



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Dec 2, 2019 – 11:13 PM EST

PDB ID : 4V8M
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 PDB ID : 4A17, 3IZ9, 3IZ6, 3IZ7, 4A18, 4A19, 3U5G, 3U5F, 3U5E, 3U5D, 3U5C, 3U5B, 3U5I, 3U5H, 2XZM, 2XZN, 3IZR, 4A1D, 4A1E, 4A1B, 4A1C, 4A1A

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB 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.

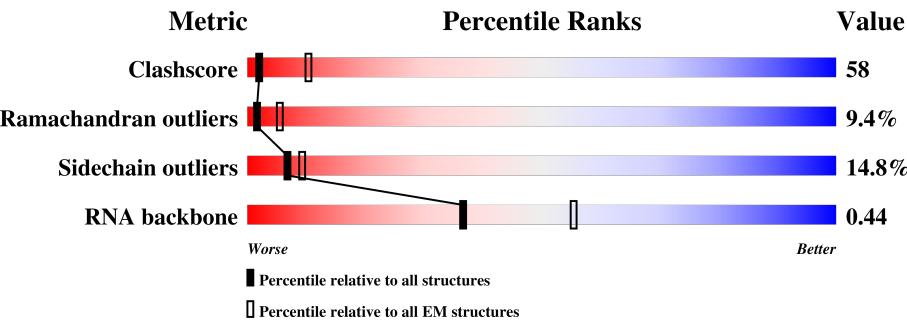
MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

1 Overall quality at a glance i

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

The reported resolution of this entry is 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.




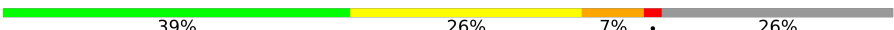

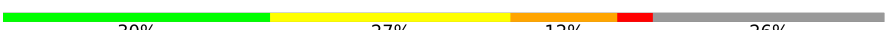

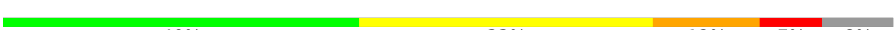




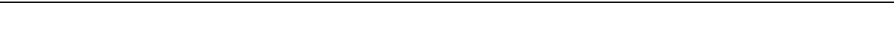

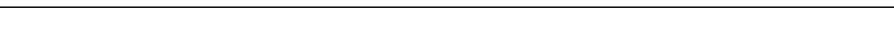
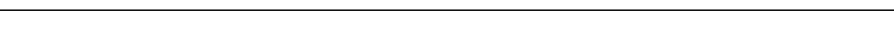






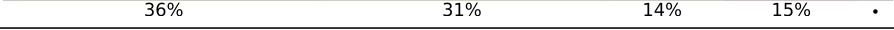




Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for $\geq 3, 2, 1$ and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A0	256	<div><div>39%</div><div>30%</div><div>14%</div><div>•</div><div>14%</div></div>
2	A1	273	<div><div>34%</div><div>40%</div><div>12%</div><div>•</div><div>9%</div></div>
3	A2	190	<div><div>53%</div><div>27%</div><div>13%</div><div>5%</div><div>•</div></div>
4	A3	250	<div><div>35%</div><div>42%</div><div>18%</div><div>5%</div></div>
5	A4	202	<div><div>35%</div><div>29%</div><div>22%</div><div>9%</div><div>5%</div></div>
6	A5	220	<div><div>40%</div><div>32%</div><div>12%</div><div>5%</div><div>11%</div></div>
7	A6	190	<div><div>41%</div><div>32%</div><div>15%</div><div>11%</div><div>•</div></div>












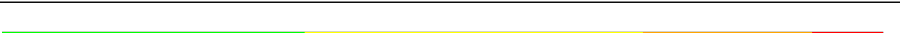




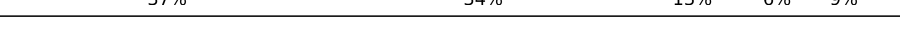
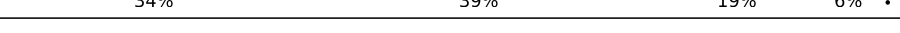
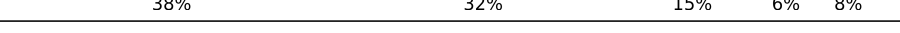
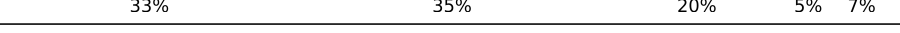
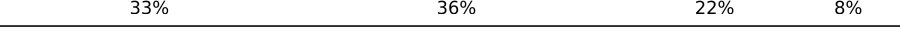
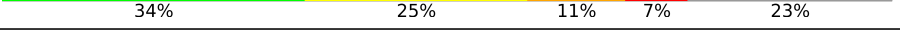



