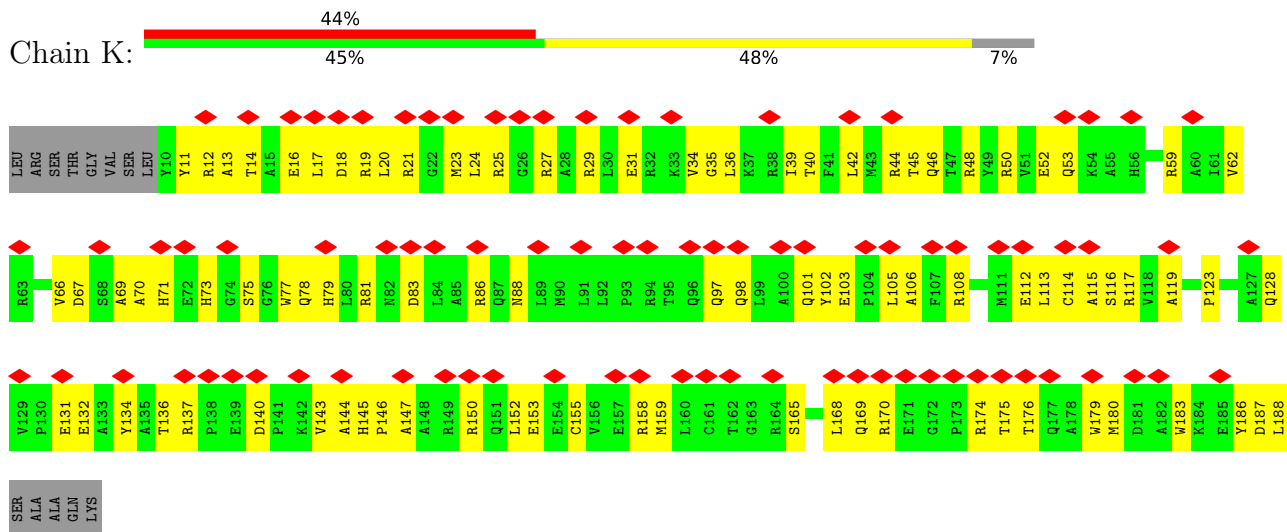




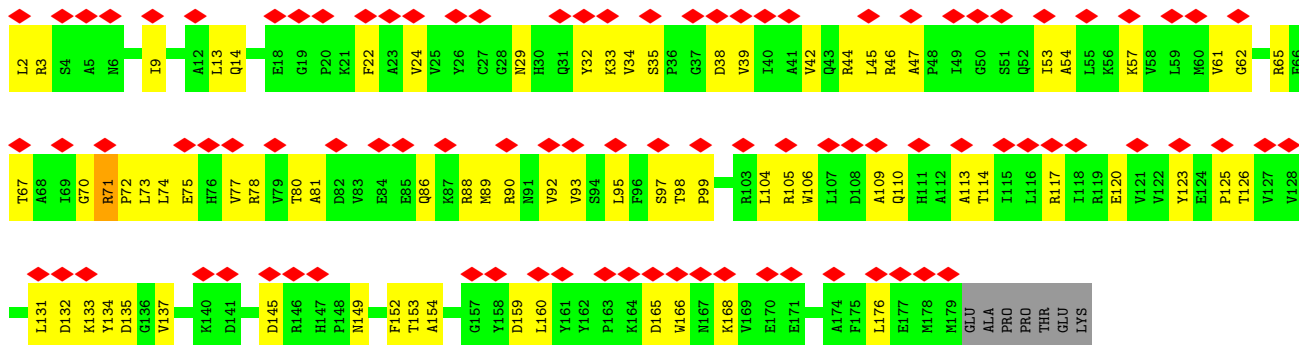
• Molecule 63: bL19m



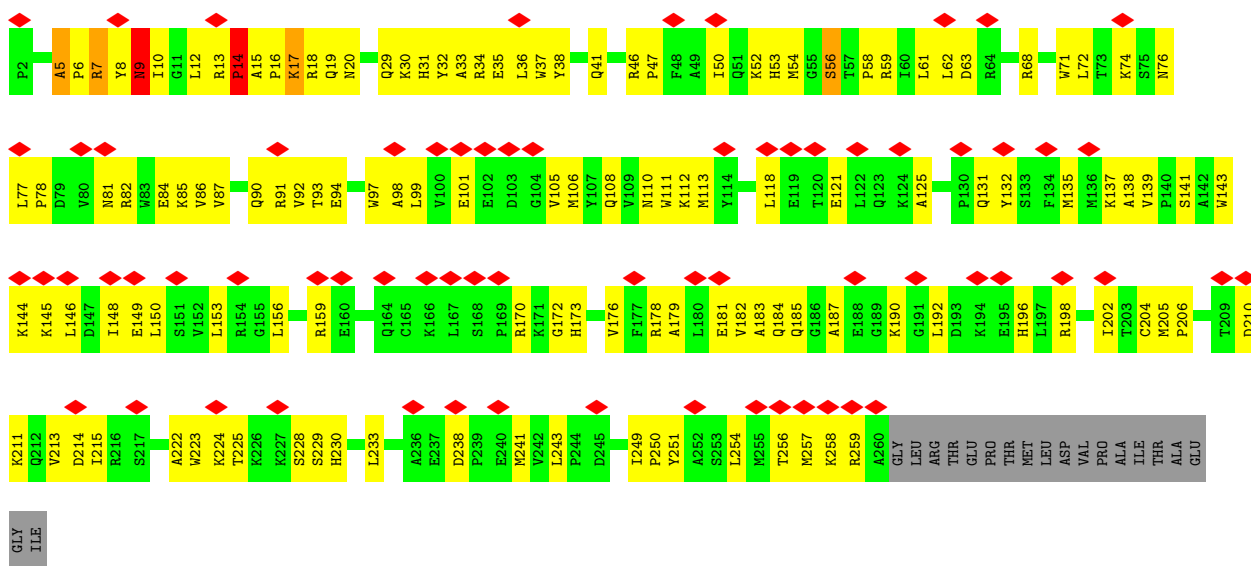
• Molecule 64: bL20m



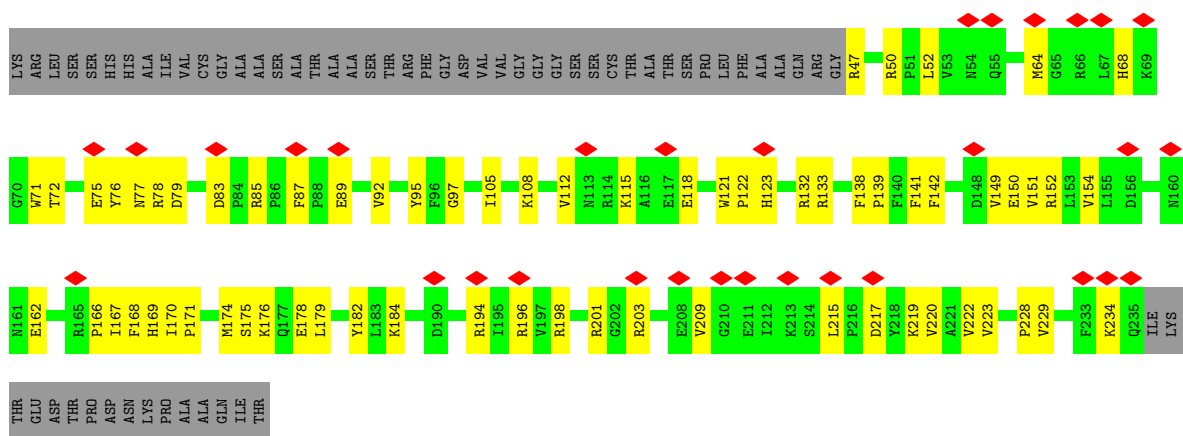
• Molecule 65: bL21m



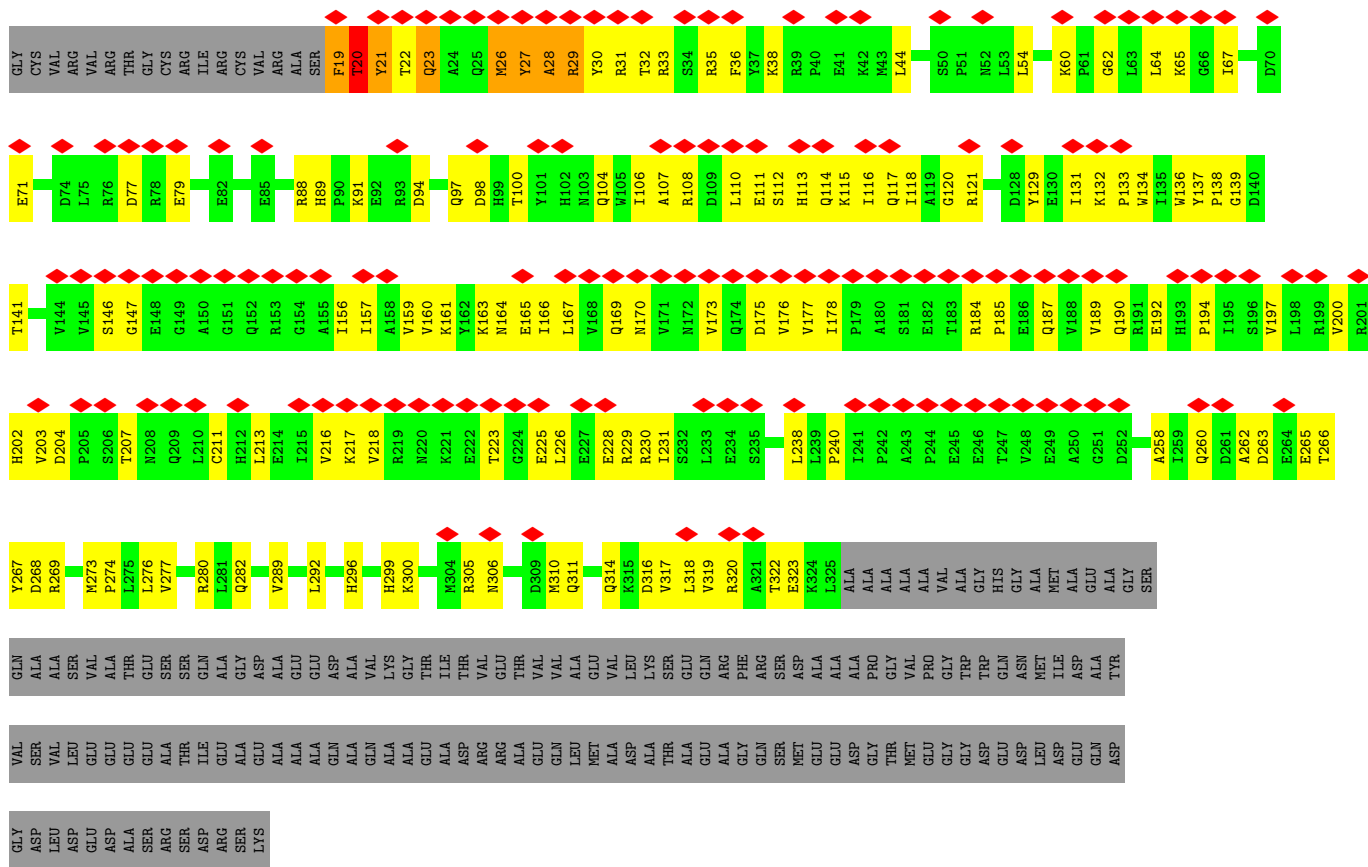
• Molecule 66: uL22m



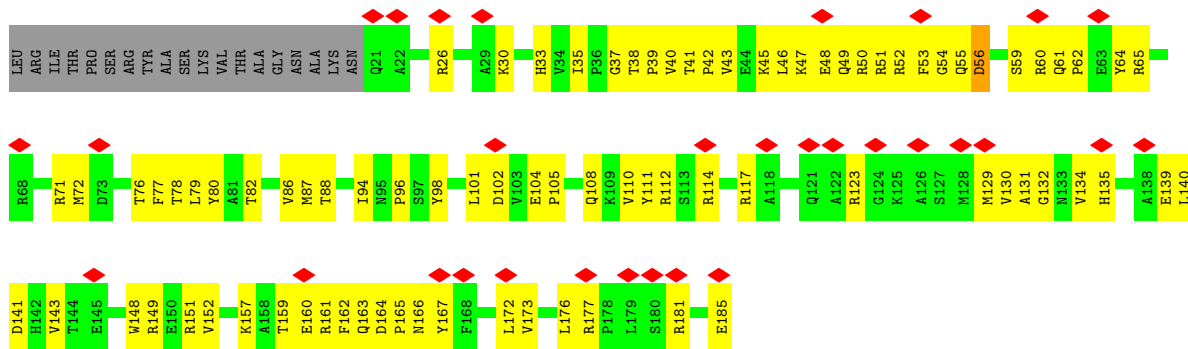
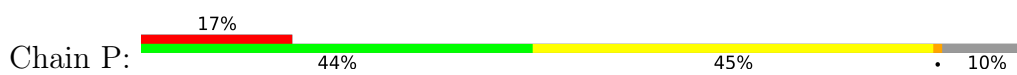
• Molecule 67: uL23m



