



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:46 AM UTC

PDB ID : 4V8M / pdb_00004v8m
EMDB ID : EMD-2239
Title : High-resolution cryo-electron microscopy structure of the Trypanosoma brucei ribosome
Authors : Hashem, Y.; des Georges, A.; Fu, J.; Buss, S.N.; Jossinet, F.; Jobe, A.; Zhang, Q.; Liao, H.Y.; Grassucci, R.A.; Bajaj, C.; Westhof, E.; Madison-Antenucci, S.; Frank, J.
Deposited on : 2012-12-09
Resolution : 5.57 Å(reported)
Based on initial models : 3U5B, 4A19, 3U5F, 3U5I, 3U5H, 4A17, 3IZ6, 3U5C, 3IZR, 3U5G, 3IZ9, 2XZN, 3U5D, 4A1B, 4A18, 4A1A, 4A1D, 3U5E, 3IZ7, 2XZM, 4A1E, 4A1C

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:

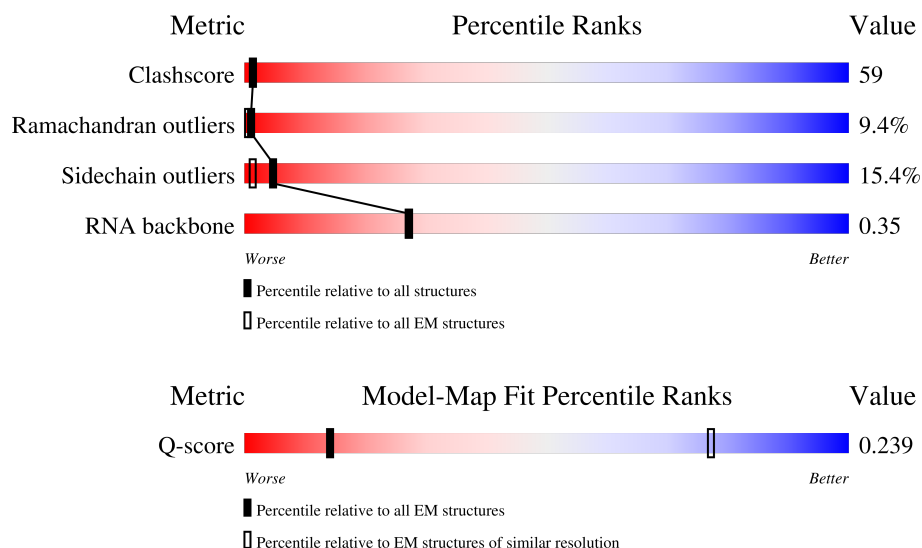
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 5.57 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	474 (5.07 - 6.07)

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	A0	256	
2	A1	273	

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Mol	Chain	Length	Quality of chain
3	A2	190	
4	A3	250	
5	A4	202	
6	A5	220	
7	A6	190	
8	A7	318	
9	A8	57	
10	A9	153	
11	AC	277	
12	AD	172	
13	AE	174	
14	AF	144	
15	AG	151	
16	AH	144	
17	AI	152	
18	AJ	130	
19	AK	149	
20	AL	142	
21	AM	153	
22	AO	167	
23	AP	266	
24	AQ	117	
25	AR	194	
26	AS	143	
27	AT	137	

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Mol	Chain	Length	Quality of chain
28	AU	113	
29	AV	111	
30	AW	86	
31	AX	214	
32	AY	66	
33	AZ	103	
34	BA	1847	
35	BB	1465	
36	BC	169	
37	BD	119	
38	BE	210	
39	BF	73	
40	BG	182	
41	BH	135	
42	BI	193	
43	BJ	214	
44	BK	213	
45	BL	194	
46	BM	164	
47	BN	218	
48	BO	222	
49	BP	189	
50	BQ	221	
51	BR	166	
52	BS	179	

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Mol	Chain	Length	Quality of chain
53	BT	260	
54	BU	159	
55	BV	130	
56	BW	139	
57	BX	164	
58	BY	125	
59	BZ	143	
60	Ba	133	
61	Bb	145	
62	Bc	146	
63	Bd	71	
64	Be	260	
65	Bf	429	
66	Bg	105	
67	Bh	188	
68	Bi	132	
69	Bj	170	
70	Bk	127	
71	Bl	149	
72	Bm	109	
73	Bn	84	
74	Bo	93	
75	Bp	82	
76	Bq	51	
77	Br	374	

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Mol	Chain	Length	Quality of chain
78	Bs	128	
79	Bt	106	
80	Bu	308	
81	Bv	192	
82	Bw	257	
83	Bx	276	
84	By	189	
85	AA	2251	
86	AB	73	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 232955 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 protein called 40S RIBOSOMAL PROTEIN S3A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A0	219	Total	C	N	O	S	0	1
			1782	1124	337	313	8		

- Molecule 2 is a protein called 40S RIBOSOMAL PROTEIN S4, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A1	248	Total	C	N	O	S	0	1
			1940	1232	360	339	9		

- Molecule 3 is a protein called 40S RIBOSOMAL PROTEIN S5, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A2	187	Total	C	N	O	S	0	0
			1484	928	286	265	5		

- Molecule 4 is a protein called 40S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A3	250	Total	C	N	O	S	0	0
			2003	1243	415	341	4		

- Molecule 5 is a protein called RIBOSOMAL PROTEIN S7, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A4	192	Total	C	N	O	S	0	1
			1592	1014	310	263	5		

- Molecule 6 is a protein called 40S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A5	195	Total	C	N	O	S	0	1
			1551	975	315	259	2		

- Molecule 7 is a protein called 40S RIBOSOMAL PROTEIN S9, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A6	187	Total	C	N	O	S	0	1
			1518	951	307	253	7		

- Molecule 8 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A7	315	Total	C	N	O	S	0	1
			2412	1508	429	462	13		

- Molecule 9 is a protein called RIBOSOMAL PROTEIN S29, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A8	42	Total	C	N	O	S	0	0
			334	204	69	57	4		

- Molecule 10 is a protein called UBIQUITIN/RIBOSOMAL PROTEIN S27A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A9	66	Total	C	N	O	S	0	1
			530	330	102	91	7		

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN SA, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AC	204	Total	C	N	O	S	0	1
			1620	1034	293	282	11		

- Molecule 12 is a protein called 40S RIBOSOMAL PROTEIN S10, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AD	104	Total	C	N	O	S	0	1
			853	553	148	147	5		

- Molecule 13 is a protein called 40S RIBOSOMAL PROTEINS S11, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AE	160	Total	C	N	O	S	0	0
			1300	812	262	220	6		

- Molecule 14 is a protein called 40S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AF	121	Total	C	N	O	S	0	0
			940	578	169	184	9		

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN S13, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AG	141	Total	C	N	O	S	0	0
			1148	724	227	190	7		

- Molecule 16 is a protein called 40S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AH	126	Total	C	N	O	S	0	1
			922	572	167	174	9		

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN S15, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AI	134	Total	C	N	O	S	0	1
			1074	679	211	181	3		

- Molecule 18 is a protein called 40S RIBOSOMAL PROTEIN S15A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AJ	129	Total	C	N	O	S	0	0
			1018	645	191	174	8		

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN S16, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AK	148	Total	C	N	O	S	0	0
			1190	757	225	205	3		

- Molecule 20 is a protein called 40S RIBOSOMAL PROTEIN S17, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AL	127	Total	C	N	O	S	0	1
			1021	641	198	177	5		

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN S18, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AM	153	Total	C	N	O	S	0	0
			1229	764	244	215	6		

- Molecule 22 is a protein called RIBOSOMAL PROTEIN S19, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AO	149	Total	C	N	O	S	0	0
			1181	746	230	196	9		

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN S2, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AP	224	Total	C	N	O	S	0	1
			1731	1103	309	310	9		

- Molecule 24 is a protein called RIBOSOMAL PROTEIN S20, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AQ	105	Total	C	N	O	S	0	1
			827	522	153	149	3		

- Molecule 25 is a protein called 40S RIBOSOMAL PROTEIN S21, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AR	81	Total	C	N	O	S	0	1
			603	374	108	118	3		

- Molecule 26 is a protein called 40S RIBOSOMAL PROTEIN S23, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AS	142	Total	C	N	O	S	0	0
			1116	706	219	189	2		

- Molecule 27 is a protein called 40S RIBOSOMAL PROTEIN S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AT	131	Total	C	N	O	S	0	0
			1050	666	206	174	4		

- Molecule 28 is a protein called 40S RIBOSOMAL PROTEIN S25, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AU	86	Total	C	N	O	S	0	1
			673	427	127	114	5		

- Molecule 29 is a protein called RIBOSOMAL PROTEIN S26, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AV	101	Total	C	N	O	S	0	1
			809	498	172	131	8		

- Molecule 30 is a protein called 40S RIBOSOMAL PROTEIN S27, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AW	83	Total	C	N	O	S	0	1
			636	396	120	111	9		

- Molecule 31 is a protein called 40S RIBOSOMAL PROTEIN S3, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AX	206	Total	C	N	O	S	0	1
			1628	1020	307	289	12		

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN S30, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AY	65	Total	C	N	O	S	0	0
			514	322	107	84	1		

- Molecule 33 is a protein called 40S RIBOSOMAL PROTEIN S33, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AZ	68	Total	C	N	O	S	0	0
			526	315	107	100	4		

- Molecule 34 is a RNA chain called ALPHA CHAIN OF THE LARGE RIBOSOMAL SUB-UNIT 28S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BA	1847	Total	C	N	O	P	0	0
			39395	17589	7008	12952	1846		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	?	-	C	deletion	GB X14553
BA	?	-	U	deletion	GB X14553
BA	?	-	U	deletion	GB X14553
BA	?	-	C	deletion	GB X14553
BA	?	-	C	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	C	deletion	GB X14553
BA	?	-	C	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	U	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	?	-	G	deletion	GB X14553
BA	799	A	-	insertion	GB X14553

- Molecule 35 is a RNA chain called BETA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT 28S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BB	1465	Total	C	N	O	P	0	0
			31164	13918	5476	10306	1464		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	484	G	-	insertion	GB X14553
BB	485	U	-	insertion	GB X14553
BB	486	G	-	insertion	GB X14553
BB	487	A	-	insertion	GB X14553

- Molecule 36 is a RNA chain called 5.8S RRNA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BC	169	Total	C	N	O	P	0	0
			3584	1604	629	1183	168		

- Molecule 37 is a RNA chain called 5S RRNA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BD	119	Total	C	N	O	P	0	0
			2533	1131	449	835	118		

- Molecule 38 is a RNA chain called SHORT RRNA-I OF THE LARGE RIBOSOMAL SUB-UNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BE	210	Total	C	N	O	P	0	0
			4441	1986	768	1478	209		

- Molecule 39 is a RNA chain called SHORT RRNA-II OF THE LARGE RIBOSOMAL SUB-UNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BF	73	Total	C	N	O	P	0	0
			1521	682	247	520	72		

- Molecule 40 is a RNA chain called SHORT RRNA-III OF THE LARGE RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BG	182	Total	C	N	O	P	0	0
			3896	1737	706	1272	181		

- Molecule 41 is a RNA chain called SHORT RRNA-IV OF THE LARGE RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BH	135	Total	C	N	O	P	0	0
			2867	1280	502	951	134		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BI	192	Total	C	N	O	S	0	0
			1527	956	315	248	8		

- Molecule 43 is a protein called RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BJ	214	Total	C	N	O	S	0	0
			1717	1086	308	307	16		

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L10, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BK	212	Total	C	N	O	S	0	0
			1725	1086	338	287	14		

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L11, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BL	170	Total	C	N	O	S	0	1
			1363	859	258	239	7		

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L12, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BM	139	Total	C	N	O	S	0	1
			1022	642	187	188	5		

- Molecule 47 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BN	216	Total	C	N	O	S	0	1
			1762	1097	366	292	7		

- Molecule 48 is a protein called 60S RIBOSOMAL PROTEIN L13A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BO	201	Total	C	N	O	S	0	1
			1627	1035	323	262	7		

- Molecule 49 is a protein called PROBABLE 60S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BP	184	Total	C	N	O	S	0	1
			1484	934	299	247	4		

- Molecule 50 is a protein called RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BQ	203	Total	C	N	O	S	0	0
			1716	1077	370	264	5		

- Molecule 51 is a protein called 60S RIBOSOMAL PROTEIN L17, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BR	155	Total	C	N	O	S	0	1
			1245	782	247	208	8		

- Molecule 52 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BS	179	Total	C	N	O	S	0	0
			1473	931	290	244	8		

- Molecule 53 is a protein called 60S RIBOSOMAL PROTEIN L19, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BT	200	Total	C	N	O	S	0	1
			1672	1025	366	273	8		

- Molecule 54 is a protein called 60S RIBOSOMAL PROTEIN L21E, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BU	158	Total	C	N	O	S	0	0
			1260	802	246	206	6		

- Molecule 55 is a protein called 60S RIBOSOMAL PROTEIN L22, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BV	104	Total	C	N	O	S	0	1
			863	558	152	150	3		

- Molecule 56 is a protein called 60S RIBOSOMAL PROTEIN L23, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BW	138	Total	C	N	O	S	0	0
			1042	659	198	180	5		

- Molecule 57 is a protein called 60S RIBOSOMAL PROTEIN L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BX	121	Total	C	N	O	S	0	0
			990	629	186	173	2		

- Molecule 58 is a protein called 60S RIBOSOMAL PROTEIN L24, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BY	100	Total	C	N	O	S	0	0
			836	530	171	130	5		

- Molecule 59 is a protein called 60S RIBOSOMAL PROTEIN L26, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BZ	125	Total	C	N	O	S	0	1
			1008	623	213	167	5		

- Molecule 60 is a protein called 60S RIBOSOMAL PROTEIN L27, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Ba	132	Total	C	N	O	S	0	0
			1091	691	222	175	3		

- Molecule 61 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Bb	144	Total	C	N	O	S	0	0
			1137	717	228	186	6		

- Molecule 62 is a protein called 60S RIBOSOMAL PROTEIN L28, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Bc	141	Total	C	N	O	S	0	1
			1129	704	226	191	8		

- Molecule 63 is a protein called 60S RIBOSOMAL PROTEIN L29, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bd	70	Total	C	N	O	S	0	0
			571	349	128	93	1		

- Molecule 64 is a protein called 60S RIBOSOMAL PROTEIN L2, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Be	186	Total	C	N	O	S	0	1
			1390	859	284	237	10		

- Molecule 65 is a protein called RIBOSOMAL PROTEIN L3, MITOCHONDRIAL, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Bf	414	Total	C	N	O	S	0	1
			3317	2084	661	559	13		

- Molecule 66 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bg	96	Total	C	N	O	S	0	0
			735	457	132	141	5		

- Molecule 67 is a protein called 60S RIBOSOMAL SUBUNIT PROTEIN L31, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bh	188	Total	C	N	O	S	0	0
			1526	961	309	250	6		

- Molecule 68 is a protein called 60S RIBOSOMAL PROTEIN L32, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Bi	129	Total	C	N	O	S	0	1
			1054	664	215	171	4		

- Molecule 69 is a protein called 60S RIBOSOMAL PROTEIN L34, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Bj	162	Total	C	N	O	S	0	1
			1293	801	286	202	4		

- Molecule 70 is a protein called 60S RIBOSOMAL PROTEIN L35, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bk	84	Total	C	N	O	S	0	0
			719	448	161	108	2		

- Molecule 71 is a protein called 60S RIBOSOMAL PROTEIN L35A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bl	116	Total	C	N	O	S	0	0
			936	589	189	155	3		

- Molecule 72 is a protein called RIBOSOMAL PROTEIN L36, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bm	107	Total	C	N	O	S	0	1
			849	530	178	139	2		

- Molecule 73 is a protein called RIBOSOMAL PROTEIN L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bn	83	Total	C	N	O	S	0	0
			699	425	161	107	6		

- Molecule 74 is a protein called 60S RIBOSOMAL PROTEIN L37A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bo	92	Total	C	N	O	S	0	1
			715	442	148	119	6		

- Molecule 75 is a protein called 60S RIBOSOMAL PROTEIN L38, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Bp	81	Total	C	N	O	S	0	0
			656	411	130	111	4		

- Molecule 76 is a protein called 60S RIBOSOMAL PROTEIN L39, PUTATIVE.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	Bq	50	Total	C	N	O	0	0
			457	297	98	62		

- Molecule 77 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Br	368	Total	C	N	O	S	0	1
			2883	1802	576	488	17		

- Molecule 78 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bs	52	Total	C	N	O	S	0	0
			427	265	88	67	7		

- Molecule 79 is a protein called 60S RIBOSOMAL PROTEIN L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bt	105	Total	C	N	O	S	0	0
			866	547	170	144	5		

- Molecule 80 is a protein called 60S RIBOSOMAL PROTEIN L5, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Bu	299	Total	C	N	O	S	0	1
			2354	1485	447	416	6		

- Molecule 81 is a protein called 60S RIBOSOMAL PROTEIN L6, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bv	158	Total	C	N	O	S	0	1
			1222	776	228	215	3		

- Molecule 82 is a protein called 60S RIBOSOMAL PROTEIN L7, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Bw	257	Total	C	N	O	S	0	0
			2066	1316	394	345	11		

- Molecule 83 is a protein called 60S RIBOSOMAL PROTEIN L7A, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Bx	240	Total	C	N	O	S	0	0
			1908	1198	375	329	6		

- Molecule 84 is a protein called 60S RIBOSOMAL PROTEIN L9, PUTATIVE.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	By	189	Total	C	N	O	S	0	0
			1540	975	284	277	4		

- Molecule 85 is a RNA chain called 18S RRNA OF THE SMALL RIBOSOMAL SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	AA	2227	Total	C	N	O	P	0	0
			47370	21162	8354	15629	2225		

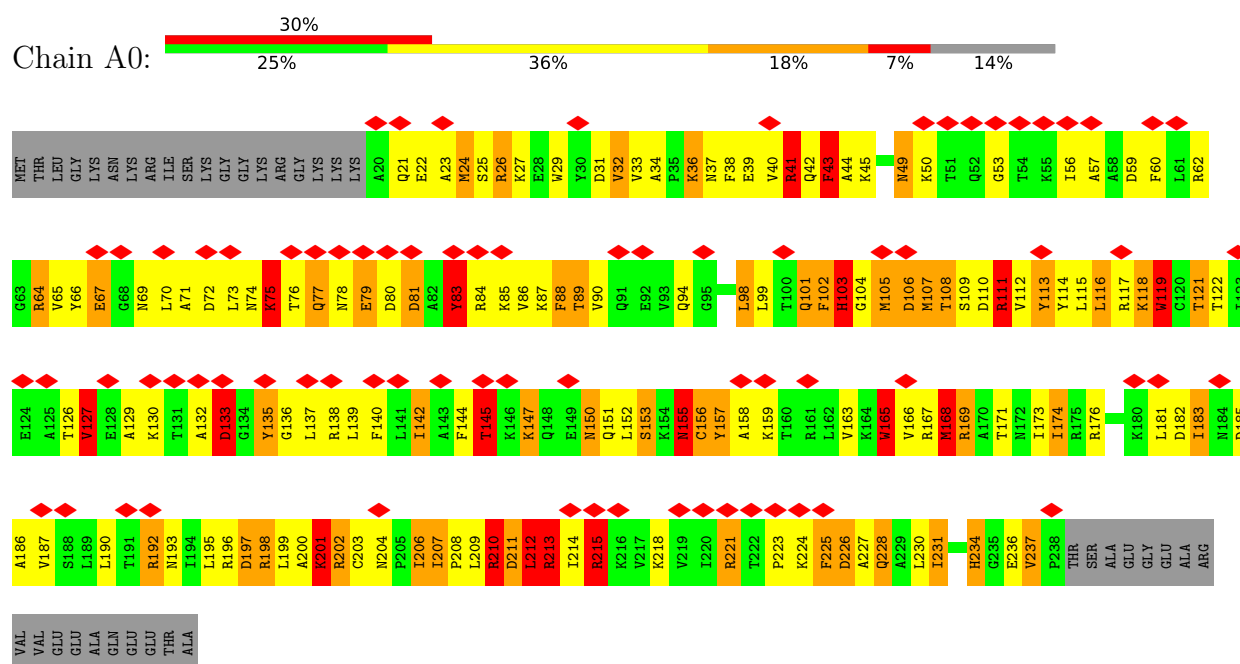
- Molecule 86 is a RNA chain called E-SITE TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
86	AB	73	1557	695	279	511	72	0	0

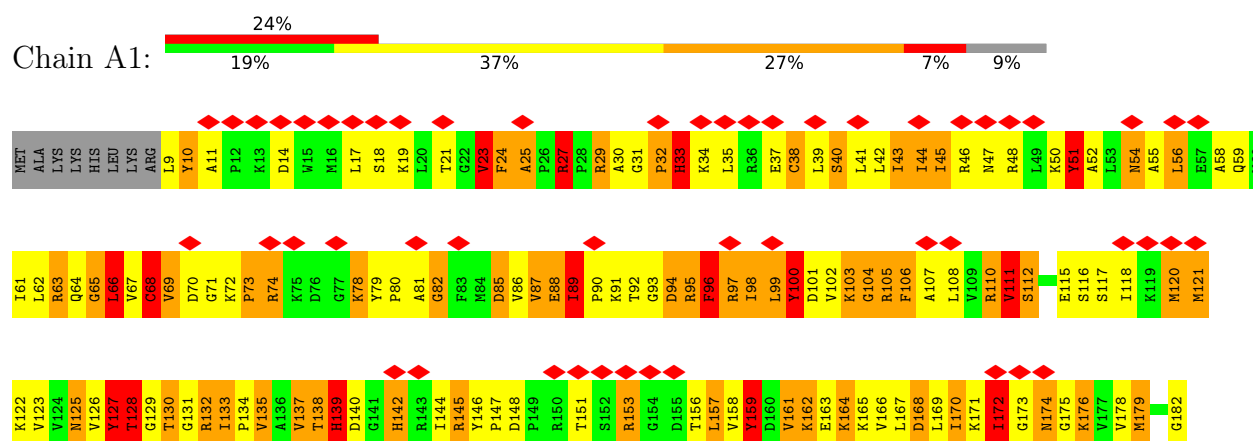
3 Residue-property plots

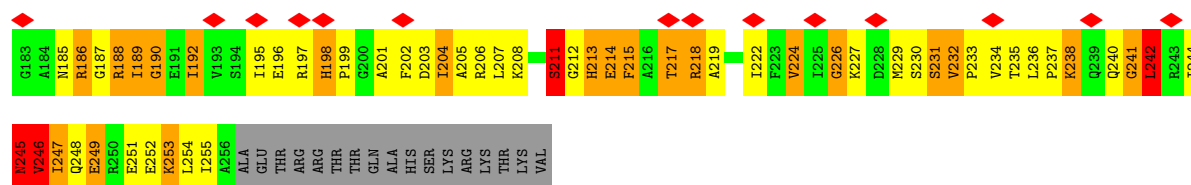
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 40S RIBOSOMAL PROTEIN S3A, PUTATIVE

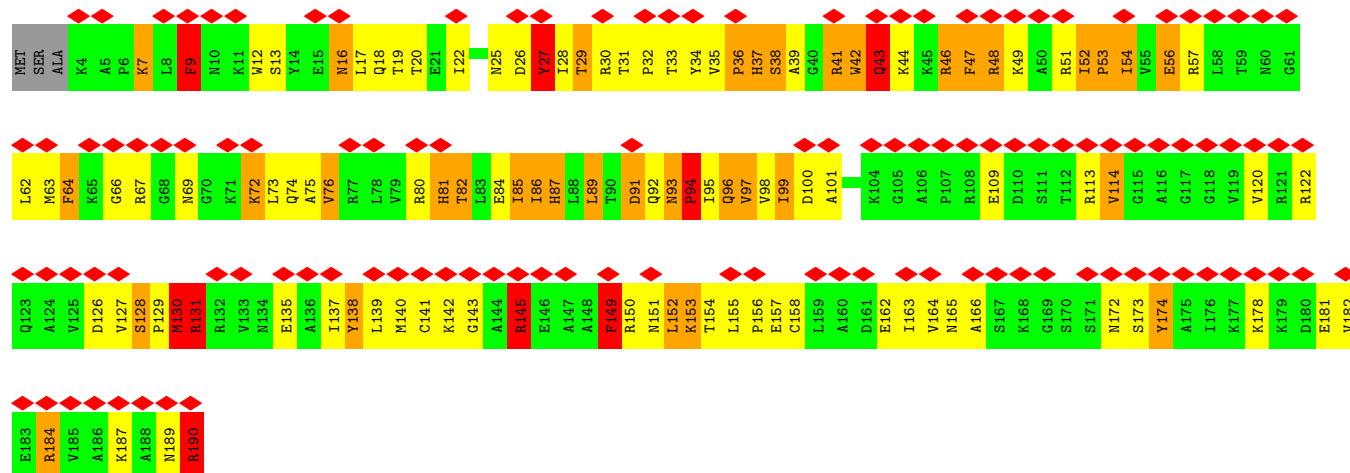


• Molecule 2: 40S RIBOSOMAL PROTEIN S4, PUTATIVE

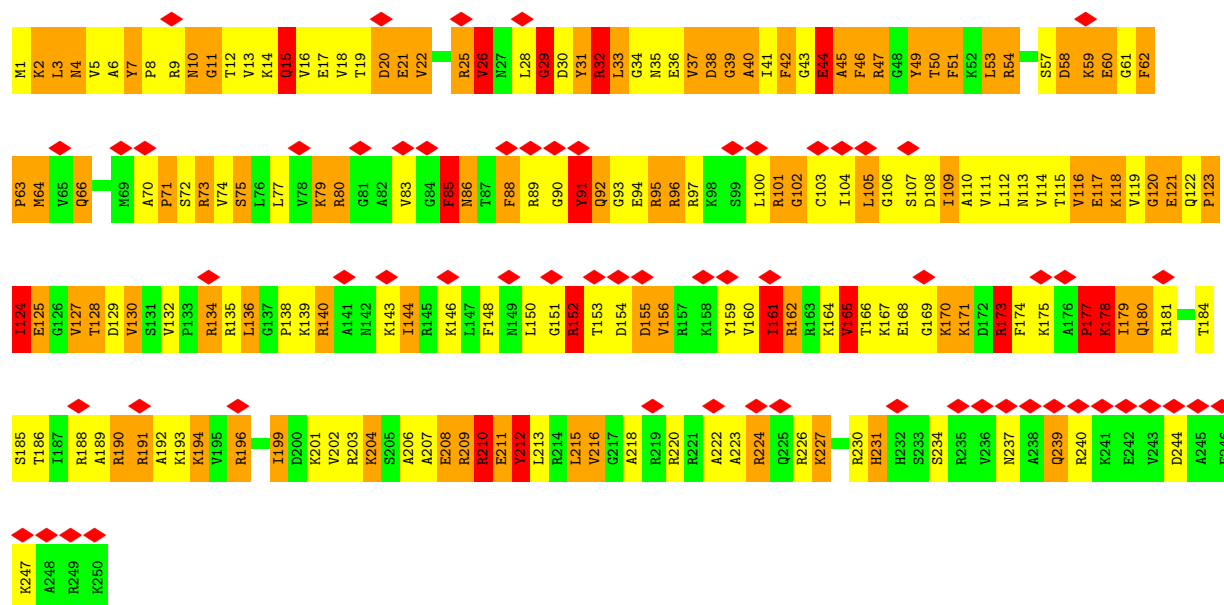
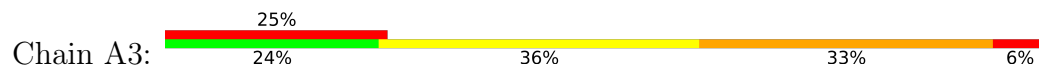




• Molecule 3: 40S RIBOSOMAL PROTEIN S5, PUTATIVE

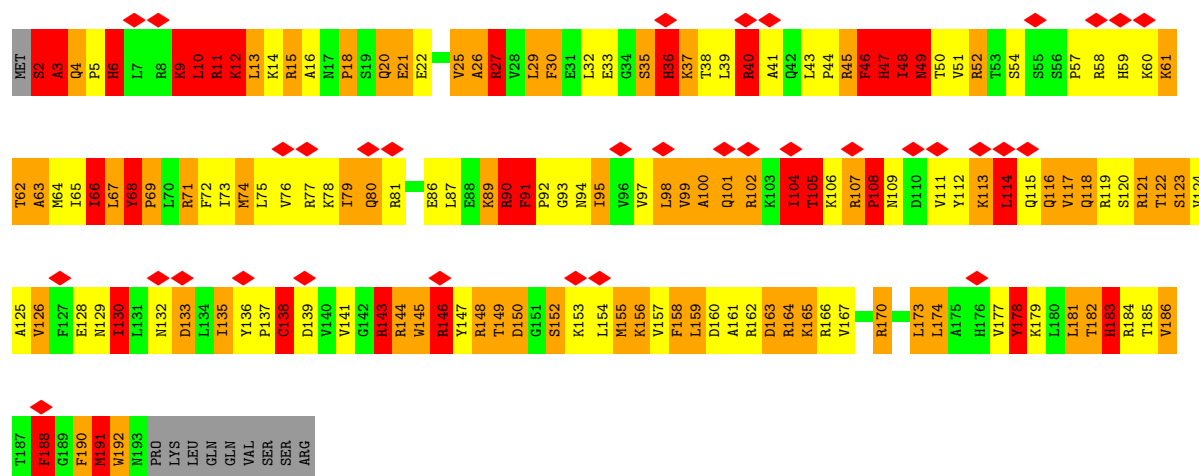


• Molecule 4: 40S RIBOSOMAL PROTEIN S6

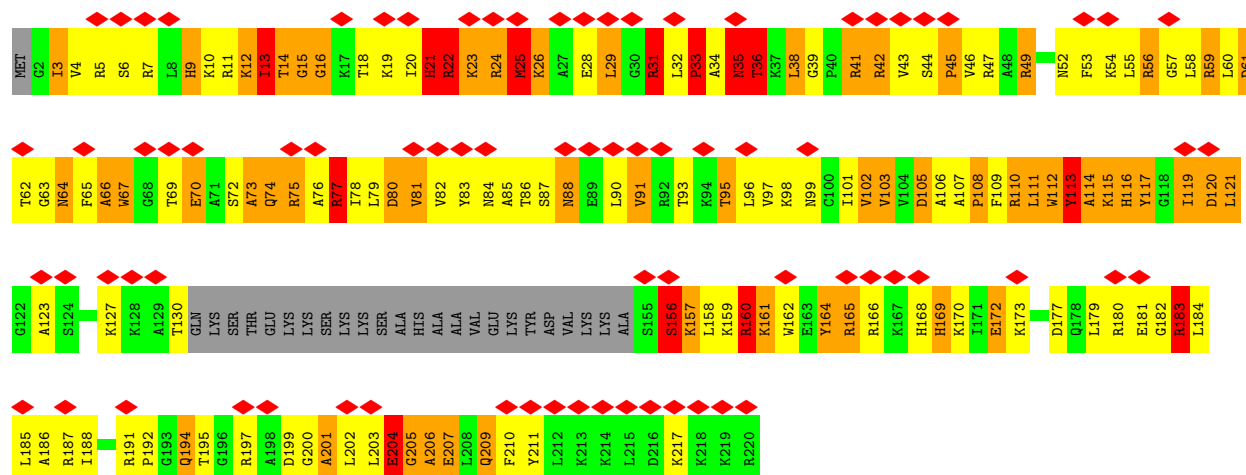
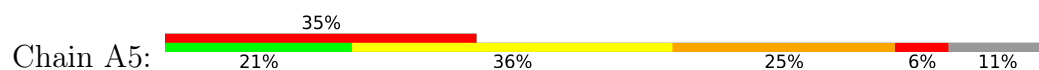