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Mol	Chain	Length	Quality of chain
8	A7	318	
9	A8	57	
10	A9	153	
11	AC	277	
12	AD	172	
13	AE	174	
14	AF	144	
15	AG	151	
16	AH	144	
17	AI	152	
18	AJ	130	
19	AK	149	
20	AL	142	
21	AM	153	
22	AO	167	
23	AP	266	
24	AQ	117	
25	AR	194	
26	AS	143	
27	AT	137	
28	AU	113	
29	AV	111	
30	AW	86	
31	AX	214	
32	AY	66	

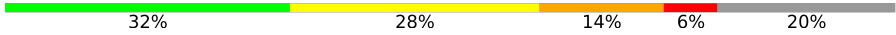
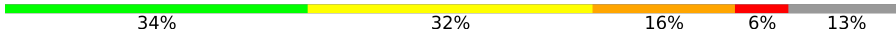


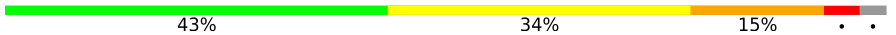

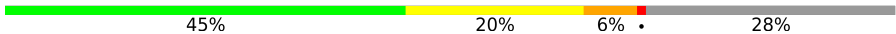





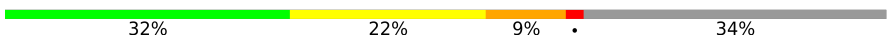
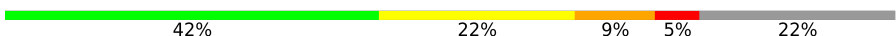











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Mol	Chain	Length	Quality of chain
33	AZ	103	
34	BA	1847	
35	BB	1465	
36	BC	169	
37	BD	119	
38	BE	210	
39	BF	73	
40	BG	182	
41	BH	135	
42	BI	193	
43	BJ	214	
44	BK	213	
45	BL	194	
46	BM	164	
47	BN	218	
48	BO	222	
49	BP	189	
50	BQ	221	
51	BR	166	
52	BS	179	
53	BT	260	
54	BU	159	
55	BV	130	
56	BW	139	
57	BX	164	

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Mol	Chain	Length	Quality of chain
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	
78	Bs	128	
79	Bt	106	
80	Bu	308	
81	Bv	192	
82	Bw	257	

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Mol	Chain	Length	Quality of chain
83	Bx	276	<div><div></div><div>57%</div><div>22%</div><div>7%</div><div>13%</div></div>
84	By	189	<div><div></div><div>56%</div><div>28%</div><div>13%</div><div></div></div>
85	AA	2251	<div><div></div><div>19%</div><div>75%</div><div></div></div>
86	AB	73	<div><div></div><div>7%</div><div>23%</div><div>70%</div></div>

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		

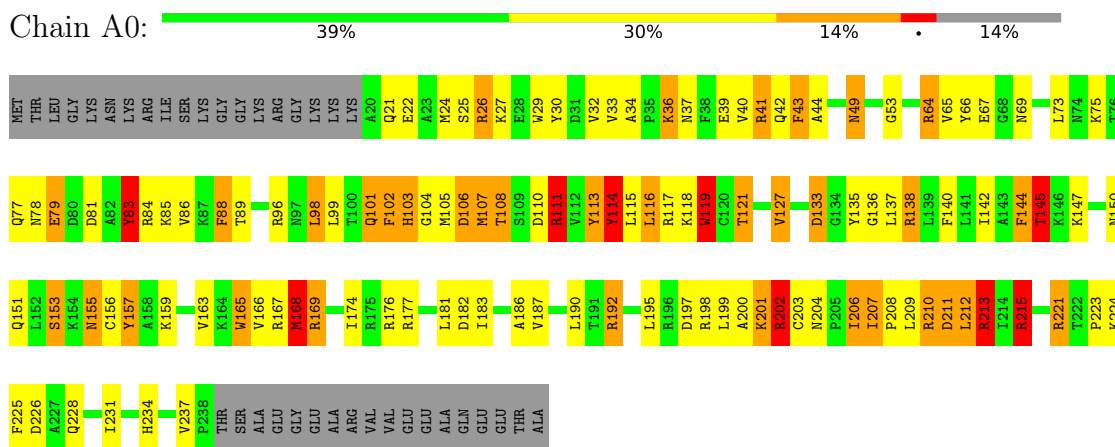
- Molecule 86 is a RNA chain called E-SITE TRNA.