• Molecule 68: uL24m

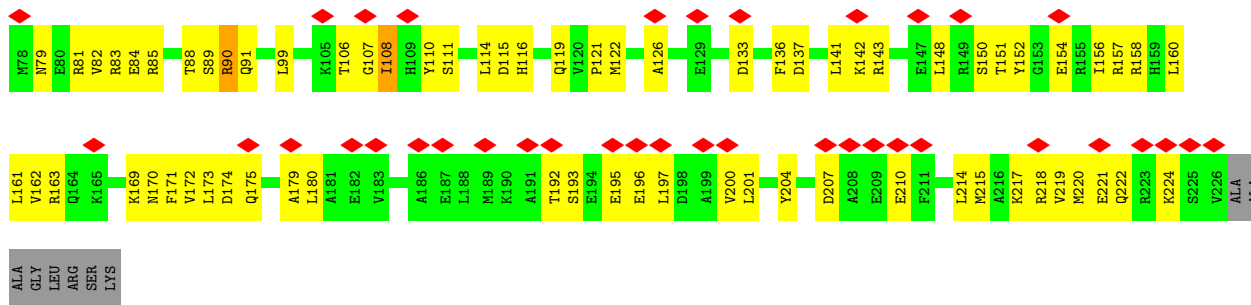


• Molecule 69: bL27m

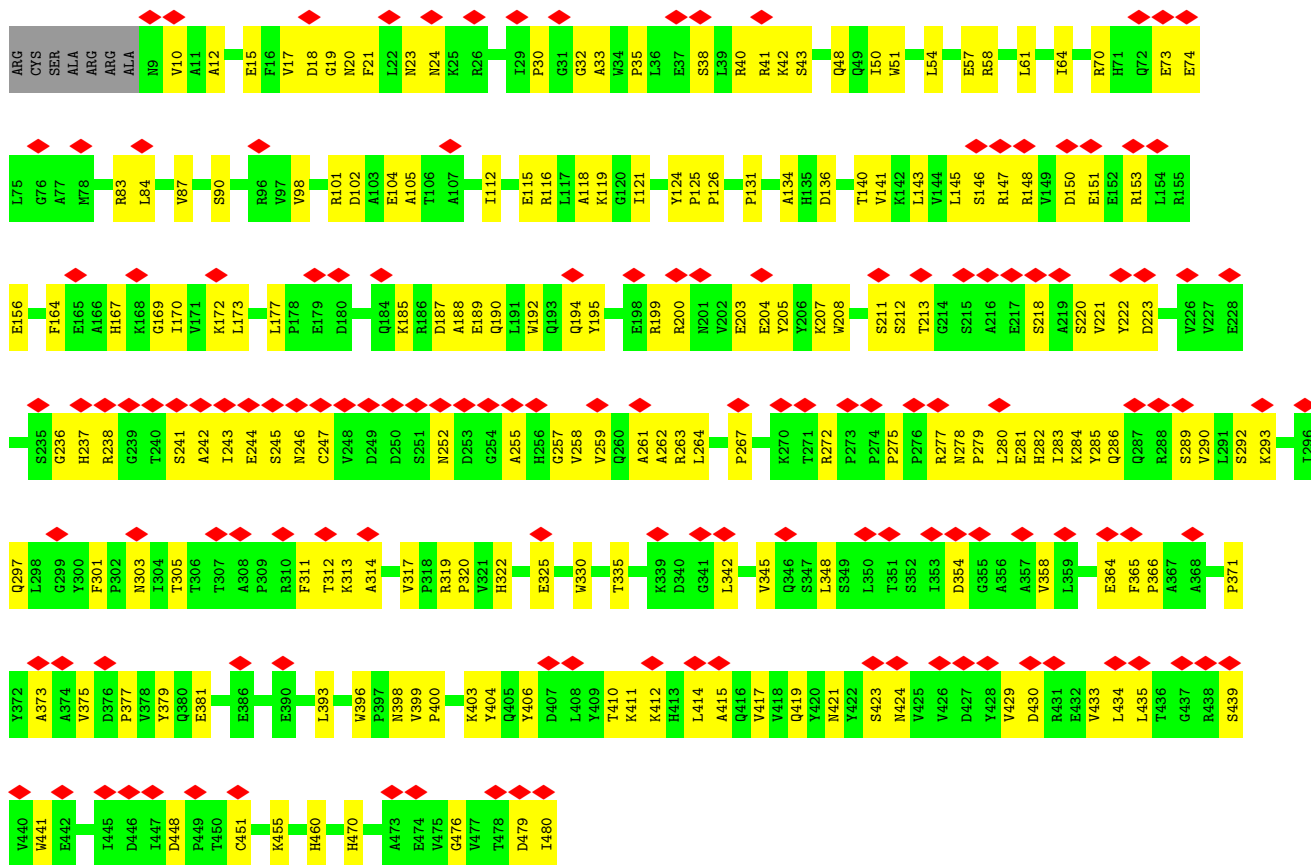


• Molecule 70: bL28m

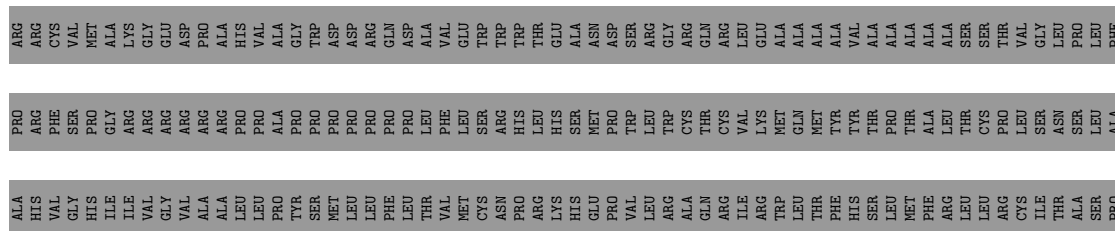


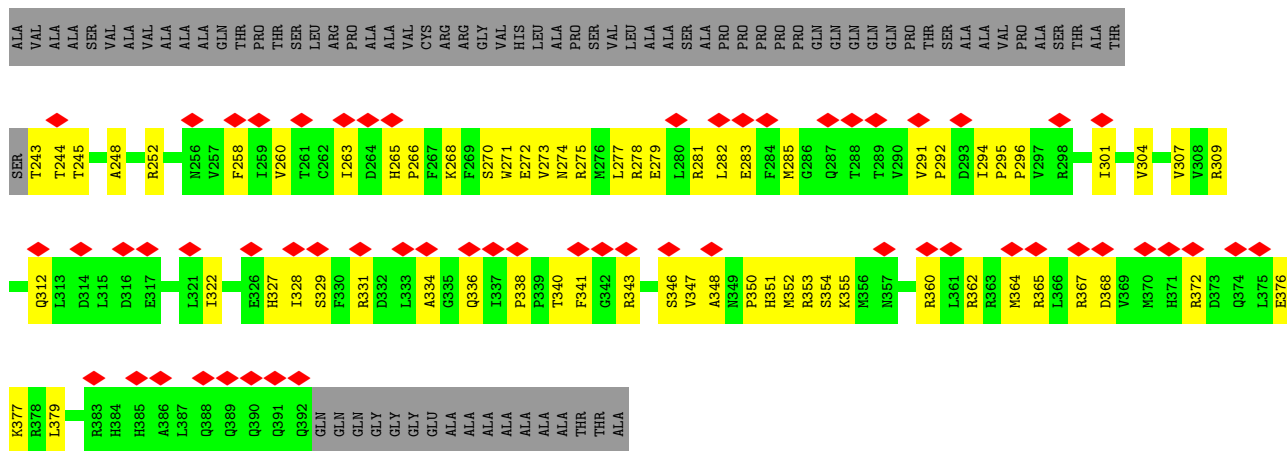


• Molecule 71: uL29m

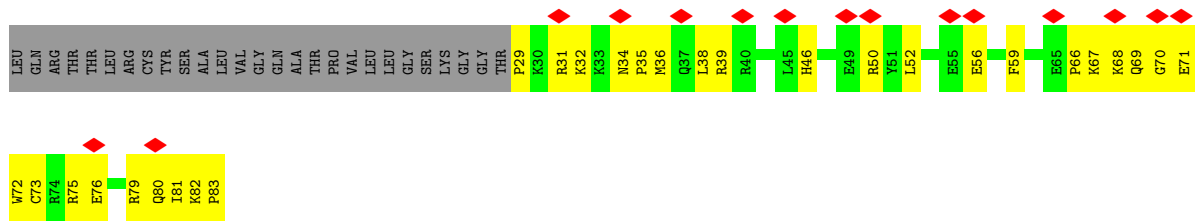


• Molecule 72: uL30m

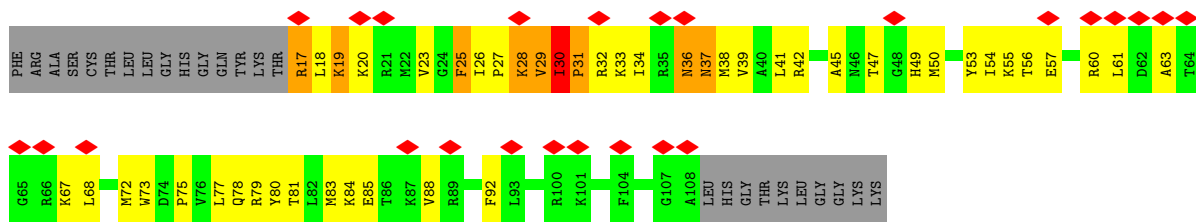




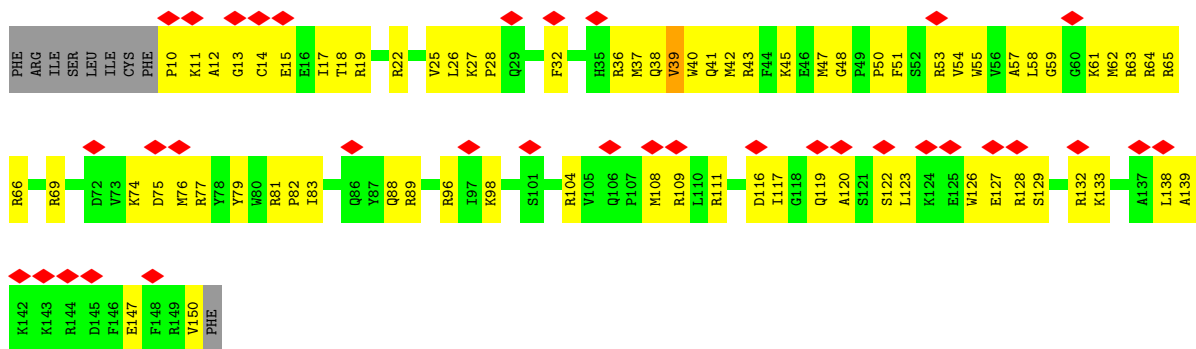
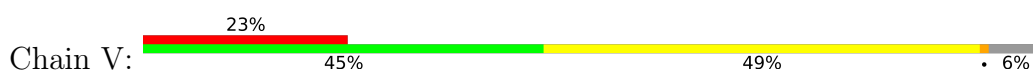
• Molecule 73: bL32m



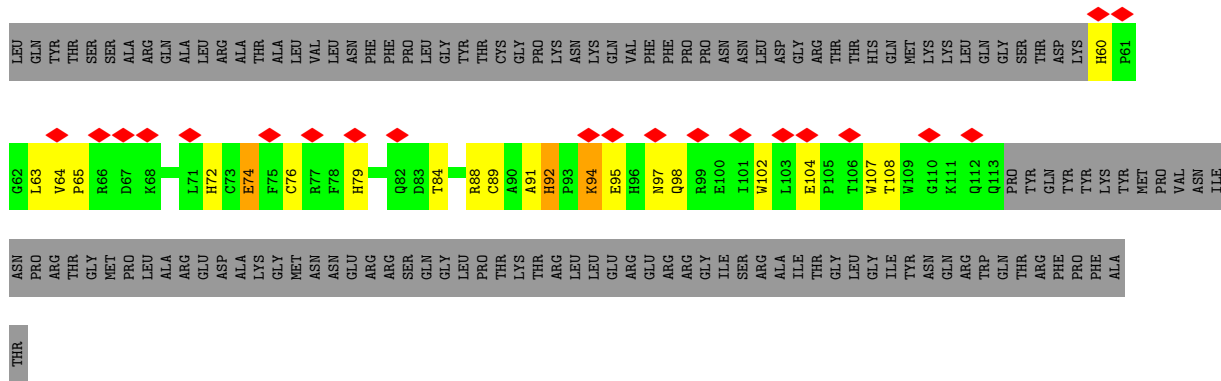
• Molecule 74: bL33m



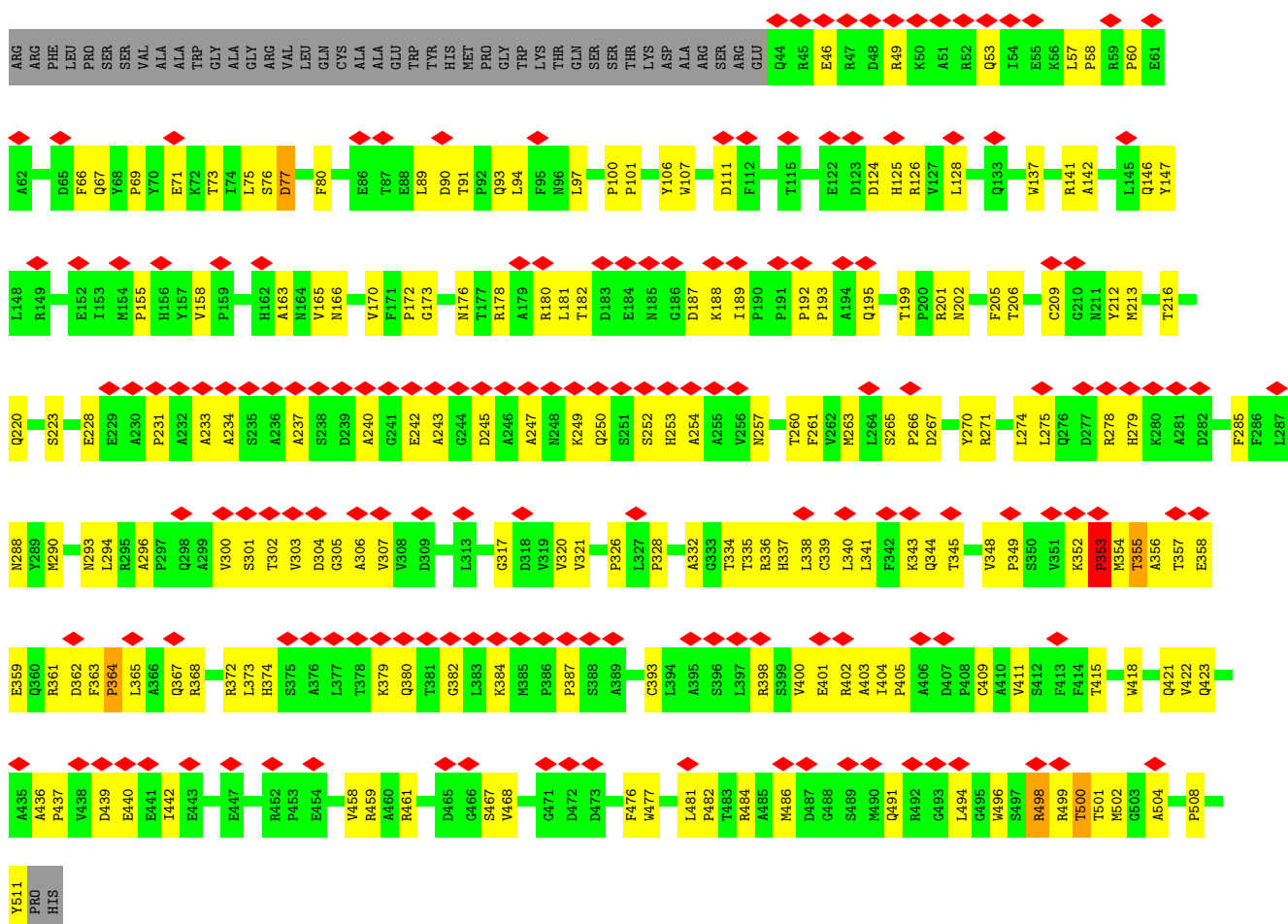
• Molecule 75: bL35m



• Molecule 76: bL36m

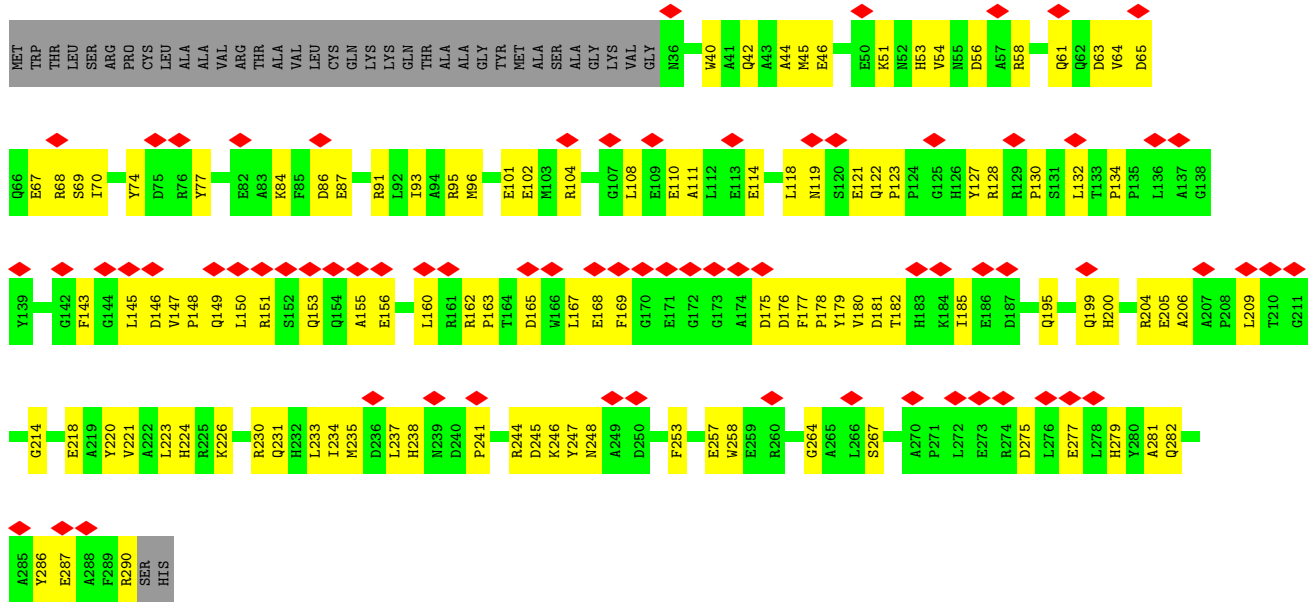


• Molecule 77: mL38

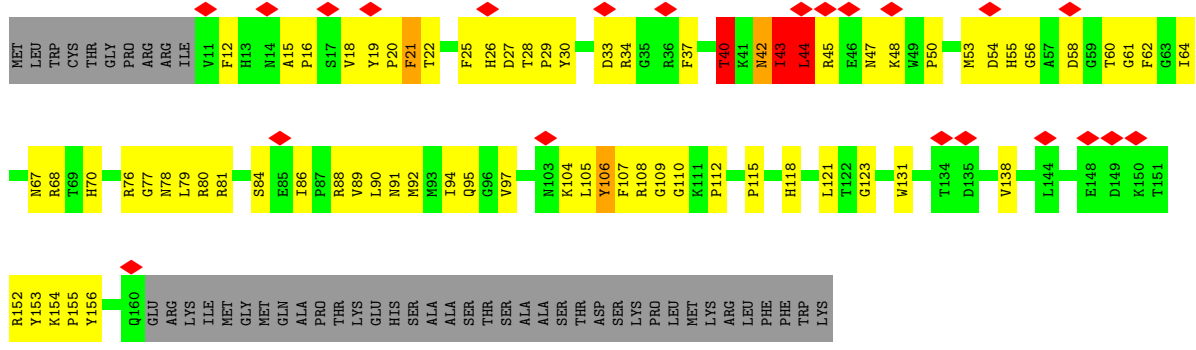


• Molecule 78: mL40

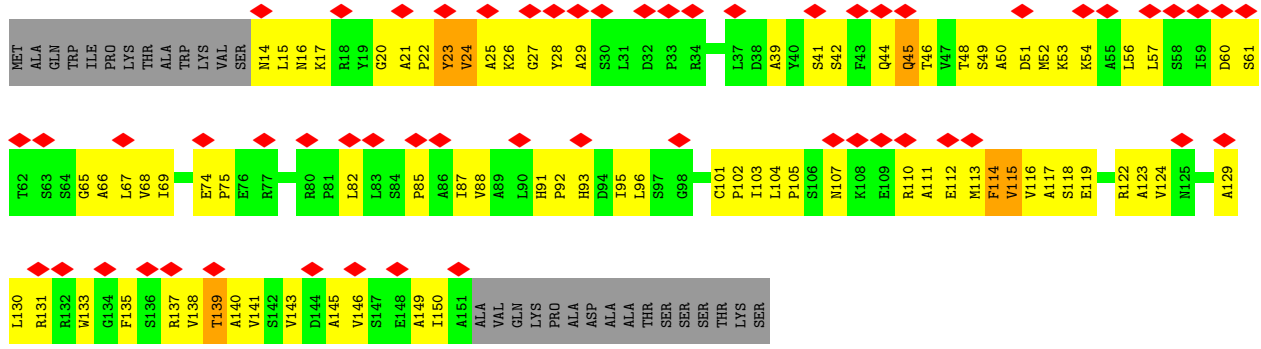




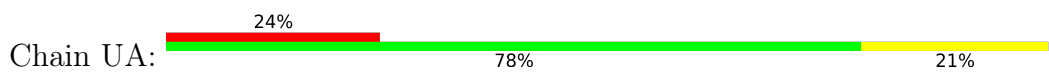
• Molecule 79: mL41

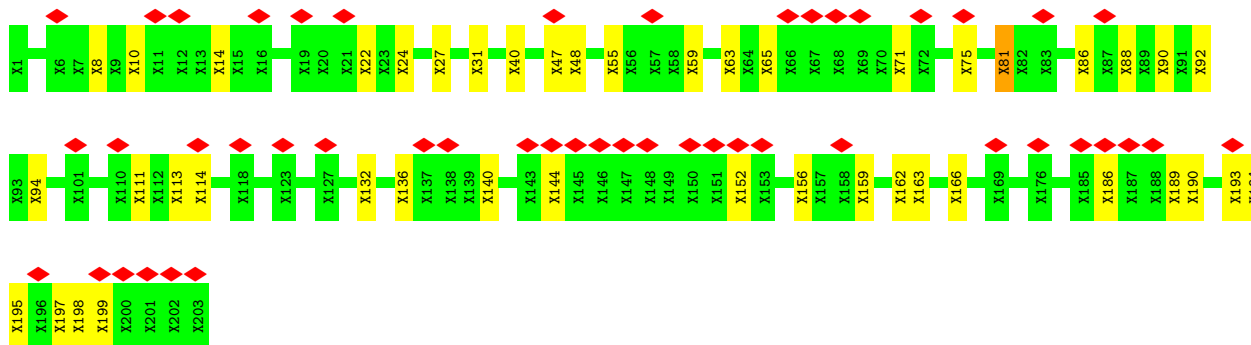


• Molecule 80: mL94

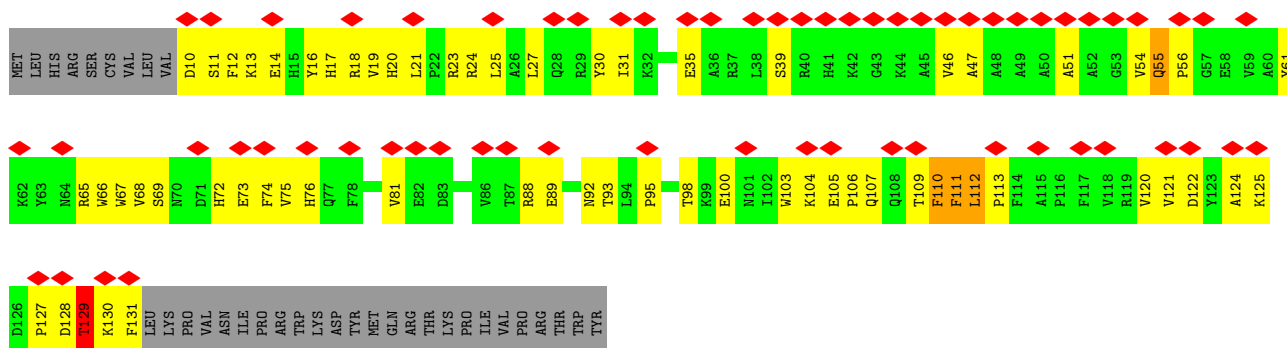
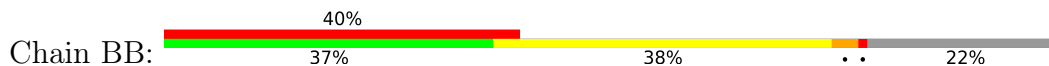


• Molecule 81: UA

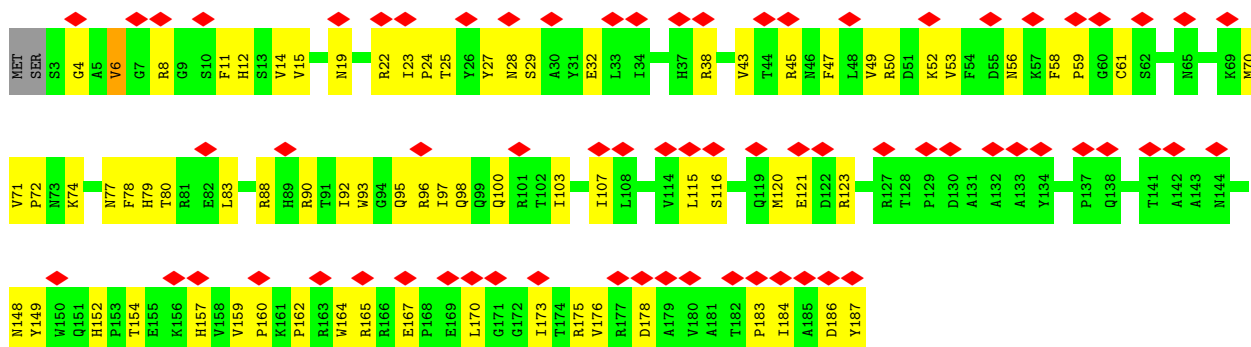
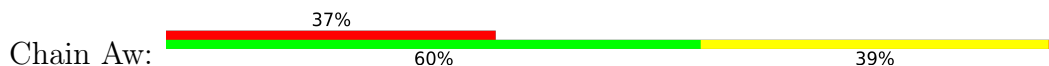