• Molecule 5: RIBOSOMAL PROTEIN S7, PUTATIVE

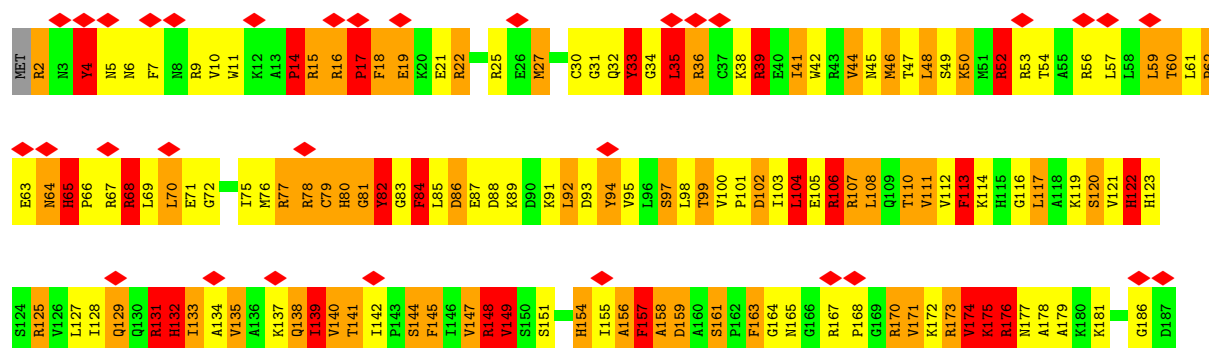
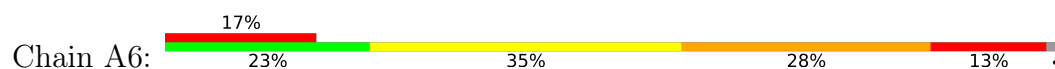




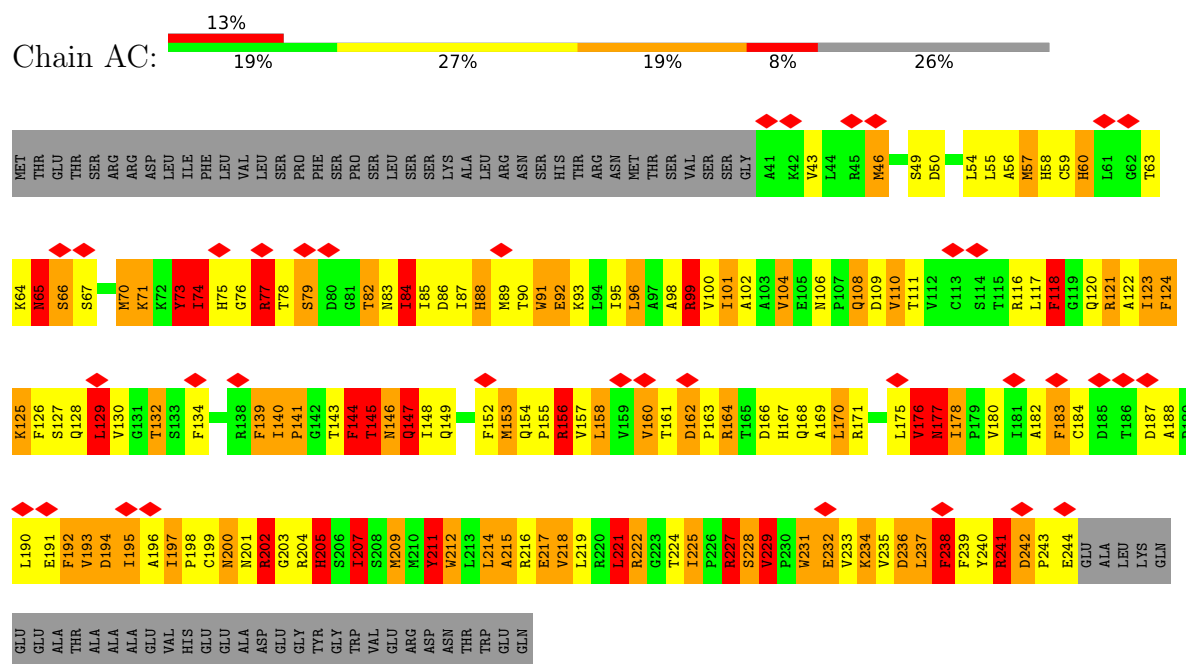
• Molecule 6: 40S RIBOSOMAL PROTEIN S8



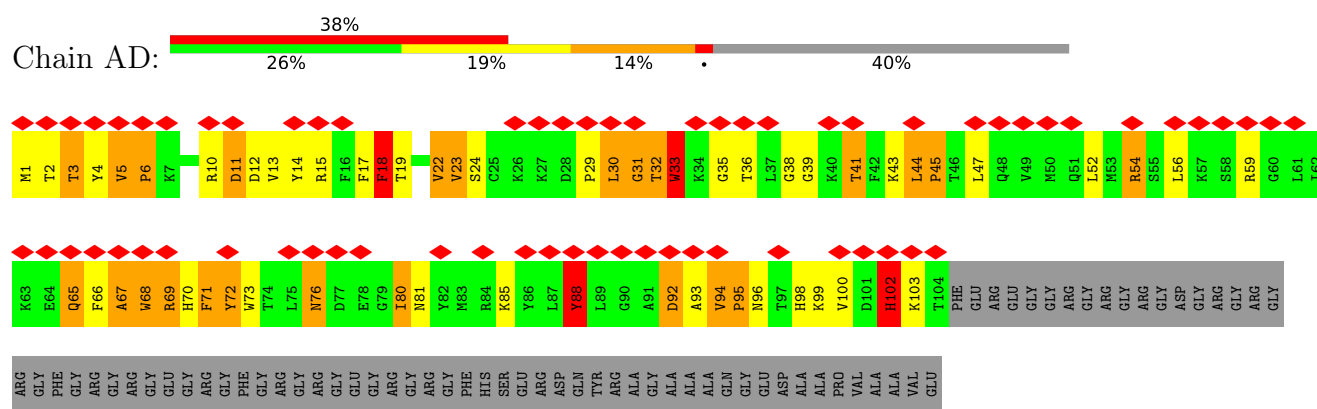
• Molecule 7: 40S RIBOSOMAL PROTEIN S9, PUTATIVE



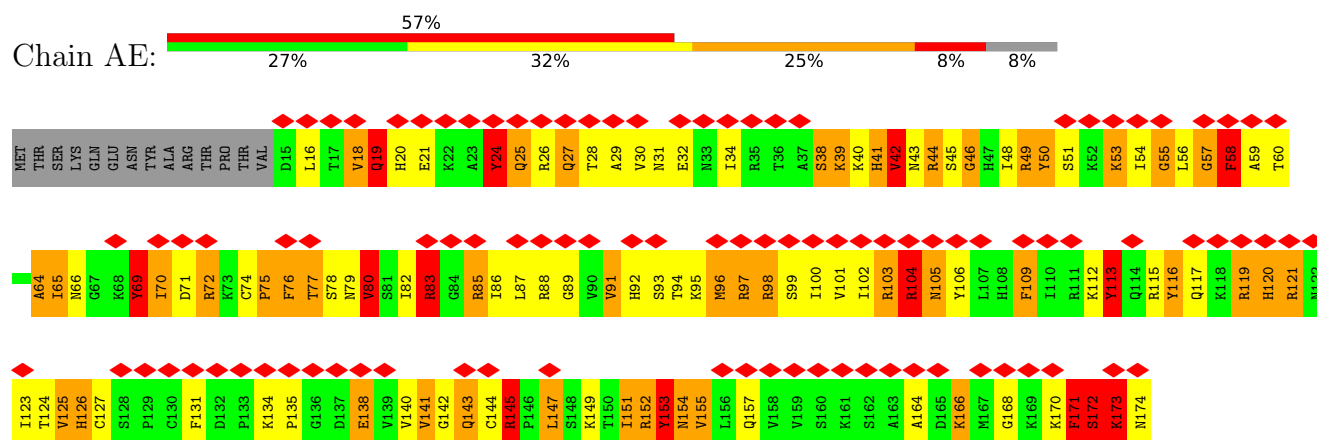
• Molecule 11: 40S RIBOSOMAL PROTEIN SA, PUTATIVE



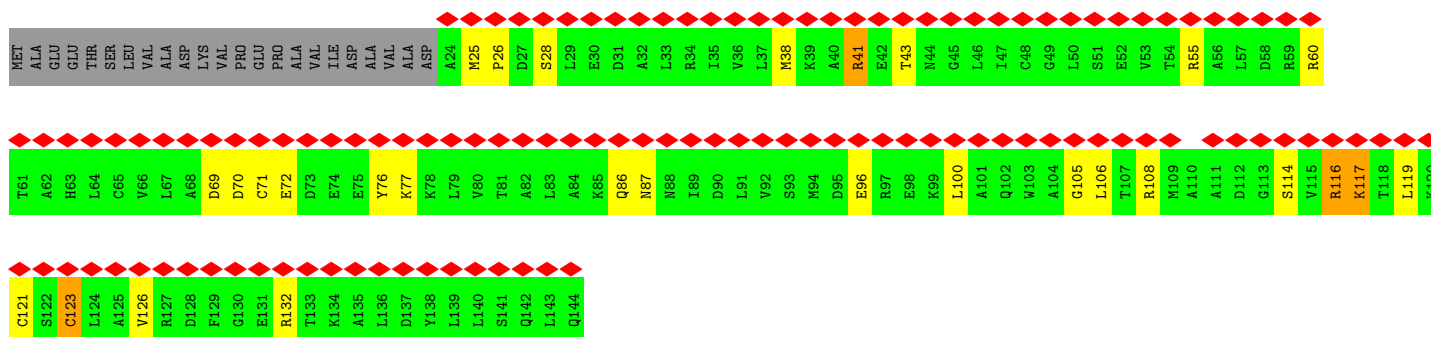
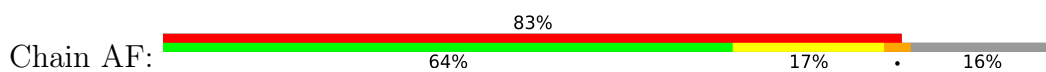
• Molecule 12: 40S RIBOSOMAL PROTEIN S10, PUTATIVE



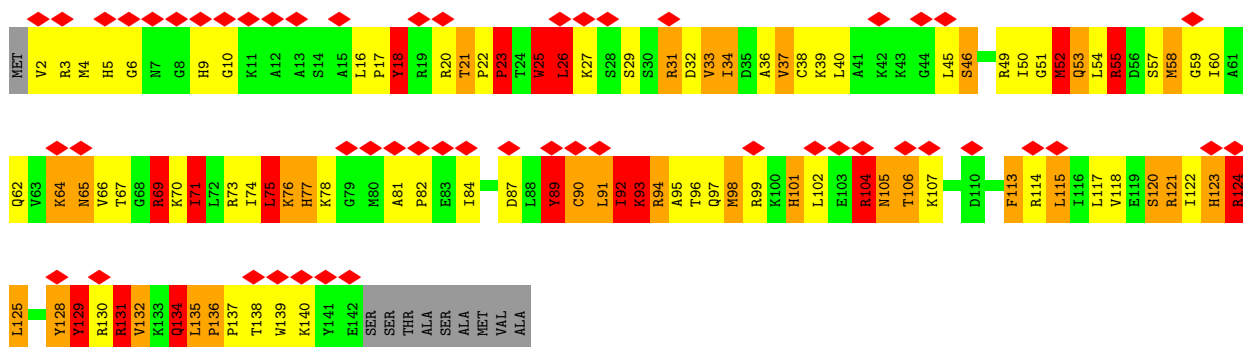
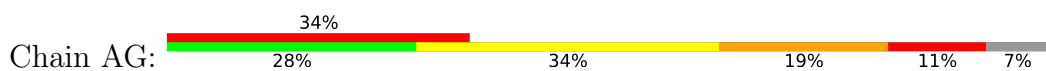
• Molecule 13: 40S RIBOSOMAL PROTEINS S11, PUTATIVE



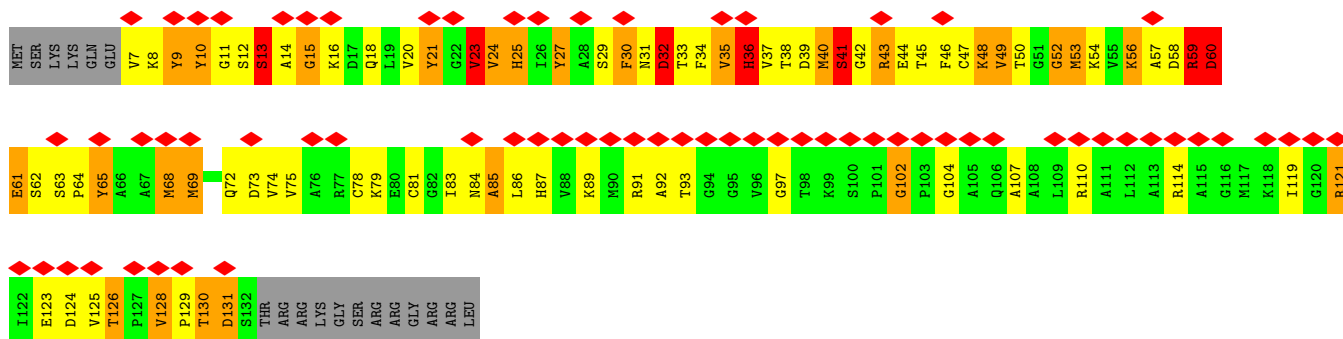
• Molecule 14: 40S RIBOSOMAL PROTEIN S12



• Molecule 15: 40S RIBOSOMAL PROTEIN S13, PUTATIVE

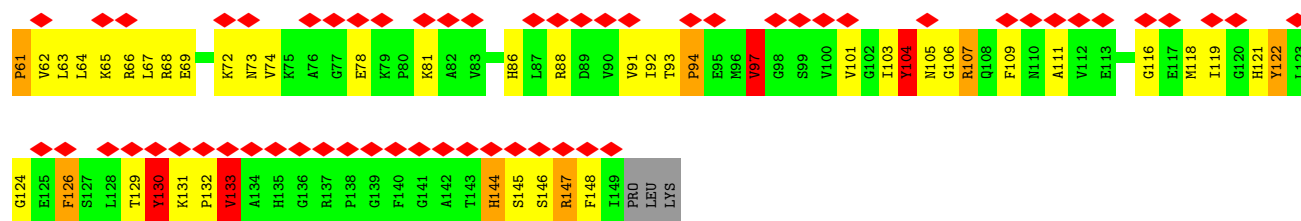


• Molecule 16: 40S RIBOSOMAL PROTEIN S14

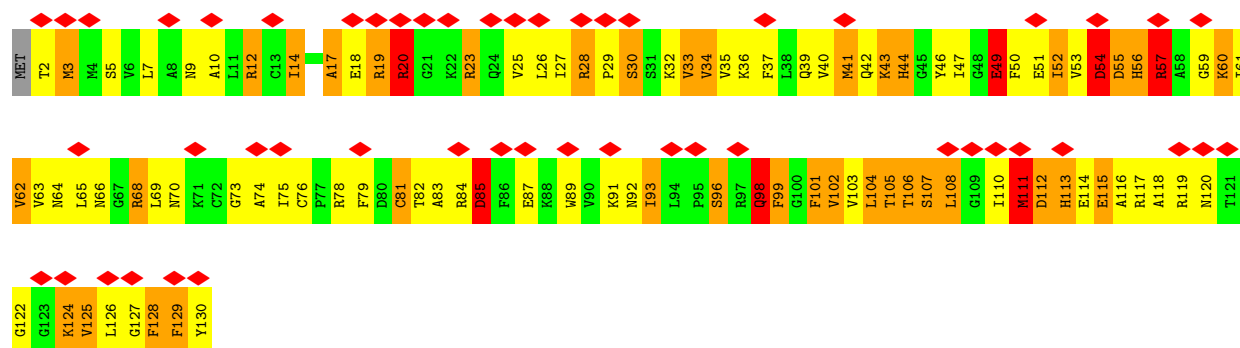
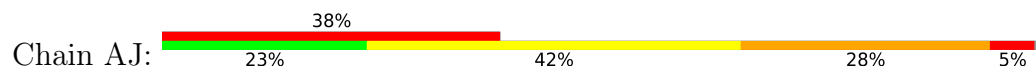


• Molecule 17: 40S RIBOSOMAL PROTEIN S15, PUTATIVE

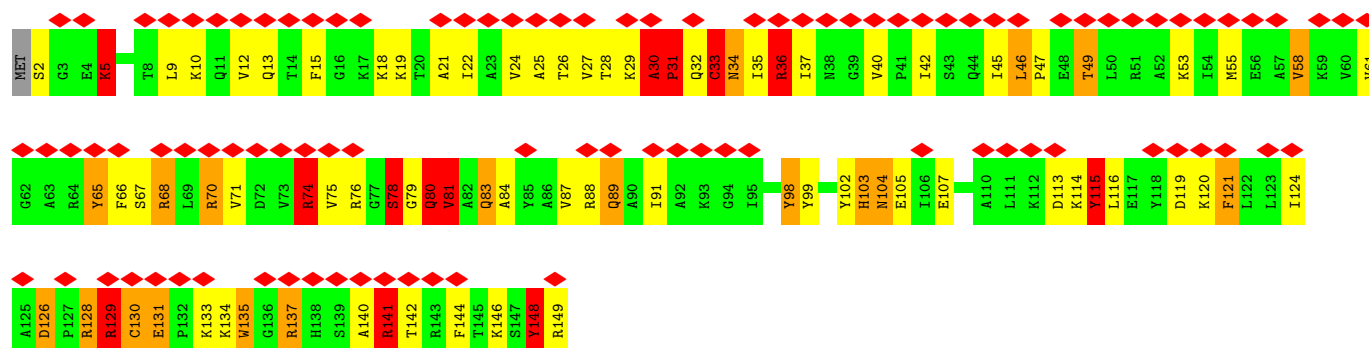




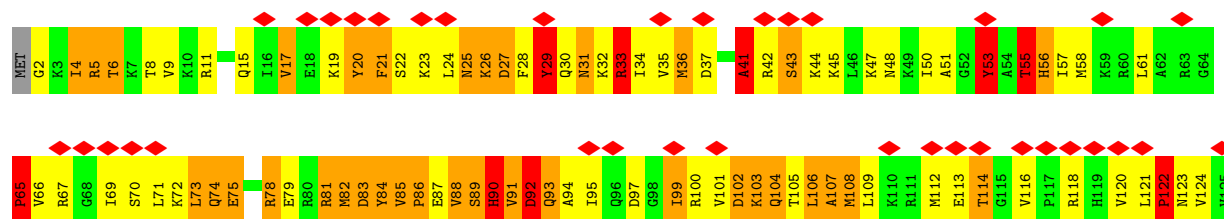
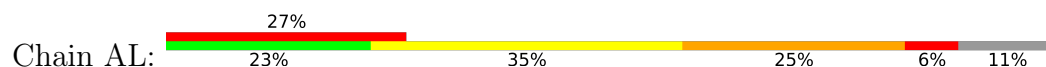
• Molecule 18: 40S RIBOSOMAL PROTEIN S15A, PUTATIVE

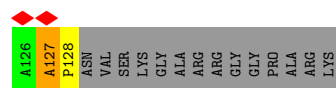


• Molecule 19: 40S RIBOSOMAL PROTEIN S16, PUTATIVE

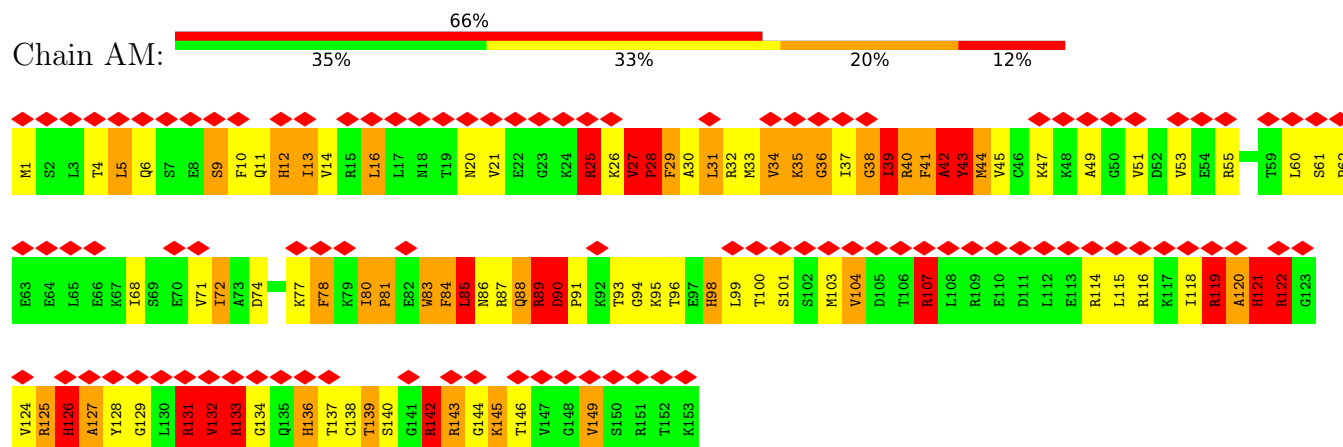


• Molecule 20: 40S RIBOSOMAL PROTEIN S17, PUTATIVE

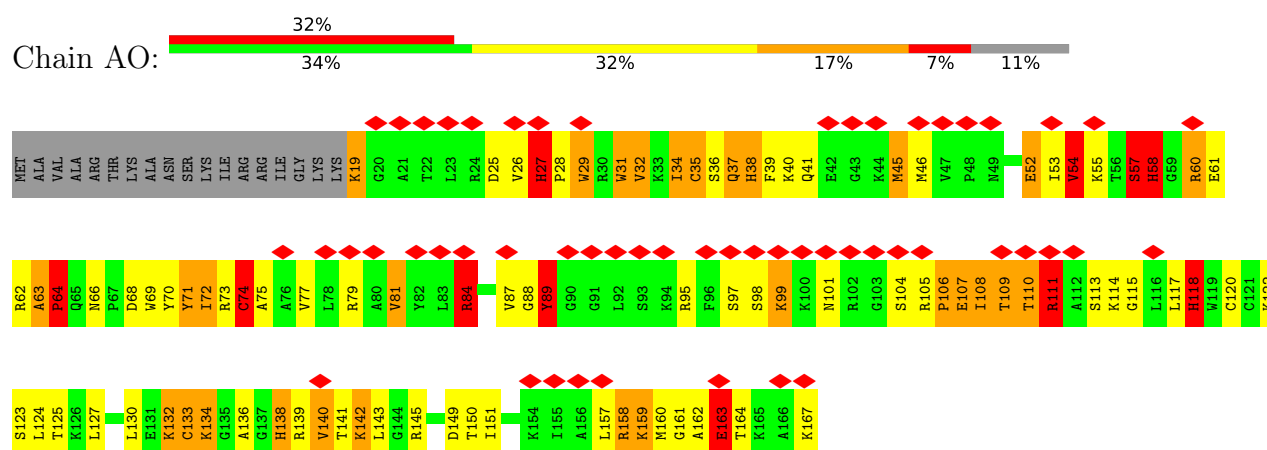




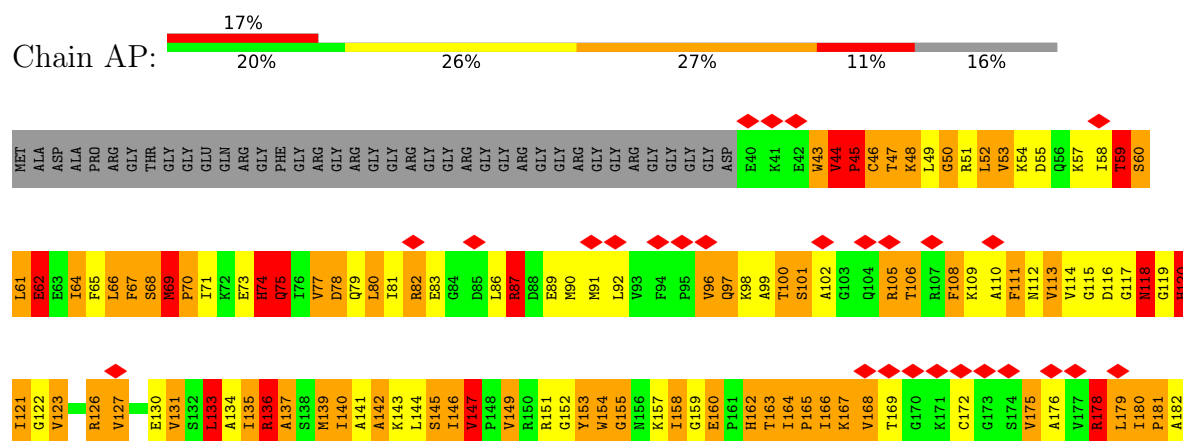
• Molecule 21: 40S RIBOSOMAL PROTEIN S18, PUTATIVE

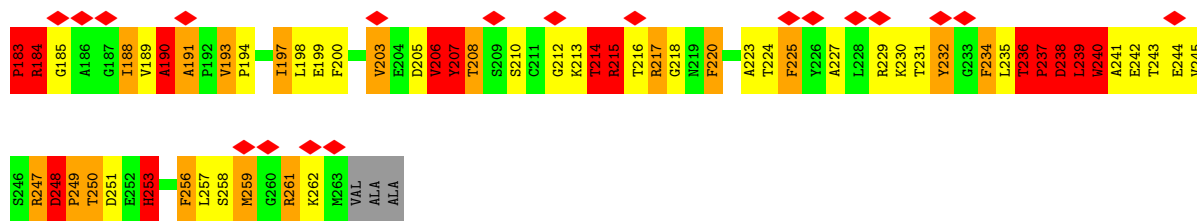


• Molecule 22: RIBOSOMAL PROTEIN S19, PUTATIVE

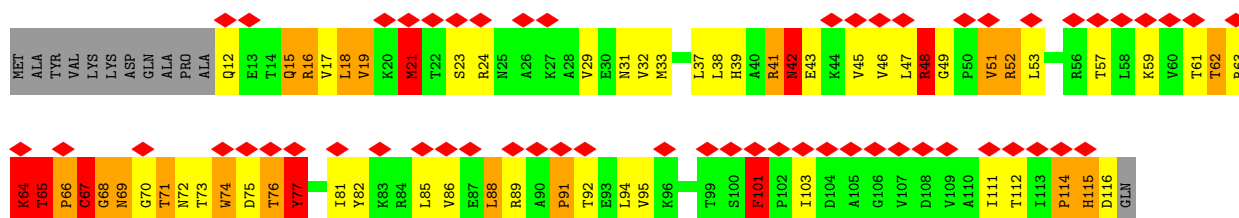


• Molecule 23: 40S RIBOSOMAL PROTEIN S2, PUTATIVE

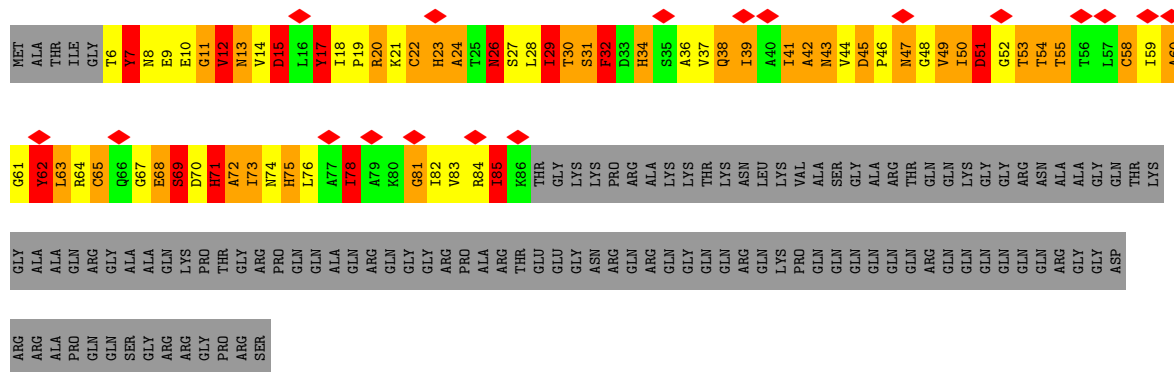
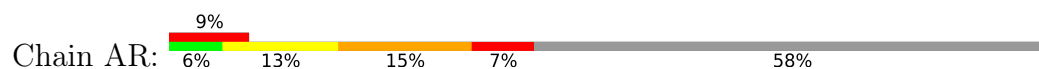




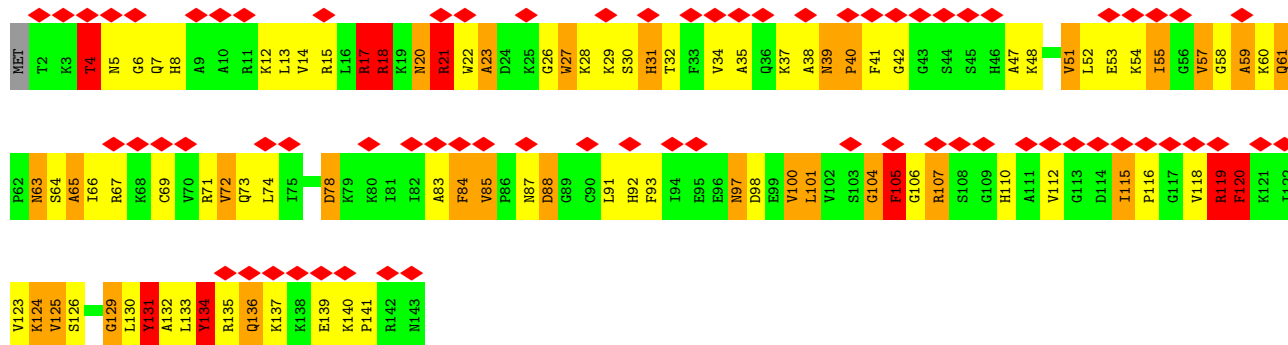
• Molecule 24: RIBOSOMAL PROTEIN S20, PUTATIVE