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

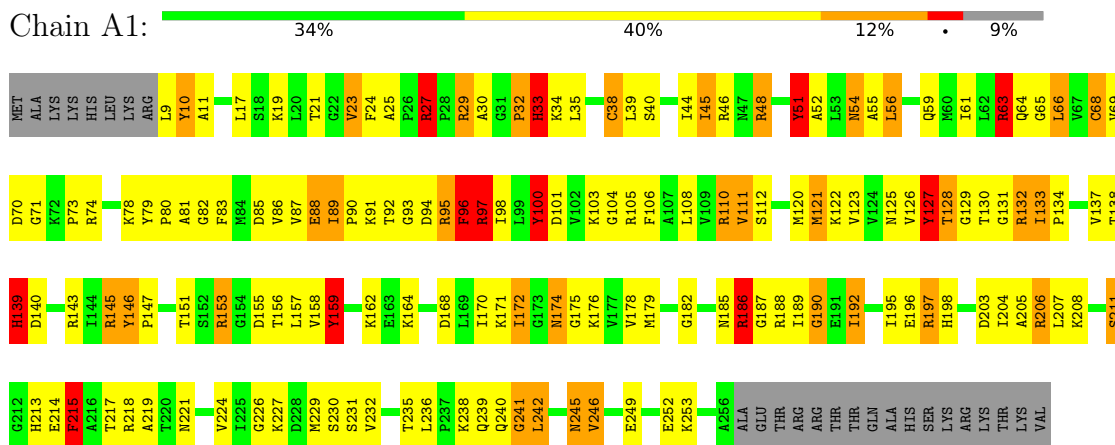
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

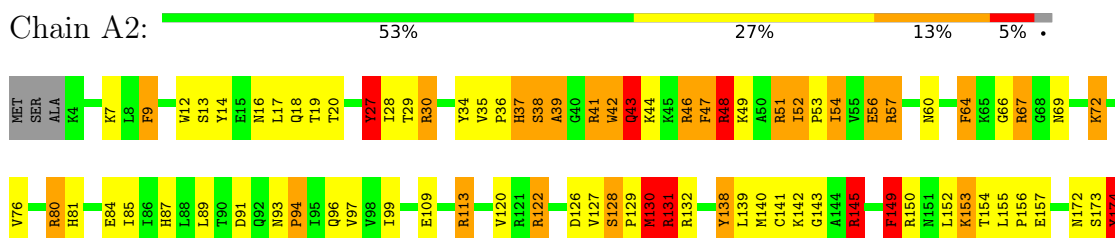
- Molecule 1: 40S RIBOSOMAL PROTEIN S3A, PUTATIVE

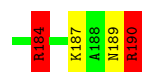


- Molecule 2: 40S RIBOSOMAL PROTEIN S4, PUTATIVE



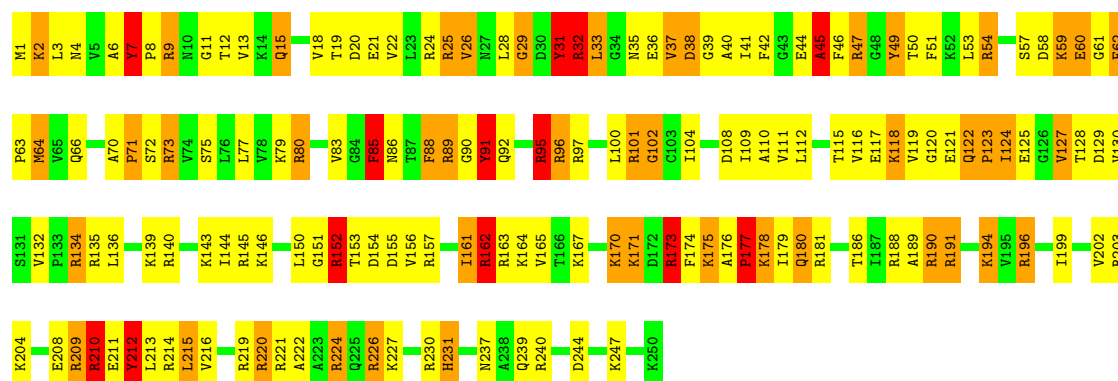
- Molecule 3: 40S RIBOSOMAL PROTEIN S5, PUTATIVE