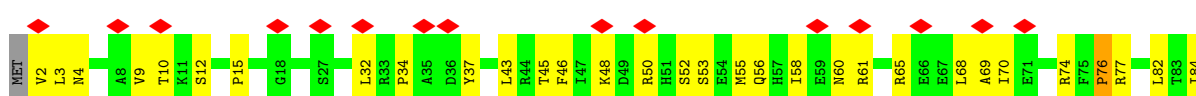
• Molecule 82: mL95



• Molecule 83: mL89

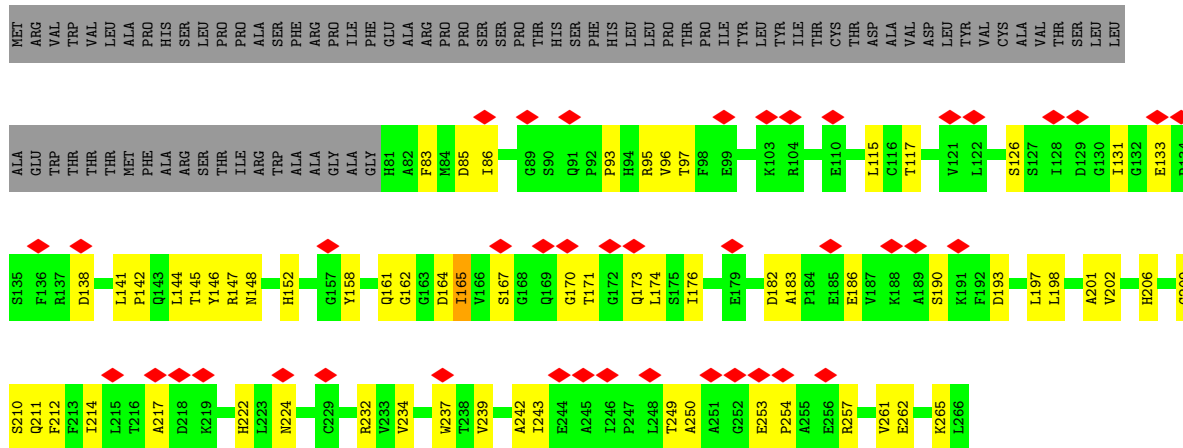


• Molecule 84: bL31m

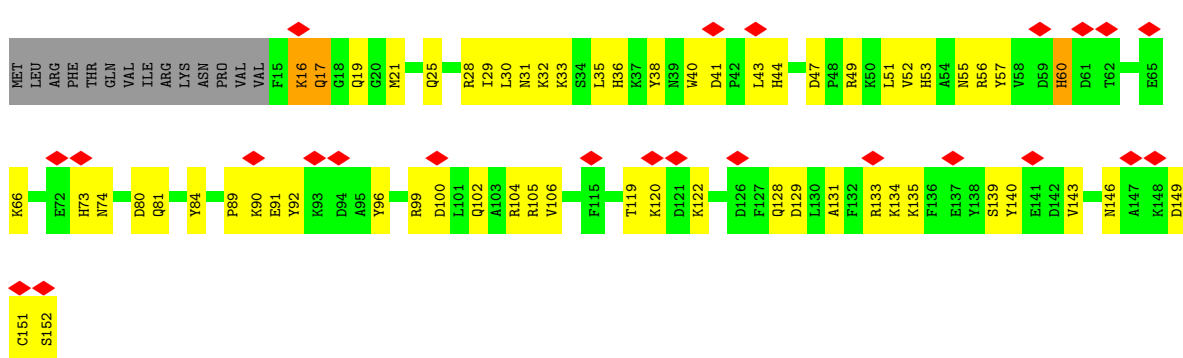


SER
GLN
SER

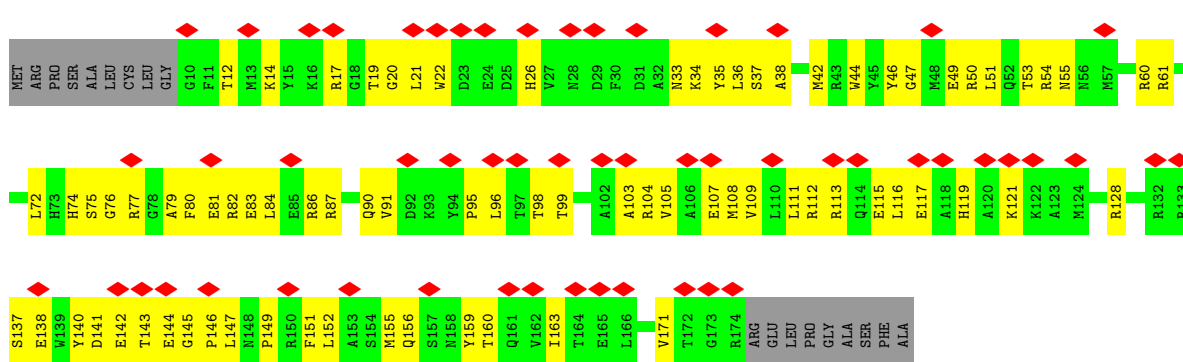
• Molecule 87: Peptidyl-prolyl cis-trans isomerase