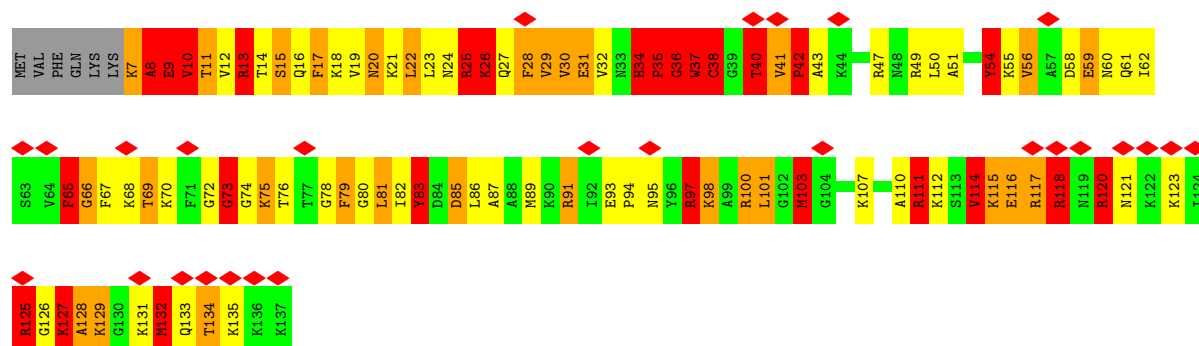
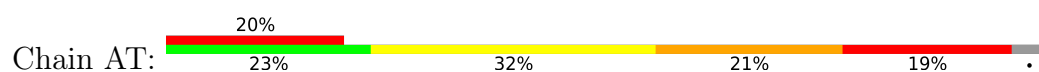
• Molecule 25: 40S RIBOSOMAL PROTEIN S21, PUTATIVE



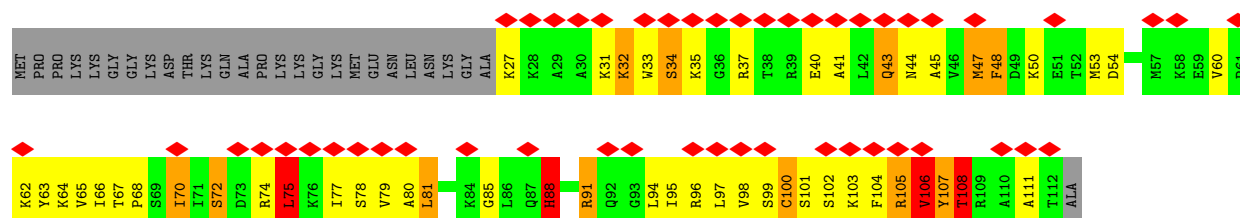
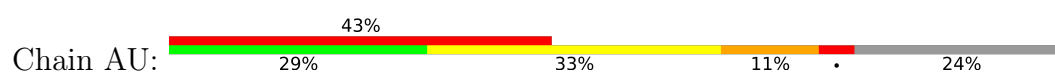
• Molecule 26: 40S RIBOSOMAL PROTEIN S23, PUTATIVE



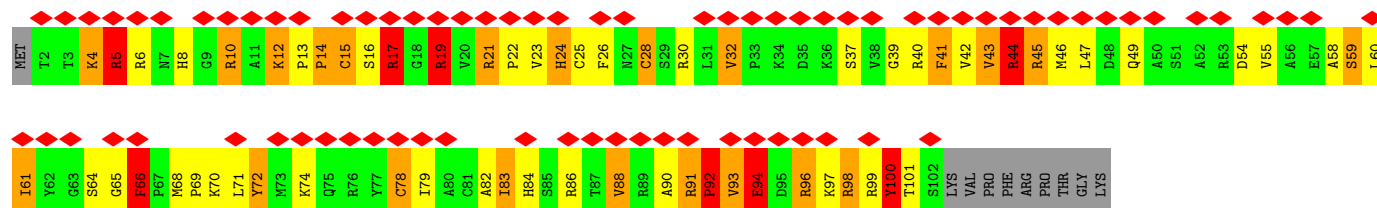
• Molecule 27: 40S RIBOSOMAL PROTEIN S24



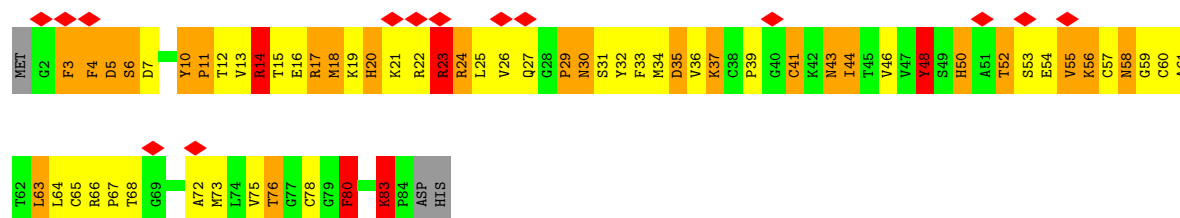
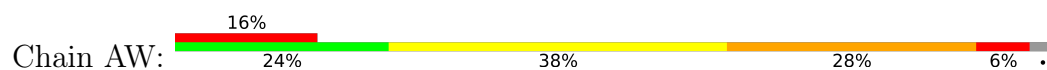
• Molecule 28: 40S RIBOSOMAL PROTEIN S25, PUTATIVE



• Molecule 29: RIBOSOMAL PROTEIN S26, PUTATIVE



• Molecule 30: 40S RIBOSOMAL PROTEIN S27, PUTATIVE



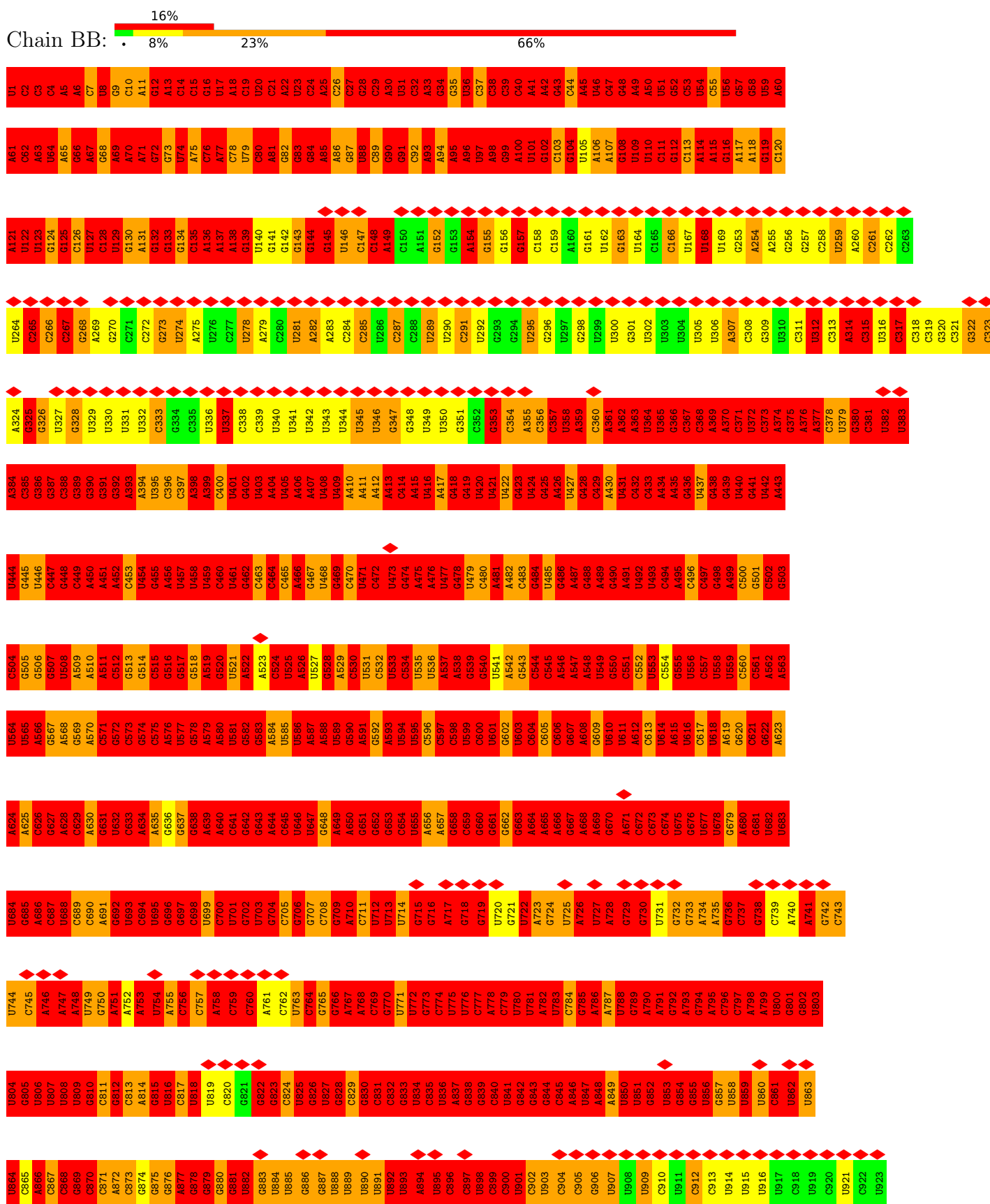
• Molecule 31: 40S RIBOSOMAL PROTEIN S3, PUTATIVE

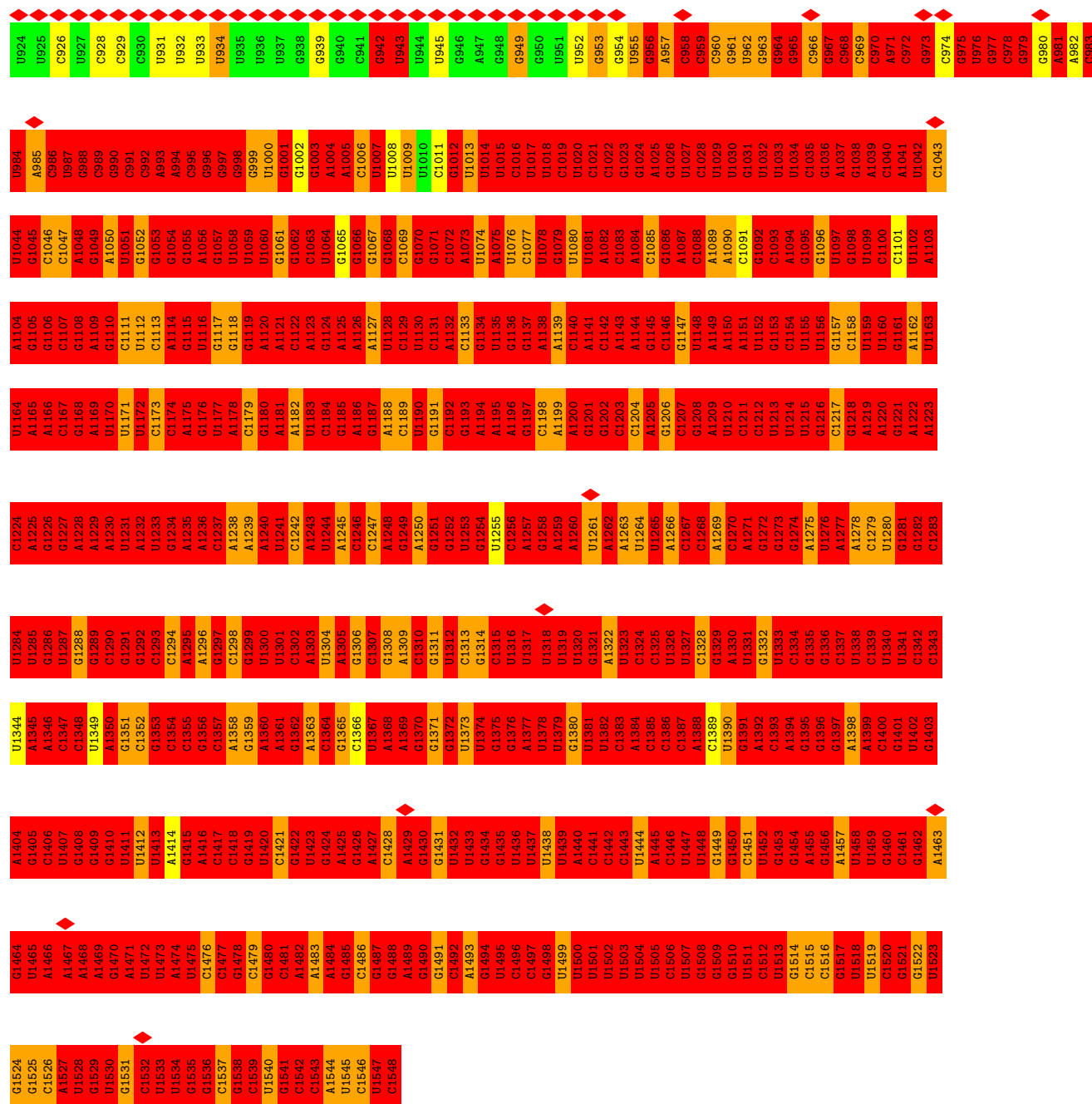


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U241	U242	C243	A244	U245	G246	U247	G248	A249	U250	U251	C252	U253	U254	U255	G256	A257	U258	C259	A260	A261	C262	G263	A264	U265	C266	A267	U268	G269	U270	C271	A272	U273	C274	C275	C276	A277	U278	U279	A280	C281	A282	U283	U284	C285	C286	U287	U288	A289	C290	C291	C292	U293	C294	U295	G296	A297	A298	G299	C300	
G181	U182	G183	C184	A185	G186	G187	C188	G189	U190	G191	C192	C193	G194	G195	A196	U197	U198	U199	C200	A201	A202	G203	U204	U205	C206	A207	U208	G209	U210	C211	A212	U213	C214	C215	C216	C217	G218	U219	U220	U221	C222	U223	U224	A225	A226	C227	U228	C229	A230	U231	U232	U233	A234	C235	A236	A237	C238	C239	C240	

G1801	U1081	G1201	G1261	G1321	A1381	C1441	U1501	C1561	U1621	U1681	G1741	G1801
C1802	U1082	G1202	C1141	A1322	G1382	A1442	G1502	G1562	U1622	A1682	G1742	C1802
A1803	A1083	U1203	C1142	A1323	U1383	U1443	G1503	G1563	U1623	C1683	U1743	A1803
A1804	A1084	U1204	A1143	G1324	U1384	U1444	A1504	U1564	U1624	A1684	G1744	A1804
C1805	G1085	A1205	G1144	G1325	U1385	U1445	G1505	U1565	C1625	G1685	G1745	C1805
A1806	G1086	C1206	U1146	U1326	U1386	U1446	G1506	G1566	U1626	G1686	G1746	A1806
G1807	A1087	A1207	C1147	G1327	U1387	C1447	C1507	G1567	U1627	G1687	G1747	G1807
A1808	G1088	U1208	U1148	U1328	A1389	U1448	U1509	A1568	U1628	G1688	C1748	A1808
G1809	U1089	A1209	U1149	U1329	U1389	U1449	G1510	G1569	A1628	G1689	C1749	G1809
A1810	A1090	A1210	A1150	G1330	C1390	G1450	C1511	C1570	A1629	U1690	A1750	A1810
A1811	U1091	G1211	A1151	G1331	U1391	A1451	G1512	C1571	A1630	G1691	A1751	A1811
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U1813	G1093	U1213	A1153	G1333	C1393	U1453	C1514	C1573	C1632	C1693	U1753	U1813
G1815	U1094	U1214	U1154	U1334	U1394	G1454	A1514	C1574	C1633	C1694	U1754	G1815
G1816	G1095	G1215	U1155	A1335	U1395	C1455	U1515	U1575	A1634	G1695	G1754	G1816
G1817	C1096	G1216	U1156	G1336	U1396	C1456	G1516	C1576	G1635	G1696	U1755	G1817
A1818	G1097	A1217	A1157	U1337	C1397	U1457	U1517	U1577	C1636	C1697	C1756	A1818
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A1821	A1100	U1220	U1160	U1340	C1399	U1460	A1520	U1580	U1639	C1700	C1759	A1821
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A1831	A1110	G1230	A1170	C1350	C1409	U1470	G1531	G1591	G1650	G1711	G1766	A1831
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G1837	G1116	U1236	C1176	U1356	C1415	G1476	U1537	G1597	A1656	G1717	G1772	G1837
U1838	G1117	U1237	C1177	C1357	C1416	G1477	G1538	U1598	A1657	C1718	U1773	U1838
G1839	C1118	C1238	U1178	A1358	C1417	U1478	A1539	A1599	G1658	G1719	U1774	G1839
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G1843	G1122	A1242	U1183	A1362	A1421	U1482	A1543	A1603	G1662	U1723	U1778	G1843
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G1846	U1126	G1246	U1186	U1365	U1424	U1485	C1546	A1606	G1665	U1726	A1781	G1846
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C1128	C1128	A1248	U1188	C1367	U1426	U1487	A1548	C1608	G1667	G1728	G1783	C1128
U1129	U1129	G1249	A1189	G1368	U1427	U1488	U1549	U1609	C1668	G1729	G1784	U1129
U1130	U1130	A1250	C1191	C1369	G1428	U1489	G1550	A1610	C1669	A1730	G1785	U1130
G1131	G1131	U1251	C1192	A1370	A1429	U1490	G1551	A1611	A1670	A1731	G1786	G1131
U1132	A1132	G1252	A1192	U1371	C1430	G1491	C1552	G1612	A1671	U1732	U1787	U1132
A1133	A1133	U1253	G1193	C1372	G1431	U1492	G1553	G1613	C1672	G1733	G1788	A1133
A1134	G1134	C1254	G1194	U1373	A1432	U1493	G1554	G1614	G1673	U1734	U1789	A1134
U1135	G1135	G1255	G1195	C1373	U1433	G1494	G1555	A1615	G1674	G1735	G1790	U1135
A1136	U1136	A1256	C1196	G1374	U1434	A1495	A1556	A1616	C1675	A1736	U1791	A1136
U1137	U1137	U1257	U1197	C1375	U1435	G1496	A1557	U1617	C1676	A1737	U1792	U1137
C1138	C1138	G1258	U1198	G1376	A1436	U1497	C1558	A1618	C1677	G1738	U1793	C1138
U1199	U1199	C1259	U1199	A1377	G1437	A1498	C1559	U1619	C1678	G1739	A1794	U1199
A1140	A1140	G1260	U1200	G1378	C1438	A1499	U1560	U1620	C1679	U1740	A1795	A1140
				A1320	G1440	G1500						

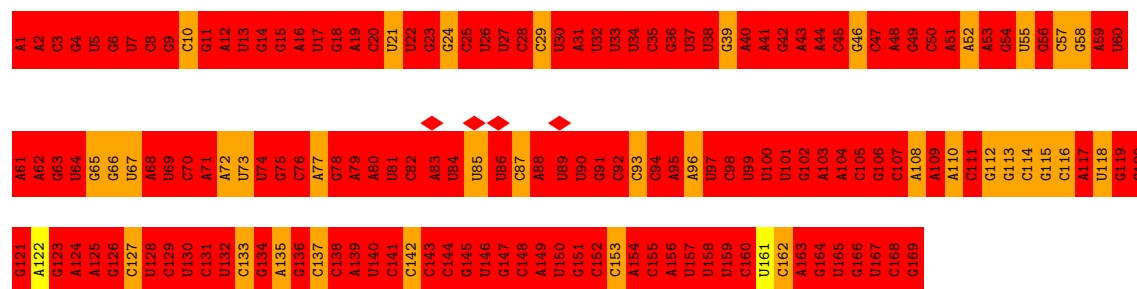
• Molecule 35: BETA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT 28S RRNA



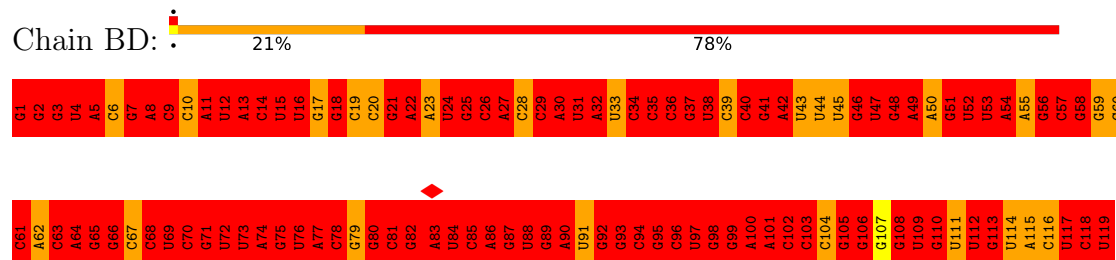


● Molecule 36: 5.8S RRNA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT

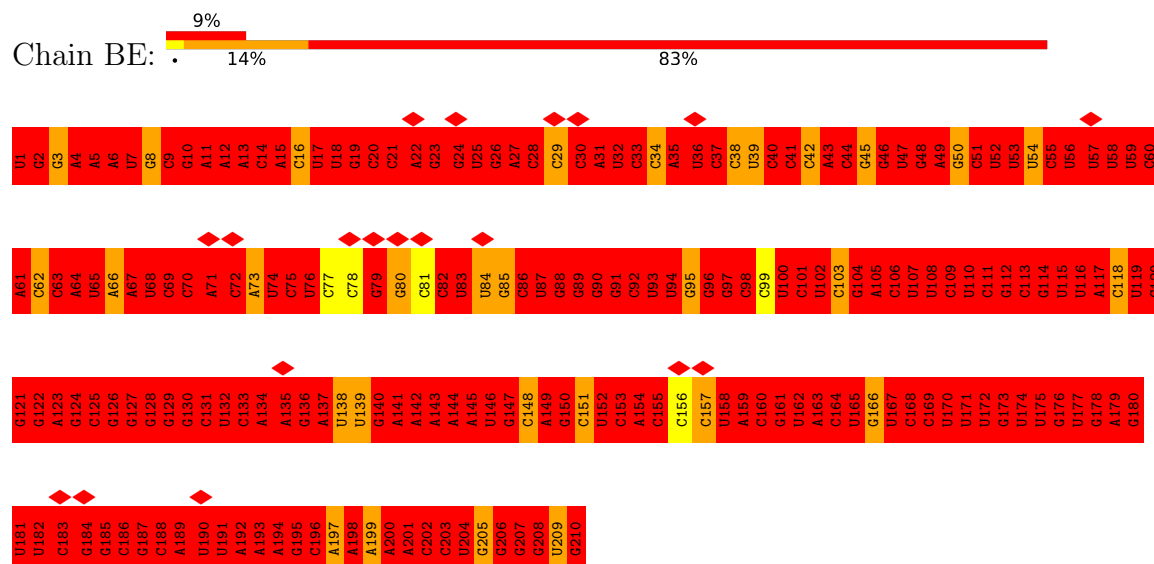
Chain BC: 21% 78%



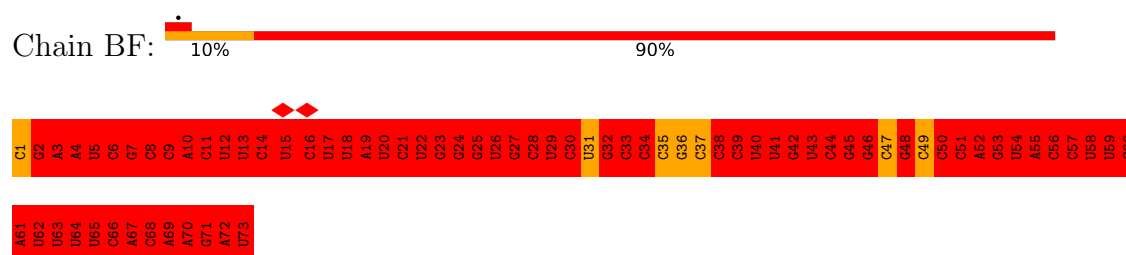
• Molecule 37: 5S RRNA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT



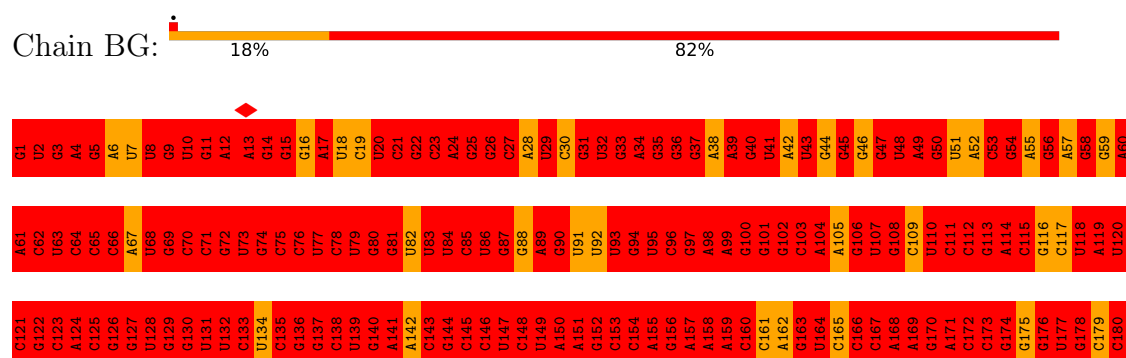
• Molecule 38: SHORT RRNA-I OF THE LARGE RIBOSOMAL SUBUNIT



• Molecule 39: SHORT RRNA-II OF THE LARGE RIBOSOMAL SUBUNIT

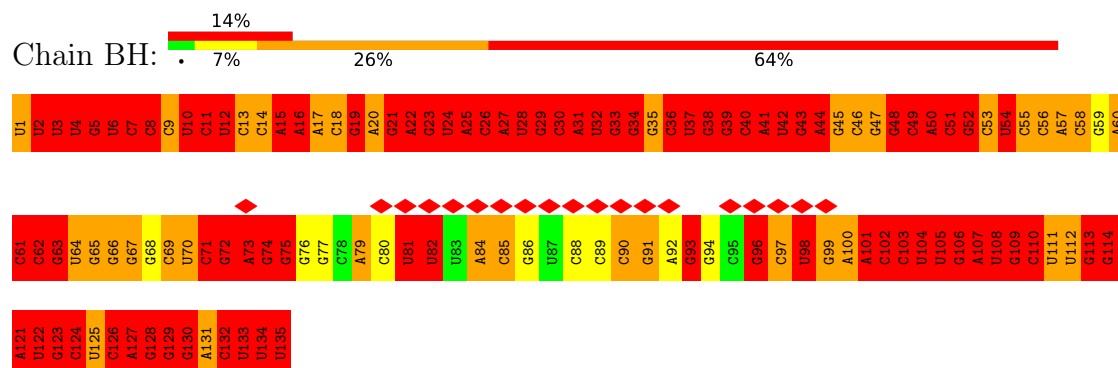


• Molecule 40: SHORT RRNA-III OF THE LARGE RIBOSOMAL SUBUNIT

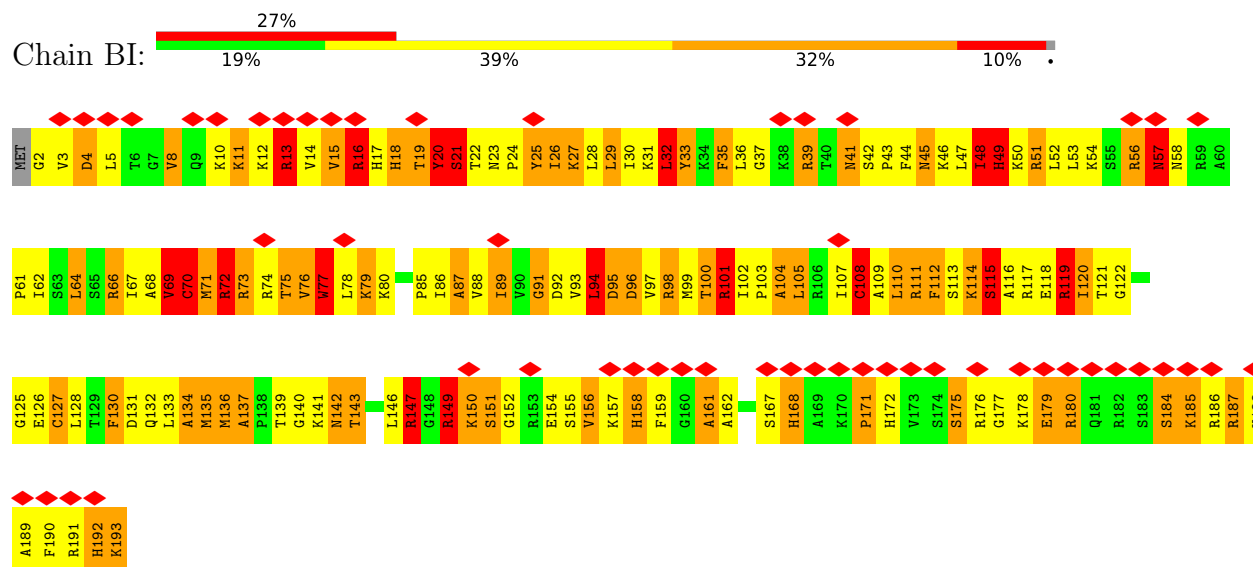


G181
G182

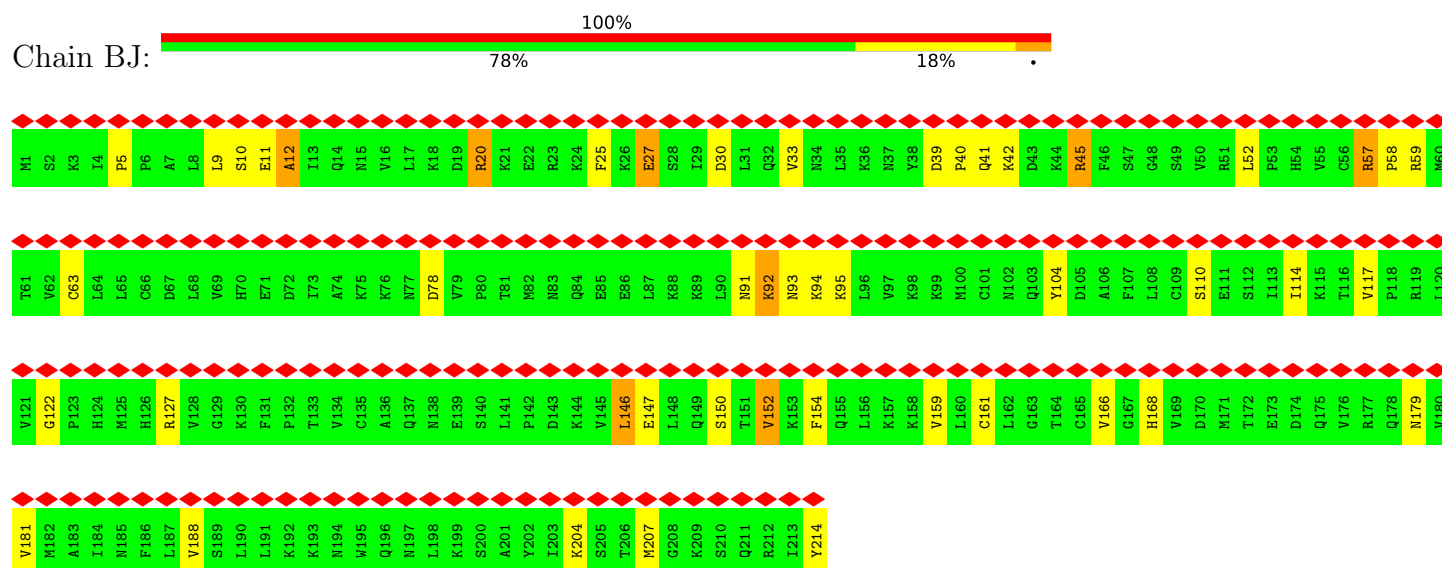
• Molecule 41: SHORT RRNA-IV OF THE LARGE RIBOSOMAL SUBUNIT