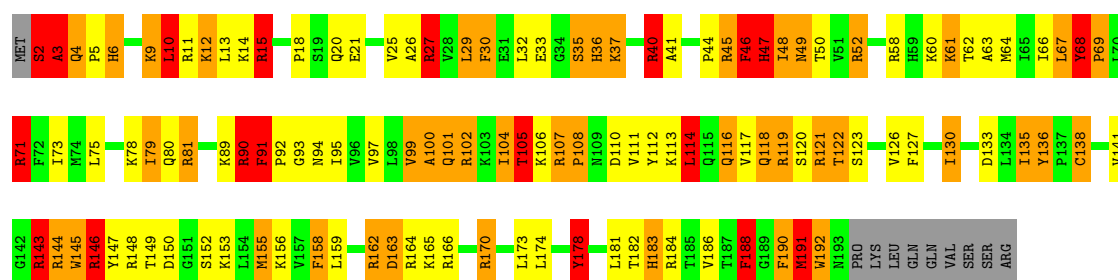
• Molecule 4: 40S RIBOSOMAL PROTEIN S6

Chain A3: 35% 42% 18% 5%



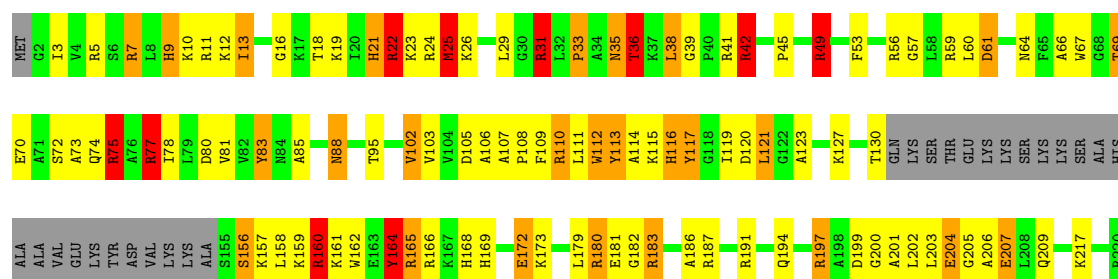
• Molecule 5: RIBOSOMAL PROTEIN S7, PUTATIVE