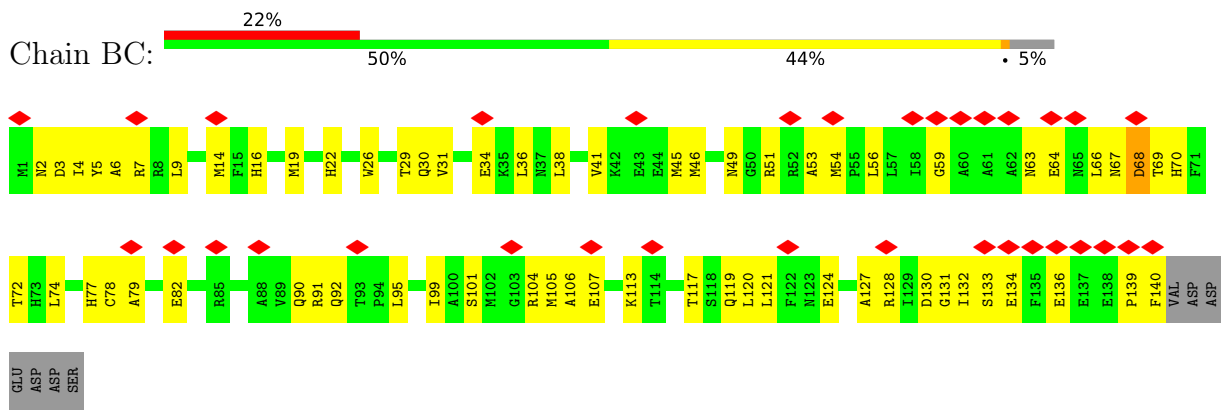
• Molecule 88: mL93



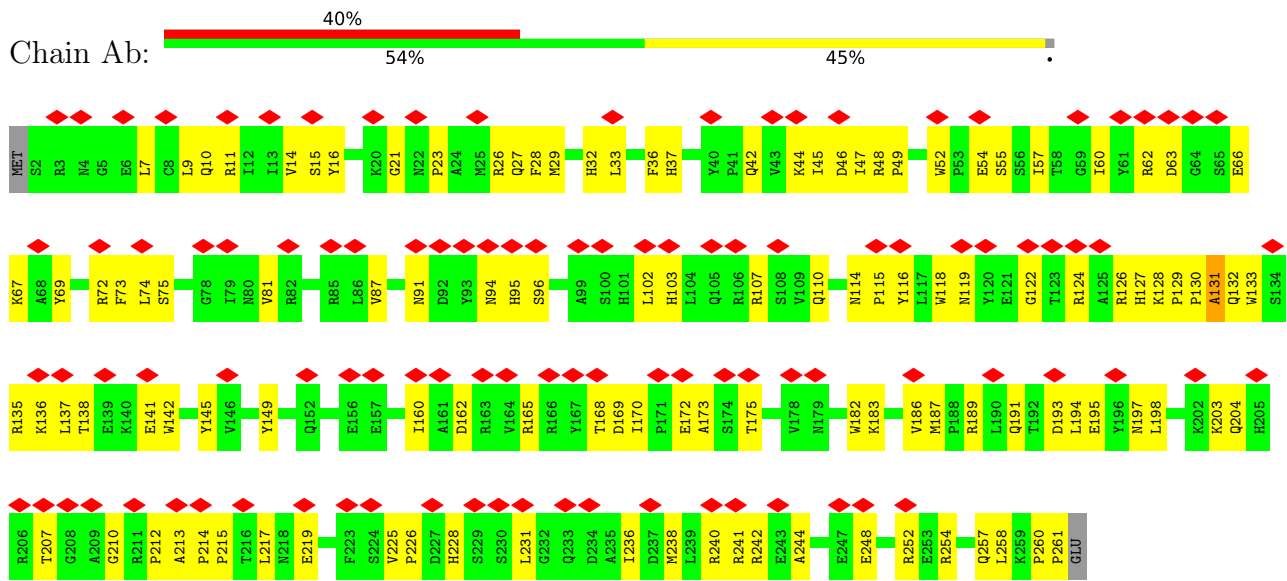
• Molecule 89: mL86



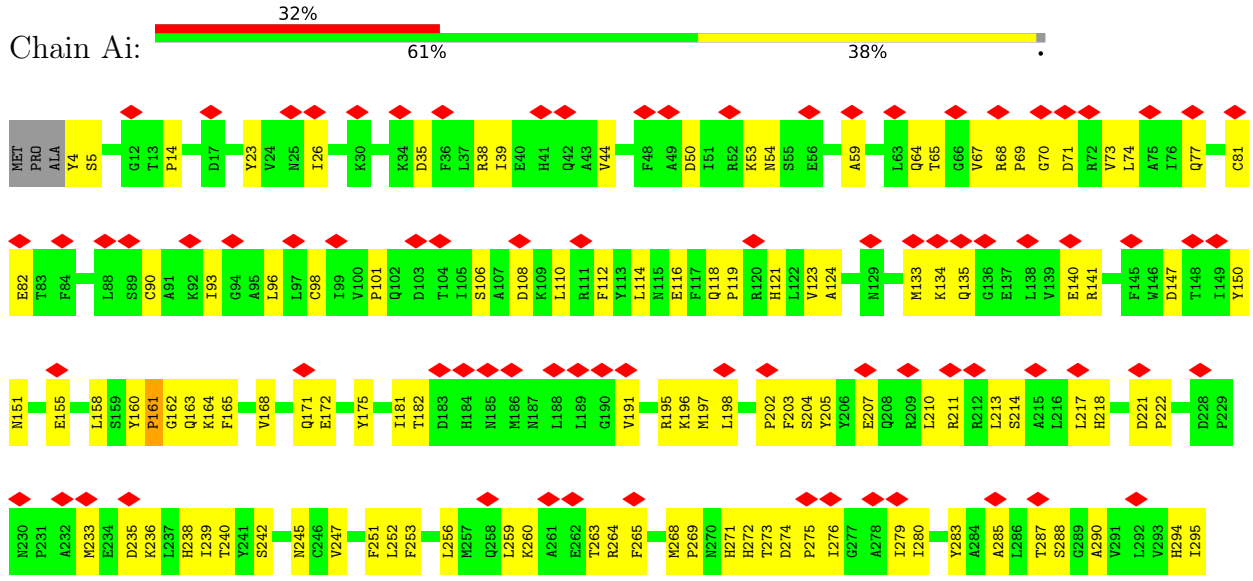
• Molecule 90: mL96

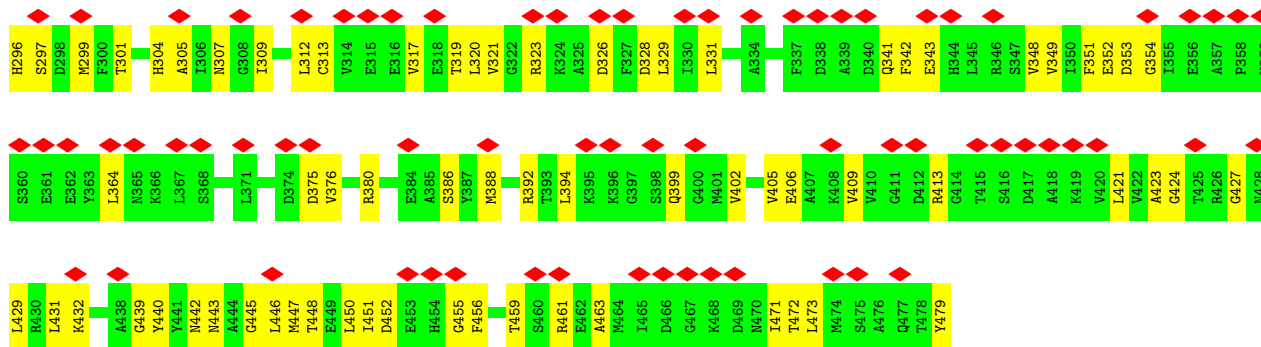


- Molecule 91: L51_S25_CI-B8 domain-containing protein

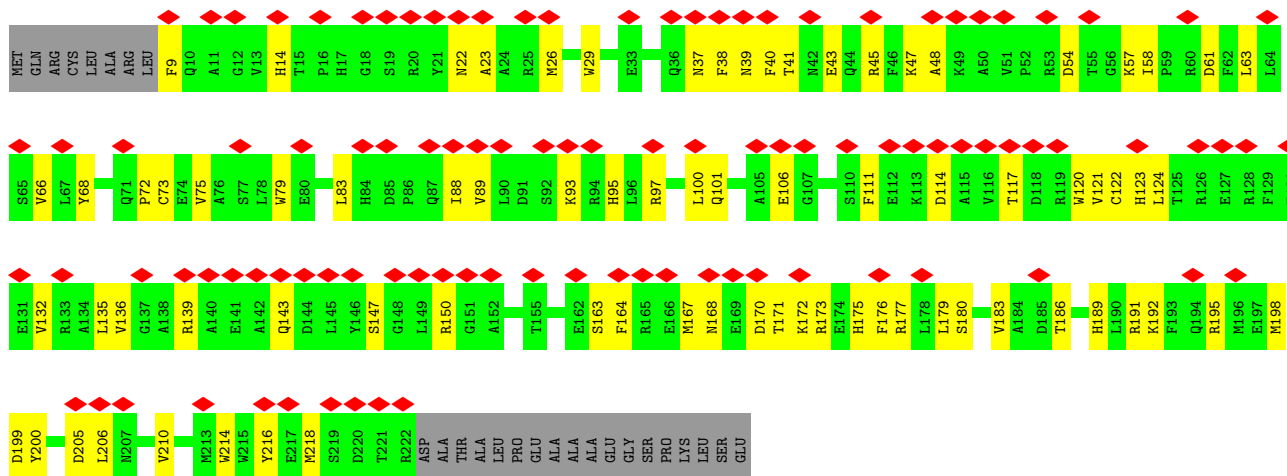


- Molecule 92: mL69

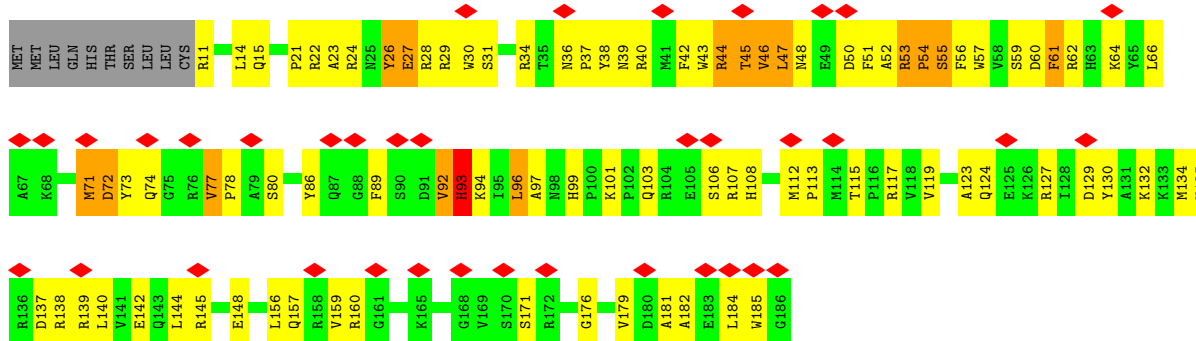




• Molecule 93: mL80

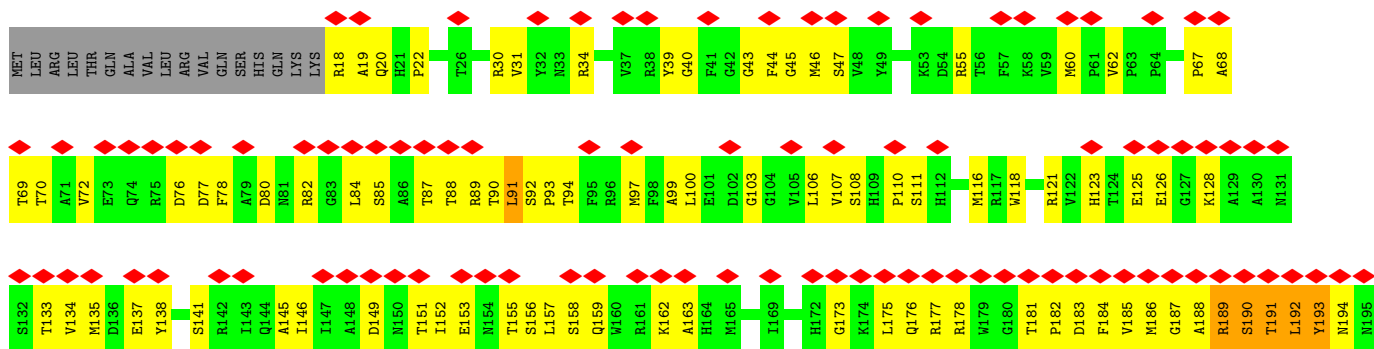


• Molecule 94: mL87

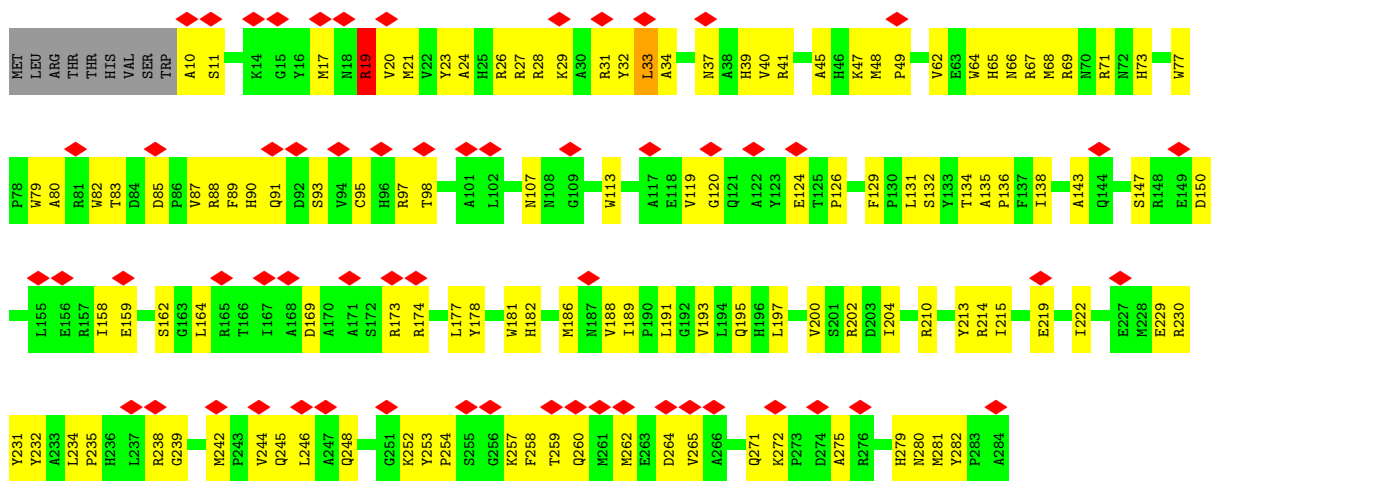


• Molecule 95: mL42

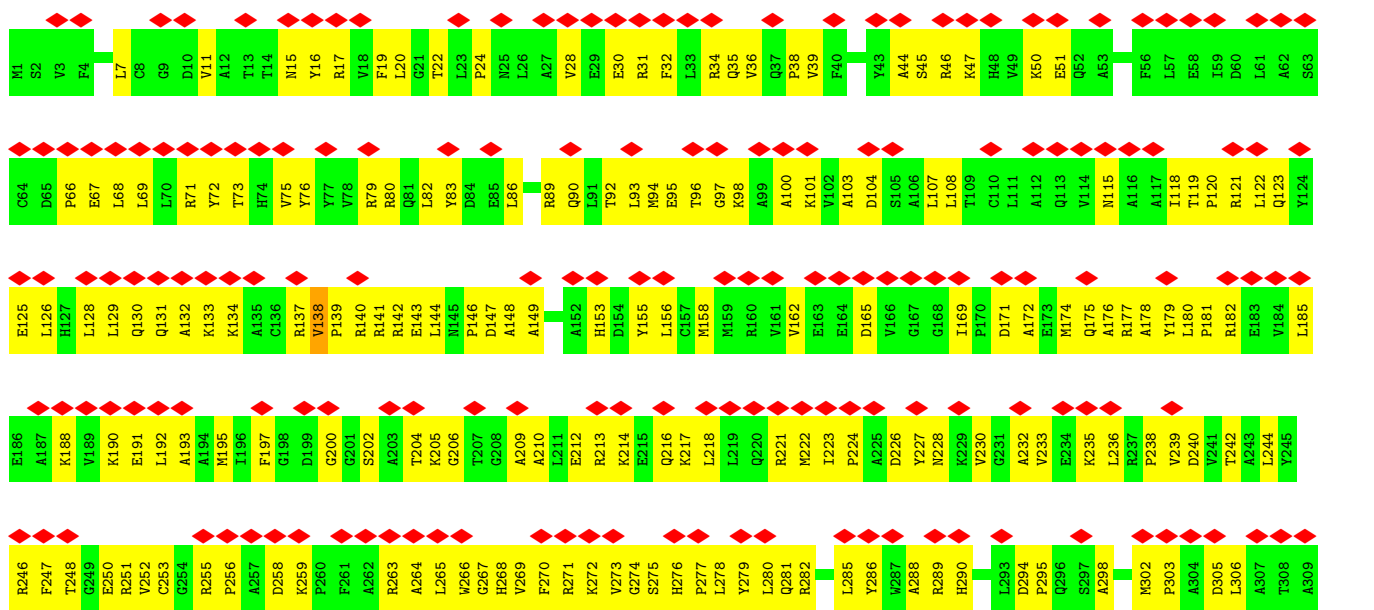


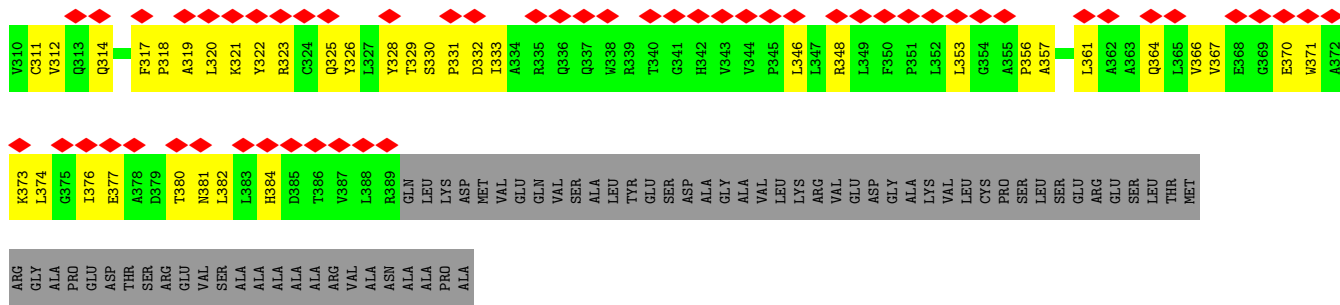


• Molecule 96: mL79

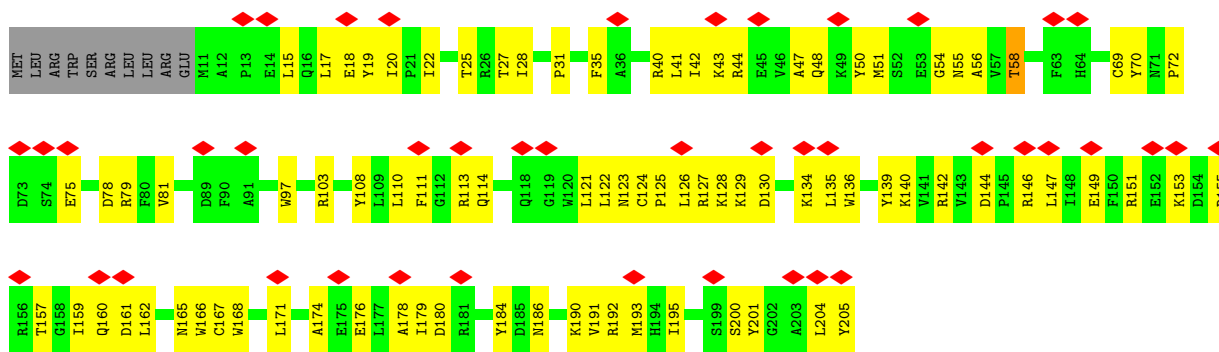


• Molecule 97: mL70

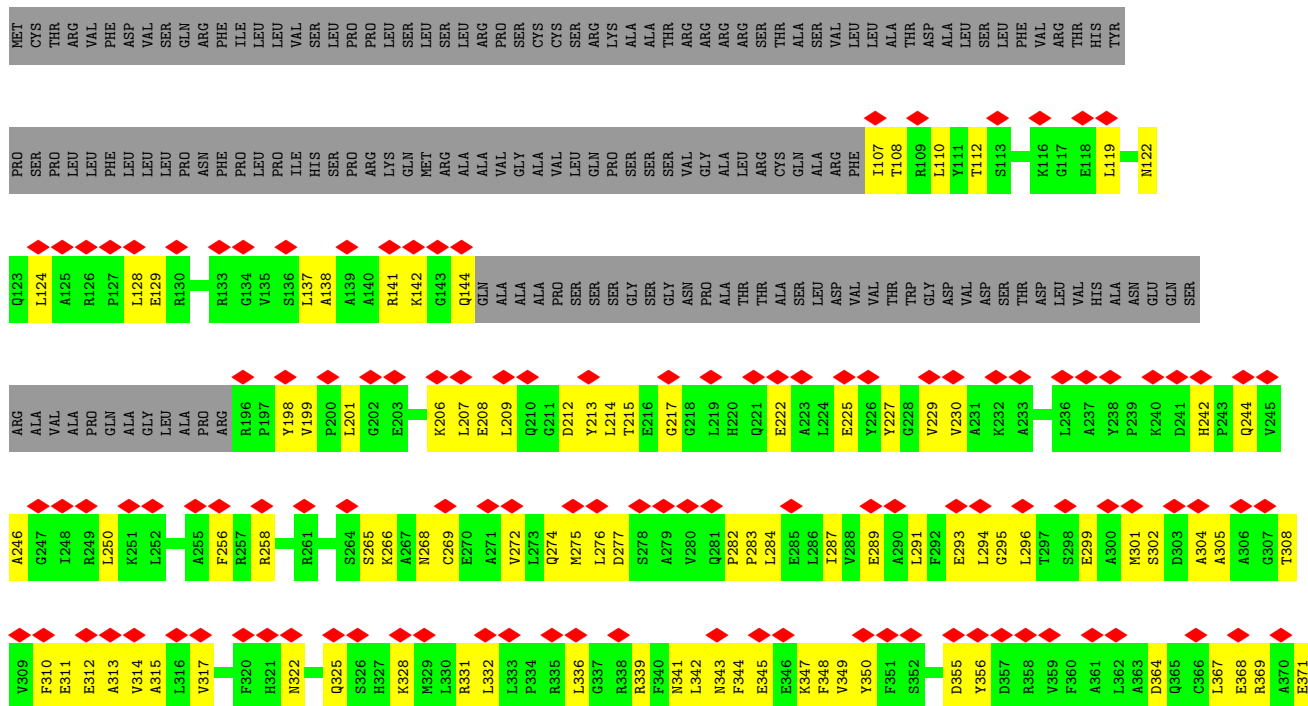


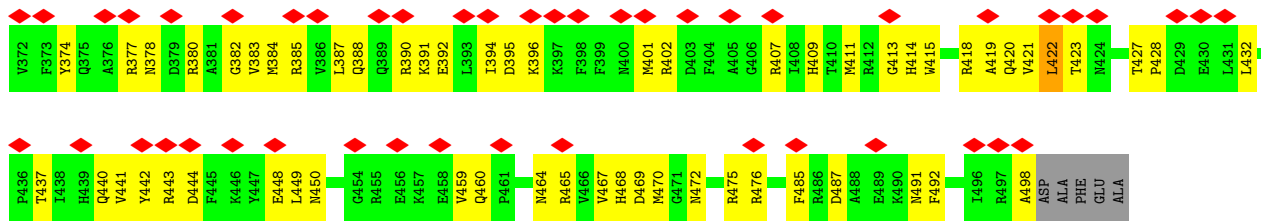


• Molecule 98: mL84

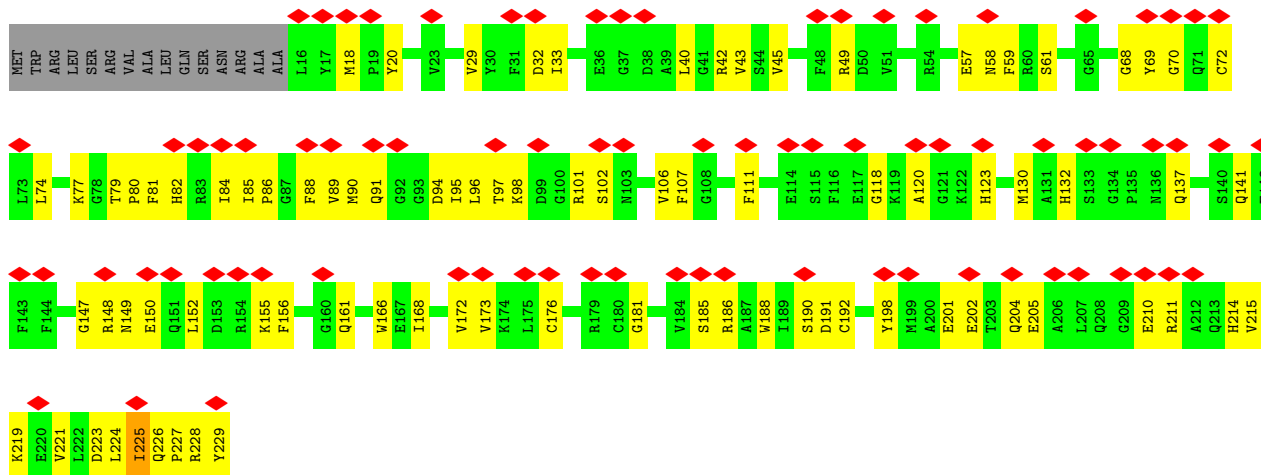


• Molecule 99: mL72

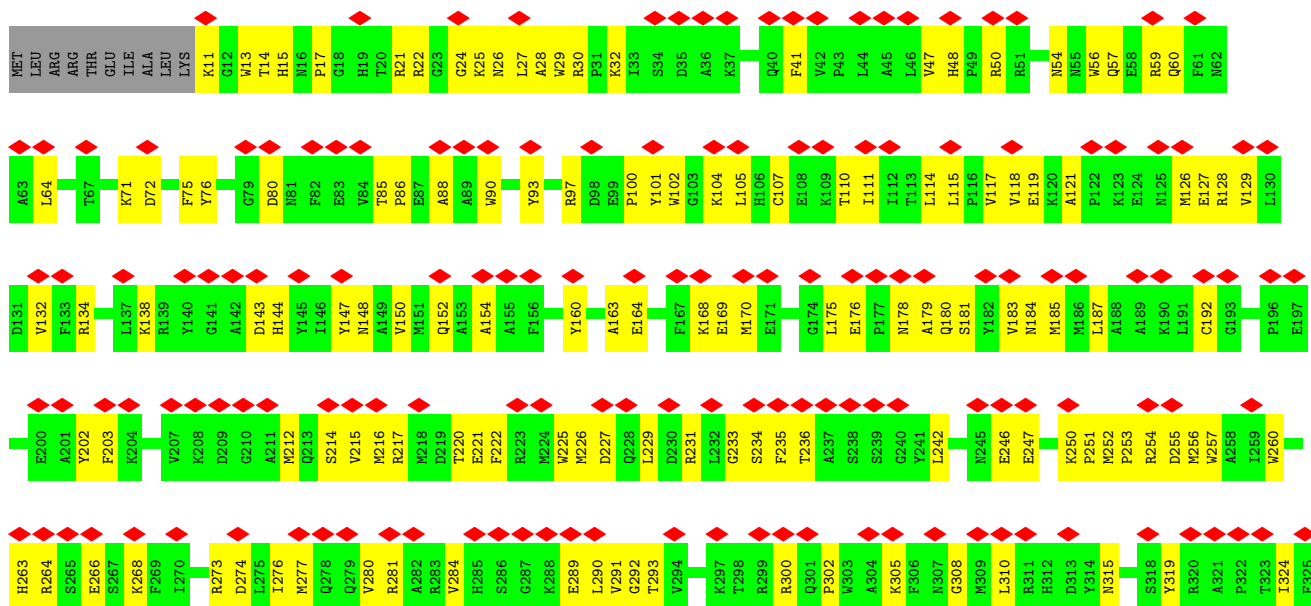


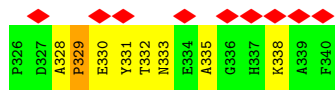


• Molecule 100: Peptidyl-prolyl cis-trans isomerase

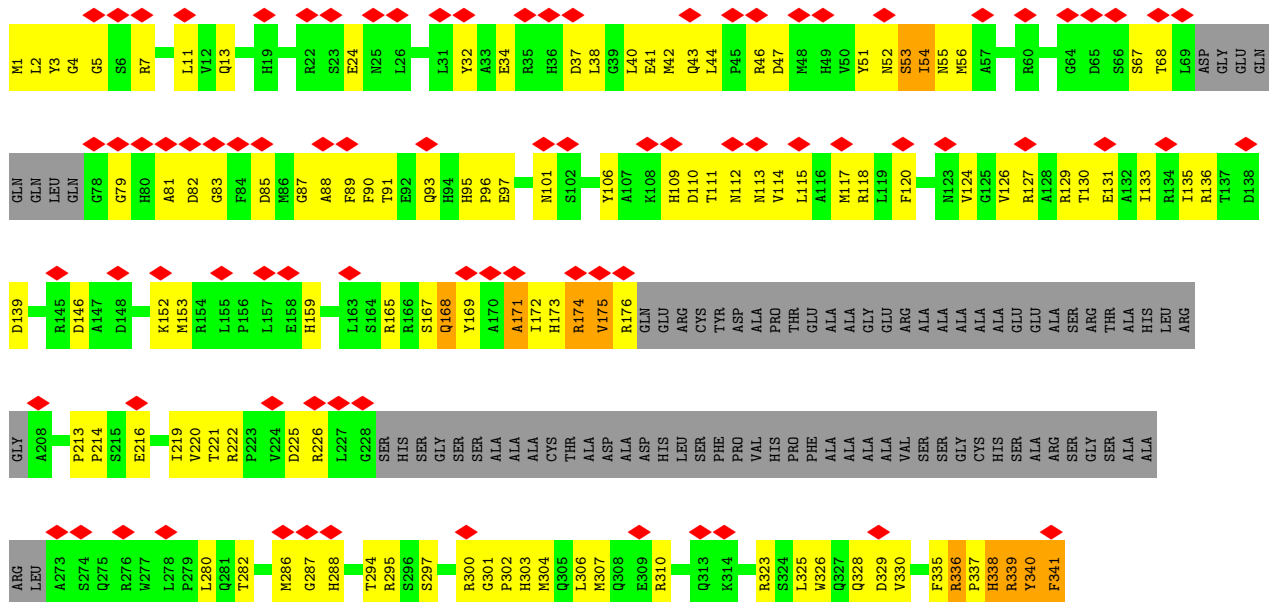
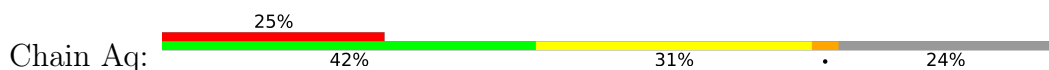


• Molecule 101: mL75

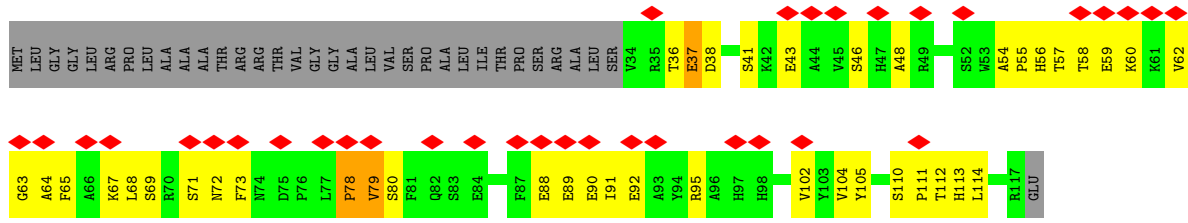




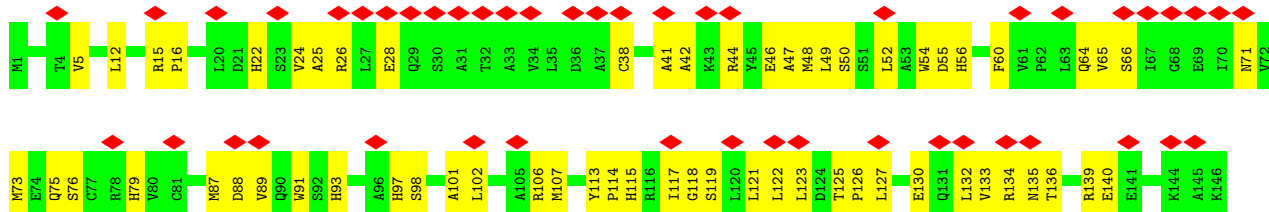
• Molecule 102: mL82

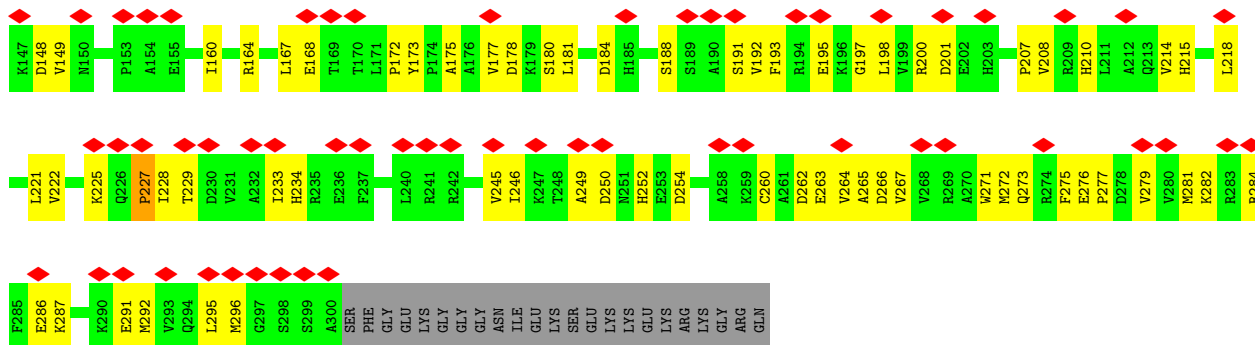


• Molecule 103: mL98

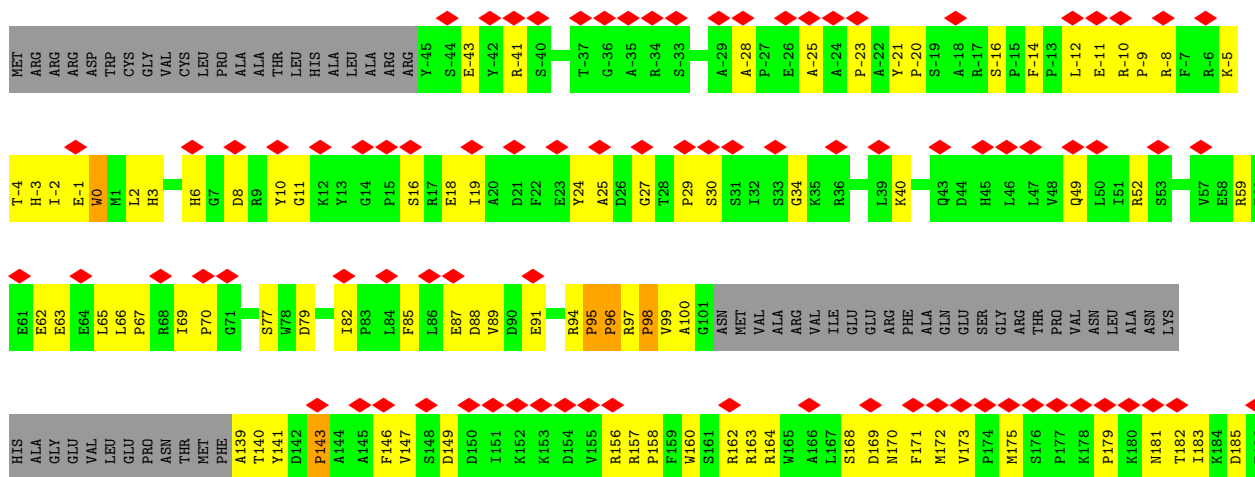


• Molecule 104: mL73

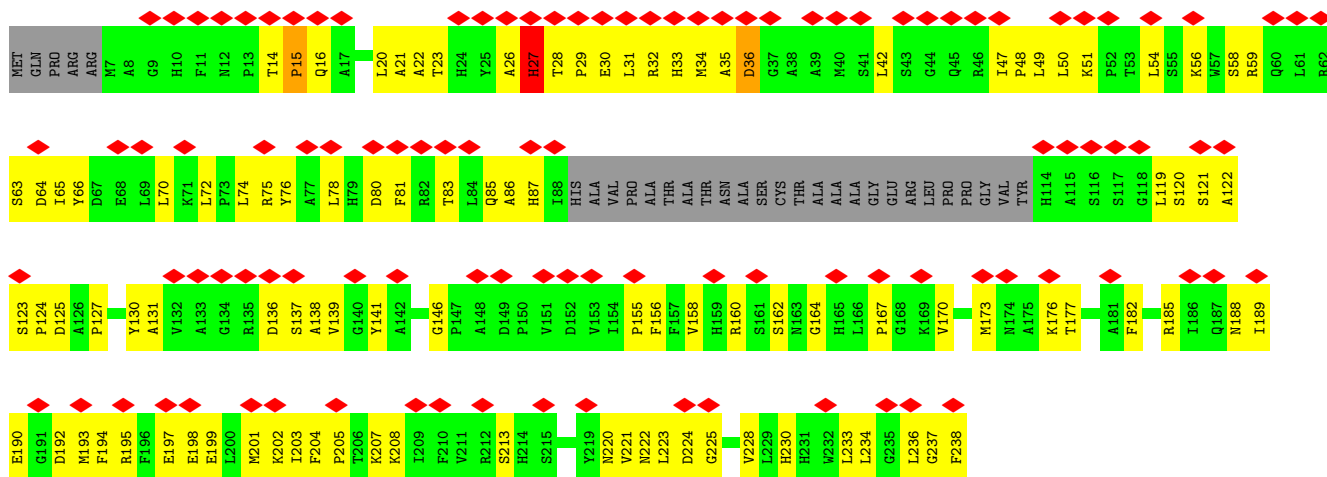
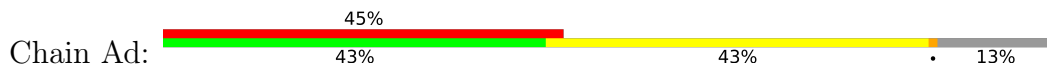