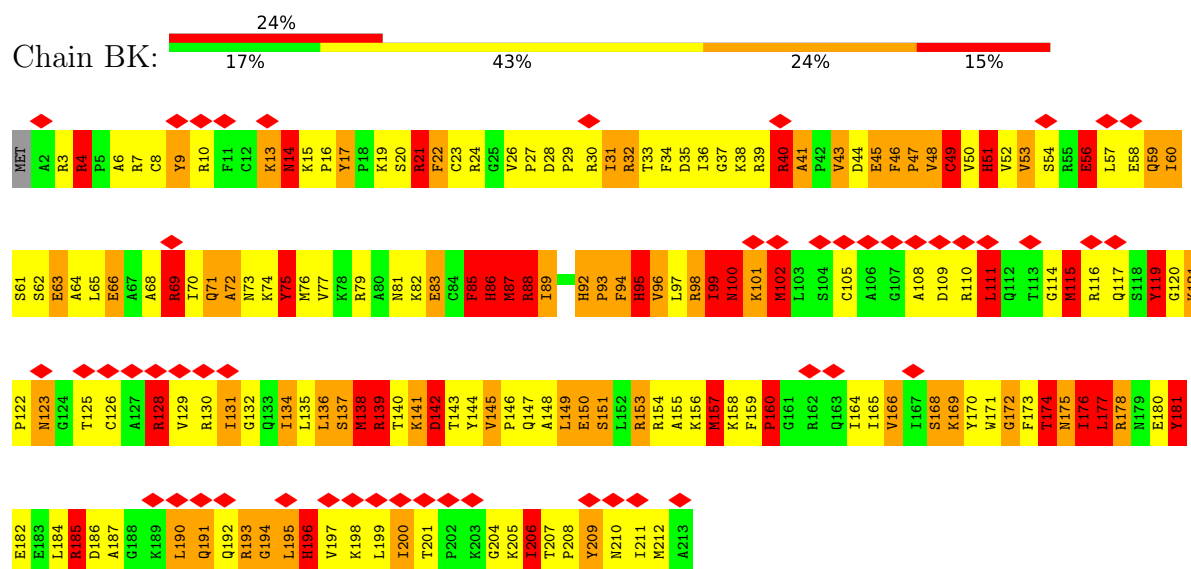
• Molecule 42: 60S RIBOSOMAL PROTEIN L18



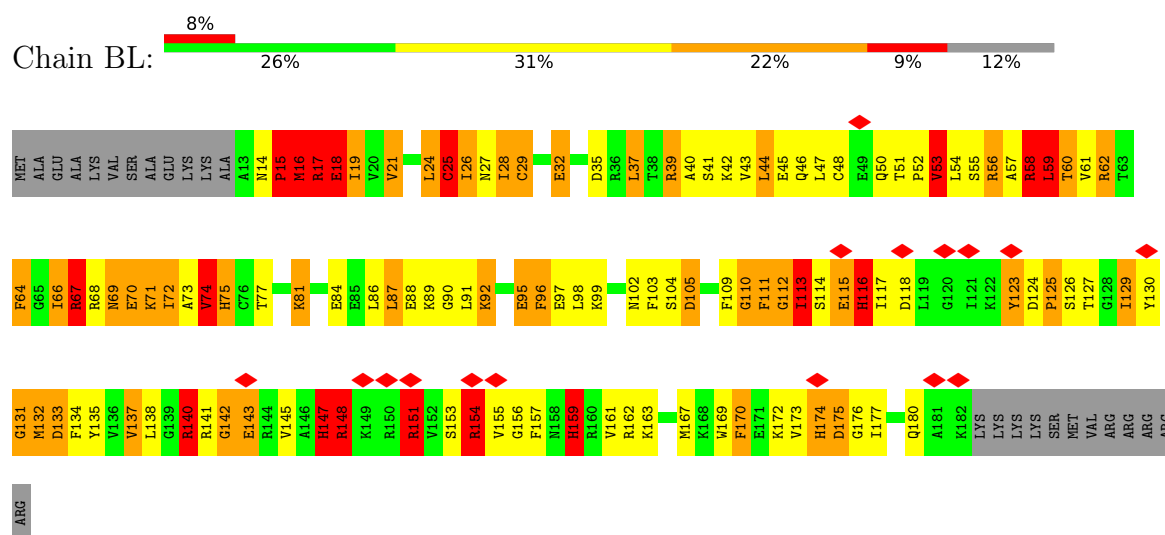
• Molecule 43: RIBOSOMAL PROTEIN



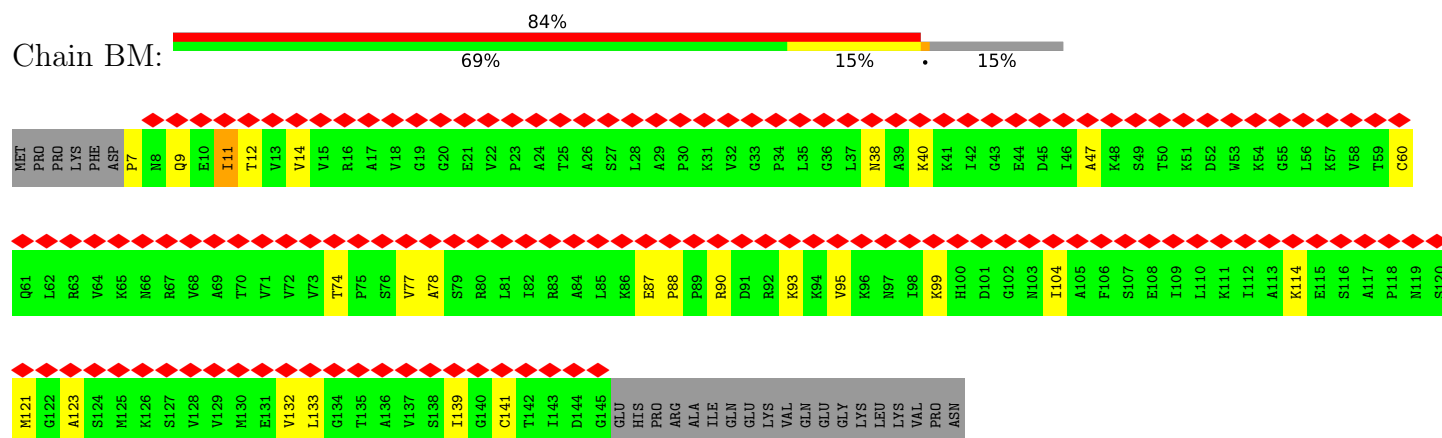
• Molecule 44: 60S RIBOSOMAL PROTEIN L10, PUTATIVE



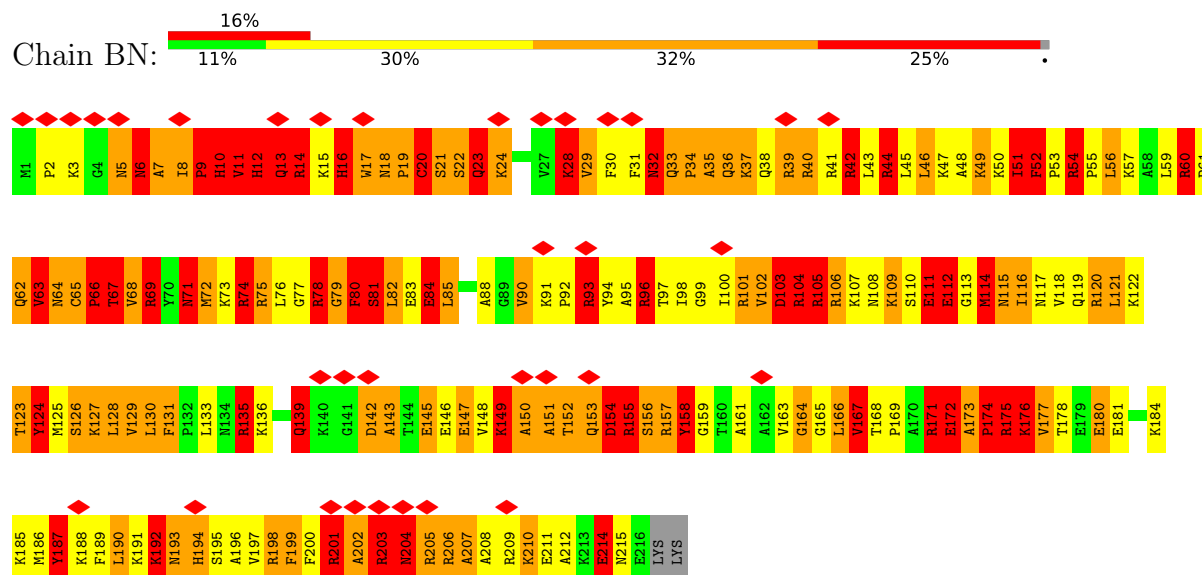
• Molecule 45: 60S RIBOSOMAL PROTEIN L11, PUTATIVE



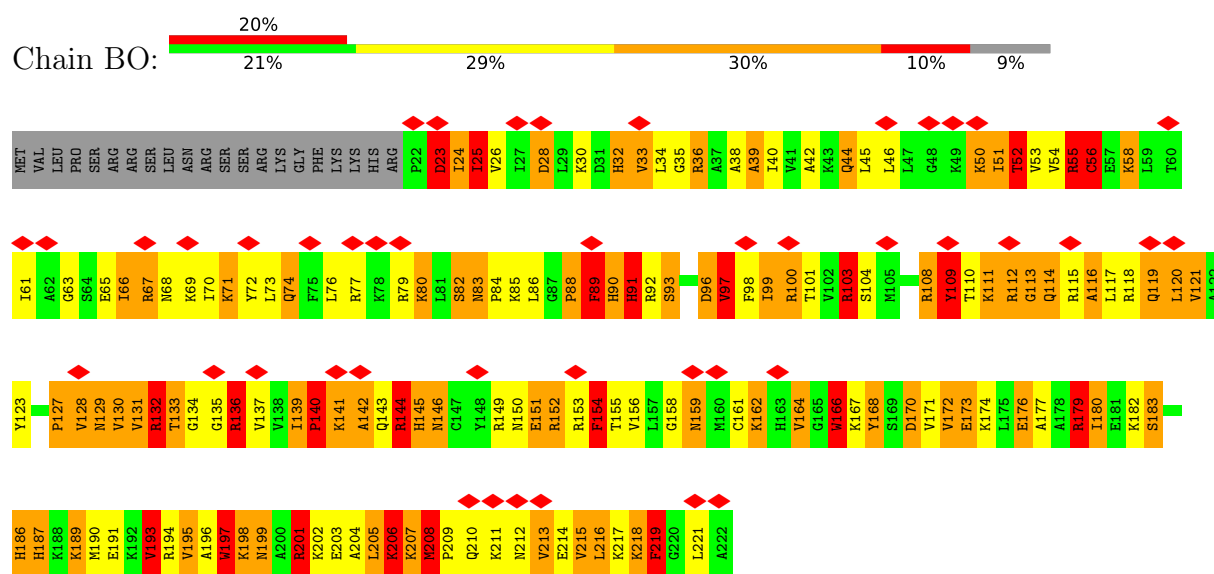
• Molecule 46: 60S RIBOSOMAL PROTEIN L12, PUTATIVE



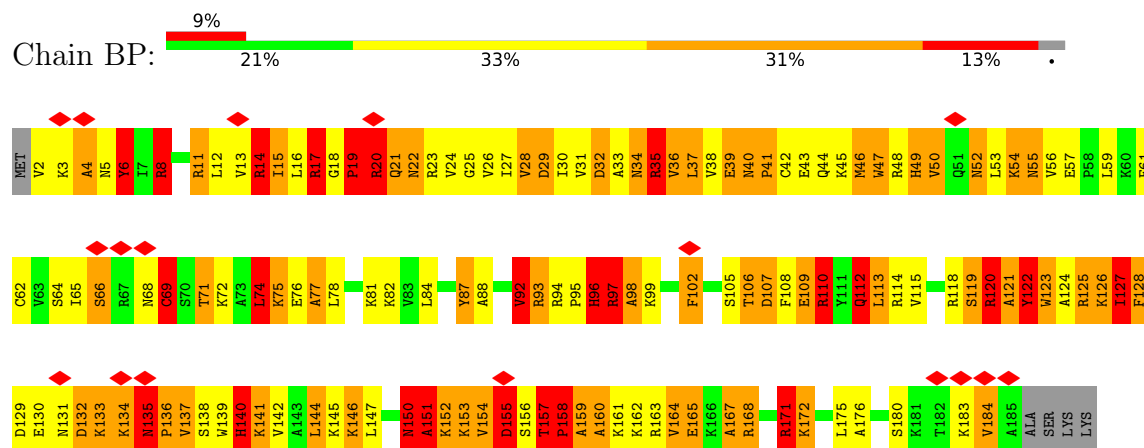
● Molecule 47: 60S RIBOSOMAL PROTEIN L13



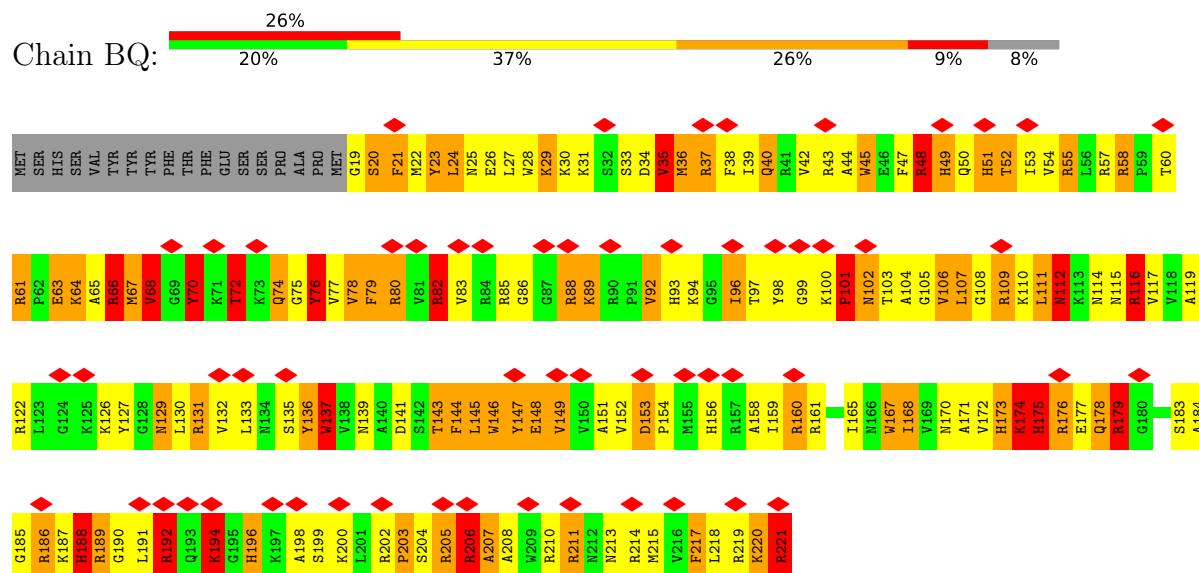
● Molecule 48: 60S RIBOSOMAL PROTEIN L13A, PUTATIVE



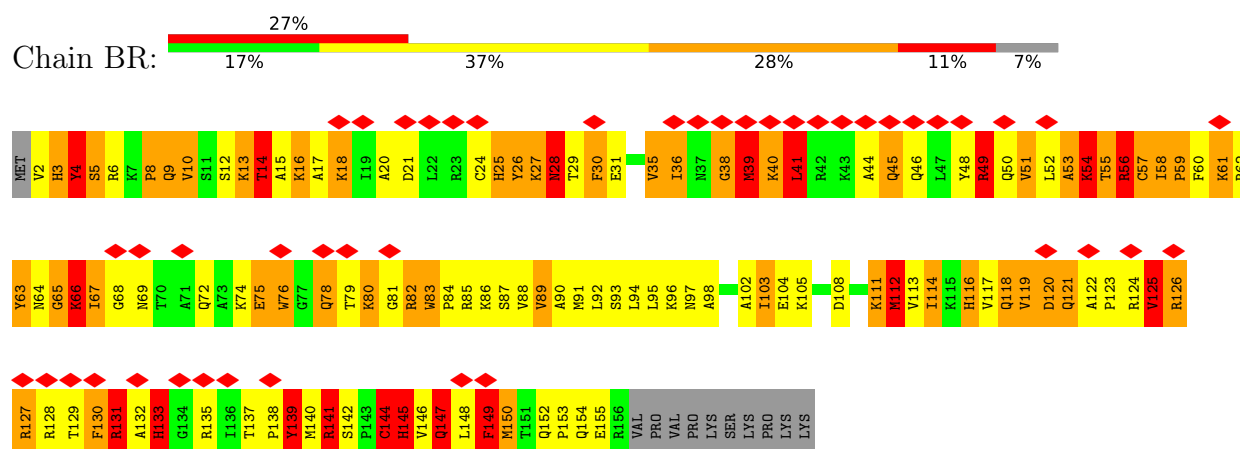
● Molecule 49: PROBABLE 60S RIBOSOMAL PROTEIN L14



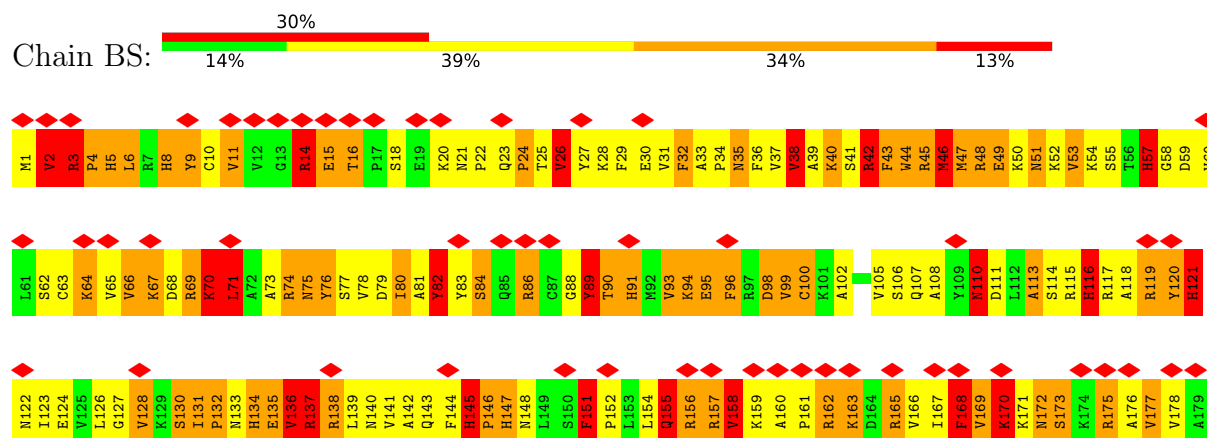
• Molecule 50: RIBOSOMAL PROTEIN L15



• Molecule 51: 60S RIBOSOMAL PROTEIN L17, PUTATIVE

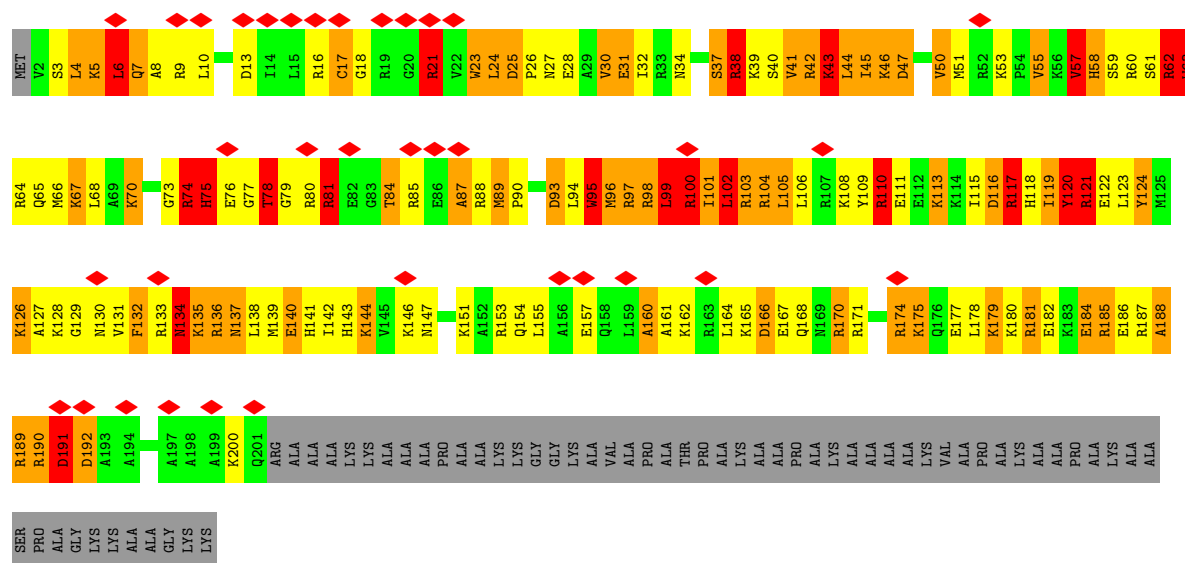


• Molecule 52: 60S RIBOSOMAL PROTEIN L18A

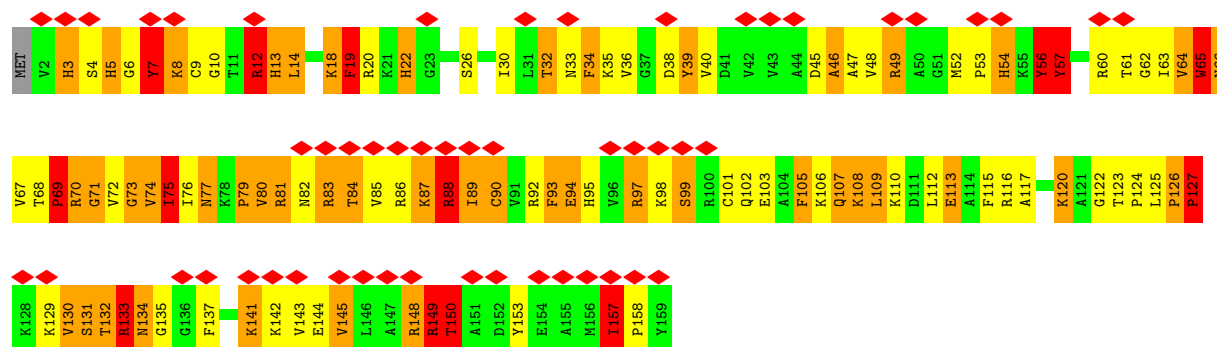


• Molecule 53: 60S RIBOSOMAL PROTEIN L19, PUTATIVE

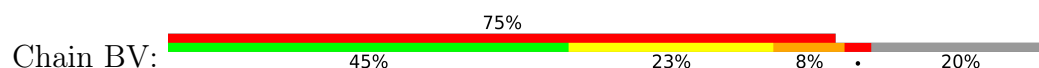




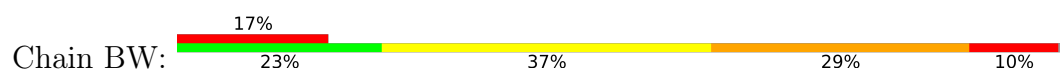
• Molecule 54: 60S RIBOSOMAL PROTEIN L21E, PUTATIVE

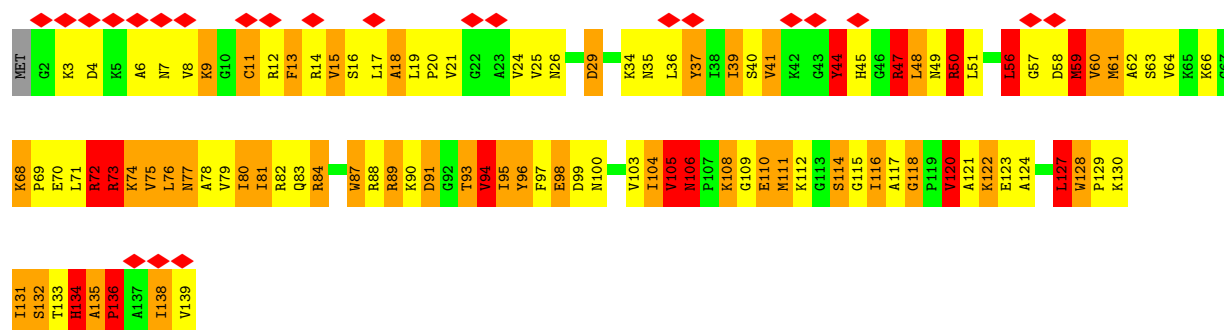


• Molecule 55: 60S RIBOSOMAL PROTEIN L22, PUTATIVE

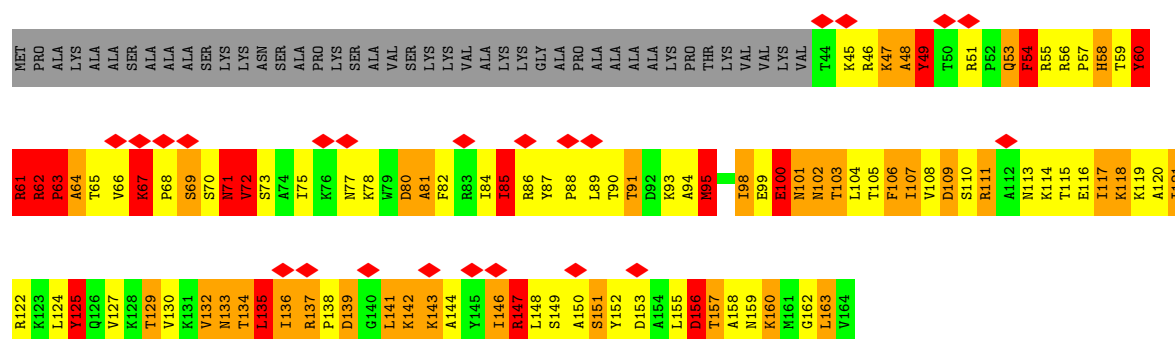


• Molecule 56: 60S RIBOSOMAL PROTEIN L23, PUTATIVE

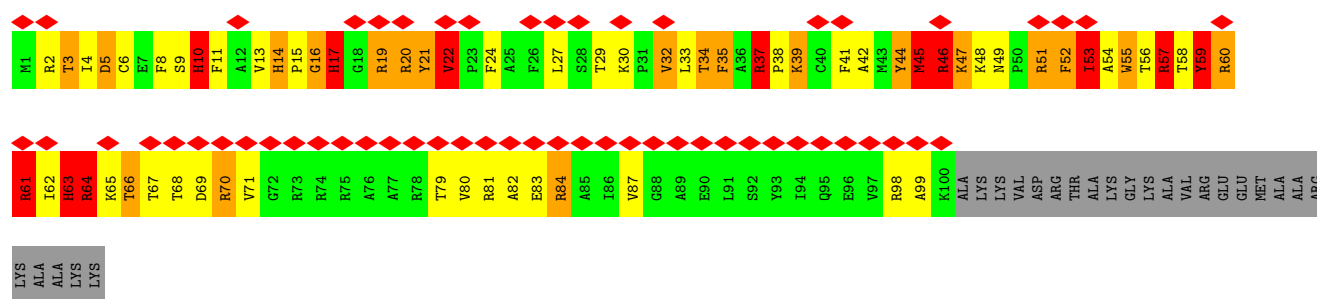
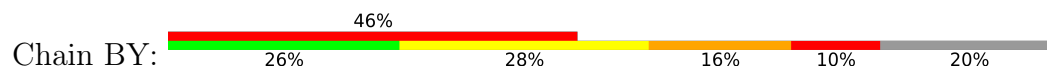




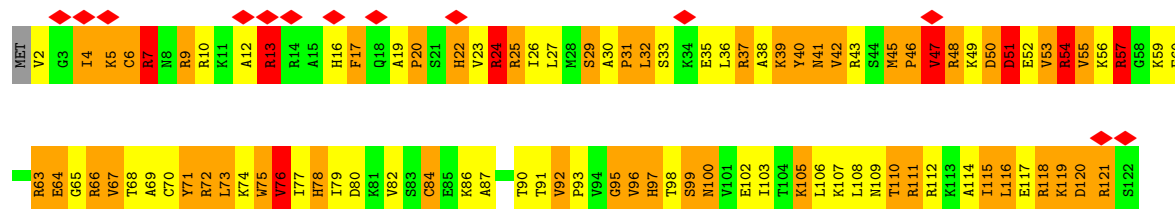
• Molecule 57: 60S RIBOSOMAL PROTEIN L23A

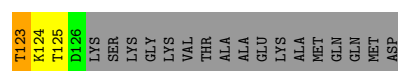


• Molecule 58: 60S RIBOSOMAL PROTEIN L24, PUTATIVE

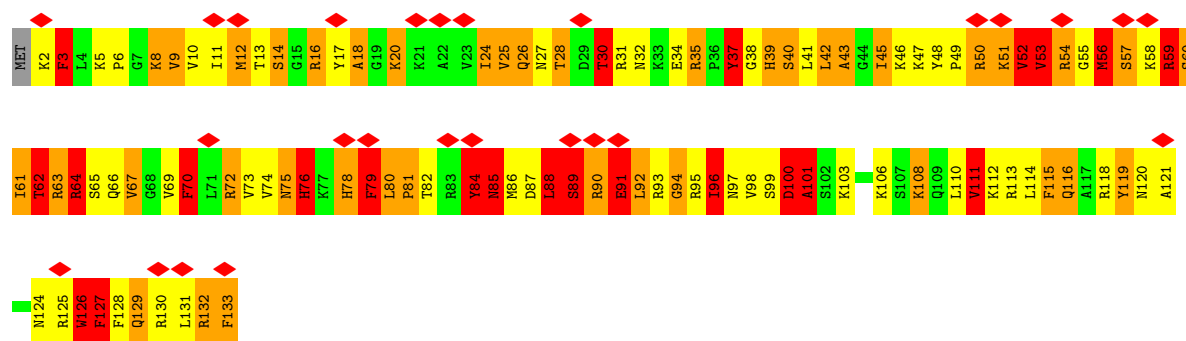


• Molecule 59: 60S RIBOSOMAL PROTEIN L26, PUTATIVE

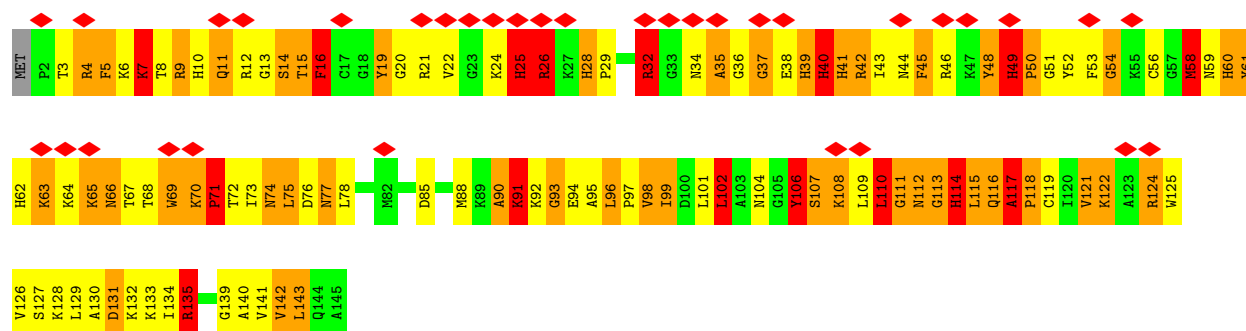
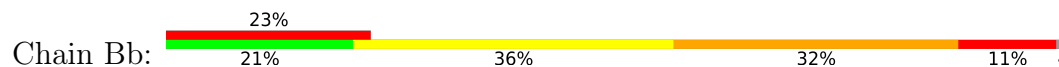