Chain A4: 35% 29% 22% 9% 5%



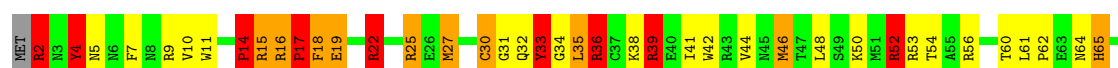
• Molecule 6: 40S RIBOSOMAL PROTEIN S8

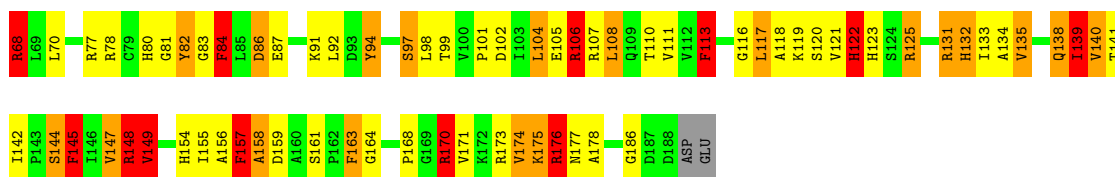
Chain A5: 40% 32% 12% 5% 11%



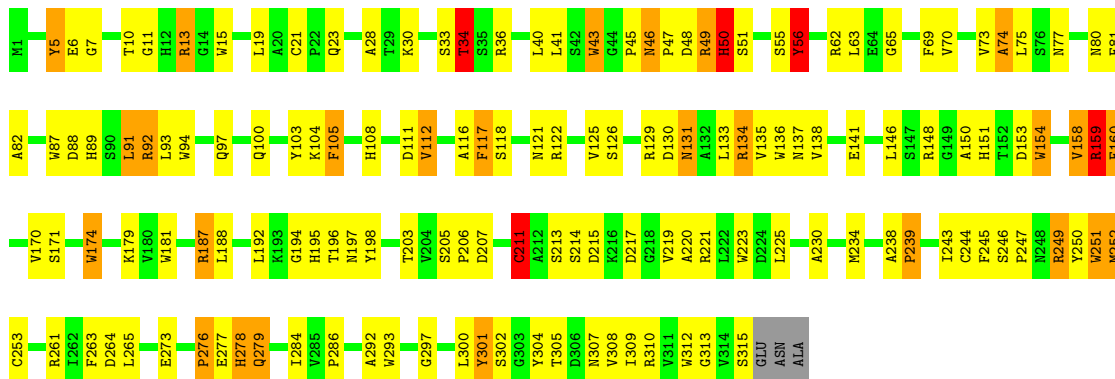
• Molecule 7: 40S RIBOSOMAL PROTEIN S9, PUTATIVE

Chain A6: 41% 32% 15% 11%

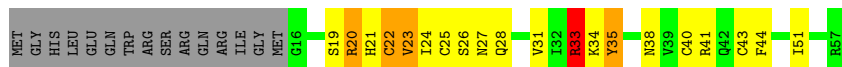




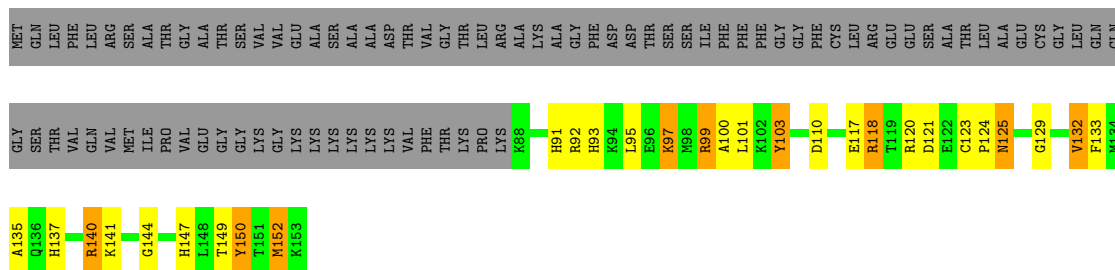
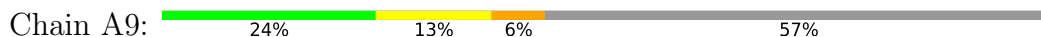
- Molecule 8: GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN



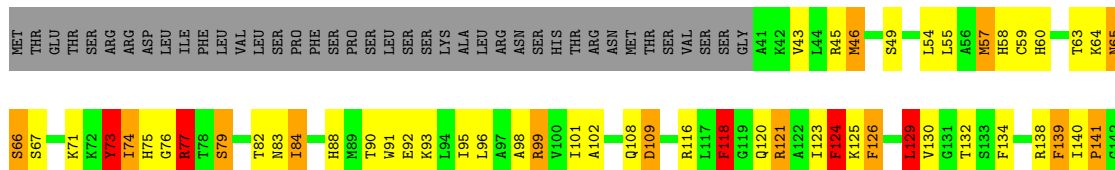
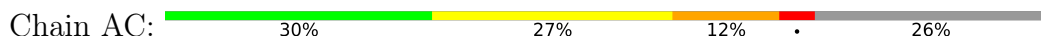
- Molecule 9: RIBOSOMAL PROTEIN S29, PUTATIVE