• Molecule 105: mL52

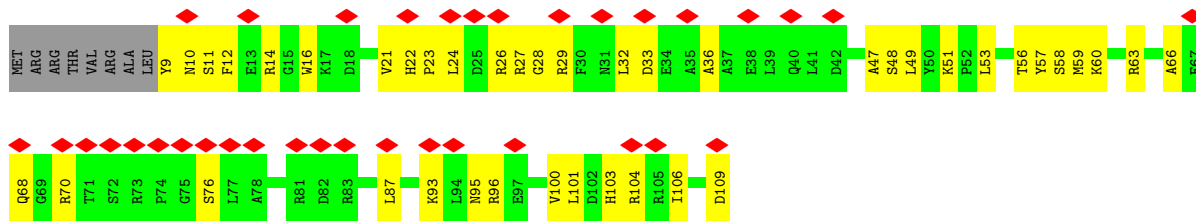


• Molecule 106: mL49



• Molecule 107: mL99

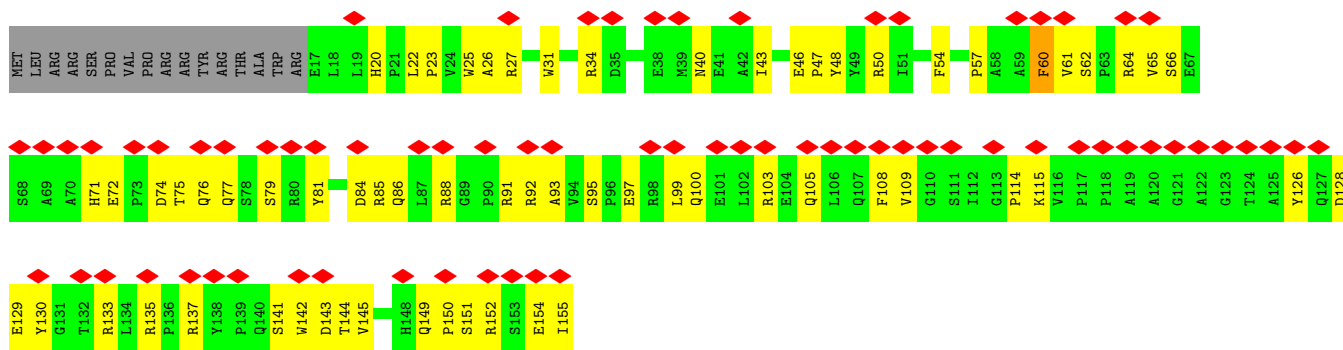




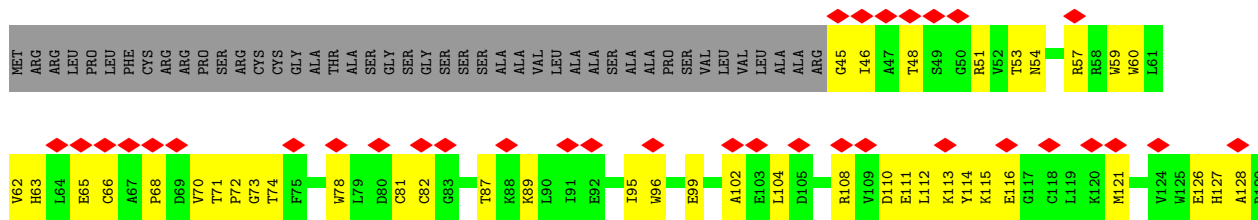
• Molecule 108: mL88

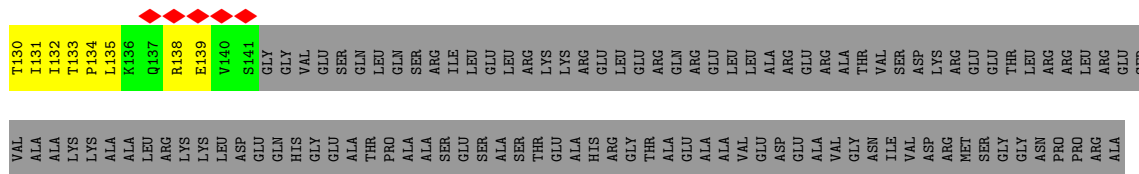


• Molecule 109: mL63

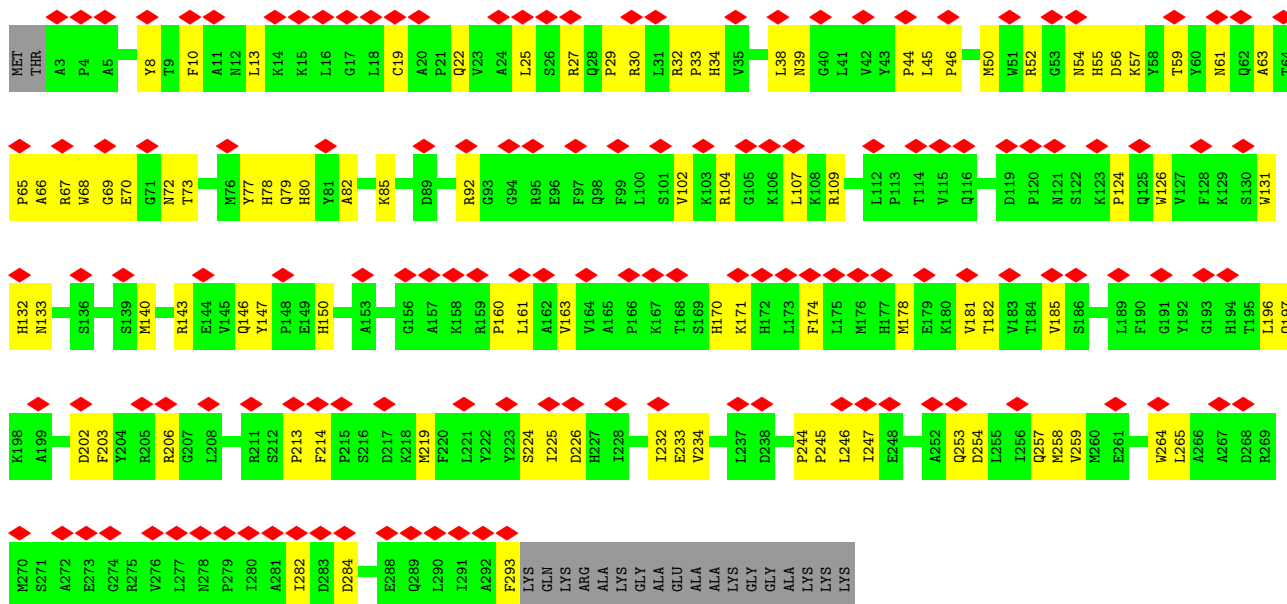


• Molecule 110: mL85

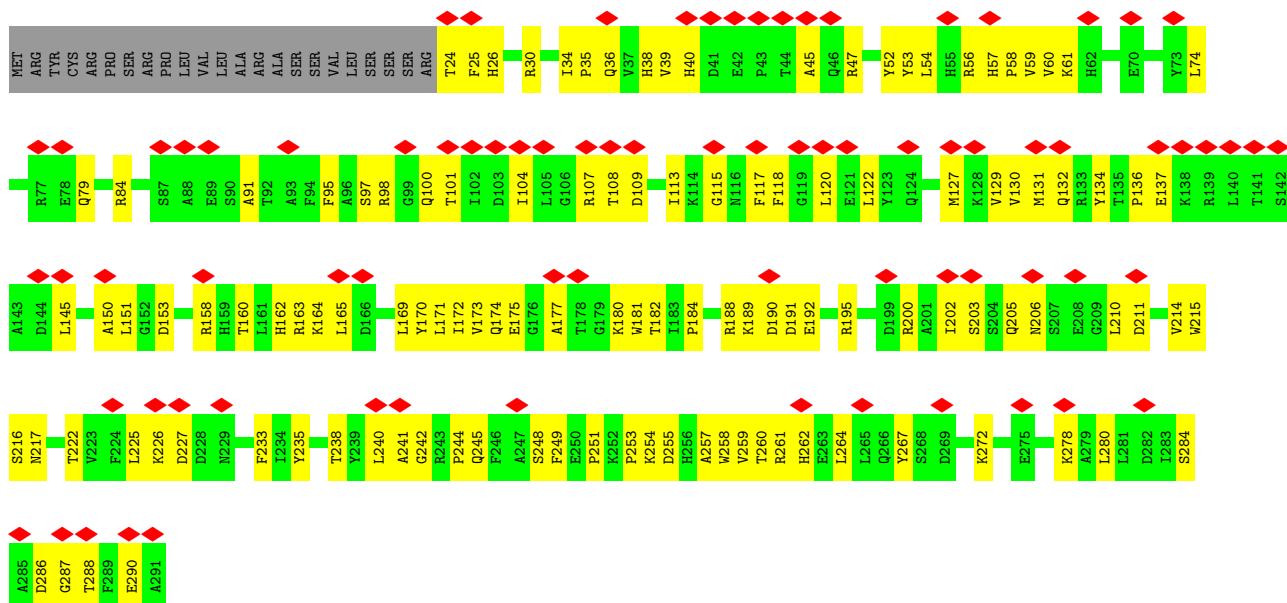


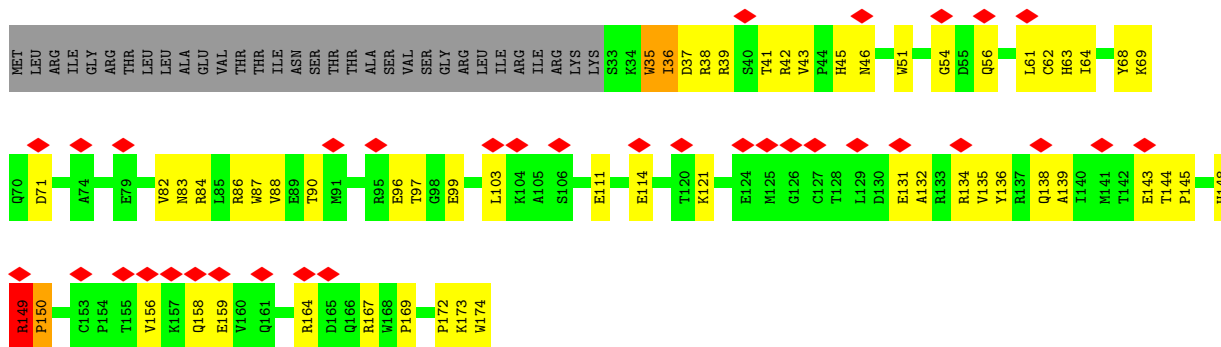


• Molecule 111: mL53

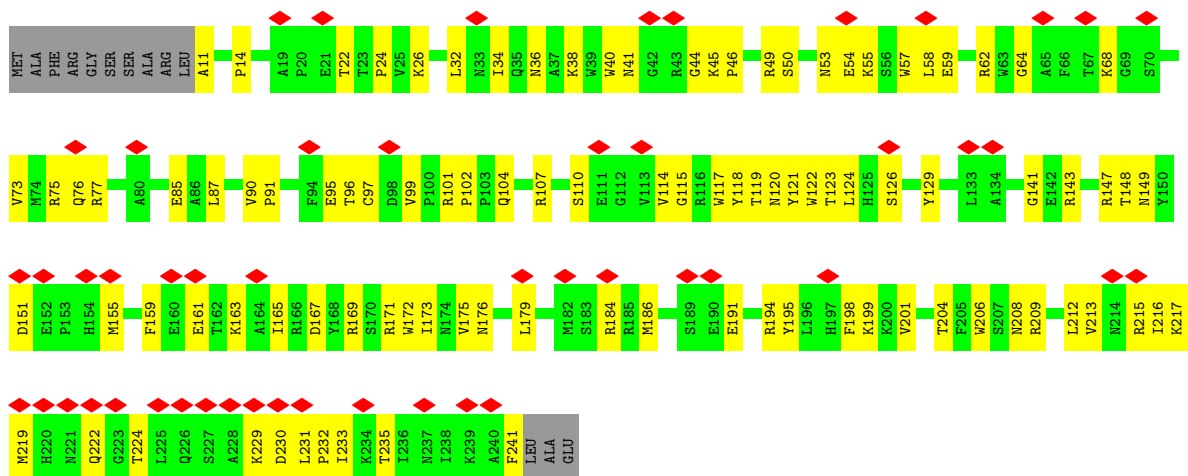


• Molecule 112: MRP-L46 domain-containing protein

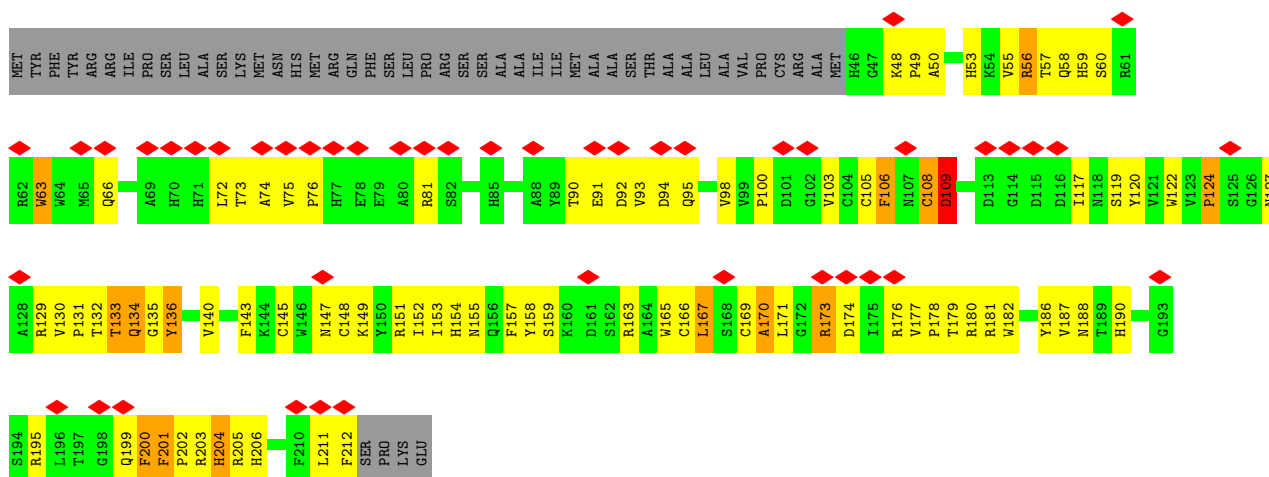




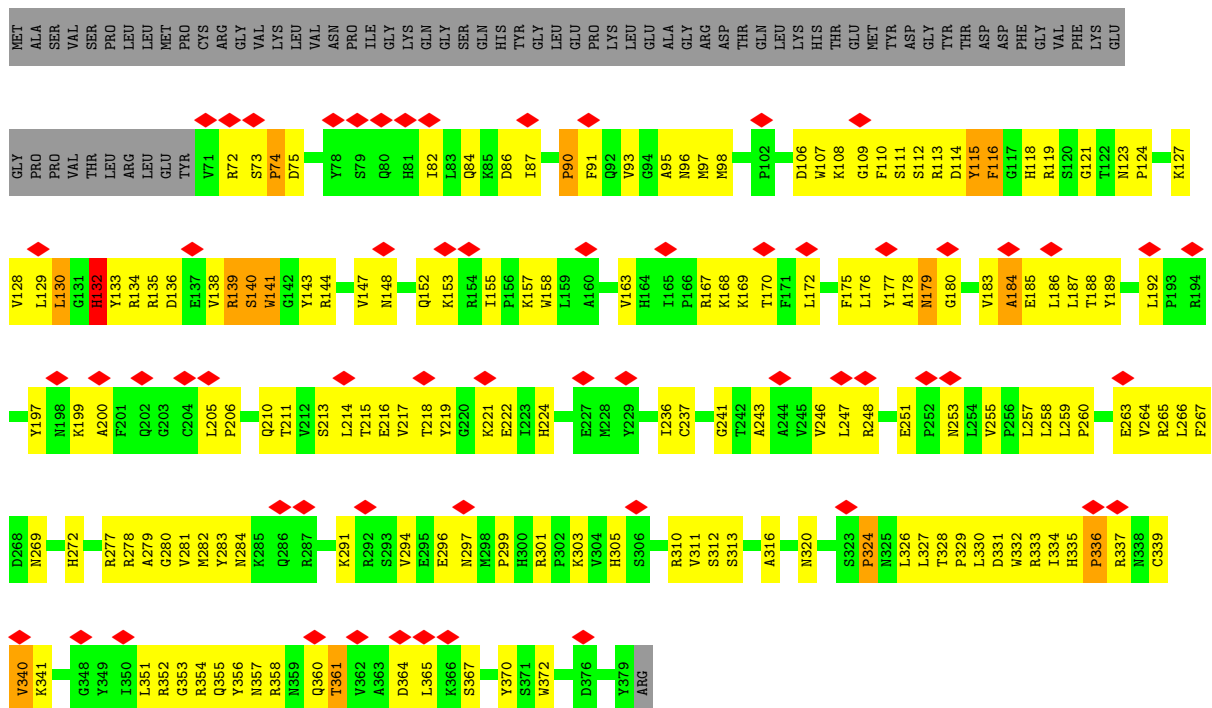
• Molecule 116: mL59/64



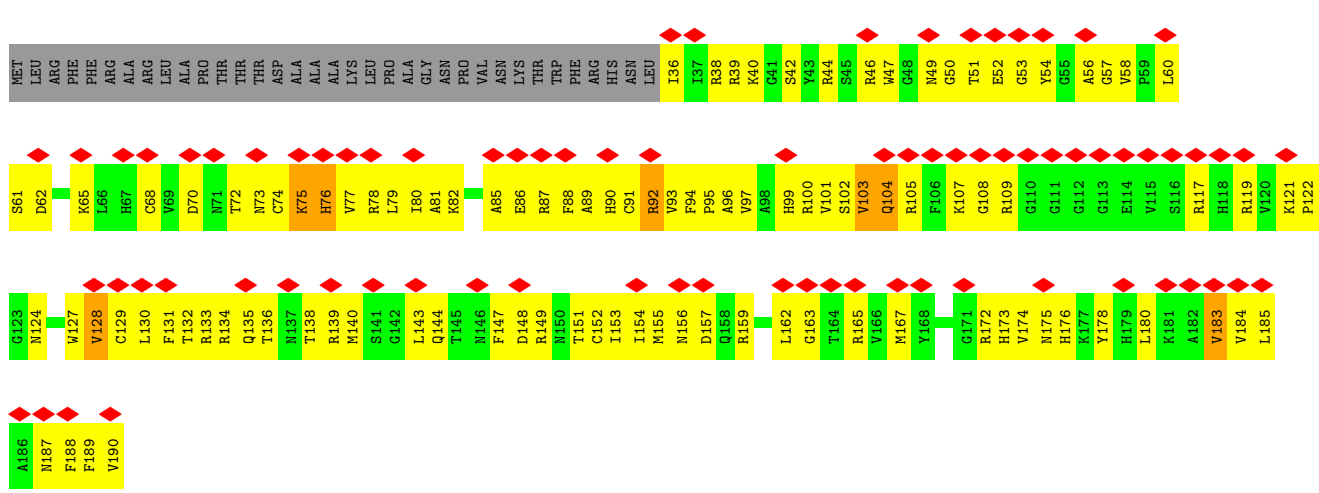
• Molecule 117: LIM zinc-binding domain-containing protein



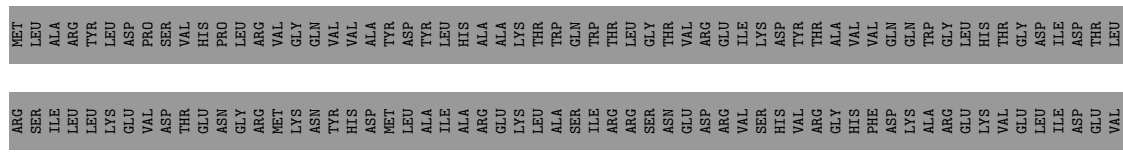
• Molecule 118: Putative ribosomal protein L2