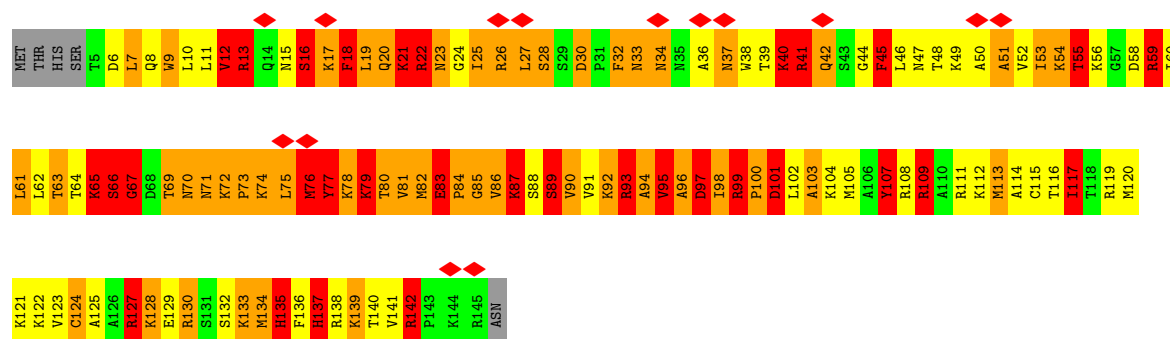
• Molecule 60: 60S RIBOSOMAL PROTEIN L27, PUTATIVE



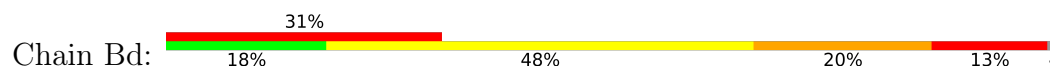
• Molecule 61: 60S RIBOSOMAL PROTEIN L27A

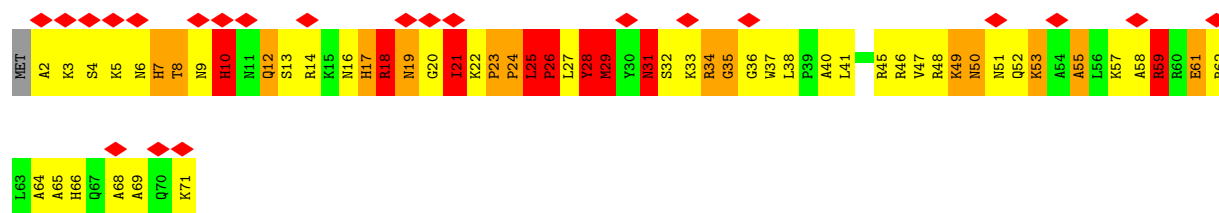


• Molecule 62: 60S RIBOSOMAL PROTEIN L28, PUTATIVE

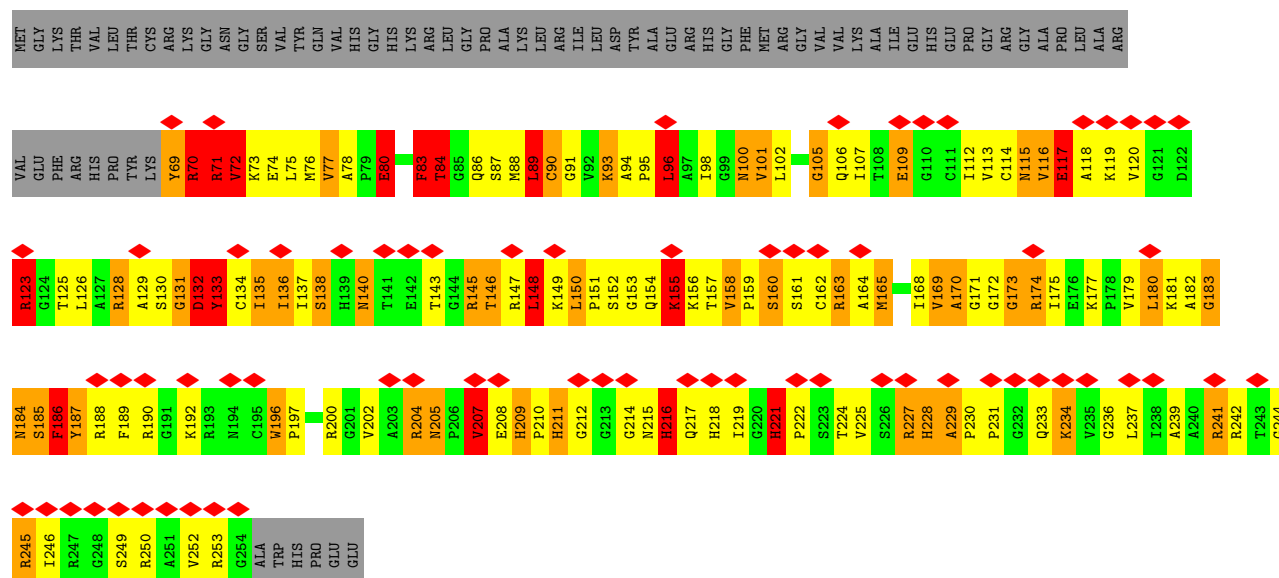


• Molecule 63: 60S RIBOSOMAL PROTEIN L29, PUTATIVE

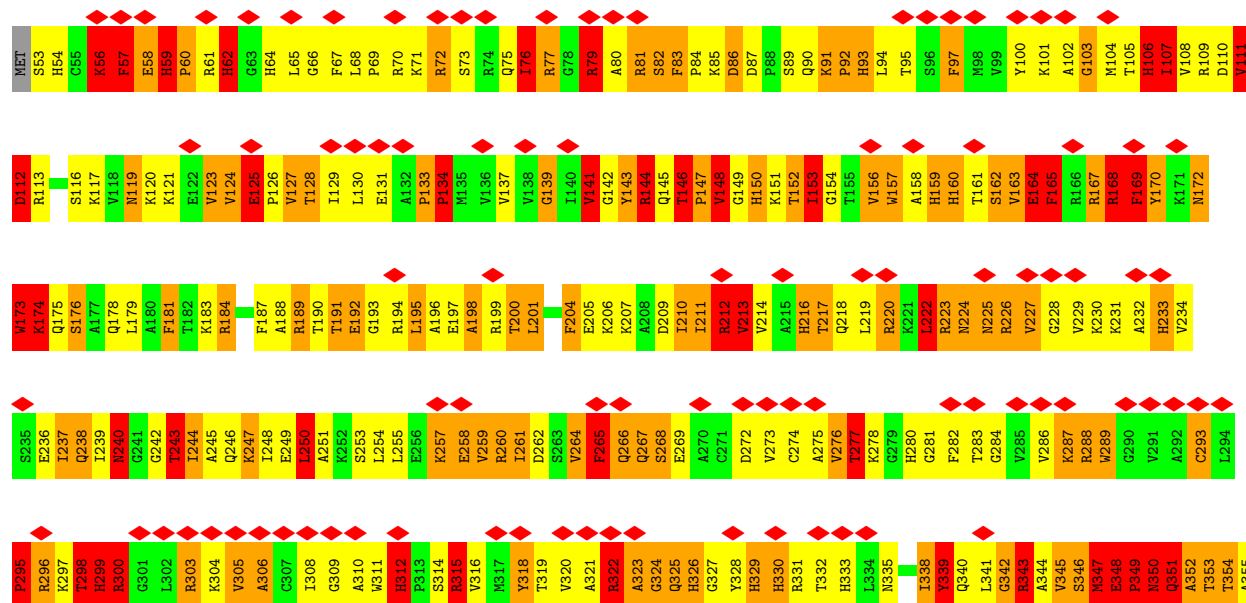
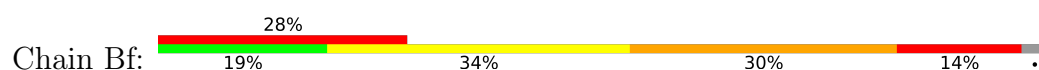




• Molecule 64: 60S RIBOSOMAL PROTEIN L2, PUTATIVE

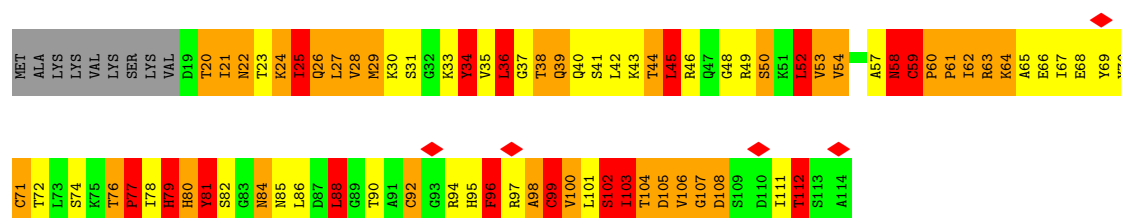


• Molecule 65: RIBOSOMAL PROTEIN L3, MITOCHONDRIAL, PUTATIVE

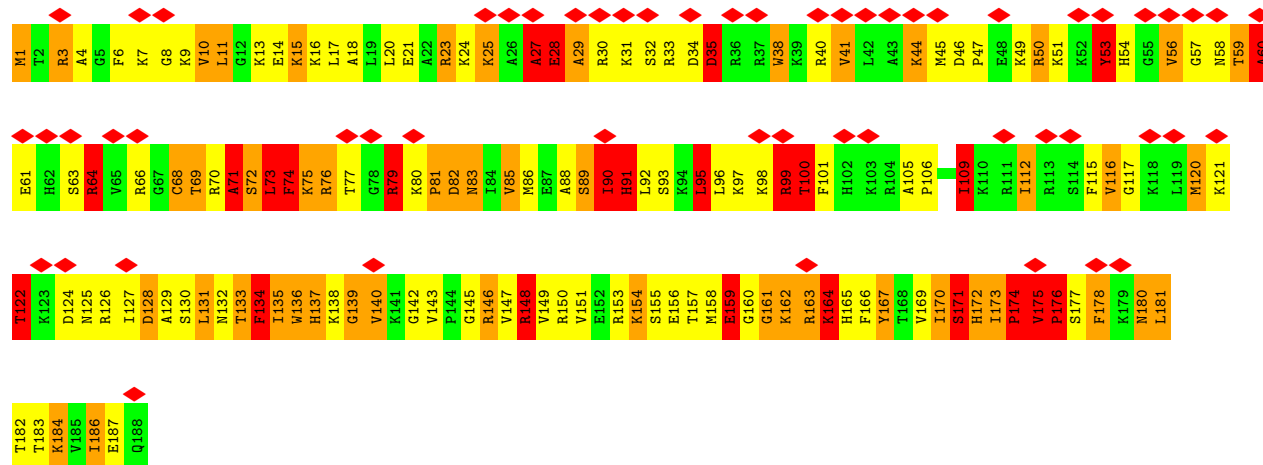
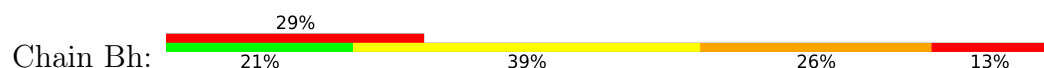




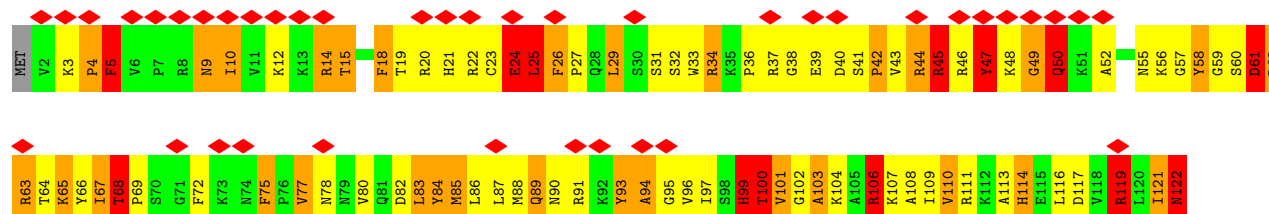
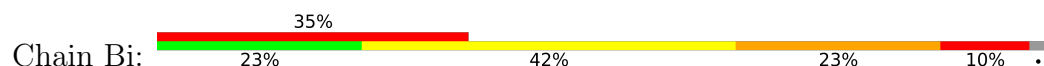
• Molecule 66: 60S RIBOSOMAL PROTEIN L30



• Molecule 67: 60S RIBOSOMAL SUBUNIT PROTEIN L31, PUTATIVE

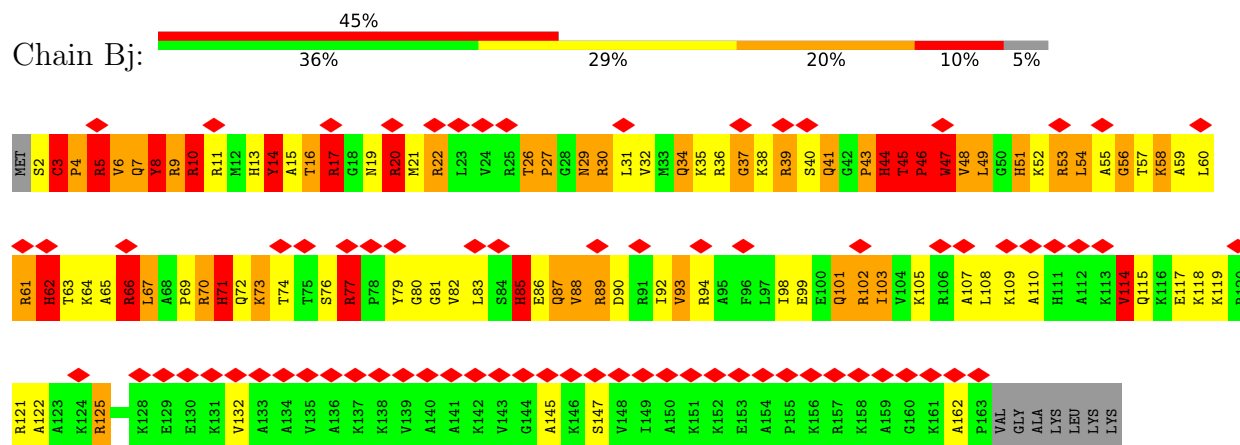


• Molecule 68: 60S RIBOSOMAL PROTEIN L32, PUTATIVE

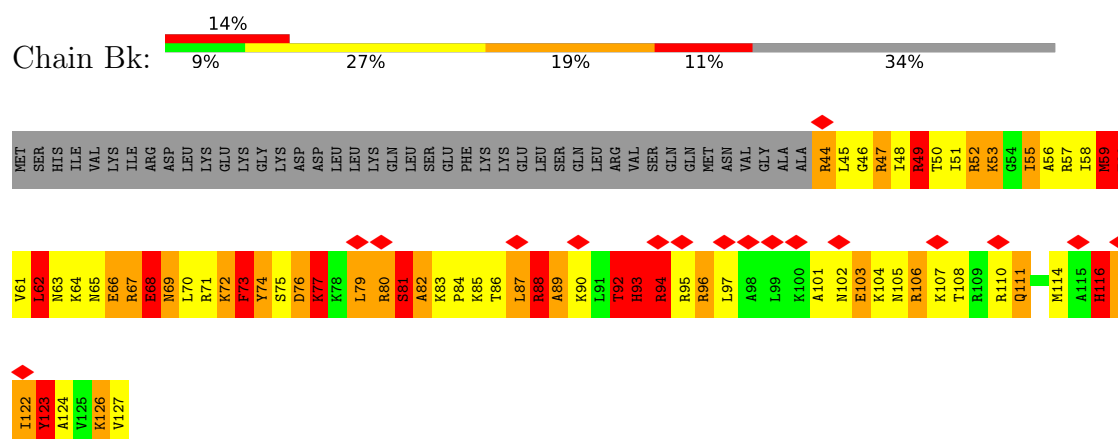




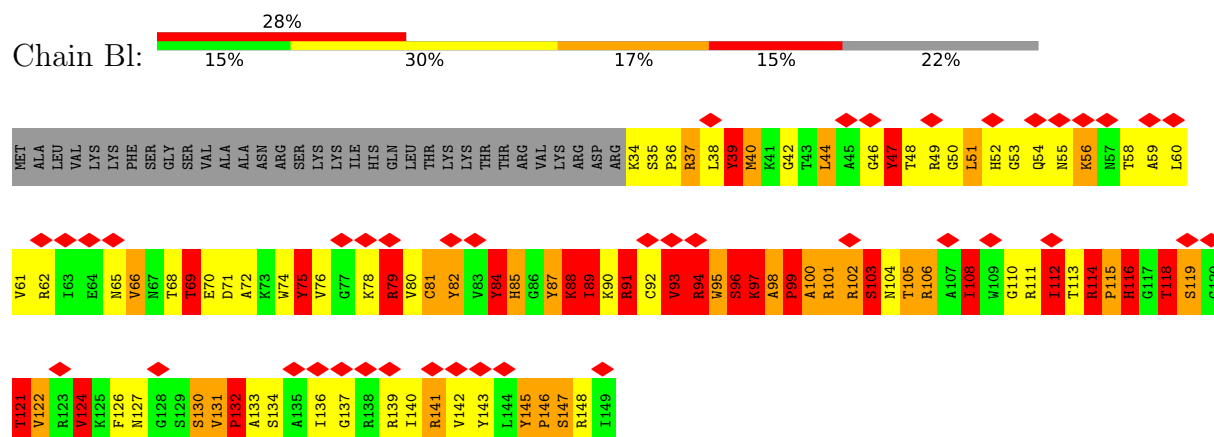
• Molecule 69: 60S RIBOSOMAL PROTEIN L34, PUTATIVE



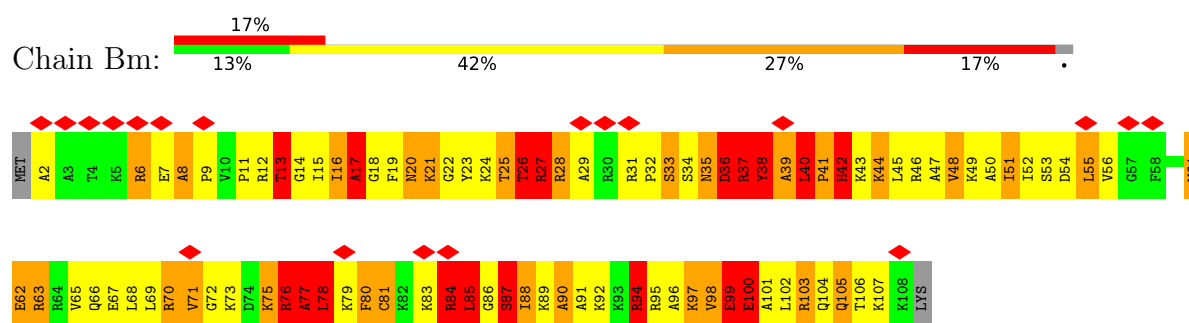
• Molecule 70: 60S RIBOSOMAL PROTEIN L35, PUTATIVE



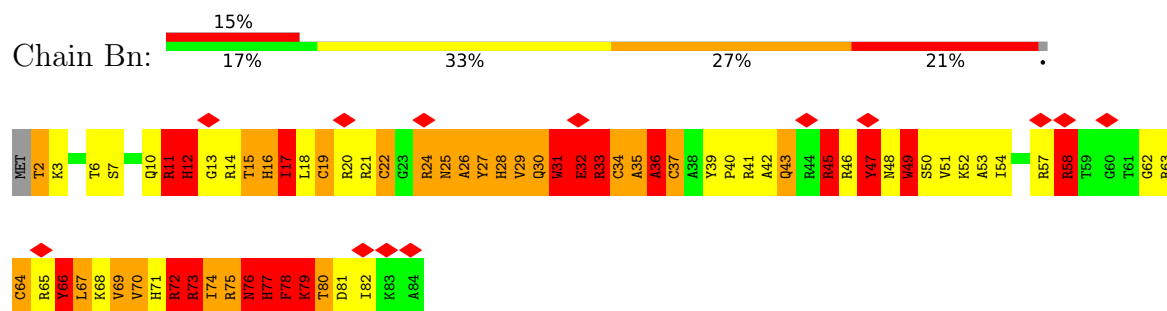
• Molecule 71: 60S RIBOSOMAL PROTEIN L35A, PUTATIVE



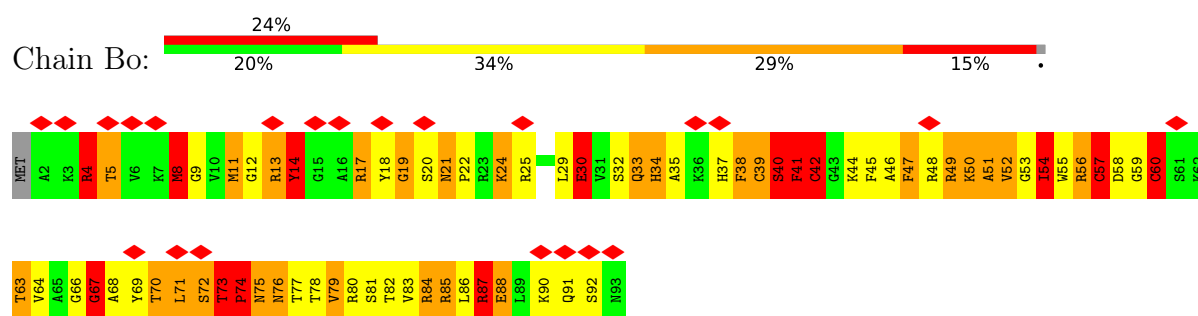
• Molecule 72: RIBOSOMAL PROTEIN L36, PUTATIVE



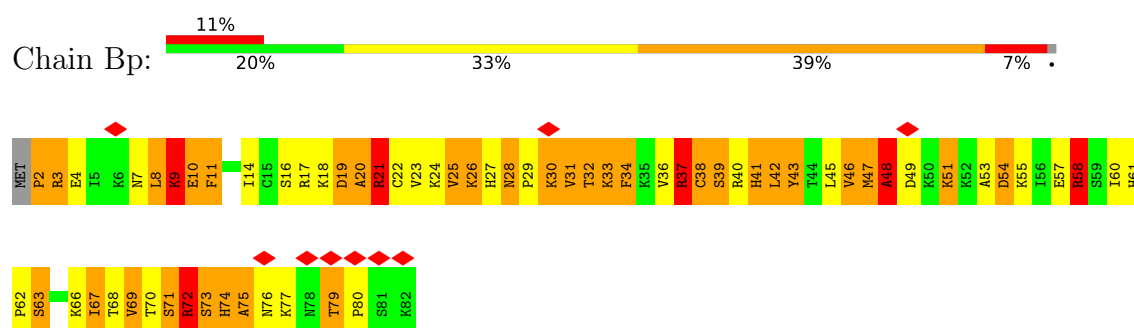
• Molecule 73: RIBOSOMAL PROTEIN L37



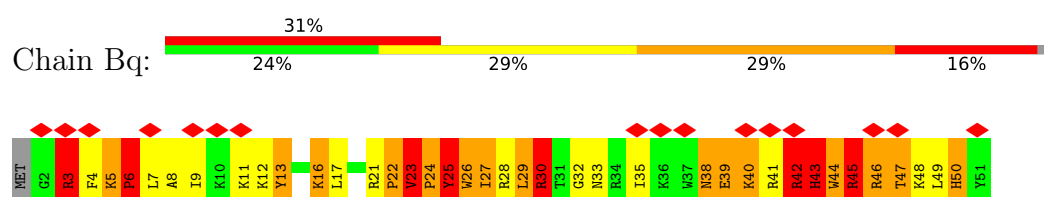
• Molecule 74: 60S RIBOSOMAL PROTEIN L37A, PUTATIVE



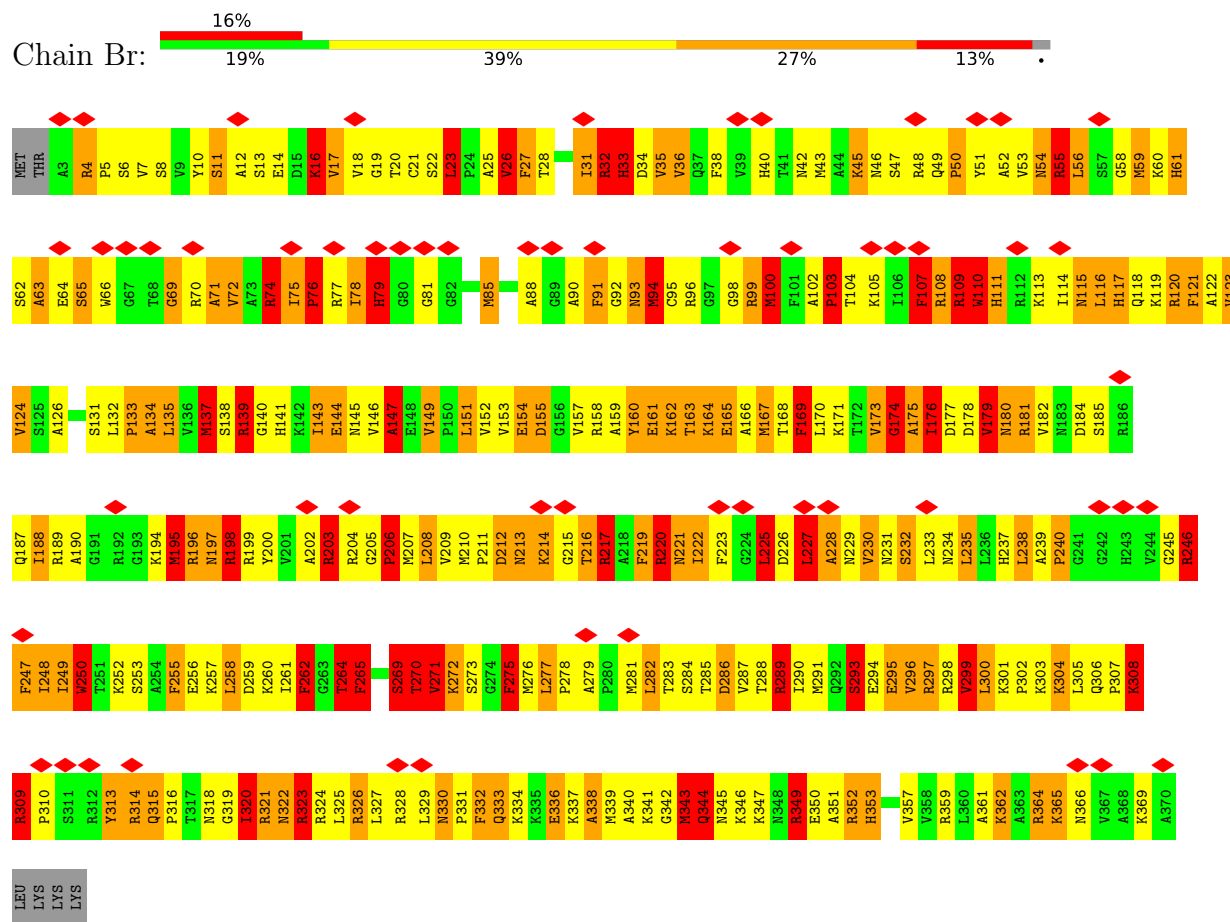
• Molecule 75: 60S RIBOSOMAL PROTEIN L38, PUTATIVE



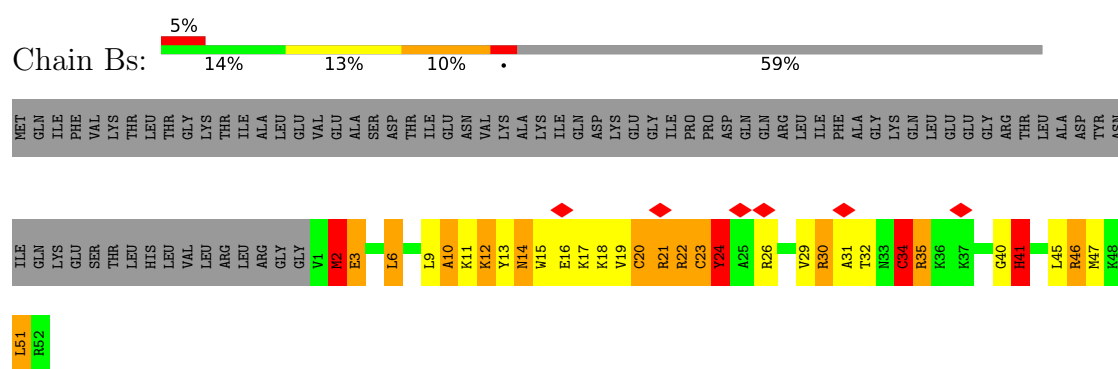
• Molecule 76: 60S RIBOSOMAL PROTEIN L39, PUTATIVE