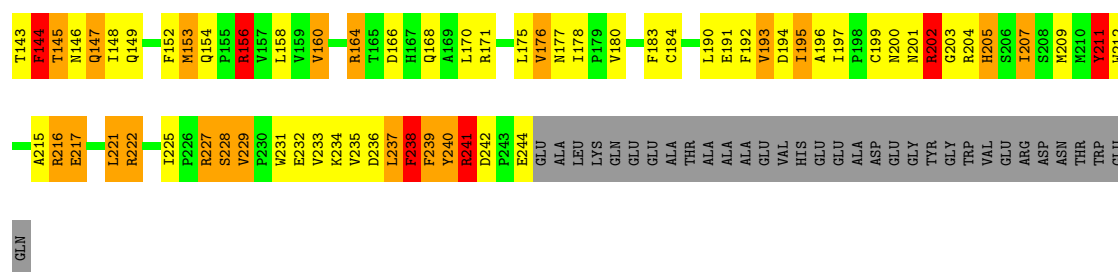


- Molecule 10: UBIQUITIN/RIBOSOMAL PROTEIN S27A, PUTATIVE



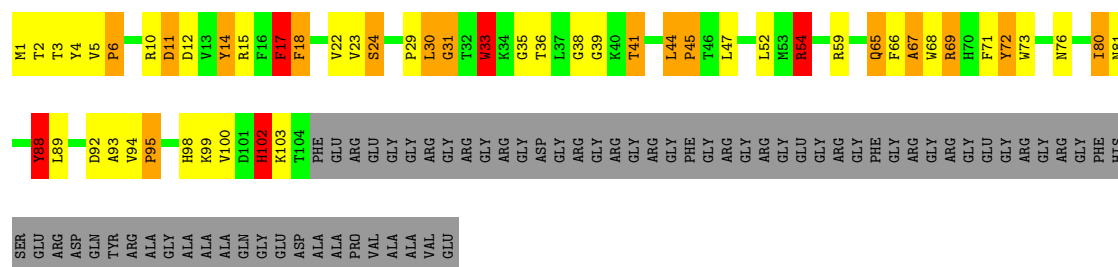
- Molecule 11: 40S RIBOSOMAL PROTEIN SA, PUTATIVE





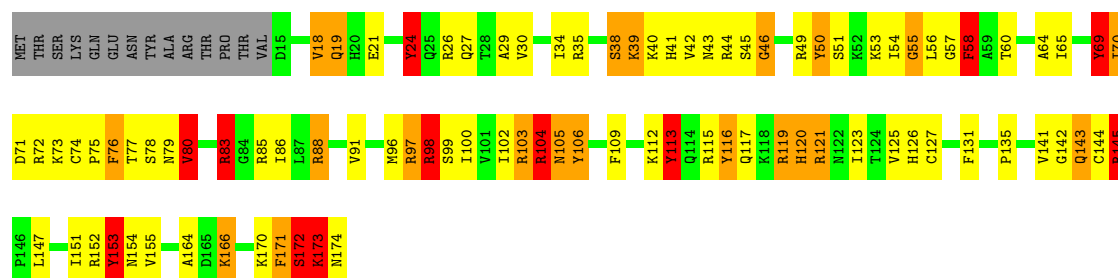
• Molecule 12: 40S RIBOSOMAL PROTEIN S10, PUTATIVE

Chain AD: 30% 19% 9% • 40%



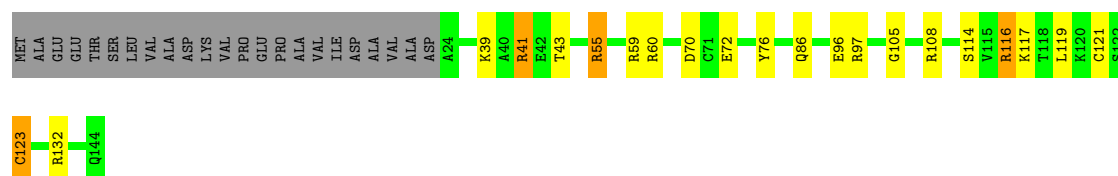
• Molecule 13: 40S RIBOSOMAL PROTEINS S11, PUTATIVE

Chain AE: 40% 33% 12% 7% 8%



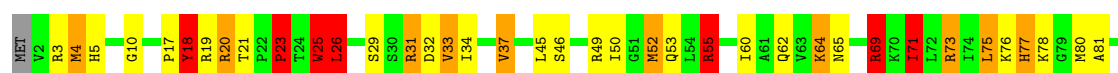
• Molecule 14: 40S RIBOSOMAL PROTEIN S12