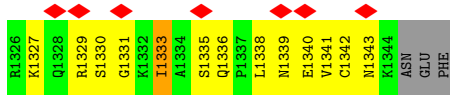


• Molecule 119: Putative ribosomal protein L14

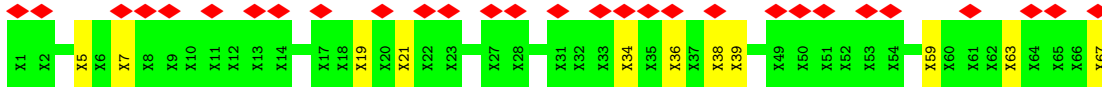
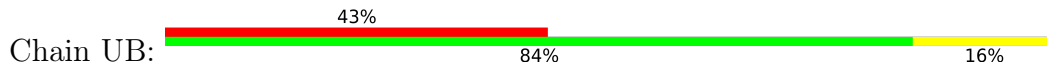


• Molecule 120: mL100

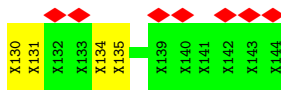
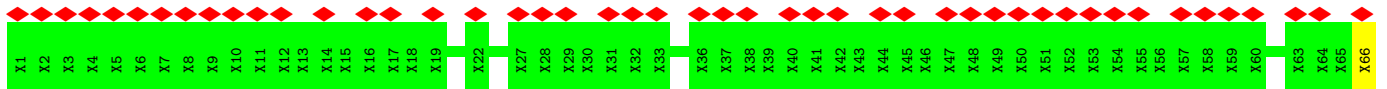
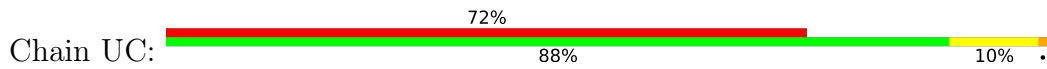




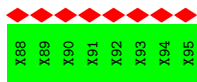
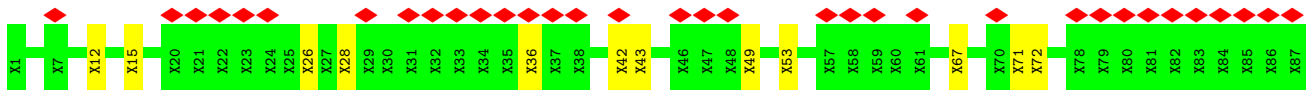
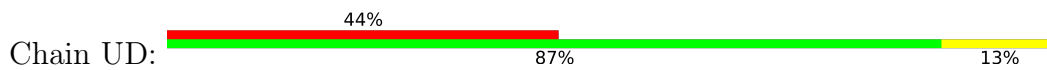
• Molecule 121: UB



• Molecule 122: UC



• Molecule 123: UD



4 Experimental information

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 ($e^-/\text{\AA}^2$)	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: NAD, MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.45	0/25559	0.60	21/39736 (0.1%)
1	2	0.78	54/14217 (0.4%)	1.18	154/22099 (0.7%)
2	h	0.23	0/1347	0.42	0/1819
3	aw	0.24	0/1172	0.47	0/1578
4	m	0.22	0/2437	0.48	0/3300
5	f	0.21	0/1239	0.52	0/1660
6	s	0.22	0/1389	0.44	0/1877
7	au	0.20	0/2140	0.41	0/2899
8	am	0.23	0/2252	0.47	0/3035
9	n	0.20	0/1209	0.45	0/1625
10	ae	0.20	0/4698	0.48	0/6385
11	ay	0.21	0/1223	0.44	0/1653
12	ag	0.21	0/4627	0.46	0/6260
13	aj	0.19	0/2641	0.44	0/3591
14	e	0.24	0/6598	0.47	1/8991 (0.0%)
15	d	0.22	0/2771	0.44	0/3733
16	az	0.24	0/1343	0.46	0/1815
17	ax	0.21	0/1405	0.42	0/1906
18	r	0.21	0/3818	0.44	0/5177
19	af	0.19	0/4802	0.44	0/6515
20	u	0.21	0/5673	0.48	1/7675 (0.0%)
21	aa	0.19	0/12362	0.44	0/16747
22	ab	0.21	0/9432	0.45	0/12775
23	ak	0.21	0/2187	0.47	0/2963
24	ac	0.19	0/8897	0.49	2/12093 (0.0%)
25	ad	0.72	2/5837 (0.0%)	0.52	5/7913 (0.1%)
26	an	0.23	0/2545	0.49	0/3443
27	ao	0.22	0/1574	0.50	0/2141
28	ap	0.21	0/1927	0.49	1/2593 (0.0%)
29	aq	0.17	0/1847	0.47	0/2506
30	as	1.50	6/2013 (0.3%)	0.58	3/2745 (0.1%)
31	at	0.18	0/1664	0.53	1/2243 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	y	0.20	0/2191	0.50	0/2965
33	w	0.18	0/1315	0.45	0/1787
34	v	0.18	0/490	0.49	0/656
35	t	0.18	0/1826	0.48	1/2488 (0.0%)
36	p	0.22	0/2002	0.47	1/2704 (0.0%)
37	j	0.20	0/1553	0.47	0/2098
38	l	0.20	0/4544	0.51	1/6158 (0.0%)
39	ar	0.19	0/2038	0.45	0/2758
40	av	0.20	0/1265	0.54	0/1716
41	ai	0.21	0/3133	0.49	0/4241
42	x	0.23	0/2091	0.47	0/2844
43	i	0.20	0/2271	0.43	0/3065
44	g	0.18	0/834	0.49	0/1115
45	o	1.04	1/3847 (0.0%)	0.48	2/5196 (0.0%)
46	c	0.24	0/2084	0.47	0/2815
47	k	0.22	0/977	0.42	0/1319
48	q	0.22	0/1748	0.48	0/2354
49	b	0.25	0/1319	0.52	0/1787
50	a	0.62	6/3377 (0.2%)	0.51	0/4558
51	ba	0.16	0/232	0.46	0/314
52	z	0.22	0/7898	0.47	0/10712
53	bd	0.33	0/358	0.68	0/487
54	A	0.50	0/3098	0.63	3/4217 (0.1%)
55	B	0.47	0/3623	0.59	3/4931 (0.1%)
56	C	0.43	0/1831	0.54	0/2498
57	D	0.34	0/1062	0.52	0/1438
58	E	0.34	0/2734	0.48	0/3687
59	F	0.47	0/1485	0.64	1/2019 (0.0%)
60	G	0.48	0/3110	0.65	4/4223 (0.1%)
61	H	0.40	0/1338	0.59	0/1808
62	I	0.45	0/2220	0.62	0/2998
63	J	0.48	0/1175	0.76	1/1582 (0.1%)
64	K	0.42	0/1499	0.52	0/2026
65	L	0.44	0/1452	0.53	0/1970
66	M	0.49	0/2168	0.74	9/2928 (0.3%)
67	N	0.46	0/1650	0.52	0/2242
68	O	0.38	0/2591	0.64	4/3507 (0.1%)
69	P	0.45	0/1402	0.60	0/1892
70	Q	0.45	0/1827	0.55	0/2463
71	R	0.35	0/3852	0.50	0/5243
72	S	0.44	0/1271	0.52	0/1712
73	T	0.42	0/501	0.49	0/665
74	U	0.59	0/756	0.95	3/1011 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	V	0.50	0/1231	0.65	0/1645
76	W	0.64	0/483	1.00	1/657 (0.2%)
77	X	0.44	0/3846	0.64	3/5250 (0.1%)
78	Y	0.32	0/2116	0.47	0/2866
79	Z	0.49	0/1268	0.82	5/1725 (0.3%)
80	BA	0.36	0/1056	0.68	0/1435
82	BB	0.52	1/1061 (0.1%)	0.76	2/1438 (0.1%)
83	Aw	0.44	0/1552	0.57	0/2107
84	Bj	0.37	0/1389	0.51	0/1878
85	An	0.50	0/2677	0.84	3/3633 (0.1%)
86	Al	0.46	0/2212	0.67	3/3013 (0.1%)
87	BI	0.35	0/1440	0.48	0/1953
88	Az	0.50	0/1259	0.56	0/1700
89	At	0.41	0/1373	0.53	0/1848
90	BC	0.36	0/1135	0.48	0/1532
91	Ab	0.42	0/2249	0.51	1/3044 (0.0%)
92	Ai	0.42	0/3879	0.49	0/5258
93	Ap	0.33	0/1819	0.48	0/2458
94	Au	0.53	0/1542	0.85	3/2082 (0.1%)
95	Aa	0.59	1/1454 (0.1%)	0.74	3/1968 (0.2%)
96	Ao	0.47	0/2351	0.69	0/3196
97	BM	0.23	0/3136	0.55	0/4259
98	Ar	0.46	0/1689	0.53	0/2280
99	Aj	0.40	0/2826	0.50	0/3807
100	BH	0.42	0/1700	0.54	0/2301
101	Am	0.41	0/2791	0.55	2/3775 (0.1%)
102	Aq	0.42	0/2128	0.72	2/2876 (0.1%)
103	BE	0.38	0/723	0.75	0/981
104	Ak	0.31	0/2403	0.50	0/3265
105	BP	0.46	0/1648	0.72	5/2238 (0.2%)
106	Ad	0.48	0/1682	0.70	0/2283
107	BF	0.38	0/871	0.61	0/1170
108	Av	0.34	0/1335	0.49	0/1797
109	Af	0.40	0/1165	0.61	0/1585
110	As	0.37	0/804	0.48	0/1093
111	Ae	0.41	0/2441	0.51	0/3324
112	Ac	0.33	0/2236	0.48	0/3038
113	Ah	0.38	0/3780	0.62	3/5125 (0.1%)
114	BD	0.41	0/826	0.47	0/1109
115	Ay	0.42	0/1269	0.58	0/1724
116	Ag	0.44	0/1968	0.51	0/2661
117	Ax	0.62	0/1439	1.03	12/1952 (0.6%)
118	BL	0.52	0/2572	0.83	6/3482 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
119	BO	0.48	0/1266	0.82	0/1702
120	BG	0.46	0/657	0.94	4/888 (0.5%)
All	All	0.42	71/311630 (0.0%)	0.60	280/430089 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
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 71 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	o	132	ARG	CB-CG	63.20	3.42	1.52
25	ad	536	THR	CA-C	52.56	2.01	1.52
30	as	215	TRP	CE3-CZ3	40.74	2.60	1.38
30	as	215	TRP	CZ3-CH2	29.25	2.13	1.40
30	as	215	TRP	CE2-CZ2	26.41	1.95	1.39

The worst 5 of 280 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	136	A	C2'-C3'-O3'	-27.81	71.99	113.70
1	2	438	G	C4'-C3'-O3'	16.53	137.80	113.00
1	2	438	G	N9-C1'-C2'	-13.62	91.57	112.00
1	2	325	U	C2'-C3'-O3'	-13.09	94.07	113.70
25	ad	536	THR	O-C-N	-12.69	107.11	121.95

All (3) chirality outliers are listed below:

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

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](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	22858	0	11435	1308	0
1	2	12723	0	6326	3541	0
2	h	1311	0	1280	200	0
3	aw	1144	0	1134	233	0
4	m	2368	0	2289	152	0
5	f	1213	0	1174	120	0
6	s	1349	0	1313	231	0
7	au	2066	0	1931	122	0
8	am	2198	0	2181	234	0
9	n	1176	0	1183	165	0
10	ae	4593	0	4568	386	0
11	ay	1187	0	1172	85	0
12	ag	4521	0	4448	278	0
13	aj	2560	0	2500	258	0
14	e	6413	0	6117	380	0
15	d	2715	0	2689	241	0
16	az	1301	0	1302	176	0
17	ax	1356	0	1341	86	0
18	r	3703	0	3597	173	0
19	af	4698	0	4613	225	0
20	u	5564	0	5606	290	0
21	aa	12070	0	11779	567	0
22	ab	9209	0	8848	451	0
23	ak	2141	0	2110	145	0
24	ac	8700	0	8511	468	0
25	ad	5676	0	5503	396	0
26	an	2480	0	2457	152	0
27	ao	1535	0	1538	85	0
28	ap	1893	0	1853	105	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	aq	1794	0	1723	206	0
30	as	1954	0	1919	148	0
31	at	1631	0	1603	82	0
32	y	2152	0	2180	107	0
33	w	1279	0	1251	181	0
34	v	486	0	469	31	0
35	t	1776	0	1723	158	0
36	p	1954	0	1923	121	0
37	j	1506	0	1504	186	0
38	l	4438	0	4408	316	0
39	ar	1993	0	1984	125	0
40	av	1237	0	1195	74	0
41	ai	3068	0	3089	130	0
42	x	2034	0	1938	102	0
43	i	2221	0	2221	209	0
44	g	818	0	818	92	0
45	o	3736	0	3614	221	0
46	c	2038	0	2000	120	0
47	k	951	0	959	64	0
48	q	1699	0	1637	194	0
49	b	1290	0	1271	131	0
50	a	3298	0	3283	267	0
51	ba	223	0	198	12	0
52	z	7713	0	7521	349	0
53	bd	350	0	380	48	0
54	A	2996	0	2807	148	0
55	B	3513	0	3413	192	0
56	C	1772	0	1734	103	0
57	D	1036	0	1038	54	0
58	E	2668	0	2697	137	0
59	F	1435	0	1396	88	0
60	G	3012	0	2917	190	0
61	H	1305	0	1315	96	0
62	I	2153	0	2089	146	0
63	J	1146	0	1145	91	0
64	K	1467	0	1469	101	0
65	L	1419	0	1443	82	0
66	M	2116	0	2150	138	0
67	N	1599	0	1591	81	0
68	O	2537	0	2530	149	0
69	P	1367	0	1374	102	0
70	Q	1785	0	1784	109	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	R	3755	0	3722	184	0
72	S	1244	0	1272	63	0
73	T	487	0	496	28	0
74	U	744	0	798	78	0
75	V	1202	0	1224	94	0
76	W	465	0	446	17	0
77	X	3733	0	3604	196	0
78	Y	2067	0	1955	116	0
79	Z	1223	0	1192	89	0
80	BA	1038	0	1052	79	0
81	UA	1015	0	213	33	0
82	BB	1028	0	1003	82	0
83	Aw	1509	0	1470	83	0
84	Bj	1358	0	1422	85	0
85	An	2605	0	2536	221	0
86	Al	2152	0	2112	132	0
87	BI	1409	0	1400	49	0
88	Az	1215	0	1144	71	0
89	At	1346	0	1299	92	0
90	BC	1114	0	1096	70	0
91	Ab	2185	0	2095	144	0
92	Ai	3789	0	3752	157	0
93	Ap	1775	0	1699	66	0
94	Au	1490	0	1450	130	0
95	Aa	1417	0	1377	126	0
96	Ao	2276	0	2176	124	0
97	BM	3069	0	3105	214	0
98	Ar	1644	0	1608	102	0
99	Aj	2766	0	2765	149	0
100	BH	1659	0	1607	73	0
101	Am	2708	0	2634	132	0
102	Aq	2074	0	2050	142	0
103	BE	700	0	665	43	0
104	Ak	2352	0	2369	109	0
105	BP	1593	0	1529	105	0
106	Ad	1632	0	1607	120	0
107	BF	851	0	831	49	0
108	Av	1300	0	1284	90	0
109	Af	1132	0	1108	63	0
110	As	787	0	777	47	0
111	Ae	2359	0	2328	97	0
112	Ac	2174	0	2096	120	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
113	Ah	3686	0	3572	212	0
114	BD	807	0	772	37	0
115	Ay	1226	0	1157	69	0
116	Ag	1916	0	1888	107	0
117	Ax	1388	0	1308	116	0
118	BL	2497	0	2489	183	0
119	BO	1239	0	1246	155	0
120	BG	643	0	617	38	0
121	UB	335	0	73	8	0
122	UC	720	0	150	10	0
123	UD	475	0	105	11	0
124	Ax	2	0	0	0	0
124	BD	1	0	0	0	0
124	BG	1	0	0	2	0
124	T	1	0	0	2	0
124	W	1	0	0	0	0
125	Ag	44	0	26	10	0
126	1	2	0	0	0	0
All	All	303111	0	278272	16534	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 29.

The worst 5 of 16534 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:502:A:C8	14:e:789:PRO:HG3	1.26	1.64
30:as:215:TRP:CZ2	30:as:215:TRP:CH2	1.77	1.64
1:2:497:A:C6	3:aw:17:ILE:HG21	1.30	1.63
1:2:175:U:C5'	48:q:11:GLN:CG	1.78	1.62
50:a:349:TRP:CZ3	50:a:349:TRP:CH2	1.75	1.62

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	43	74
11	ay	139/169 (82%)	129 (93%)	10 (7%)	0	100	100
12	ag	555/564 (98%)	520 (94%)	33 (6%)	2 (0%)	30	64
13	aj	314/397 (79%)	297 (95%)	17 (5%)	0	100	100
14	e	805/822 (98%)	736 (91%)	67 (8%)	2 (0%)	43	74
15	d	339/351 (97%)	317 (94%)	22 (6%)	0	100	100
16	az	152/163 (93%)	148 (97%)	4 (3%)	0	100	100
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	64
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%)	24	59
25	ad	688/811 (85%)	643 (94%)	43 (6%)	2 (0%)	36	69
26	an	300/302 (99%)	272 (91%)	26 (9%)	2 (1%)	18	53
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	64
37	j	178/189 (94%)	158 (89%)	20 (11%)	0	100	100
38	l	535/677 (79%)	489 (91%)	44 (8%)	2 (0%)	30	64
39	ar	248/282 (88%)	235 (95%)	13 (5%)	0	100	100
40	av	148/236 (63%)	124 (84%)	23 (16%)	1 (1%)	18	53
41	ai	377/379 (100%)	346 (92%)	31 (8%)	0	100	100
42	x	253/268 (94%)	236 (93%)	16 (6%)	1 (0%)	30	64
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%)	43	74
46	c	249/311 (80%)	223 (90%)	26 (10%)	0	100	100
47	k	114/312 (36%)	107 (94%)	7 (6%)	0	100	100
48	q	194/425 (46%)	189 (97%)	5 (3%)	0	100	100
49	b	153/159 (96%)	127 (83%)	25 (16%)	1 (1%)	18	53
50	a	406/431 (94%)	373 (92%)	32 (8%)	1 (0%)	43	74
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	38
55	B	433/435 (100%)	380 (88%)	52 (12%)	1 (0%)	43	74
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%)	21	55
60	G	363/373 (97%)	314 (86%)	47 (13%)	2 (1%)	21	55
61	H	160/167 (96%)	144 (90%)	14 (9%)	2 (1%)	9	40
62	I	255/304 (84%)	224 (88%)	31 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	J	139/143 (97%)	102 (73%)	36 (26%)	1 (1%)	18	53
64	K	177/193 (92%)	158 (89%)	19 (11%)	0	100	100
65	L	176/185 (95%)	157 (89%)	18 (10%)	1 (1%)	21	55
66	M	257/278 (92%)	217 (84%)	38 (15%)	2 (1%)	16	50
67	N	187/251 (74%)	163 (87%)	24 (13%)	0	100	100
68	O	305/475 (64%)	273 (90%)	29 (10%)	3 (1%)	12	45
69	P	163/184 (89%)	145 (89%)	17 (10%)	1 (1%)	21	55
70	Q	215/233 (92%)	192 (89%)	22 (10%)	1 (0%)	24	59
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	31
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%)	21	55
78	Y	253/292 (87%)	233 (92%)	20 (8%)	0	100	100
79	Z	148/197 (75%)	114 (77%)	31 (21%)	3 (2%)	6	32
80	BA	136/167 (81%)	103 (76%)	29 (21%)	4 (3%)	3	26
82	BB	120/156 (77%)	95 (79%)	23 (19%)	2 (2%)	7	35
83	Aw	183/187 (98%)	161 (88%)	22 (12%)	0	100	100
84	Bj	166/185 (90%)	143 (86%)	22 (13%)	1 (1%)	21	55
85	An	312/331 (94%)	253 (81%)	52 (17%)	7 (2%)	5	31
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	37
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%)	43	74
93	Ap	212/240 (88%)	188 (89%)	24 (11%)	0	100	100
94	Au	174/186 (94%)	131 (75%)	37 (21%)	6 (3%)	3	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
95	Aa	176/195 (90%)	142 (81%)	31 (18%)	3 (2%)	7	35
96	Ao	273/284 (96%)	232 (85%)	39 (14%)	2 (1%)	18	53
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%)	4	29
103	BE	82/118 (70%)	56 (68%)	25 (30%)	1 (1%)	10	41
104	Ak	298/323 (92%)	254 (85%)	44 (15%)	0	100	100
105	BP	191/254 (75%)	161 (84%)	28 (15%)	2 (1%)	12	45
106	Ad	203/237 (86%)	163 (80%)	38 (19%)	2 (1%)	12	45
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%)	18	53
110	As	95/249 (38%)	87 (92%)	8 (8%)	0	100	100
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	47
114	BD	95/102 (93%)	85 (90%)	10 (10%)	0	100	100
115	Ay	140/174 (80%)	118 (84%)	18 (13%)	4 (3%)	3	26
116	Ag	229/244 (94%)	204 (89%)	25 (11%)	0	100	100
117	Ax	165/216 (76%)	129 (78%)	33 (20%)	3 (2%)	6	34
118	BL	307/380 (81%)	233 (76%)	67 (22%)	7 (2%)	5	30
119	BO	153/190 (80%)	104 (68%)	46 (30%)	3 (2%)	6	32
120	BG	83/1347 (6%)	57 (69%)	23 (28%)	3 (4%)	2	23
All	All	32374/40717 (80%)	28909 (89%)	3346 (10%)	119 (0%)	31	64