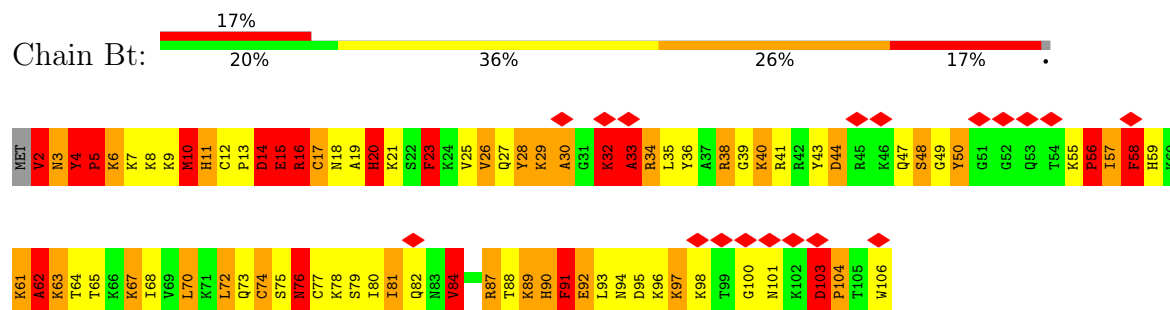
• Molecule 77: 60S RIBOSOMAL PROTEIN L4



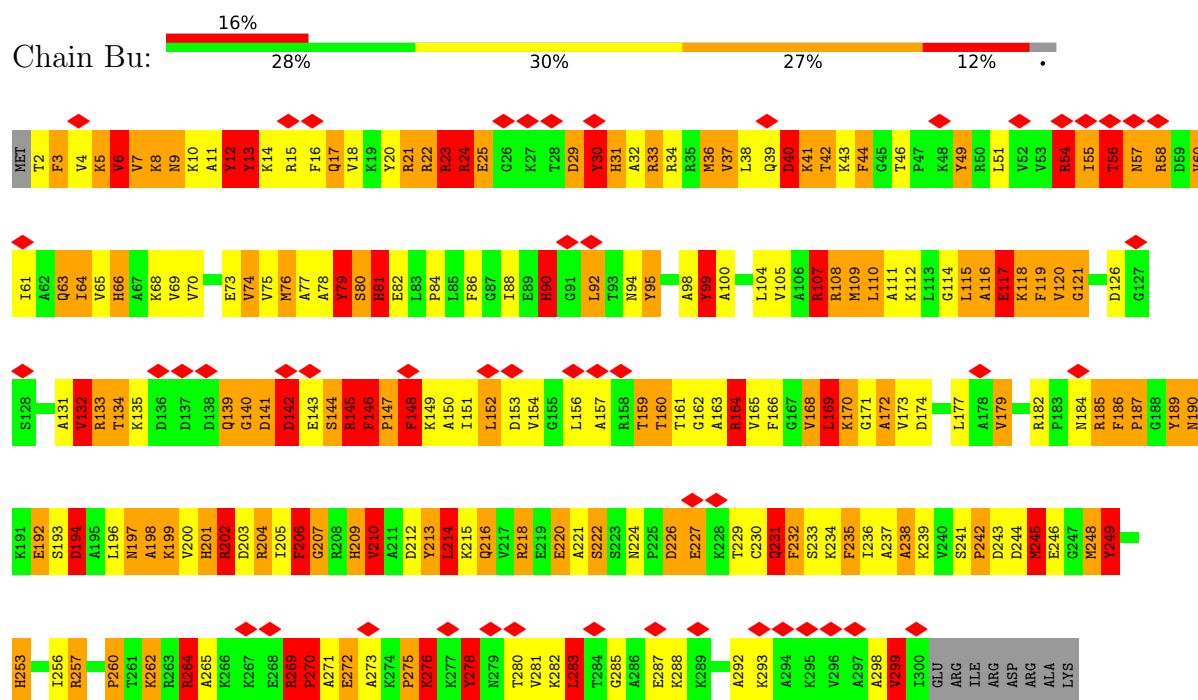
• Molecule 78: UBIQUITIN-60S RIBOSOMAL PROTEIN L40



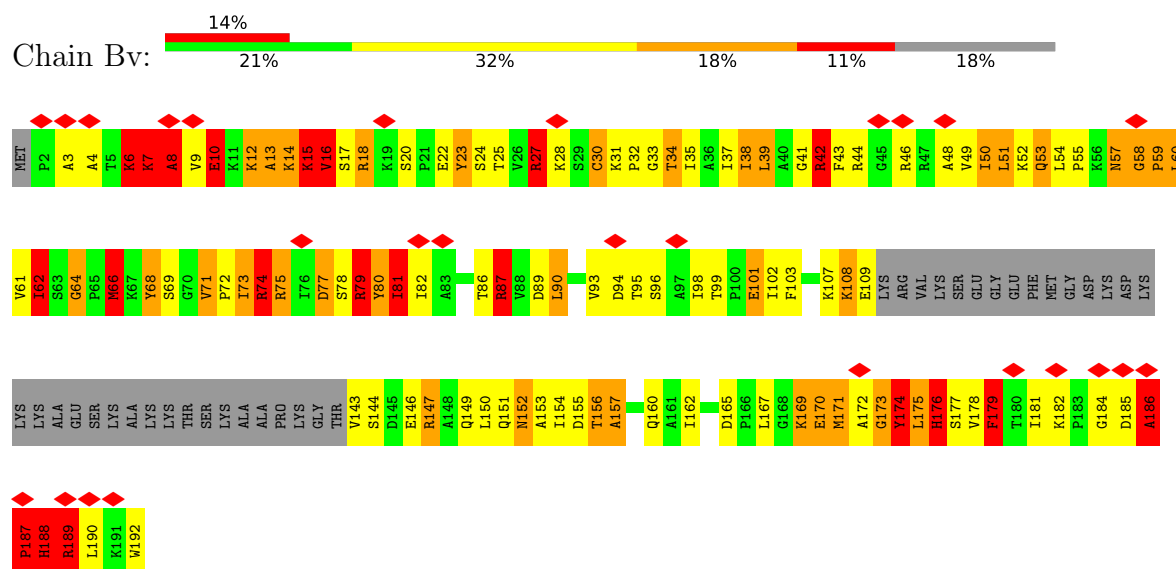
• Molecule 79: 60S RIBOSOMAL PROTEIN L44



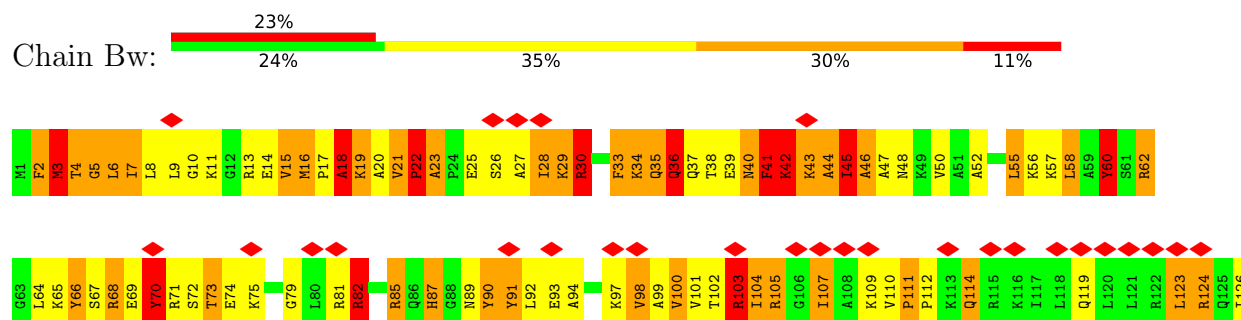
• Molecule 80: 60S RIBOSOMAL PROTEIN L5, PUTATIVE

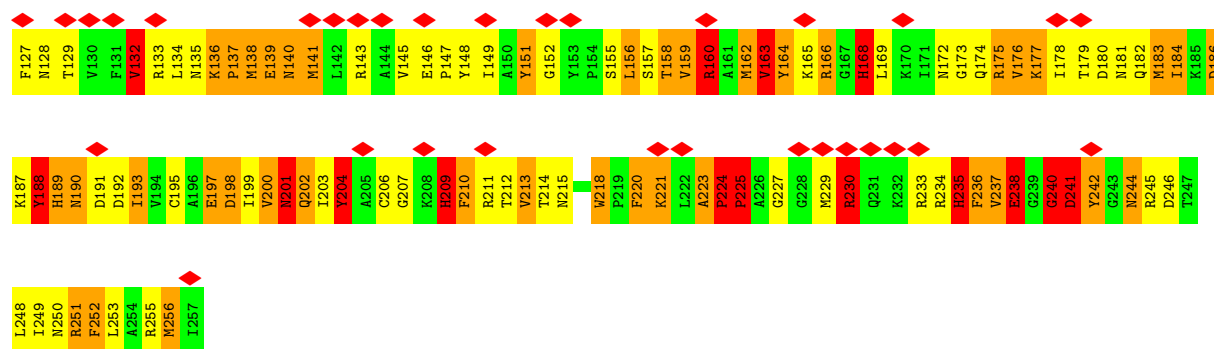


• Molecule 81: 60S RIBOSOMAL PROTEIN L6, PUTATIVE

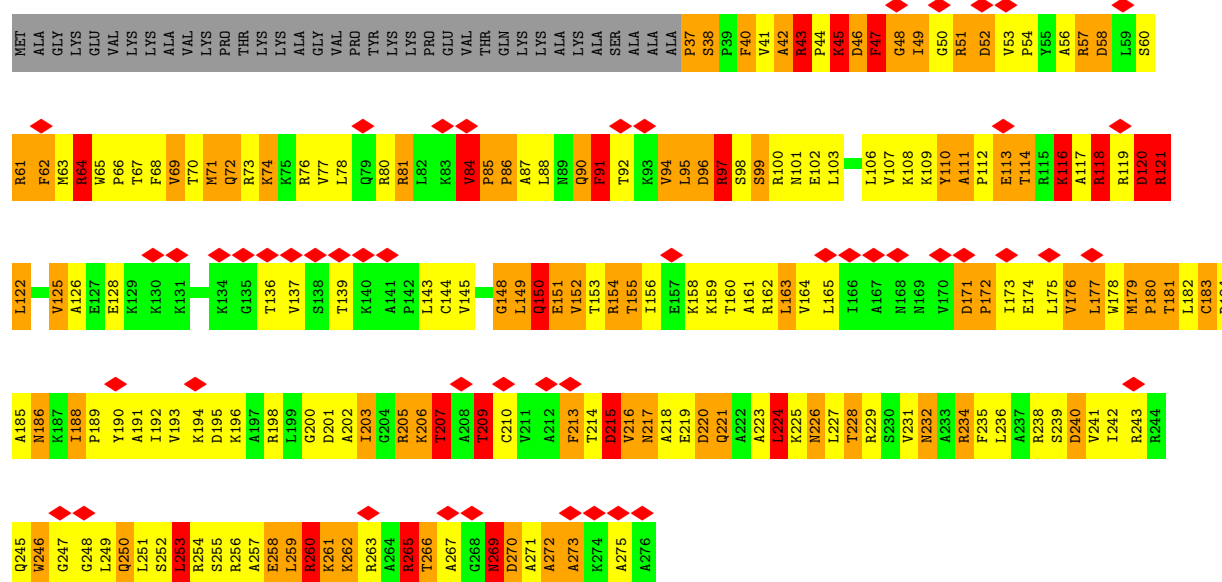
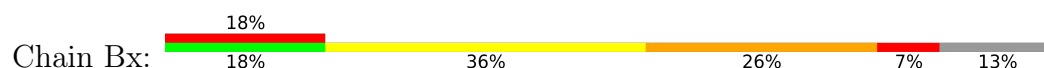


• Molecule 82: 60S RIBOSOMAL PROTEIN L7, PUTATIVE

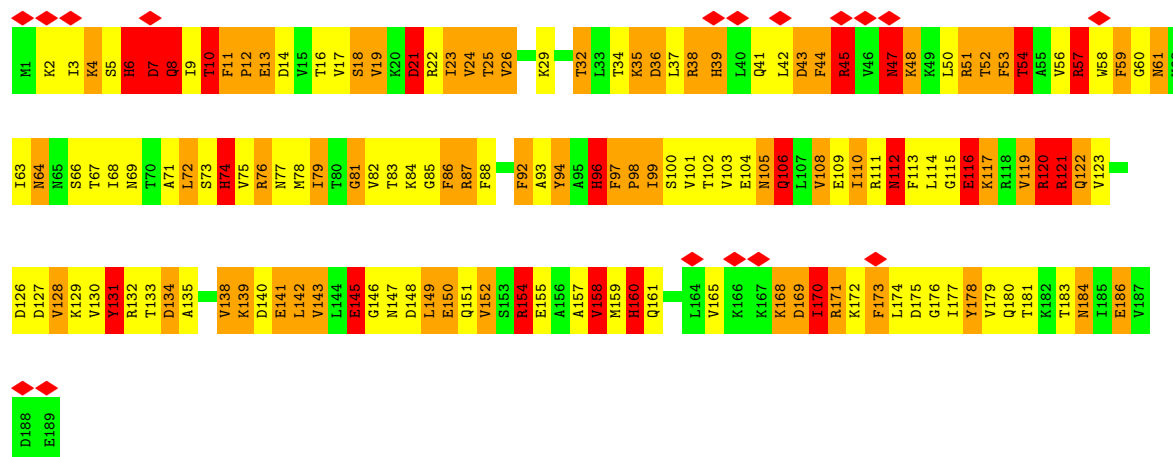
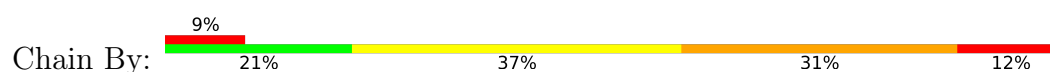




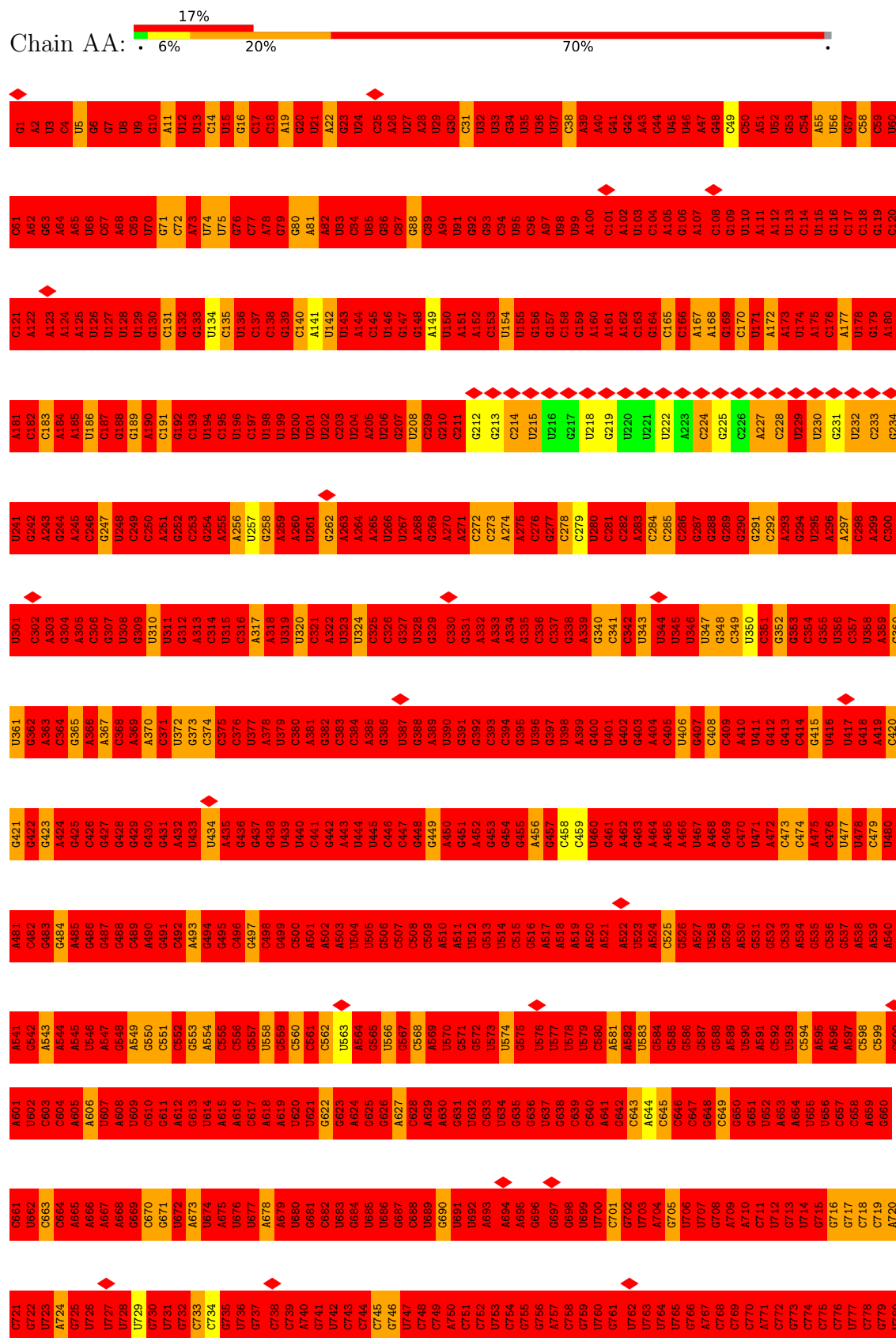
• Molecule 83: 60S RIBOSOMAL PROTEIN L7A, PUTATIVE



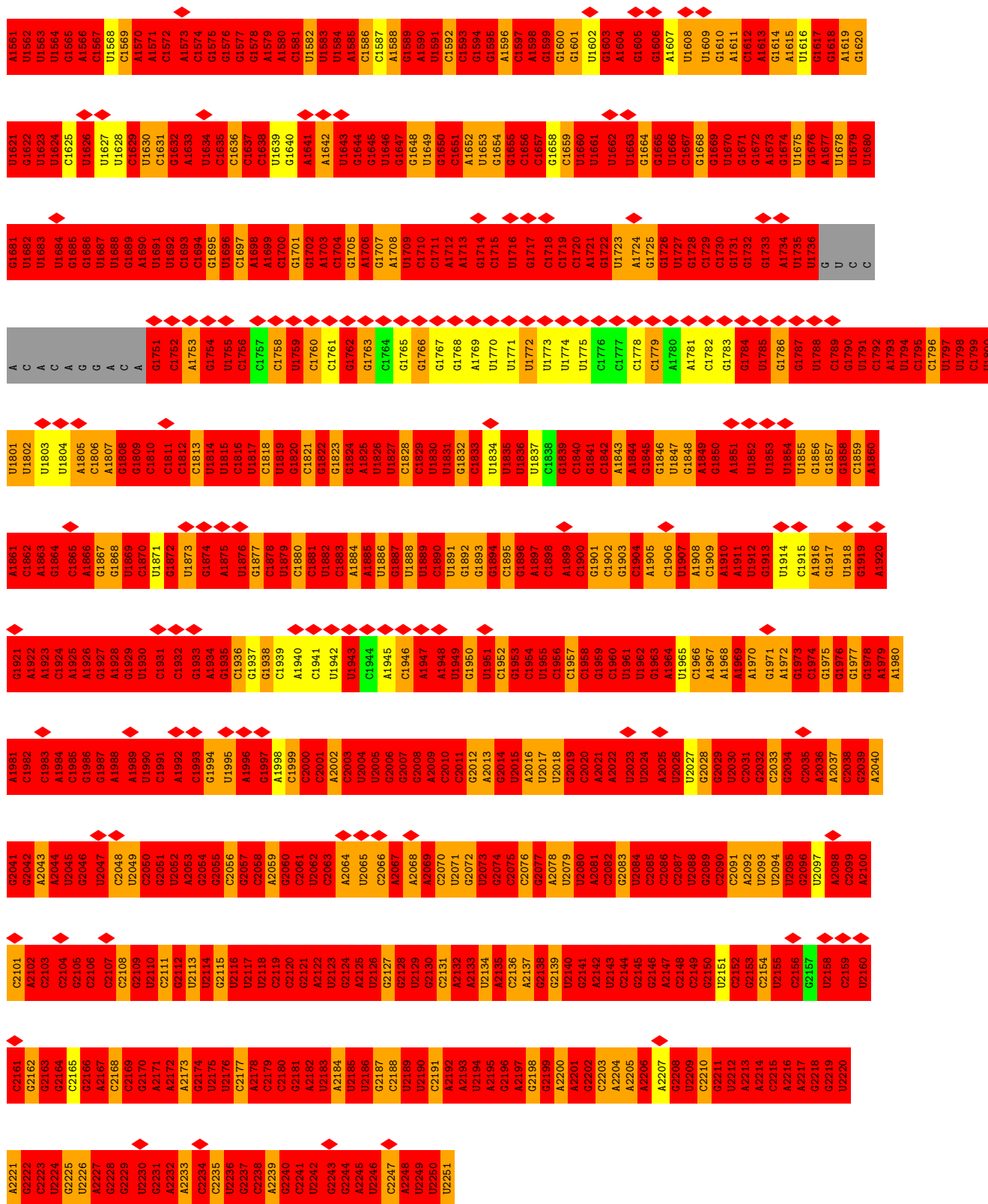
• Molecule 84: 60S RIBOSOMAL PROTEIN L9, PUTATIVE

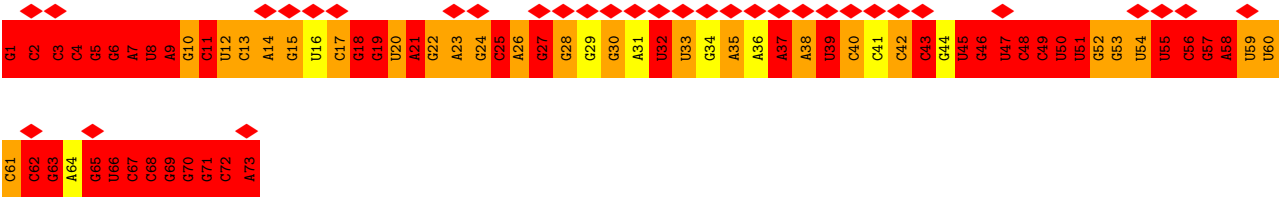


● Molecule 85: 18S RRNA OF THE SMALL RIBOSOMAL SUBUNIT



A1501	G1441	U1261	A1201	U1081	G1021	U961	C901	U841	G781
A1502	U1442	A1262	G1202	U1082	G1022	U962	A901	G842	G782
A1503	U1443	G1263	G1203	G1083	U1023	U963	G903	G843	G783
A1504	U1444	U1264	A1204	G1083	U1023	G964	U904	C844	G784
A1505	C1445	C1265	U1205	A1084	G1024	G965	C905	C845	C785
U1506	U1446	C1266	A1206	U1085	U1025	G966	U906	U846	C786
G1507	U1447	A1267	C1207	U1086	U1026	C967	G907	G847	U787
A1508	A1448	C1268	U1208	G1087	U1027	U968	C908	C848	G788
A1509	U1449	A1269	U1209	G1088	U1028	U969	C909	A849	A789
A1510	U1450	G1270	G1210	G1089	C1029	U970	G910	U850	U790
C1511	U1451	U1271	C1211	A1090	G1029	U971	A911	G851	C791
U1512	C1452	G1272	C1212	A1090	U1030	U972	C912	C852	A792
U1513	U1453	A1273	U1213	C1091	U1030	U973	U913	G853	C793
U1514	U1454	U1274	C1214	G1092	G1031	U974	U914	A854	A794
A1515	C1455	A1275	A1215	C1093	U1032	G975	G915	G855	C795
A1516	A1456	A1276	U1216	G1094	C1033	G976	A916	G856	U796
G1517	C1457	C1277	C1217	C1095	U1034	U977	A917	G857	C797
A1518	G1458	C1278	A1218	G1096	C1035	U978	U918	G858	A798
A1519	C1459	U1279	U1219	G1097	A1036	U979	G919	G859	G799
U1520	G1460	G1280	A1220	U1098	U1037	U980	A920	A860	A800
A1521	A1461	G1281	C1221	U1099	U1038	A981	C921	G861	U801
U1522	A1462	A1282	A1222	U1100	U1039	G982	A922	U862	A802
G1523	A1463	C1283	U1223	C1101	U1039	A983	C923	C863	C803
A1524	G1464	C1284	C1224	C1102	U1040	A984	A924	C864	A804
C1525	U1465	A1285	C1225	A1103	U1041	G985	G925	G865	A805
G1526	U1466	A1286	A1226	G1104	U1041	U986	C926	U866	G806
G1527	U1467	C1287	A1227	G1105	G1042	C987	A927	G867	A807
A1528	G1468	U1288	G1228	A1106	U1043	C988	U928	A868	A808
A1529	G1469	U1289	U1230	A1107	U1044	U989	G929	A869	A809
U1530	U1470	G1290	G1231	U1108	G1045	U990	G930	U870	A810
G1531	G1471	A1291	C1232	U1109	C1046	G991	C931	G871	A811
G1532	U1472	U1292	U1233	A1110	G1047	G992	A932	U872	C812
A1533	U1473	U1293	G1233	A1111	C1048	G993	U933	U873	C813
A1534	U1474	U1294	G1234	A1112	U1048	A994	A934	A874	G814
C1535	A1475	U1295	G1235	G1113	G1049	G995	A935	C875	G815
C1536	C1476	G1296	G1236	A1114	C1050	A996	C936	U876	A816
A1537	A1477	G1297	A1237	G1115	A1051	U997	A937	G877	G817
C1538	U1478	U1298	U1238	C1116	U1052	U998	A938	U878	A818
A1539	U1479	A1299	C1239	G1117	C1053	A999	A939	G879	C819
A1540	A1480	A1300	A1240	U1118	A1054	U1000	G940	A880	G819
U1541	U1481	C1301	A1241	A1119	U1054	G1001	C941	C881	C820
A1542	C1482	A1302	A1242	U1120	U1055	G1002	A942	C882	U821
C1543	G1483	U1303	G1243	U1121	C1056	G1003	A943	A883	U822
G1544	U1484	C1304	A1244	U1122	G1057	G1004	C944	A884	C823
U1545	G1485	A1305	U1245	C1123	C1058	C1005	A945	A885	G824
G1546	C1486	C1306	U1246	G1124	G1059	U1006	G946	A886	U825
G1547	U1487	U1307	G1247	G1125	C1060	G1007	C947	A887	C826
A1548	G1488	U1308	U1248	G1126	U1061	C1008	A948	A888	C827
G1549	U1489	G1309	U1249	G1127	U1062	G1009	U949	A889	U828
C1550	A1490	U1310	A1250	G1128	U1063	U1010	C950	U890	C829
G1551	U1491	G1311	G1251	A1129	C1064	G1011	C951	C891	A830
U1552	A1361	U1312	C1252	G1130	G1065	C1012	C952	C892	C831
G1553	U1363	U1313	A1253	A1131	U1066	C1013	C953	G893	U832
C1554	U1364	G1312	G1254	A1132	U1067	U1014	C954	A894	U833
G1555	A1366	C1313	A1255	C1133	G1068	U1015	C956	C895	U834
U1556	C1367	C1314	C1256	U1136	A1068	U1016	C957	C896	A836
U1557	G1368	C1315	C1257	U1137	U1069	G1017	A897	A897	C837
A1558	U1369	G1316	U1258	A1138	U1070	G1018	C958	G898	G838
G1499	G1370	U1317	U1259	U1139	U1071	U1019	C959	A899	C839
A1428	C1371	G1371	U1318	G1140	U1072	C1020	G960	G900	A840
U1429	C1372	G1318	U1319		U1073				
A1430	U1373	G1319			U1074				
U1431	U1374				U1075				
C1432	U1375				U1076				
C1433	U1376				U1077				
U1434	C1377				U1078				
C1435	A1379				U1079				
A1436	U1380								
G1437									
A1438									
A1439									
C1440									





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	164000	Depositor
Resolution determination method	Not provided	
CTF correction method	PHASE-FLIPPING	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	483783.781	Depositor
Minimum map value	-202702.703	Depositor
Average map value	7679.429	Depositor
Map value standard deviation	33729.660	Depositor
Recommended contour level	108000	Depositor
Map size ($\text{\AA}$)	391.31, 391.31, 391.31	wwPDB
Map dimensions	359, 359, 359	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.09, 1.09, 1.09	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	A0	1.88	45/1808 (2.5%)	2.39	110/2432 (4.5%)
2	A1	2.11	72/1973 (3.6%)	2.43	144/2657 (5.4%)
3	A2	1.67	22/1507 (1.5%)	2.28	73/2027 (3.6%)
4	A3	2.03	60/2026 (3.0%)	2.31	110/2699 (4.1%)
5	A4	2.09	60/1623 (3.7%)	2.61	132/2185 (6.0%)
6	A5	2.22	75/1574 (4.8%)	2.40	98/2100 (4.7%)
7	A6	2.19	67/1548 (4.3%)	2.42	93/2076 (4.5%)
8	A7	1.62	36/2471 (1.5%)	2.13	108/3368 (3.2%)
9	A8	1.47	2/337 (0.6%)	2.26	17/445 (3.8%)
10	A9	1.33	2/542 (0.4%)	1.91	17/722 (2.4%)
11	AC	2.24	70/1655 (4.2%)	2.30	86/2240 (3.8%)
12	AD	1.53	8/877 (0.9%)	1.93	20/1182 (1.7%)
13	AE	2.04	43/1324 (3.2%)	2.26	61/1771 (3.4%)
14	AF	1.07	0/946	1.79	19/1270 (1.5%)
15	AG	2.33	61/1170 (5.2%)	2.39	64/1567 (4.1%)
16	AH	1.91	20/937 (2.1%)	2.30	48/1263 (3.8%)
17	AI	1.32	3/1098 (0.3%)	2.11	39/1473 (2.6%)
18	AJ	2.06	39/1035 (3.8%)	2.32	55/1386 (4.0%)
19	AK	1.61	15/1211 (1.2%)	2.24	55/1625 (3.4%)
20	AL	1.97	36/1033 (3.5%)	2.55	87/1380 (6.3%)
21	AM	1.57	16/1247 (1.3%)	2.30	72/1666 (4.3%)
22	AO	1.61	15/1206 (1.2%)	2.38	77/1613 (4.8%)
23	AP	2.21	76/1766 (4.3%)	2.33	94/2383 (3.9%)
24	AQ	1.74	11/839 (1.3%)	2.25	39/1139 (3.4%)
25	AR	2.52	43/612 (7.0%)	2.83	63/835 (7.5%)
26	AS	1.88	29/1137 (2.6%)	2.21	63/1520 (4.1%)
27	AT	1.74	18/1065 (1.7%)	2.58	85/1411 (6.0%)
28	AU	1.54	5/681 (0.7%)	2.08	29/907 (3.2%)
29	AV	1.68	12/825 (1.5%)	2.40	52/1105 (4.7%)
30	AW	2.06	28/648 (4.3%)	2.34	33/868 (3.8%)
31	AX	1.66	18/1649 (1.1%)	2.15	59/2203 (2.7%)
32	AY	1.80	14/521 (2.7%)	2.31	30/685 (4.4%)
33	AZ	1.88	13/527 (2.5%)	2.16	18/702 (2.6%)
34	BA	2.68	3553/44057 (8.1%)	2.41	3746/68678 (5.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	BB	2.44	2231/34826 (6.4%)	2.17	2268/54269 (4.2%)
36	BC	2.85	400/4004 (10.0%)	2.44	355/6235 (5.7%)
37	BD	2.73	249/2830 (8.8%)	2.40	237/4410 (5.4%)
38	BE	2.61	360/4956 (7.3%)	2.59	492/7716 (6.4%)
39	BF	2.55	120/1691 (7.1%)	2.73	181/2627 (6.9%)
40	BG	2.92	447/4358 (10.3%)	2.42	385/6797 (5.7%)
41	BH	2.53	215/3201 (6.7%)	2.42	245/4987 (4.9%)
42	BI	2.34	89/1553 (5.7%)	2.59	129/2070 (6.2%)
43	BJ	1.00	0/1743	1.74	29/2339 (1.2%)
44	BK	2.19	79/1760 (4.5%)	2.36	111/2359 (4.7%)
45	BL	2.06	45/1385 (3.2%)	2.23	64/1851 (3.5%)
46	BM	0.90	0/1033	1.73	15/1394 (1.1%)
47	BN	4.31	97/1793 (5.4%)	2.76	193/2392 (8.1%)
48	BO	2.29	96/1655 (5.8%)	2.44	98/2214 (4.4%)
49	BP	2.37	85/1506 (5.6%)	2.45	99/2014 (4.9%)
50	BQ	2.33	79/1755 (4.5%)	2.30	85/2346 (3.6%)
51	BR	2.14	62/1270 (4.9%)	2.56	93/1705 (5.5%)
52	BS	2.09	59/1508 (3.9%)	2.58	121/2028 (6.0%)
53	BT	2.33	98/1689 (5.8%)	2.32	78/2232 (3.5%)
54	BU	2.05	41/1290 (3.2%)	2.30	64/1734 (3.7%)
55	BV	1.32	3/878 (0.3%)	2.13	37/1169 (3.2%)
56	BW	2.25	51/1059 (4.8%)	2.41	68/1424 (4.8%)
57	BX	2.39	65/1007 (6.5%)	2.52	84/1353 (6.2%)
58	BY	1.90	25/857 (2.9%)	2.19	41/1150 (3.6%)
59	BZ	2.31	54/1021 (5.3%)	2.66	79/1362 (5.8%)
60	Ba	2.14	44/1111 (4.0%)	2.37	67/1479 (4.5%)
61	Bb	2.06	38/1165 (3.3%)	2.52	88/1554 (5.7%)
62	Bc	2.81	49/1145 (4.3%)	2.94	147/1528 (9.6%)
63	Bd	1.78	15/582 (2.6%)	2.73	58/777 (7.5%)
64	Be	2.29	70/1416 (4.9%)	2.48	98/1905 (5.1%)
65	Bf	2.23	157/3387 (4.6%)	2.51	231/4548 (5.1%)
66	Bg	2.83	68/745 (9.1%)	2.69	63/1005 (6.3%)
67	Bh	1.97	42/1551 (2.7%)	2.63	127/2059 (6.2%)
68	Bi	2.11	43/1076 (4.0%)	2.40	75/1439 (5.2%)
69	Bj	1.84	35/1312 (2.7%)	2.36	71/1743 (4.1%)
70	Bk	2.31	41/726 (5.6%)	2.48	49/957 (5.1%)
71	Bl	2.17	37/958 (3.9%)	2.49	67/1290 (5.2%)
72	Bm	2.45	63/859 (7.3%)	2.33	49/1141 (4.3%)
73	Bn	2.46	53/713 (7.4%)	2.44	48/949 (5.1%)
74	Bo	2.68	57/727 (7.8%)	2.31	36/968 (3.7%)
75	Bp	2.40	43/666 (6.5%)	2.49	46/885 (5.2%)
76	Bq	1.92	8/471 (1.7%)	2.15	19/626 (3.0%)
77	Br	2.29	155/2937 (5.3%)	2.52	226/3943 (5.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	Bs	2.10	18/433 (4.2%)	2.25	20/572 (3.5%)
79	Bt	2.09	32/883 (3.6%)	2.35	54/1170 (4.6%)
80	Bu	2.02	85/2397 (3.5%)	2.40	138/3219 (4.3%)
81	Bv	2.01	48/1242 (3.9%)	2.36	81/1667 (4.9%)
82	Bw	2.24	91/2105 (4.3%)	2.39	138/2823 (4.9%)
83	Bx	2.32	100/1936 (5.2%)	2.42	102/2603 (3.9%)
84	By	2.15	69/1561 (4.4%)	2.49	115/2098 (5.5%)
85	AA	2.29	2855/52940 (5.4%)	2.27	3947/82489 (4.8%)
86	AB	1.66	26/1740 (1.5%)	1.96	89/2712 (3.3%)
All	All	2.36	13979/250887 (5.6%)	2.34	17796/369909 (4.8%)

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	A0	0	19
2	A1	0	18
3	A2	0	11
4	A3	0	23
5	A4	0	27
6	A5	0	23
7	A6	0	26
8	A7	0	17
9	A8	0	4
10	A9	0	4
11	AC	0	21
12	AD	0	10
13	AE	0	25
14	AF	0	6
15	AG	0	17
16	AH	0	8
17	AI	0	10
18	AJ	0	11
19	AK	0	20
20	AL	0	6
21	AM	0	18
22	AO	0	17
23	AP	0	14
24	AQ	0	7
25	AR	0	12

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Mol	Chain	#Chirality outliers	#Planarity outliers
26	AS	0	7
27	AT	0	27
28	AU	0	7
29	AV	0	13
30	AW	0	13
31	AX	0	10
32	AY	0	13
33	AZ	0	3
34	BA	0	1404
35	BB	0	967
36	BC	0	128
37	BD	0	89
38	BE	0	169
39	BF	0	61
40	BG	0	144
41	BH	0	87
42	BI	0	19
43	BJ	0	7
44	BK	0	26
45	BL	0	15
47	BN	1	31
48	BO	0	21
49	BP	0	24
50	BQ	0	28
51	BR	0	21
52	BS	0	21
53	BT	0	24
54	BU	0	21
55	BV	0	6
56	BW	0	10
57	BX	0	7
58	BY	0	15
59	BZ	0	12
60	Ba	0	20
61	Bb	0	15
62	Bc	0	27
63	Bd	0	10
64	Be	0	21
65	Bf	0	48
66	Bg	0	8
67	Bh	0	23
68	Bi	0	13

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Mol	Chain	#Chirality outliers	#Planarity outliers
69	Bj	1	23
70	Bk	0	12
71	Bl	0	23
72	Bm	0	16
73	Bn	0	14
74	Bo	0	12
75	Bp	0	6
76	Bq	0	9
77	Br	0	46
78	Bs	0	5
79	Bt	0	13
80	Bu	0	34
81	Bv	0	22
82	Bw	0	32
83	Bx	0	19
84	By	1	27
85	AA	0	1567
86	AB	0	45
All	All	3	5934

The worst 5 of 13979 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	BN	7	ALA	CA-C	154.18	3.59	1.52
62	Bc	78	LYS	CD-CE	57.86	3.26	1.52
34	BA	546	U	O3'-P	33.85	2.12	1.61
85	AA	469	G	C5-C4	28.05	1.94	1.38
34	BA	743	A	N9-C4	22.26	1.82	1.37

The worst 5 of 17796 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	BF	32	G	P-O3'-C3'	32.58	169.07	120.20
34	BA	692	U	P-O3'-C3'	30.17	165.46	120.20
34	BA	517	A	P-O5'-C5'	29.31	164.87	120.90
38	BE	175	U	P-O3'-C3'	28.24	162.56	120.20
34	BA	557	U	C4'-C3'-C2'	-27.90	74.70	102.60

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
47	BN	66	PRO	CA

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Mol	Chain	Res	Type	Atom
69	Bj	5	ARG	CA
84	By	7	ASP	CA

5 of 5934 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A0	103	HIS	Sidechain
1	A0	41	ARG	Sidechain
1	A0	43	PHE	Sidechain
1	A0	64	ARG	Sidechain
1	A0	83	TYR	Sidechain

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	A0	1782	0	1855	90	0
2	A1	1940	0	2043	95	0
3	A2	1484	0	1547	87	0
4	A3	2003	0	2138	161	0
5	A4	1592	0	1688	145	0
6	A5	1551	0	1660	87	0
7	A6	1518	0	1571	106	0
8	A7	2412	0	2334	82	0
9	A8	334	0	343	13	0
10	A9	530	0	527	18	0
11	AC	1620	0	1660	90	0
12	AD	853	0	857	38	0
13	AE	1300	0	1359	77	0
14	AF	940	0	962	6	0
15	AG	1148	0	1226	89	0
16	AH	922	0	923	47	0
17	AI	1074	0	1097	49	0
18	AJ	1018	0	1050	63	0
19	AK	1190	0	1254	35	0
20	AL	1021	0	1096	50	0
21	AM	1229	0	1291	94	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	AO	1181	0	1240	52	0
23	AP	1731	0	1782	141	0
24	AQ	827	0	883	41	0
25	AR	603	0	593	56	0
26	AS	1116	0	1170	42	0
27	AT	1050	0	1141	102	0
28	AU	673	0	735	26	0
29	AV	809	0	841	38	0
30	AW	636	0	648	34	0
31	AX	1628	0	1695	45	0
32	AY	514	0	571	55	0
33	AZ	526	0	550	26	0
34	BA	39395	0	19108	6454	0
35	BB	31164	0	15283	4032	0
36	BC	3584	0	1759	750	0
37	BD	2533	0	1235	422	0
38	BE	4441	0	2194	750	0
39	BF	1521	0	773	253	0
40	BG	3896	0	1874	666	0
41	BH	2867	0	1408	507	0
42	BI	1527	0	1646	122	0
43	BJ	1717	0	1815	9	0
44	BK	1725	0	1797	143	0
45	BL	1363	0	1402	86	0
46	BM	1022	0	1109	3	0
47	BN	1762	0	1869	242	0
48	BO	1627	0	1761	102	0
49	BP	1484	0	1601	148	0
50	BQ	1716	0	1796	97	0
51	BR	1245	0	1301	82	0
52	BS	1473	0	1512	98	0
53	BT	1672	0	1799	142	0
54	BU	1260	0	1315	79	0
55	BV	863	0	908	53	0
56	BW	1042	0	1106	60	0
57	BX	990	0	1059	75	0
58	BY	836	0	863	138	0
59	BZ	1008	0	1088	56	0
60	Ba	1091	0	1162	76	0
61	Bb	1137	0	1174	94	0
62	Bc	1129	0	1214	130	0
63	Bd	571	0	595	82	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	Be	1390	0	1444	97	0
65	Bf	3317	0	3451	225	0
66	Bg	735	0	754	61	0
67	Bh	1526	0	1654	120	0
68	Bi	1054	0	1113	50	0
69	Bj	1293	0	1420	105	0
70	Bk	719	0	811	66	0
71	Bl	936	0	968	75	0
72	Bm	849	0	934	55	0
73	Bn	699	0	718	61	0
74	Bo	715	0	743	49	0
75	Bp	656	0	717	52	0
76	Bq	457	0	495	34	0
77	Br	2883	0	3011	197	0
78	Bs	427	0	465	16	0
79	Bt	866	0	922	72	0
80	Bu	2354	0	2425	165	0
81	Bv	1222	0	1318	76	0
82	Bw	2066	0	2180	148	0
83	Bx	1908	0	2047	123	0
84	By	1540	0	1608	98	0
85	AA	47370	0	23451	5919	0
86	AB	1557	0	775	109	0
All	All	232955	0	167280	23332	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 59.

The worst 5 of 23332 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)
34:BA:214:A:C6	34:BA:214:A:C5	1.79	1.69
21:AM:13:ILE:HG23	45:BL:123:TYR:CE2	1.20	1.68
34:BA:547:C:C4'	34:BA:547:C:C3'	1.78	1.59
21:AM:13:ILE:CG2	45:BL:123:TYR:HE2	1.06	1.57
34:BA:214:A:N3	34:BA:214:A:C2	1.70	1.56

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A0	217/256 (85%)	180 (83%)	22 (10%)	15 (7%)	1	11
2	A1	246/273 (90%)	189 (77%)	38 (15%)	19 (8%)	1	9
3	A2	185/190 (97%)	159 (86%)	17 (9%)	9 (5%)	1	15
4	A3	248/250 (99%)	204 (82%)	24 (10%)	20 (8%)	1	9
5	A4	190/202 (94%)	148 (78%)	24 (13%)	18 (10%)	0	8
6	A5	191/220 (87%)	158 (83%)	18 (9%)	15 (8%)	1	9
7	A6	185/190 (97%)	135 (73%)	30 (16%)	20 (11%)	0	6
8	A7	313/318 (98%)	256 (82%)	39 (12%)	18 (6%)	1	13
9	A8	40/57 (70%)	34 (85%)	3 (8%)	3 (8%)	1	10
10	A9	64/153 (42%)	50 (78%)	9 (14%)	5 (8%)	1	9
11	AC	202/277 (73%)	162 (80%)	25 (12%)	15 (7%)	1	10
12	AD	102/172 (59%)	79 (78%)	9 (9%)	14 (14%)	0	3
13	AE	158/174 (91%)	126 (80%)	12 (8%)	20 (13%)	0	4
14	AF	119/144 (83%)	105 (88%)	11 (9%)	3 (2%)	4	25
15	AG	139/151 (92%)	120 (86%)	12 (9%)	7 (5%)	1	15
16	AH	124/144 (86%)	99 (80%)	14 (11%)	11 (9%)	0	8
17	AI	132/152 (87%)	100 (76%)	21 (16%)	11 (8%)	0	9
18	AJ	127/130 (98%)	114 (90%)	7 (6%)	6 (5%)	2	16
19	AK	146/149 (98%)	118 (81%)	18 (12%)	10 (7%)	1	11
20	AL	125/142 (88%)	94 (75%)	19 (15%)	12 (10%)	0	7
21	AM	151/153 (99%)	114 (76%)	16 (11%)	21 (14%)	0	3
22	AO	147/167 (88%)	128 (87%)	10 (7%)	9 (6%)	1	12
23	AP	222/266 (84%)	171 (77%)	29 (13%)	22 (10%)	0	7
24	AQ	103/117 (88%)	86 (84%)	10 (10%)	7 (7%)	1	11
25	AR	79/194 (41%)	59 (75%)	12 (15%)	8 (10%)	0	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	AS	140/143 (98%)	111 (79%)	18 (13%)	11 (8%)	1	9
27	AT	129/137 (94%)	100 (78%)	15 (12%)	14 (11%)	0	5
28	AU	84/113 (74%)	66 (79%)	12 (14%)	6 (7%)	1	10
29	AV	99/111 (89%)	64 (65%)	20 (20%)	15 (15%)	0	3
30	AW	81/86 (94%)	61 (75%)	11 (14%)	9 (11%)	0	5
31	AX	204/214 (95%)	176 (86%)	17 (8%)	11 (5%)	1	14
32	AY	63/66 (96%)	46 (73%)	8 (13%)	9 (14%)	0	3
33	AZ	66/103 (64%)	56 (85%)	7 (11%)	3 (4%)	2	16
42	BI	190/193 (98%)	126 (66%)	37 (20%)	27 (14%)	0	3
43	BJ	212/214 (99%)	186 (88%)	20 (9%)	6 (3%)	4	24
44	BK	210/213 (99%)	161 (77%)	26 (12%)	23 (11%)	0	5
45	BL	168/194 (87%)	134 (80%)	21 (12%)	13 (8%)	1	9
46	BM	137/164 (84%)	103 (75%)	25 (18%)	9 (7%)	1	11
47	BN	214/218 (98%)	158 (74%)	20 (9%)	36 (17%)	0	2
48	BO	199/222 (90%)	164 (82%)	21 (11%)	14 (7%)	1	10
49	BP	182/189 (96%)	149 (82%)	19 (10%)	14 (8%)	1	9
50	BQ	201/221 (91%)	160 (80%)	21 (10%)	20 (10%)	0	7
51	BR	153/166 (92%)	121 (79%)	21 (14%)	11 (7%)	1	10
52	BS	177/179 (99%)	133 (75%)	15 (8%)	29 (16%)	0	2
53	BT	198/260 (76%)	168 (85%)	20 (10%)	10 (5%)	1	14
54	BU	156/159 (98%)	118 (76%)	19 (12%)	19 (12%)	0	4
55	BV	102/130 (78%)	84 (82%)	13 (13%)	5 (5%)	1	15
56	BW	136/139 (98%)	103 (76%)	18 (13%)	15 (11%)	0	5
57	BX	119/164 (73%)	97 (82%)	9 (8%)	13 (11%)	0	5
58	BY	98/125 (78%)	81 (83%)	9 (9%)	8 (8%)	0	9
59	BZ	123/143 (86%)	104 (85%)	12 (10%)	7 (6%)	1	13
60	Ba	130/133 (98%)	93 (72%)	21 (16%)	16 (12%)	0	4
61	Bb	142/145 (98%)	108 (76%)	19 (13%)	15 (11%)	0	6
62	Bc	139/146 (95%)	103 (74%)	18 (13%)	18 (13%)	0	4
63	Bd	68/71 (96%)	50 (74%)	8 (12%)	10 (15%)	0	3
64	Be	184/260 (71%)	135 (73%)	32 (17%)	17 (9%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	Bf	412/429 (96%)	296 (72%)	66 (16%)	50 (12%)	0	4
66	Bg	94/105 (90%)	88 (94%)	5 (5%)	1 (1%)	11	45
67	Bh	186/188 (99%)	155 (83%)	13 (7%)	18 (10%)	0	7
68	Bi	127/132 (96%)	98 (77%)	18 (14%)	11 (9%)	0	8
69	Bj	160/170 (94%)	123 (77%)	22 (14%)	15 (9%)	0	8
70	Bk	82/127 (65%)	56 (68%)	14 (17%)	12 (15%)	0	3
71	Bl	114/149 (76%)	84 (74%)	10 (9%)	20 (18%)	0	2
72	Bm	105/109 (96%)	79 (75%)	8 (8%)	18 (17%)	0	2
73	Bn	81/84 (96%)	56 (69%)	15 (18%)	10 (12%)	0	4
74	Bo	90/93 (97%)	71 (79%)	6 (7%)	13 (14%)	0	3
75	Bp	79/82 (96%)	59 (75%)	10 (13%)	10 (13%)	0	4
76	Bq	48/51 (94%)	34 (71%)	6 (12%)	8 (17%)	0	2
77	Br	366/374 (98%)	274 (75%)	56 (15%)	36 (10%)	0	7
78	Bs	50/128 (39%)	44 (88%)	4 (8%)	2 (4%)	2	18
79	Bt	103/106 (97%)	75 (73%)	16 (16%)	12 (12%)	0	4
80	Bu	297/308 (96%)	216 (73%)	46 (16%)	35 (12%)	0	4
81	Bv	154/192 (80%)	114 (74%)	25 (16%)	15 (10%)	0	7
82	Bw	255/257 (99%)	200 (78%)	33 (13%)	22 (9%)	0	8
83	Bx	238/276 (86%)	188 (79%)	26 (11%)	24 (10%)	0	7
84	By	187/189 (99%)	155 (83%)	15 (8%)	17 (9%)	0	8
All	All	11687/13211 (88%)	9172 (78%)	1415 (12%)	1100 (9%)	1	8

5 of 1100 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A0	37	ASN
1	A0	119	TRP
1	A0	145	THR
1	A0	212	LEU
1	A0	225	PHE

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A0	189/218 (87%)	158 (84%)	31 (16%)	2	11
2	A1	209/231 (90%)	167 (80%)	42 (20%)	1	8
3	A2	158/160 (99%)	132 (84%)	26 (16%)	2	11
4	A3	207/207 (100%)	174 (84%)	33 (16%)	2	12
5	A4	176/187 (94%)	145 (82%)	31 (18%)	2	10
6	A5	158/180 (88%)	135 (85%)	23 (15%)	3	13
7	A6	162/166 (98%)	137 (85%)	25 (15%)	2	12
8	A7	264/267 (99%)	231 (88%)	33 (12%)	4	17
9	A8	36/49 (74%)	31 (86%)	5 (14%)	3	14
10	A9	57/126 (45%)	52 (91%)	5 (9%)	9	28
11	AC	179/243 (74%)	145 (81%)	34 (19%)	1	8
12	AD	92/131 (70%)	80 (87%)	12 (13%)	4	16
13	AE	143/156 (92%)	121 (85%)	22 (15%)	2	12
14	AF	102/120 (85%)	98 (96%)	4 (4%)	28	49
15	AG	124/131 (95%)	107 (86%)	17 (14%)	3	14
16	AH	95/112 (85%)	82 (86%)	13 (14%)	3	14
17	AI	110/128 (86%)	102 (93%)	8 (7%)	13	34
18	AJ	108/109 (99%)	87 (81%)	21 (19%)	1	8
19	AK	123/124 (99%)	106 (86%)	17 (14%)	3	14
20	AL	111/122 (91%)	98 (88%)	13 (12%)	5	18
21	AM	133/133 (100%)	115 (86%)	18 (14%)	4	15
22	AO	123/137 (90%)	107 (87%)	16 (13%)	4	16
23	AP	185/204 (91%)	154 (83%)	31 (17%)	2	10
24	AQ	94/104 (90%)	80 (85%)	14 (15%)	3	13
25	AR	66/150 (44%)	52 (79%)	14 (21%)	1	6
26	AS	117/118 (99%)	101 (86%)	16 (14%)	3	14
27	AT	110/116 (95%)	83 (76%)	27 (24%)	1	4
28	AU	73/94 (78%)	62 (85%)	11 (15%)	3	13
29	AV	87/97 (90%)	74 (85%)	13 (15%)	3	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	AW	71/75 (95%)	57 (80%)	14 (20%)	1	8
31	AX	173/180 (96%)	152 (88%)	21 (12%)	5	17
32	AY	52/53 (98%)	41 (79%)	11 (21%)	1	6
33	AZ	57/84 (68%)	53 (93%)	4 (7%)	14	35
42	BI	164/165 (99%)	143 (87%)	21 (13%)	4	16
43	BJ	201/201 (100%)	192 (96%)	9 (4%)	24	46
44	BK	184/185 (100%)	155 (84%)	29 (16%)	2	12
45	BL	146/167 (87%)	118 (81%)	28 (19%)	1	8
46	BM	114/137 (83%)	109 (96%)	5 (4%)	25	47
47	BN	185/188 (98%)	147 (80%)	38 (20%)	1	7
48	BO	175/195 (90%)	148 (85%)	27 (15%)	2	12
49	BP	156/160 (98%)	140 (90%)	16 (10%)	7	23
50	BQ	176/193 (91%)	145 (82%)	31 (18%)	2	10
51	BR	132/144 (92%)	107 (81%)	25 (19%)	1	8
52	BS	160/160 (100%)	129 (81%)	31 (19%)	1	8
53	BT	170/198 (86%)	142 (84%)	28 (16%)	2	11
54	BU	133/134 (99%)	114 (86%)	19 (14%)	3	13
55	BV	95/116 (82%)	88 (93%)	7 (7%)	13	33
56	BW	107/108 (99%)	85 (79%)	22 (21%)	1	7
57	BX	108/136 (79%)	90 (83%)	18 (17%)	2	11
58	BY	85/102 (83%)	78 (92%)	7 (8%)	10	30
59	BZ	110/125 (88%)	94 (86%)	16 (14%)	3	13
60	Ba	116/117 (99%)	97 (84%)	19 (16%)	2	11
61	Bb	115/116 (99%)	96 (84%)	19 (16%)	2	11
62	Bc	124/130 (95%)	93 (75%)	31 (25%)	0	4
63	Bd	58/59 (98%)	50 (86%)	8 (14%)	3	14
64	Be	145/204 (71%)	121 (83%)	24 (17%)	2	11
65	Bf	349/360 (97%)	299 (86%)	50 (14%)	3	13
66	Bg	84/92 (91%)	69 (82%)	15 (18%)	2	9
67	Bh	162/162 (100%)	133 (82%)	29 (18%)	2	9
68	Bi	113/117 (97%)	97 (86%)	16 (14%)	3	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Bj	130/137 (95%)	109 (84%)	21 (16%)	2	11
70	Bk	75/114 (66%)	61 (81%)	14 (19%)	1	9
71	Bl	97/126 (77%)	78 (80%)	19 (20%)	1	8
72	Bm	87/90 (97%)	73 (84%)	14 (16%)	2	11
73	Bn	70/71 (99%)	56 (80%)	14 (20%)	1	7
74	Bo	74/76 (97%)	64 (86%)	10 (14%)	4	15
75	Bp	76/77 (99%)	67 (88%)	9 (12%)	5	18
76	Bq	46/47 (98%)	37 (80%)	9 (20%)	1	8
77	Br	304/310 (98%)	252 (83%)	52 (17%)	2	10
78	Bs	46/111 (41%)	40 (87%)	6 (13%)	4	16
79	Bt	94/95 (99%)	81 (86%)	13 (14%)	3	14
80	Bu	238/247 (96%)	196 (82%)	42 (18%)	2	10
81	Bv	132/160 (82%)	110 (83%)	22 (17%)	2	11
82	Bw	213/213 (100%)	182 (85%)	31 (15%)	3	13
83	Bx	203/229 (89%)	172 (85%)	31 (15%)	3	12
84	By	172/172 (100%)	138 (80%)	34 (20%)	1	8
All	All	10068/11158 (90%)	8514 (85%)	1554 (15%)	5	12

5 of 1554 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	BU	97	ARG
65	Bf	377	ASN
56	BW	94	VAL
54	BU	88	ARG
62	Bc	8	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 205 such sidechains are listed below:

Mol	Chain	Res	Type
51	BR	154	GLN
64	Be	216	HIS
84	By	8	GLN
52	BS	145	HIS
58	BY	17	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	BA	1846/1847 (99%)	629 (34%)	225 (12%)
35	BB	1464/1465 (99%)	464 (31%)	143 (9%)
36	BC	169/169 (100%)	48 (28%)	20 (11%)
37	BD	118/119 (99%)	31 (26%)	9 (7%)
38	BE	209/210 (99%)	81 (38%)	27 (12%)
39	BF	73/73 (100%)	49 (67%)	23 (31%)
40	BG	181/182 (99%)	40 (22%)	8 (4%)
41	BH	134/135 (99%)	51 (38%)	16 (11%)
85	AA	2226/2251 (98%)	781 (35%)	312 (14%)
86	AB	72/73 (98%)	30 (41%)	7 (9%)
All	All	6492/6524 (99%)	2204 (33%)	790 (12%)

5 of 2204 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	BA	11	U
34	BA	13	U
34	BA	22	C
34	BA	23	A
34	BA	37	A

5 of 790 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
41	BH	62	C
85	AA	687	G
85	AA	33	U
41	BH	42	U
85	AA	326	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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
34	BA	3
40	BG	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BA	546:U	O3'	547:C	P	2.11
1	BA	557:U	O3'	558:C	P	1.87
1	BA	547:C	O3'	548:G	P	1.78
1	BG	24:A	O3'	25:G	P	1.39
1	BG	9:G	O3'	10:U	P	1.37

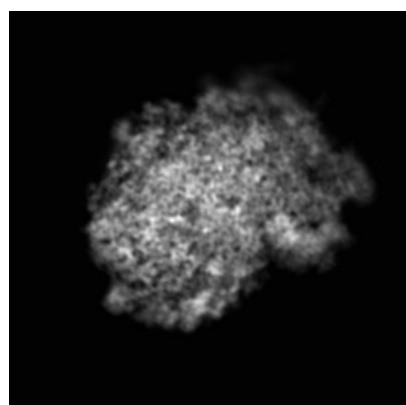
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2239. These allow visual inspection of the internal detail of the map and identification of artifacts.

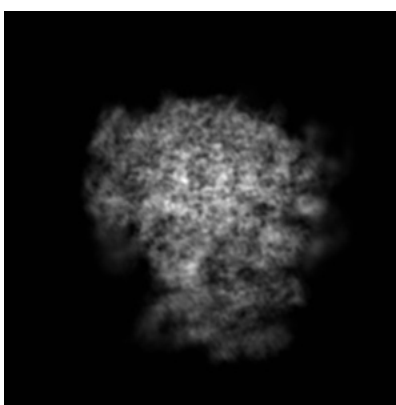
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

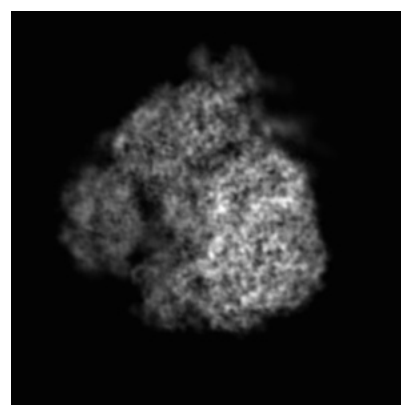
6.1.1 Primary map



X



Y

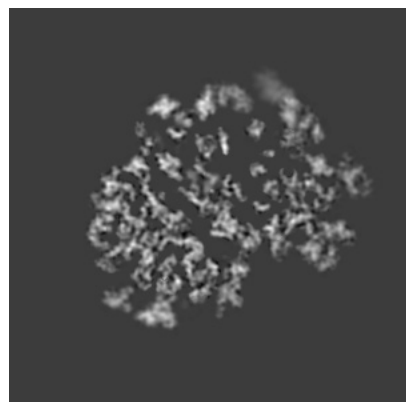


Z

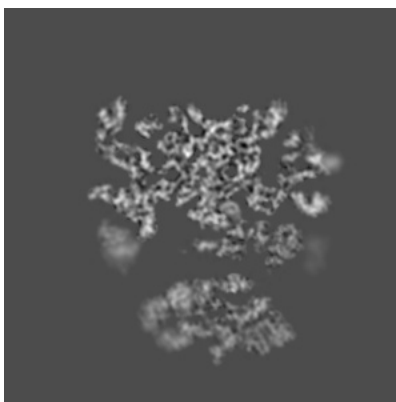
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

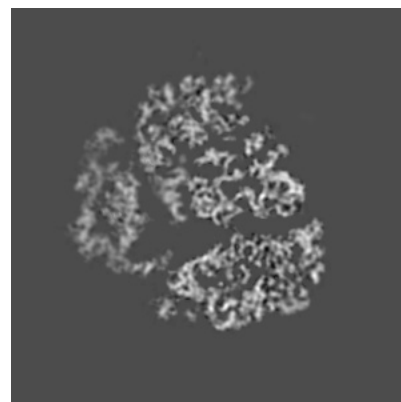
6.2.1 Primary map



X Index: 179



Y Index: 179

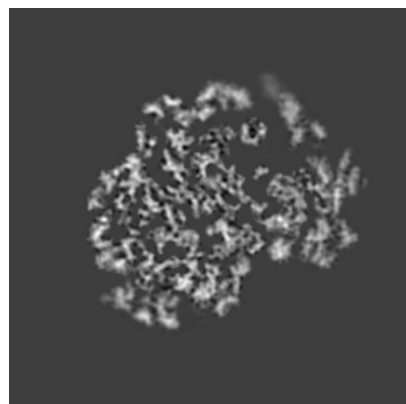


Z Index: 179

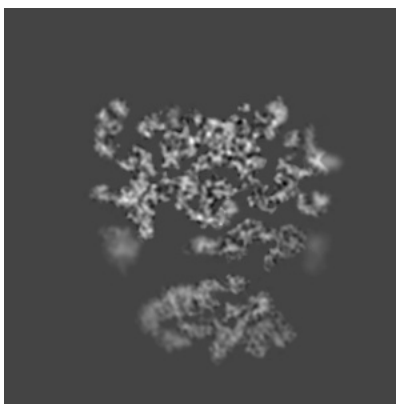
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

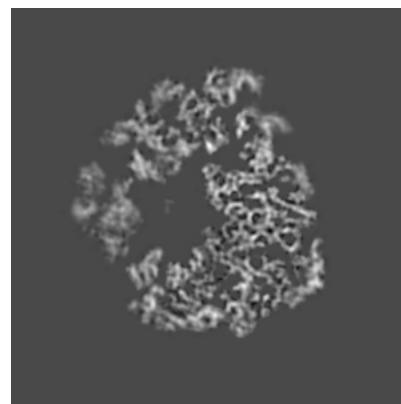
6.3.1 Primary map



X Index: 184



Y Index: 182

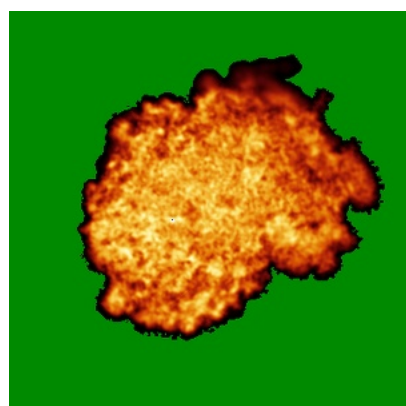


Z Index: 161

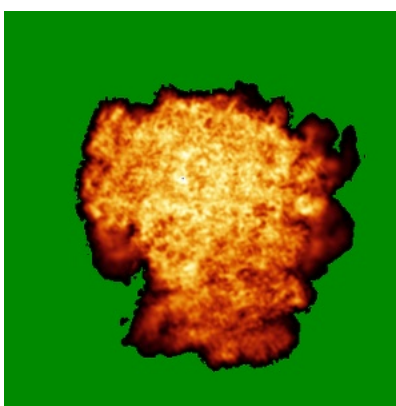
The images above show the largest variance slices of the map in three orthogonal directions.