5 of 119 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	ac	685	LEU
54	A	289	ARG

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Mol	Chain	Res	Type
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%)	250 (100%)	0	100	100
5	f	122/292 (42%)	120 (98%)	2 (2%)	55	69
6	s	143/157 (91%)	142 (99%)	1 (1%)	76	78
7	au	217/223 (97%)	217 (100%)	0	100	100
8	am	228/262 (87%)	228 (100%)	0	100	100
9	n	127/147 (86%)	127 (100%)	0	100	100
10	ae	479/532 (90%)	479 (100%)	0	100	100
11	ay	126/149 (85%)	125 (99%)	1 (1%)	73	77
12	ag	478/484 (99%)	477 (100%)	1 (0%)	87	87
13	aj	275/345 (80%)	275 (100%)	0	100	100
14	e	688/700 (98%)	687 (100%)	1 (0%)	88	89
15	d	289/296 (98%)	289 (100%)	0	100	100
16	az	137/144 (95%)	137 (100%)	0	100	100
17	ax	146/166 (88%)	145 (99%)	1 (1%)	76	78
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%)	580 (100%)	2 (0%)	86	85
21	aa	1266/1465 (86%)	1264 (100%)	2 (0%)	87	87
22	ab	951/971 (98%)	950 (100%)	1 (0%)	88	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	ak	224/268 (84%)	224 (100%)	0	100	100
24	ac	889/1002 (89%)	889 (100%)	0	100	100
25	ad	595/699 (85%)	593 (100%)	2 (0%)	86	85
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%)	191 (100%)	0	100	100
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%)	171 (99%)	1 (1%)	78	80
32	y	230/379 (61%)	230 (100%)	0	100	100
33	w	140/170 (82%)	140 (100%)	0	100	100
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%)	209 (100%)	0	100	100
37	j	163/172 (95%)	163 (100%)	0	100	100
38	l	465/552 (84%)	465 (100%)	0	100	100
39	ar	217/237 (92%)	217 (100%)	0	100	100
40	av	136/208 (65%)	136 (100%)	0	100	100
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%)	393 (100%)	0	100	100
46	c	217/260 (84%)	217 (100%)	0	100	100
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%)	140 (100%)	0	100	100
50	a	346/365 (95%)	346 (100%)	0	100	100
51	ba	21/82 (26%)	21 (100%)	0	100	100
52	z	817/979 (84%)	816 (100%)	1 (0%)	88	89
53	bd	39/85 (46%)	39 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	A	314/393 (80%)	313 (100%)	1 (0%)	86	85
55	B	380/380 (100%)	375 (99%)	5 (1%)	61	71
56	C	190/226 (84%)	189 (100%)	1 (0%)	81	82
57	D	106/154 (69%)	106 (100%)	0	100	100
58	E	285/300 (95%)	285 (100%)	0	100	100
59	F	151/152 (99%)	149 (99%)	2 (1%)	61	71
60	G	315/322 (98%)	307 (98%)	8 (2%)	42	62
61	H	138/142 (97%)	138 (100%)	0	100	100
62	I	223/261 (85%)	222 (100%)	1 (0%)	84	83
63	J	119/121 (98%)	115 (97%)	4 (3%)	32	55
64	K	151/161 (94%)	151 (100%)	0	100	100
65	L	151/157 (96%)	151 (100%)	0	100	100
66	M	226/241 (94%)	222 (98%)	4 (2%)	51	67
67	N	175/219 (80%)	175 (100%)	0	100	100
68	O	278/396 (70%)	274 (99%)	4 (1%)	59	71
69	P	147/162 (91%)	145 (99%)	2 (1%)	59	71
70	Q	191/203 (94%)	189 (99%)	2 (1%)	68	75
71	R	406/411 (99%)	405 (100%)	1 (0%)	87	87
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%)	74 (92%)	6 (8%)	12	38
75	V	125/134 (93%)	124 (99%)	1 (1%)	73	77
76	W	50/163 (31%)	46 (92%)	4 (8%)	11	35
77	X	402/437 (92%)	397 (99%)	5 (1%)	63	72
78	Y	209/236 (89%)	209 (100%)	0	100	100
79	Z	132/172 (77%)	129 (98%)	3 (2%)	44	63
80	BA	112/135 (83%)	111 (99%)	1 (1%)	70	75
82	BB	106/140 (76%)	105 (99%)	1 (1%)	70	75
83	Aw	157/159 (99%)	155 (99%)	2 (1%)	61	71
84	Bj	150/165 (91%)	149 (99%)	1 (1%)	76	78
85	An	274/289 (95%)	265 (97%)	9 (3%)	33	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
86	Al	236/299 (79%)	228 (97%)	8 (3%)	32	55
87	BI	153/221 (69%)	152 (99%)	1 (1%)	76	78
88	Az	129/143 (90%)	128 (99%)	1 (1%)	73	77
89	At	140/153 (92%)	140 (100%)	0	100	100
90	BC	117/124 (94%)	116 (99%)	1 (1%)	70	75
91	Ab	233/235 (99%)	232 (100%)	1 (0%)	84	83
92	Ai	408/410 (100%)	407 (100%)	1 (0%)	87	87
93	Ap	189/208 (91%)	188 (100%)	1 (0%)	81	82
94	Au	154/164 (94%)	148 (96%)	6 (4%)	28	52
95	Aa	150/166 (90%)	150 (100%)	0	100	100
96	Ao	236/245 (96%)	235 (100%)	1 (0%)	84	83
97	BM	319/370 (86%)	318 (100%)	1 (0%)	86	85
98	Ar	169/179 (94%)	168 (99%)	1 (1%)	78	80
99	Aj	286/420 (68%)	284 (99%)	2 (1%)	76	78
100	BH	177/189 (94%)	176 (99%)	1 (1%)	78	80
101	Am	278/287 (97%)	276 (99%)	2 (1%)	76	78
102	Aq	221/276 (80%)	218 (99%)	3 (1%)	59	71
103	BE	76/100 (76%)	76 (100%)	0	100	100
104	Ak	254/272 (93%)	254 (100%)	0	100	100
105	BP	167/215 (78%)	166 (99%)	1 (1%)	78	80
106	Ad	172/193 (89%)	170 (99%)	2 (1%)	63	72
107	BF	88/95 (93%)	87 (99%)	1 (1%)	65	74
108	Av	141/169 (83%)	140 (99%)	1 (1%)	76	78
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%)	247 (99%)	2 (1%)	73	77
112	Ac	232/253 (92%)	232 (100%)	0	100	100
113	Ah	385/485 (79%)	380 (99%)	5 (1%)	61	71
114	BD	85/90 (94%)	85 (100%)	0	100	100
115	Ay	130/158 (82%)	129 (99%)	1 (1%)	73	77
116	Ag	202/211 (96%)	201 (100%)	1 (0%)	81	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
117	Ax	150/190 (79%)	144 (96%)	6 (4%)	28	51
118	BL	268/329 (82%)	262 (98%)	6 (2%)	45	64
119	BO	130/158 (82%)	129 (99%)	1 (1%)	73	77
120	BG	67/1047 (6%)	66 (98%)	1 (2%)	57	70
All	All	27983/34364 (81%)	27840 (100%)	143 (0%)	78	82

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
105	BP	0	TRP
108	Av	42	THR
117	Ax	109	ASP
70	Q	49	VAL
69	P	134	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 716 such sidechains are listed below:

Mol	Chain	Res	Type
70	Q	222	GLN
92	Ai	248	ASN
72	S	256	ASN
70	Q	170	ASN
84	Bj	57	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1082/18998 (5%)	639 (59%)	129 (11%)
1	2	602/18998 (3%)	496 (82%)	200 (33%)
All	All	1684/37996 (4%)	1135 (67%)	329 (19%)

5 of 1135 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	U
1	2	3	C
1	2	4	A
1	2	6	U
1	2	7	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	-	46,48,48	0.50	0	64,73,73	0.79	3 (4%)

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	-	-	11/30/62/62	0/5/5/5

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
125	Ag	301	NAD	C4D-O4D-C1D	-3.26	106.94	109.92
125	Ag	301	NAD	C6N-N1N-C2N	-2.24	119.97	121.88
125	Ag	301	NAD	O4B-C4B-C3B	-2.10	100.98	105.15

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

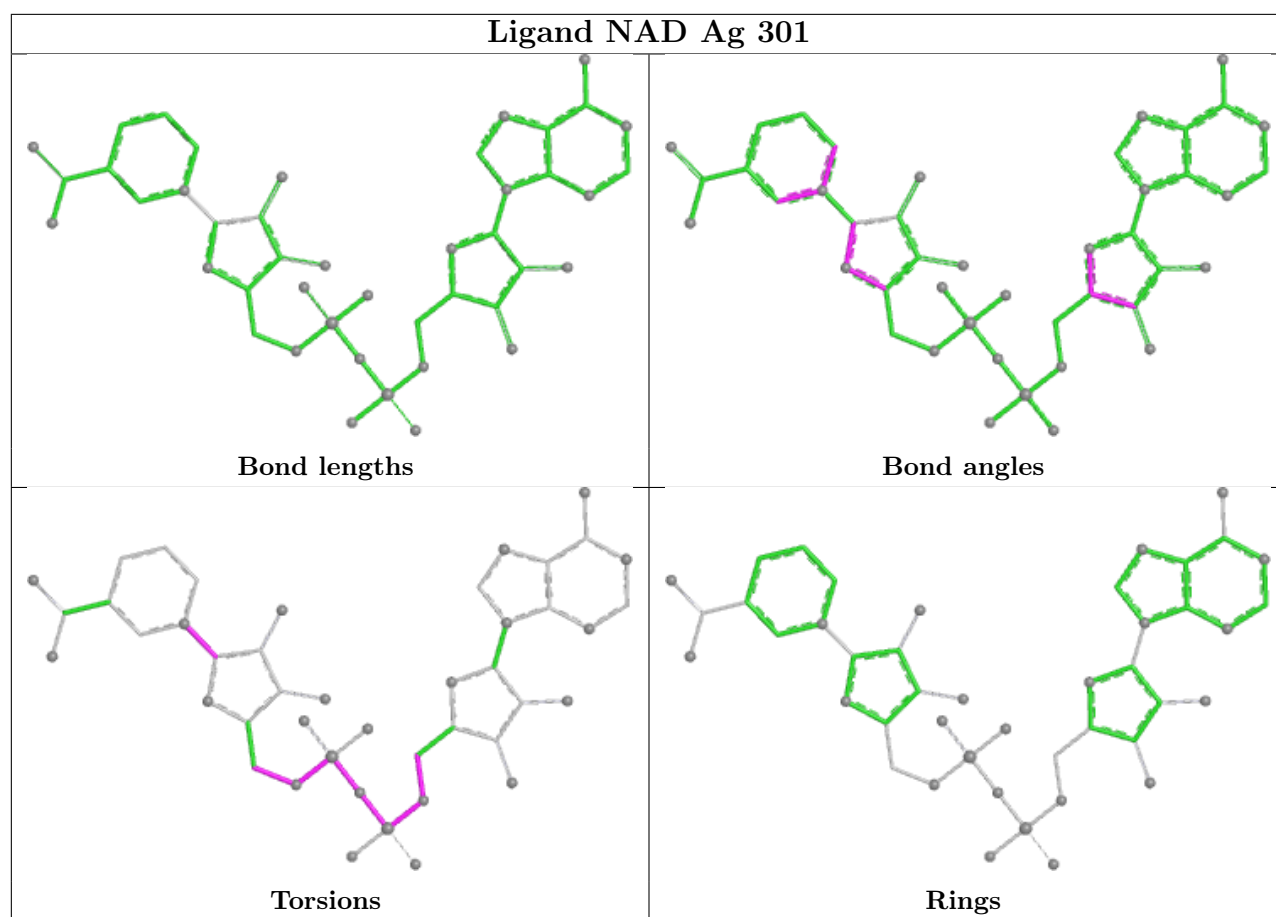
Mol	Chain	Res	Type	Atoms
125	Ag	301	NAD	C5B-O5B-PA-O3
125	Ag	301	NAD	C2D-C1D-N1N-C2N
125	Ag	301	NAD	C4B-C5B-O5B-PA
125	Ag	301	NAD	PN-O3-PA-O5B
125	Ag	301	NAD	PA-O3-PN-O5D

There are no ring outliers.

1 monomer is involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
125	Ag	301	NAD	10	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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

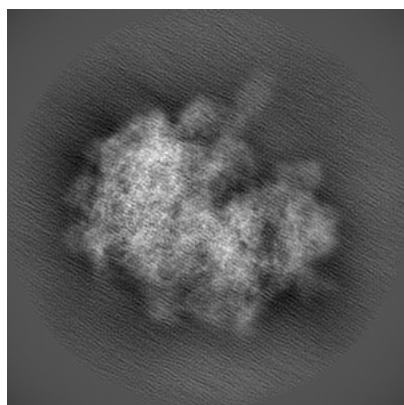
6 Map visualisation [i](#)

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.

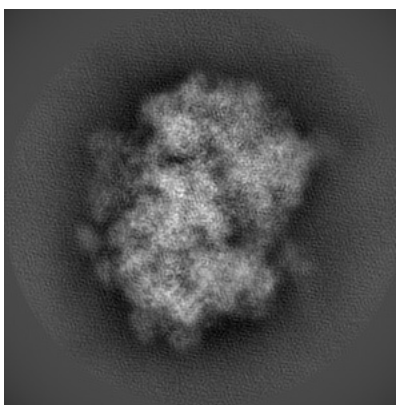
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

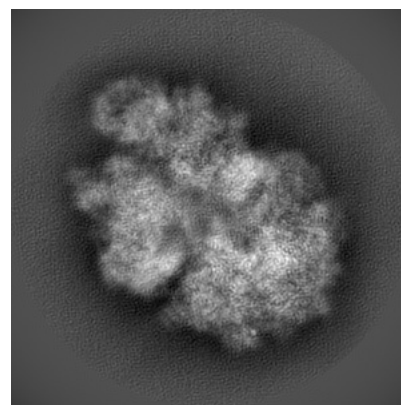
6.1.1 Primary map



X



Y

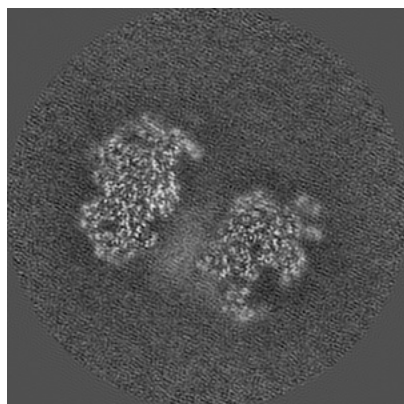


Z

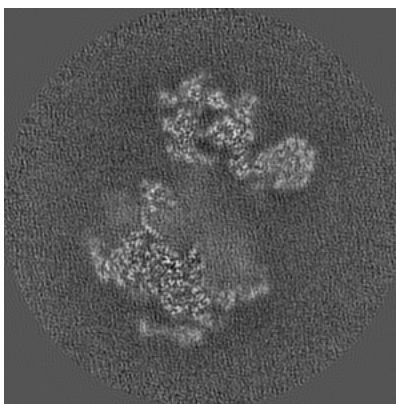
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

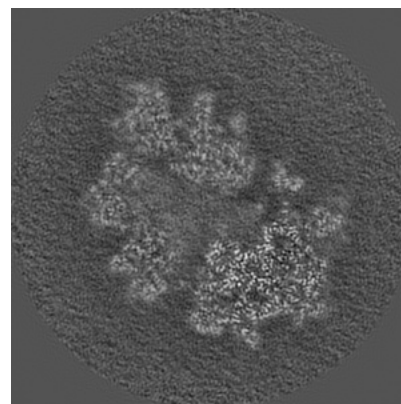
6.2.1 Primary map



X Index: 200



Y Index: 200

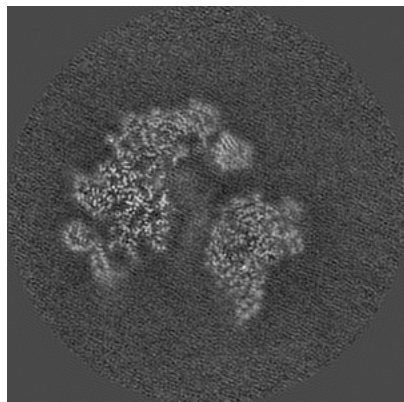


Z Index: 200

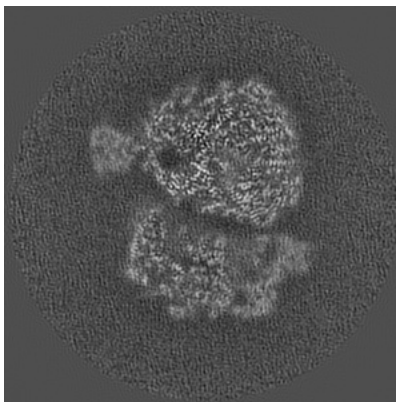
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

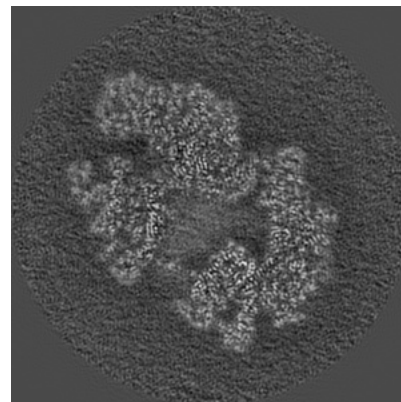
6.3.1 Primary map



X Index: 224



Y Index: 150

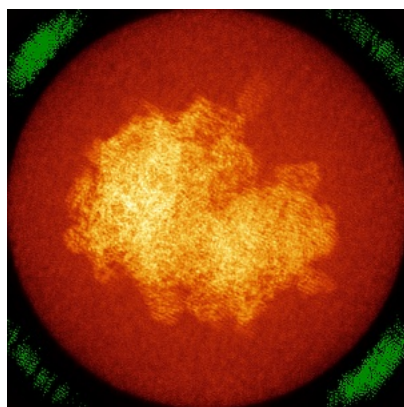


Z Index: 173

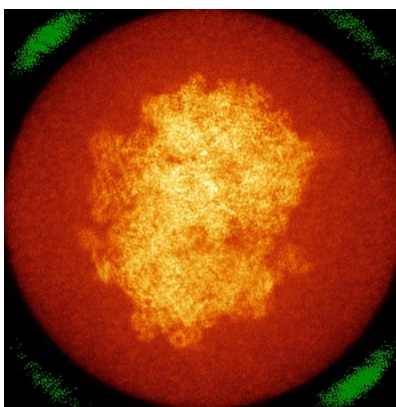
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

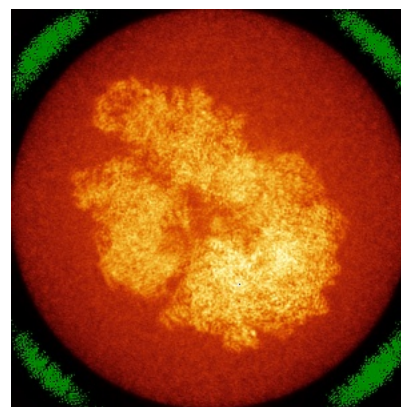
6.4.1 Primary map



X



Y

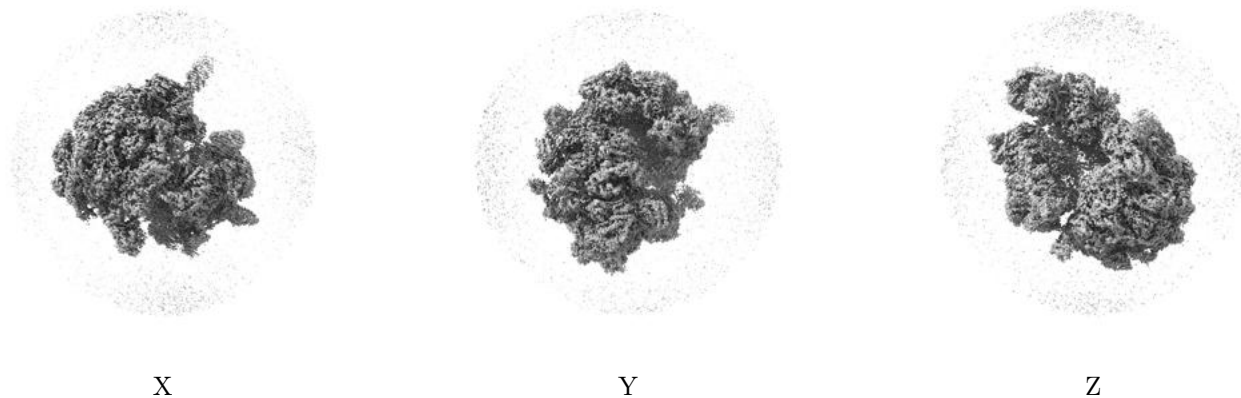


Z

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



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.