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

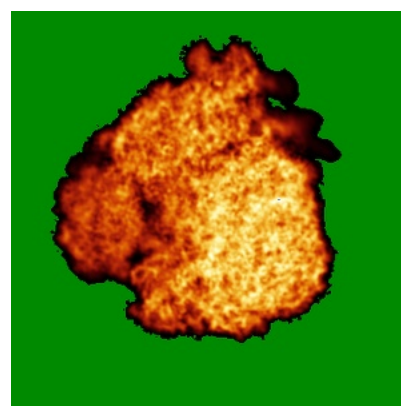
6.4.1 Primary map



X



Y

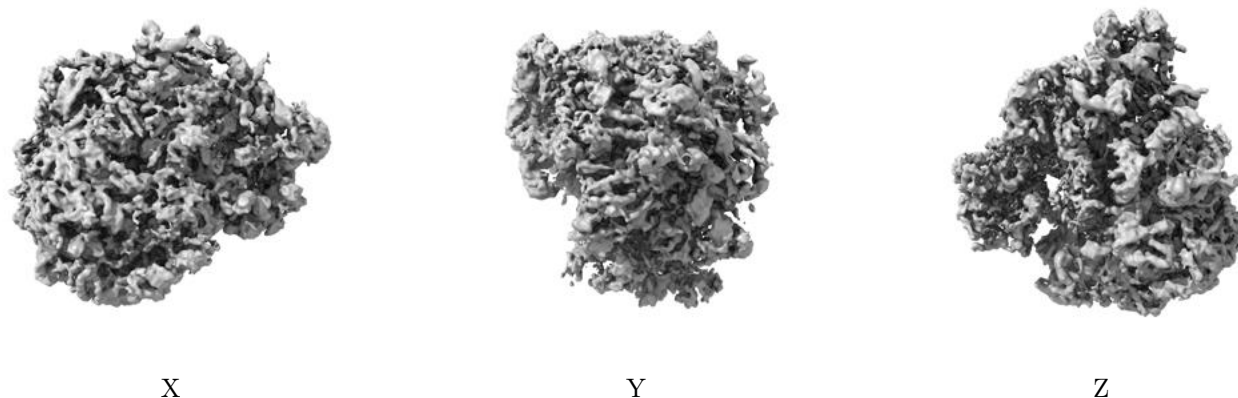


Z

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 108000.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

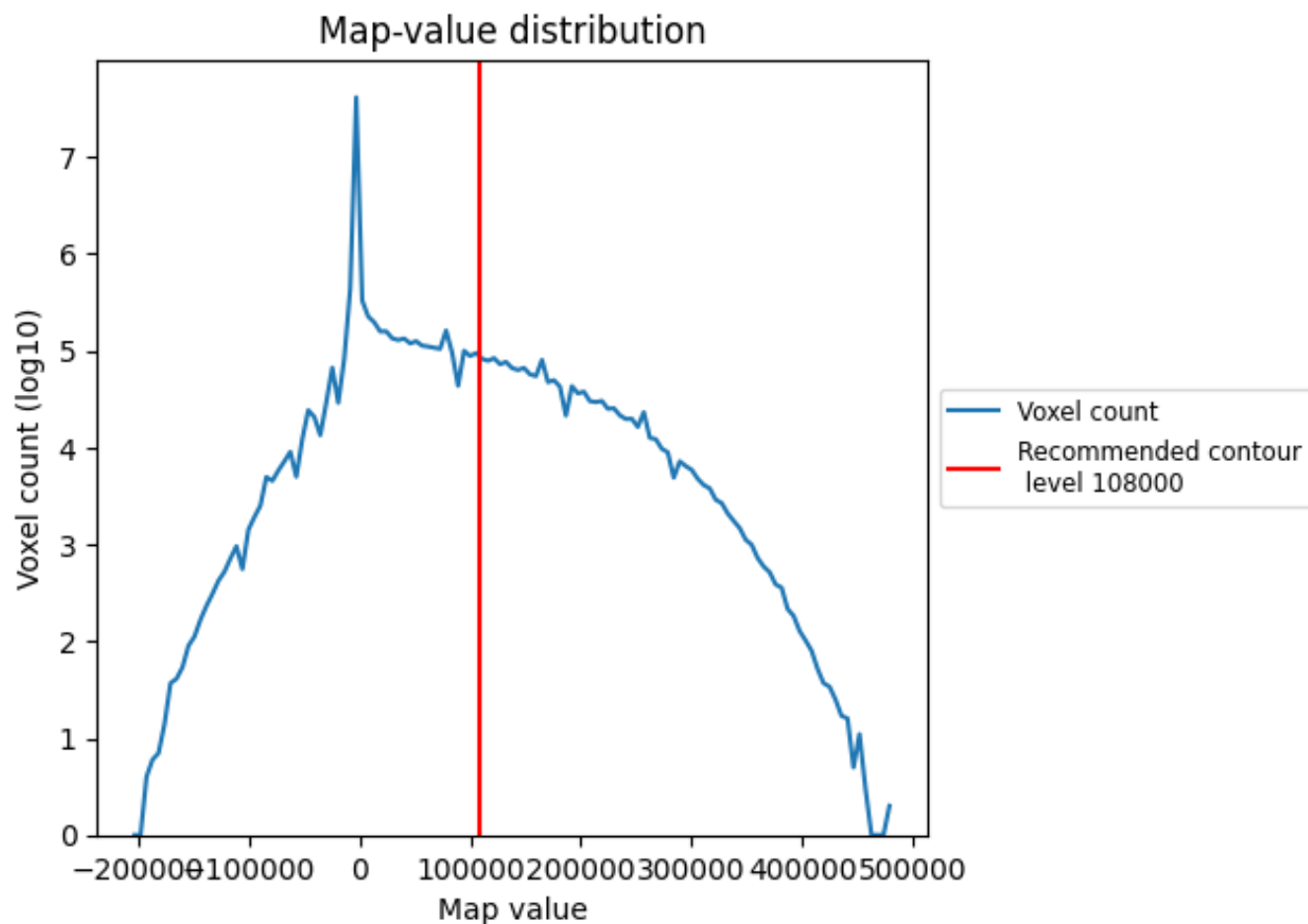
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

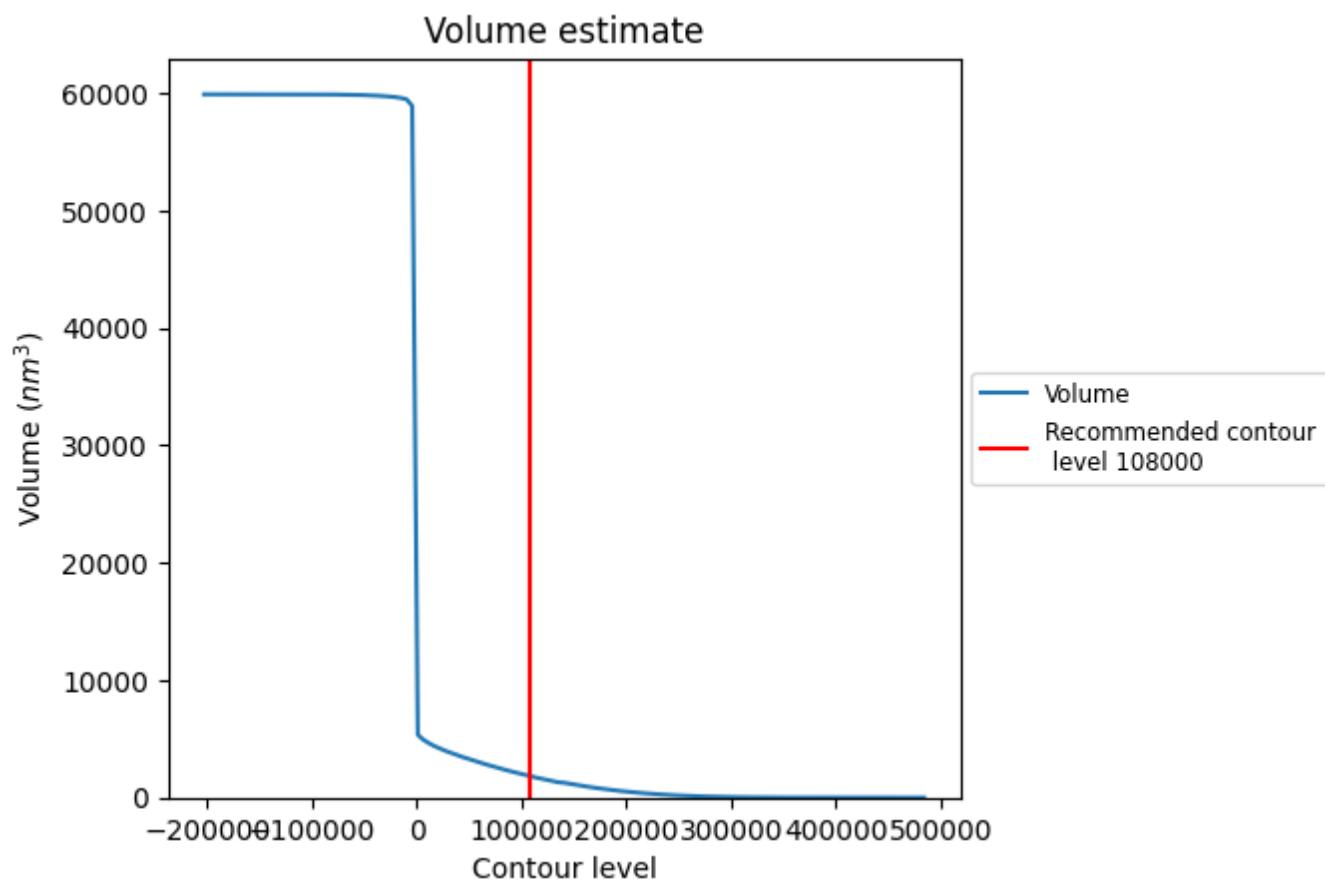
This section contains the results of statistical analysis of the map.

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.

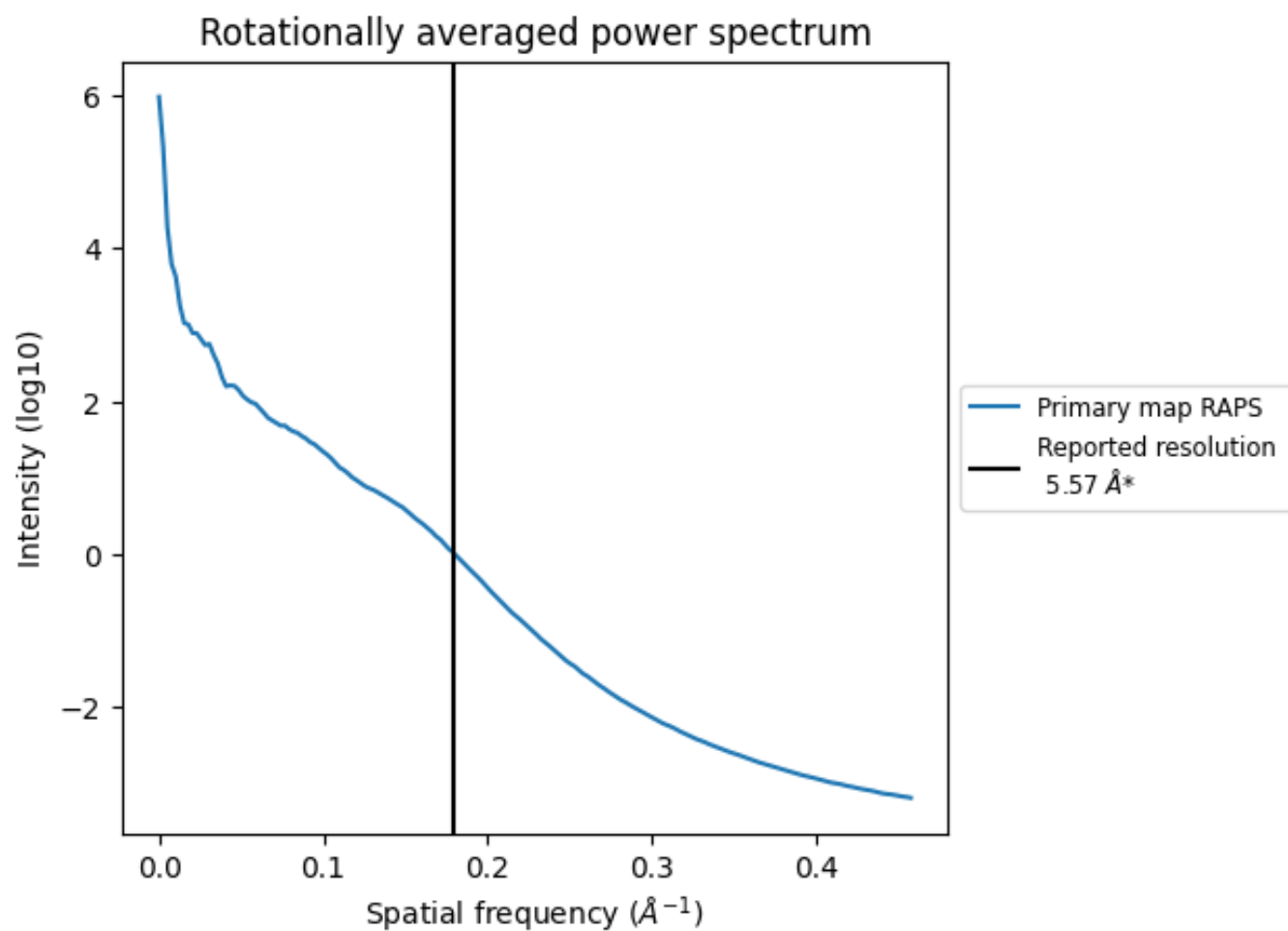
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1820 nm³; this corresponds to an approximate mass of 1644 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

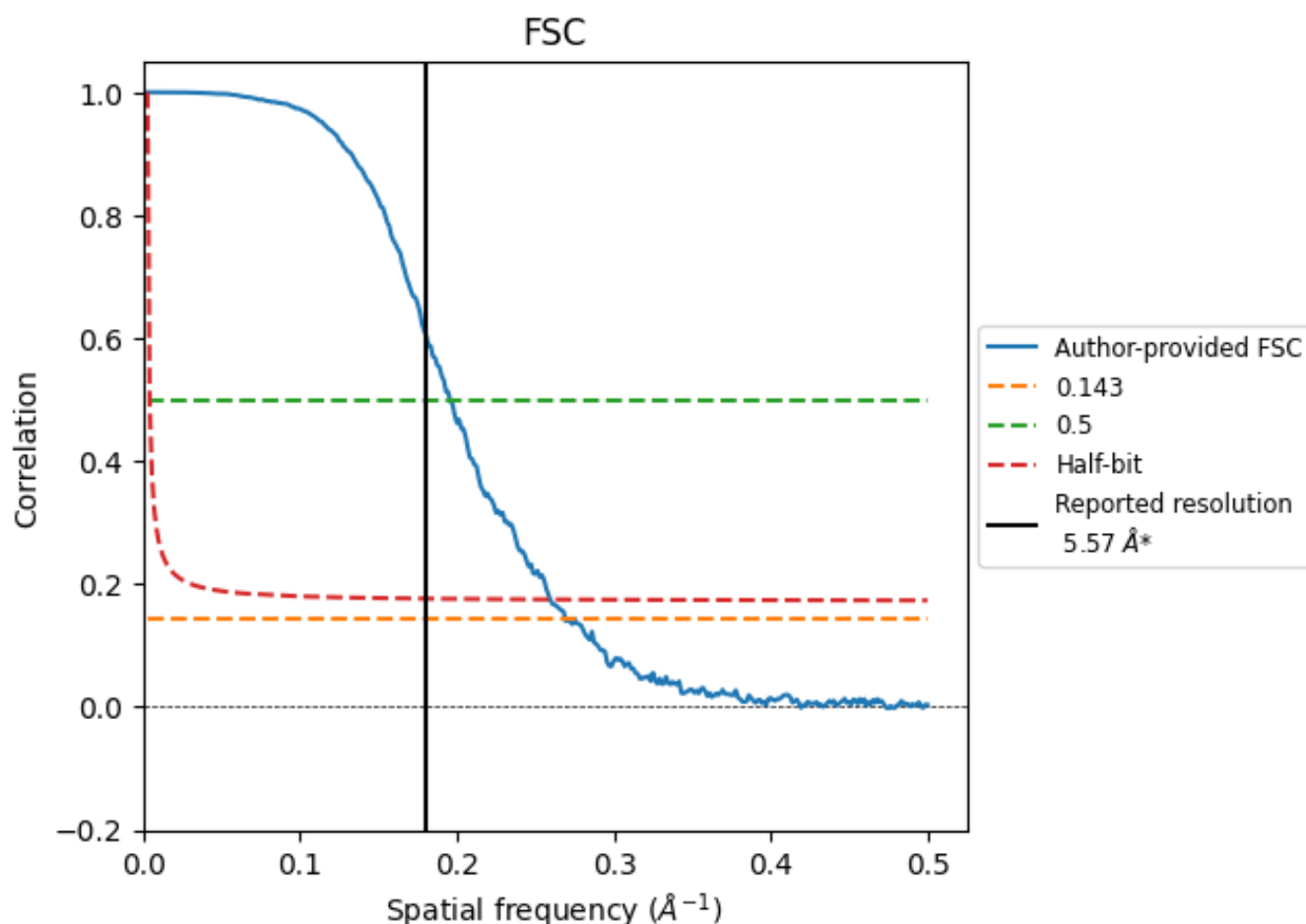


*Reported resolution corresponds to spatial frequency of 0.180 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.180 Å⁻¹

8.2 Resolution estimates [i](#)

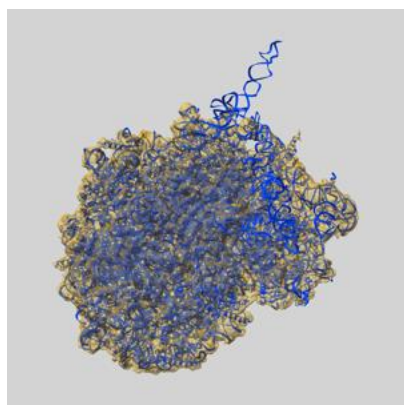
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	3.72	5.11	3.85
Unmasked-calculated*	-	-	-

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

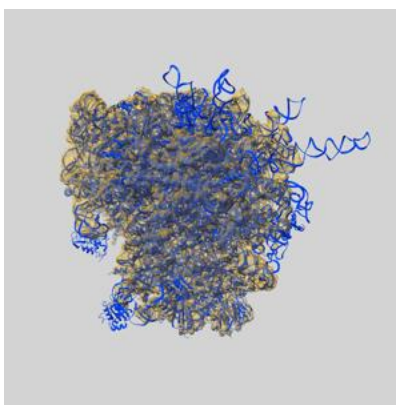
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2239 and PDB model 4V8M. Per-residue inclusion information can be found in section 3 on page 21.

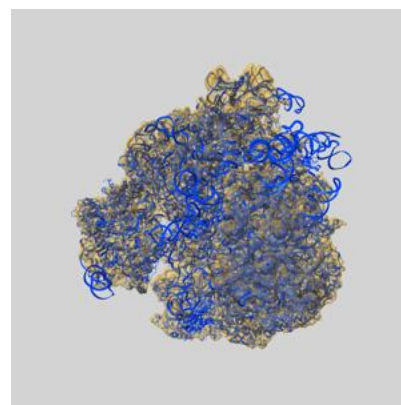
9.1 Map-model overlay [i](#)



X



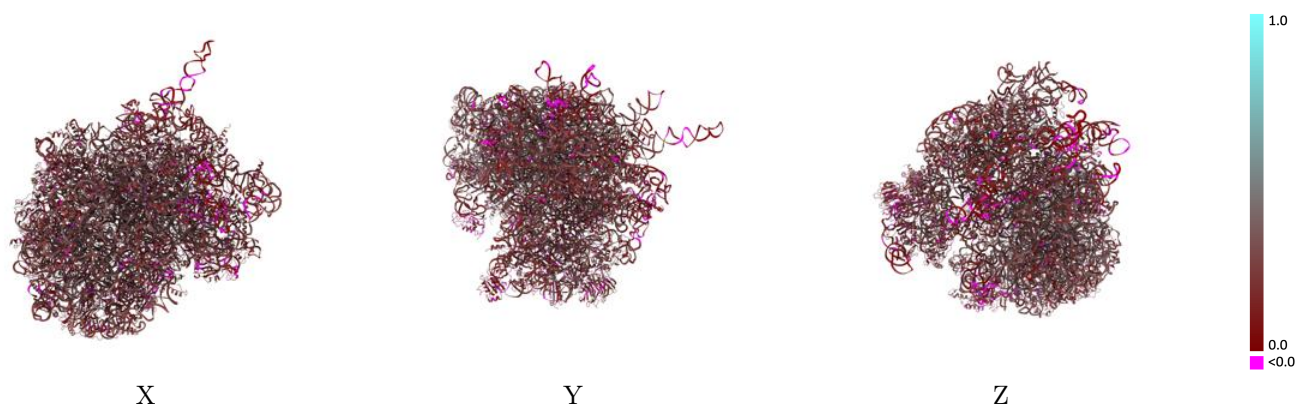
Y



Z

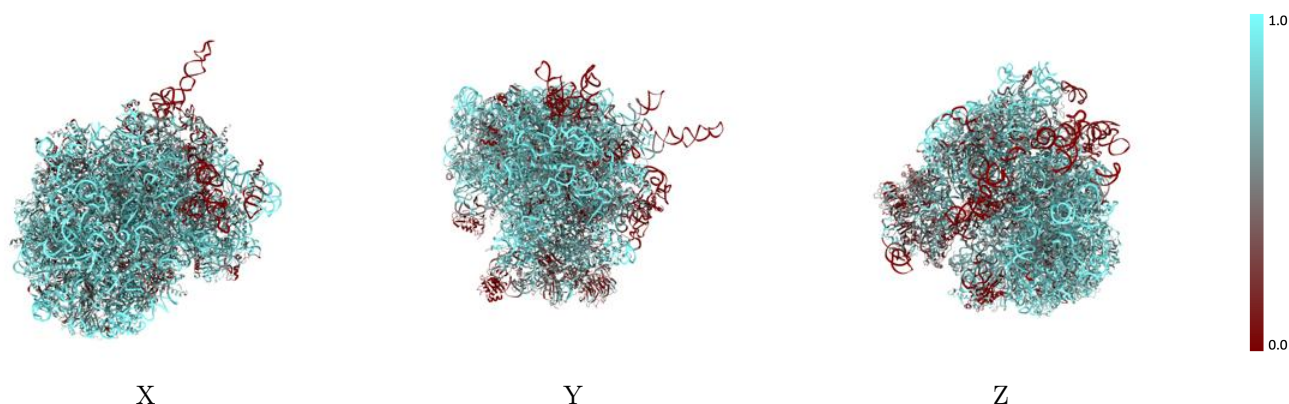
The images above show the 3D surface view of the map at the recommended contour level 108000.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



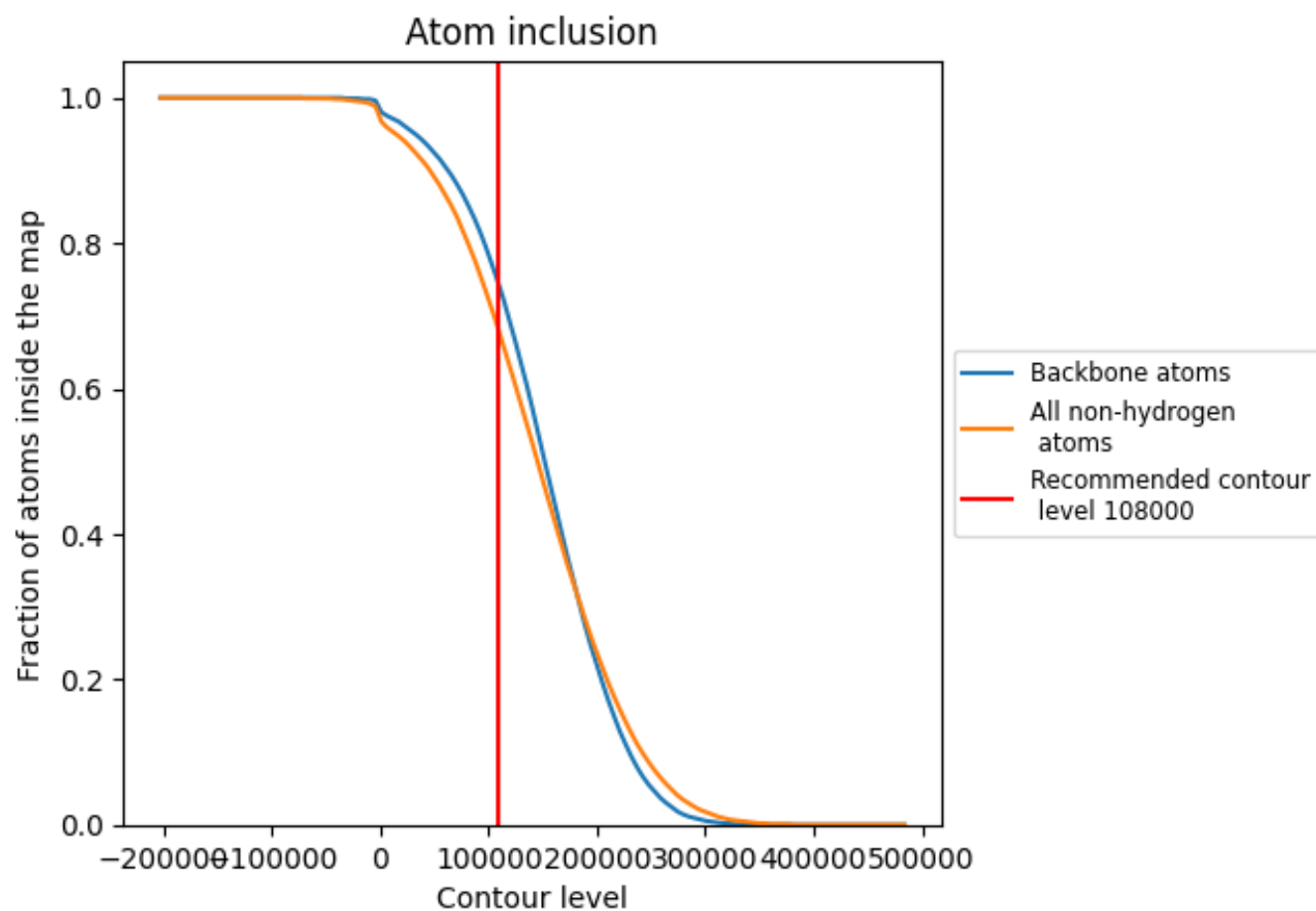
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (108000).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 69% 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 (108000) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6860	 0.2390
A0	 0.5170	 0.2360
A1	 0.5980	 0.2390
A2	 0.3430	 0.1910
A3	 0.6080	 0.2070
A4	 0.6130	 0.2320
A5	 0.4740	 0.2180
A6	 0.6720	 0.2270
A7	 0.3000	 0.1870
A8	 0.1980	 0.1170
A9	 0.1860	 0.1310
AA	 0.7340	 0.2390
AB	 0.4690	 0.1630
AC	 0.6380	 0.2440
AD	 0.3260	 0.1670
AE	 0.3730	 0.2080
AF	 0.0100	 0.1110
AG	 0.5170	 0.2330
AH	 0.3730	 0.1990
AI	 0.2750	 0.1480
AJ	 0.4700	 0.2300
AK	 0.3240	 0.2000
AL	 0.5290	 0.2220
AM	 0.2880	 0.1420
AO	 0.4990	 0.1980
AP	 0.6320	 0.2360
AQ	 0.3770	 0.1720
AR	 0.6530	 0.2550
AS	 0.4020	 0.1980
AT	 0.6470	 0.2000
AU	 0.3200	 0.1280
AV	 0.2260	 0.2090
AW	 0.6460	 0.2790
AX	 0.3660	 0.1860
AY	 0.5460	 0.1940



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Chain	Atom inclusion	Q-score
AZ	 0.4490	 0.2050
BA	 0.8610	 0.2760
BB	 0.7680	 0.2580
BC	 0.9190	 0.3090
BD	 0.9510	 0.2740
BE	 0.8330	 0.2680
BF	 0.8680	 0.2620
BG	 0.9360	 0.2990
BH	 0.7890	 0.2190
BI	 0.5580	 0.2150
BJ	 0.0020	 0.0510
BK	 0.6170	 0.2440
BL	 0.7250	 0.2310
BM	 0.0060	 0.0470
BN	 0.6690	 0.2310
BO	 0.5960	 0.2140
BP	 0.7160	 0.2300
BQ	 0.5560	 0.2370
BR	 0.5830	 0.2270
BS	 0.5430	 0.2280
BT	 0.6370	 0.2260
BU	 0.5080	 0.2240
BV	 0.0750	 0.0940
BW	 0.6440	 0.2610
BX	 0.6060	 0.2500
BY	 0.3600	 0.1320
BZ	 0.6920	 0.2300
Ba	 0.5800	 0.2450
Bb	 0.5890	 0.2360
Bc	 0.7570	 0.2500
Bd	 0.5270	 0.1590
Be	 0.4990	 0.2320
Bf	 0.5470	 0.2240
Bg	 0.7180	 0.2600
Bh	 0.5850	 0.2040
Bi	 0.4600	 0.2010
Bj	 0.4200	 0.1440
Bk	 0.6270	 0.2390
Bl	 0.5120	 0.2040
Bm	 0.6440	 0.2360
Bn	 0.6380	 0.2130
Bo	 0.5410	 0.2050

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Chain	Atom inclusion	Q-score
Bp	 0.7110	 0.2480
Bq	 0.5520	 0.2310
Br	 0.6450	 0.2410
Bs	 0.6410	 0.2440
Bt	 0.6610	 0.2570
Bu	 0.6820	 0.2240
Bv	 0.6580	 0.2470
Bw	 0.5990	 0.2310
Bx	 0.6090	 0.2340
By	 0.7460	 0.2370