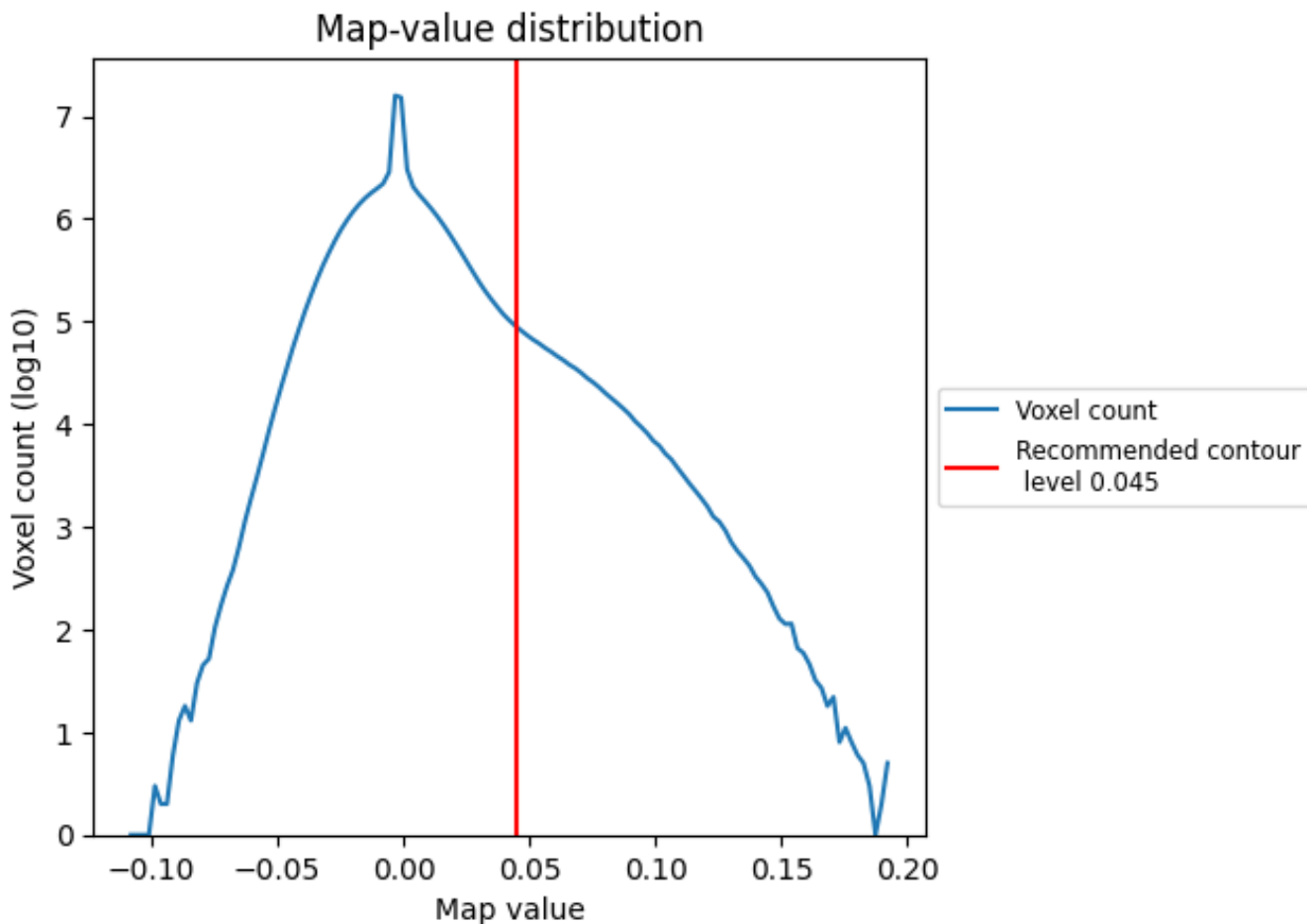
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

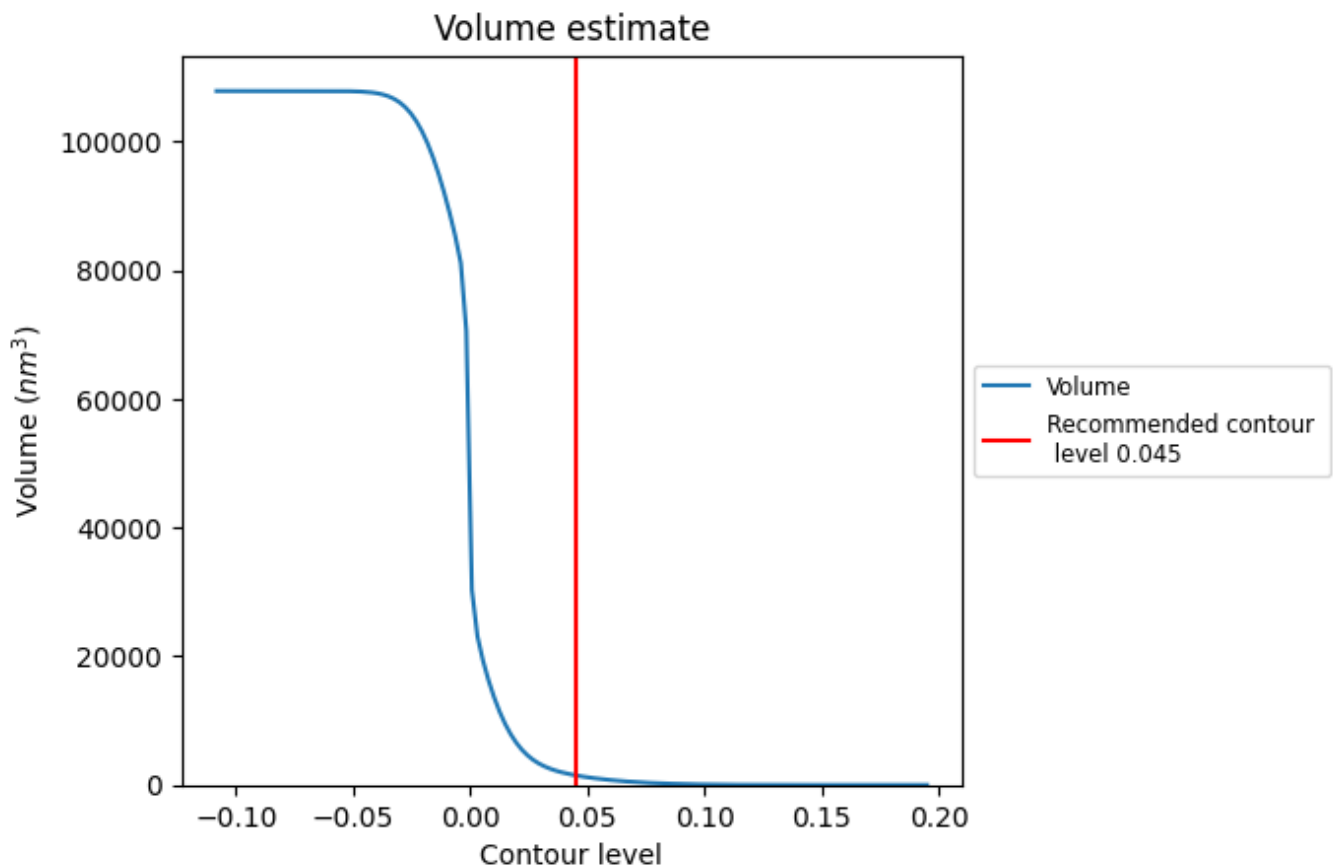
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

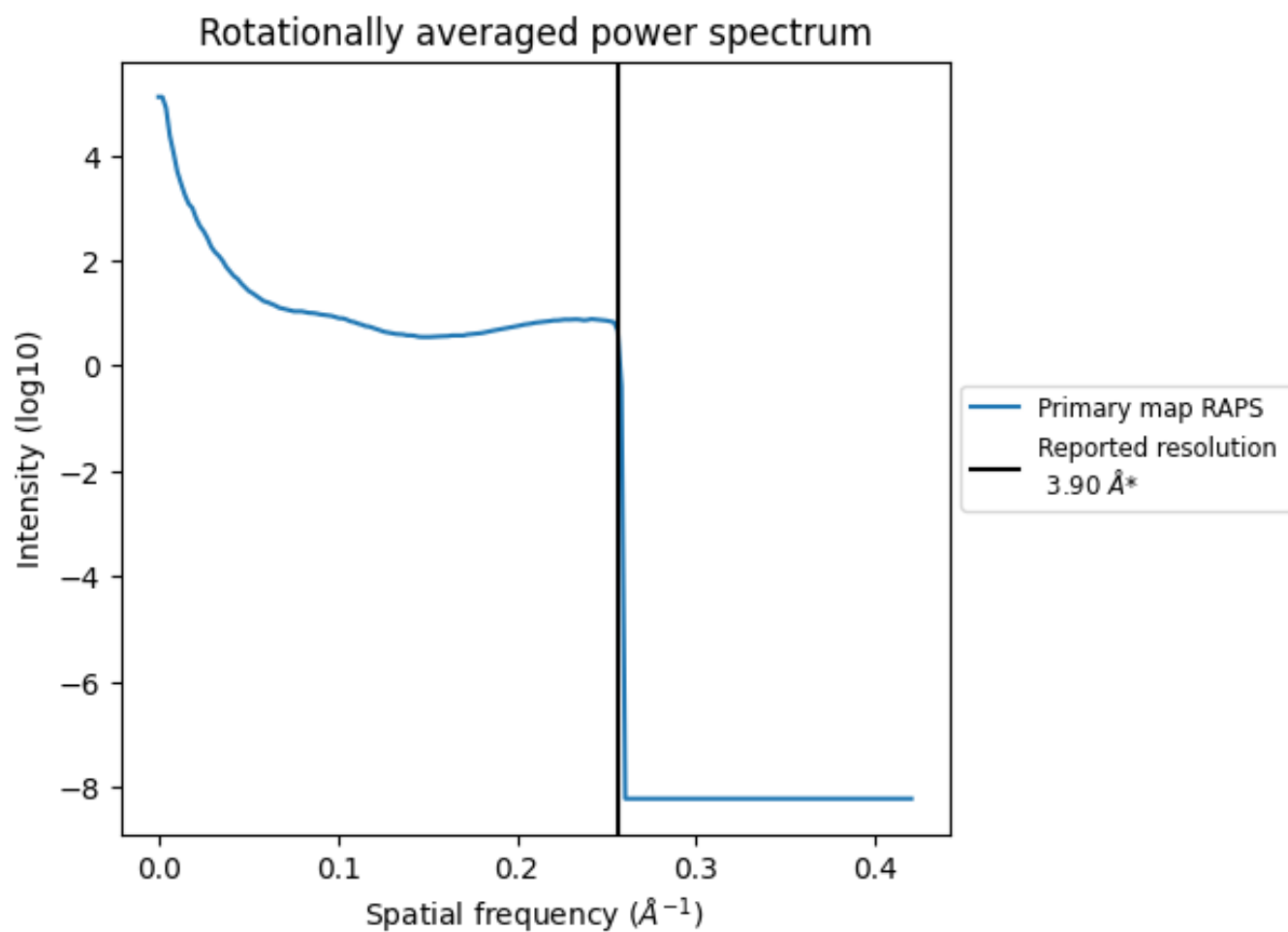
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1487 nm³; 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 \AA^{-1}

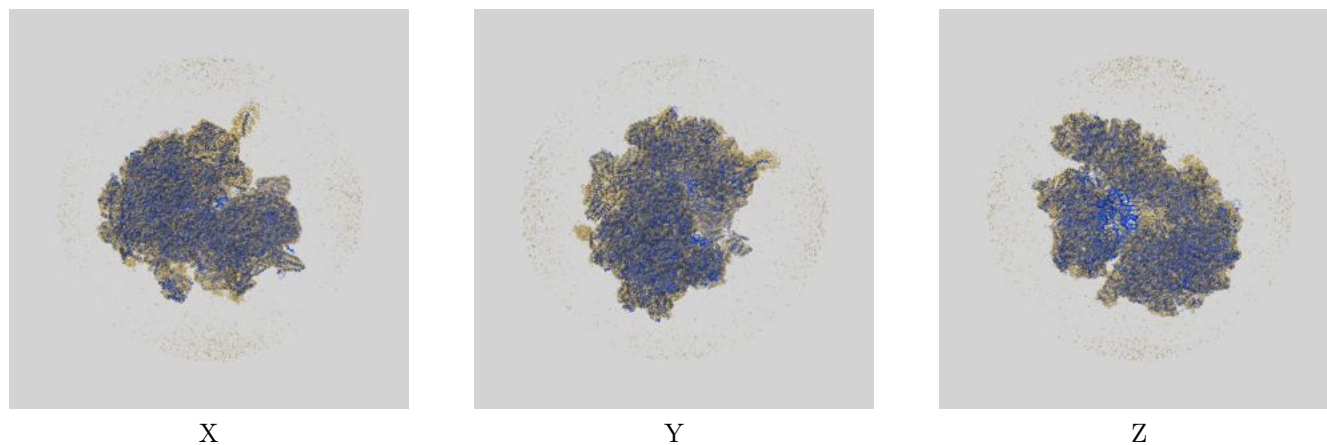
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

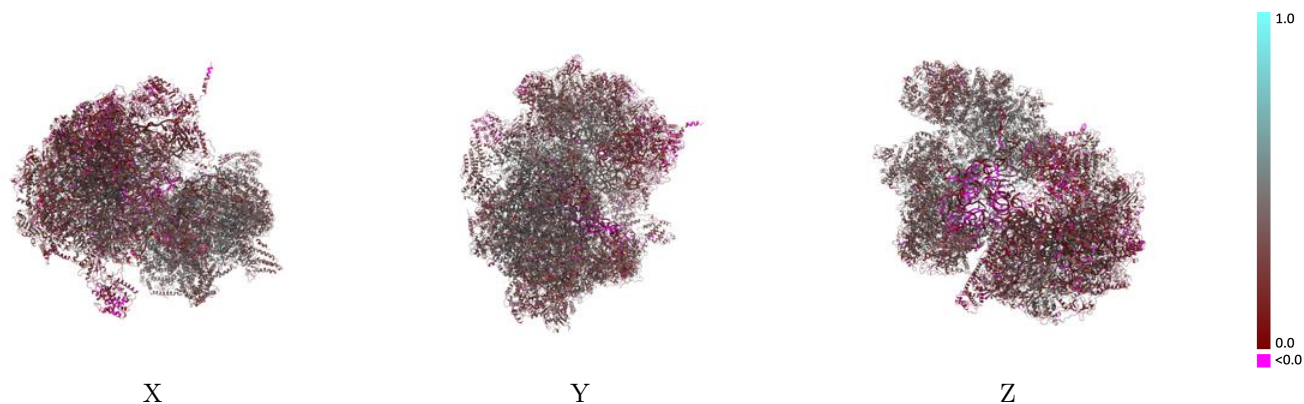
This section contains information regarding the fit between EMDB map EMD-11829 and PDB model 7ANE. Per-residue inclusion information can be found in section 3 on page 27.

9.1 Map-model overlay [i](#)



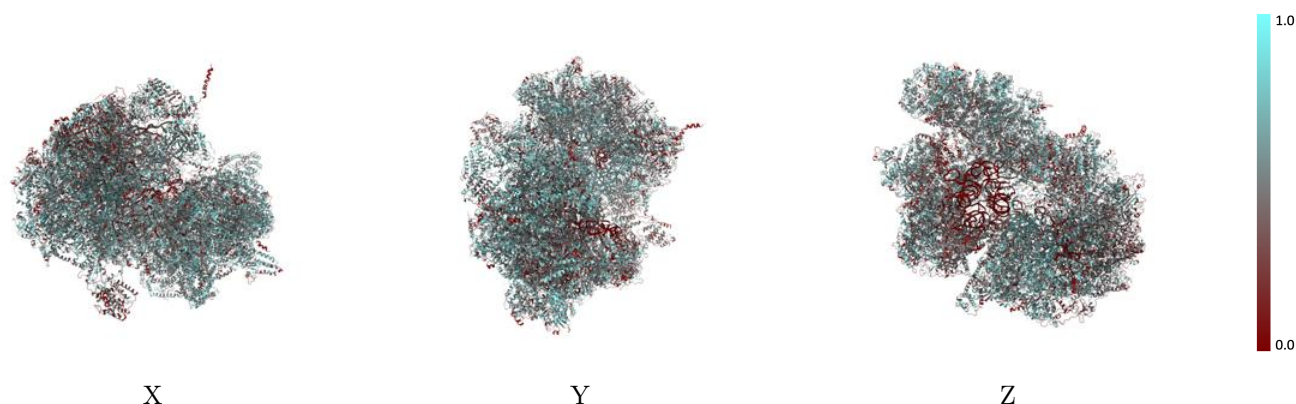
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



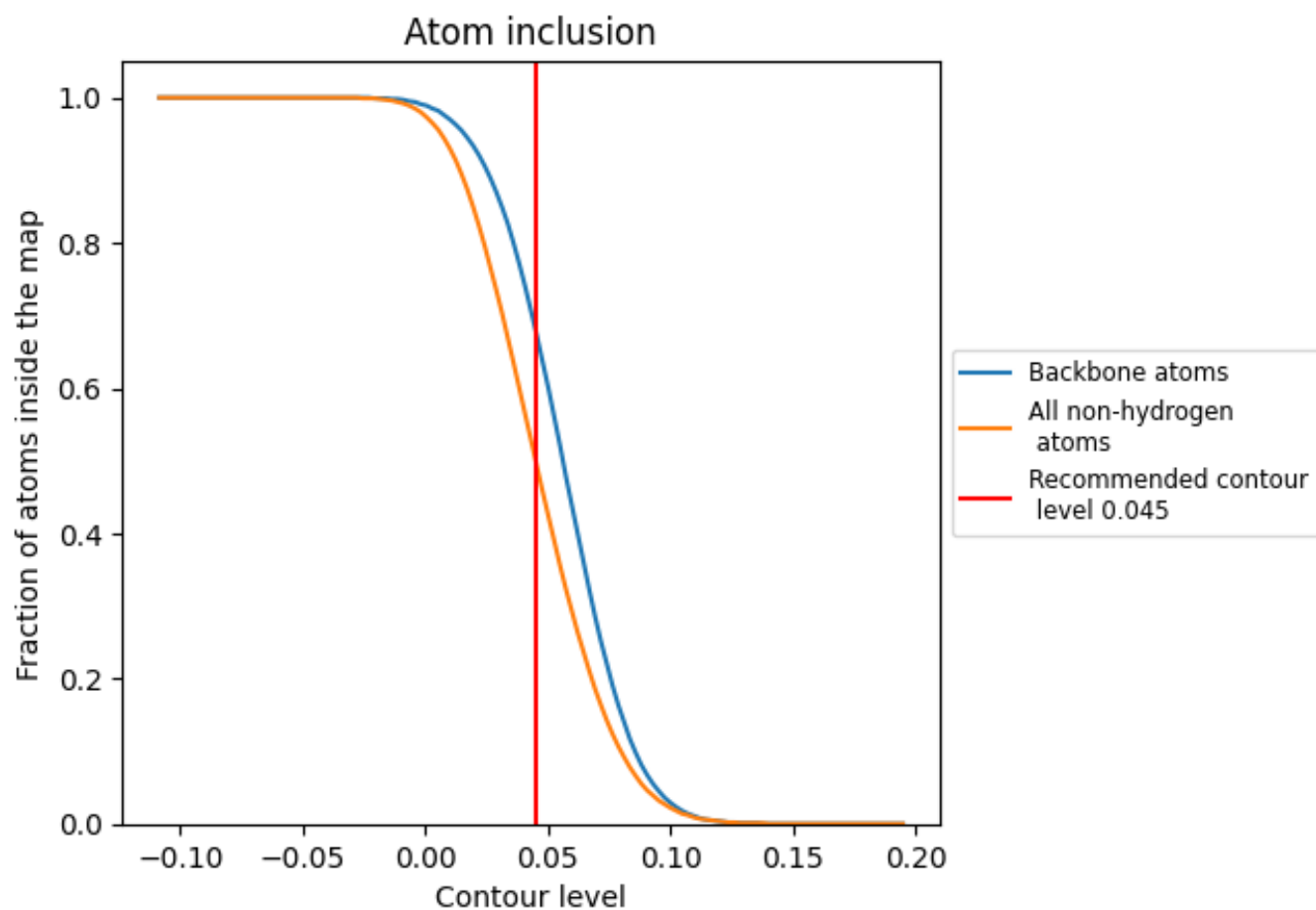
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



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







































































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