Chain AF: 69% 12% • 16%

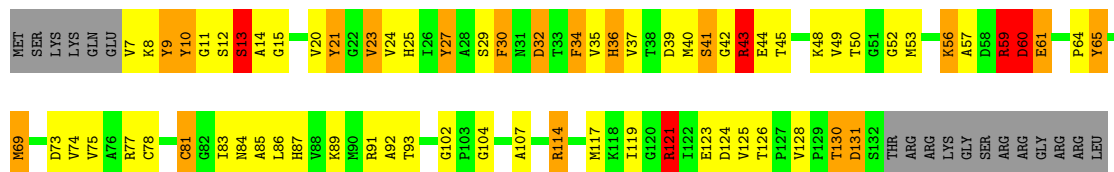


• Molecule 15: 40S RIBOSOMAL PROTEIN S13, PUTATIVE

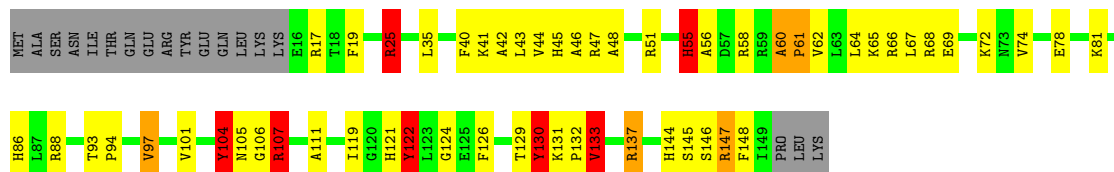
Chain AG: 46% 25% 15% 7% 7%



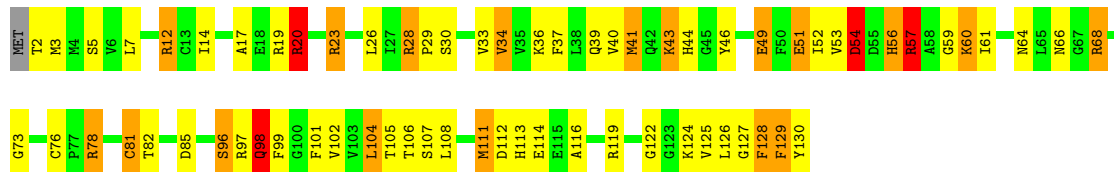
• Molecule 16: 40S RIBOSOMAL PROTEIN S14



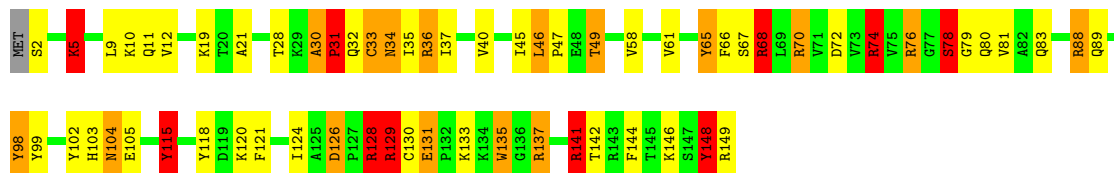
- Molecule 17: 40S RIBOSOMAL PROTEIN S15, PUTATIVE



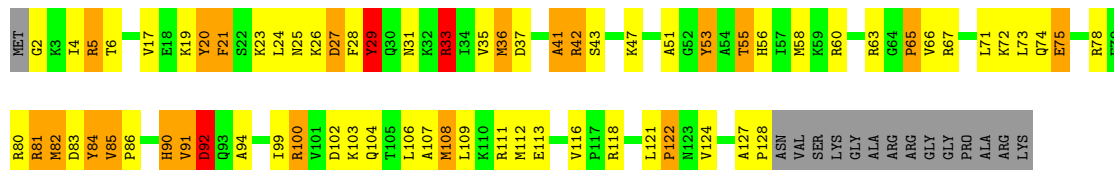
- Molecule 18: 40S RIBOSOMAL PROTEIN S15A, PUTATIVE



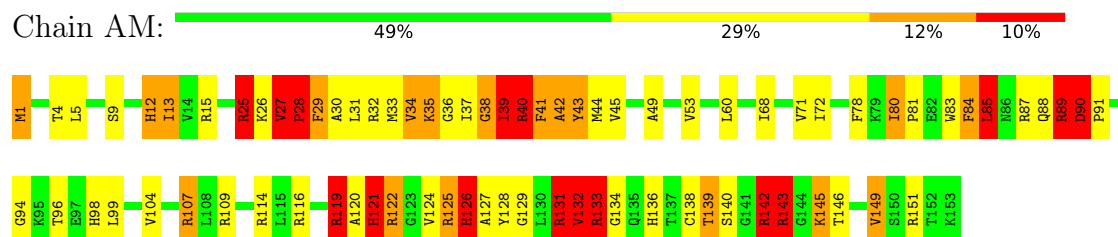
- Molecule 19: 40S RIBOSOMAL PROTEIN S16, PUTATIVE



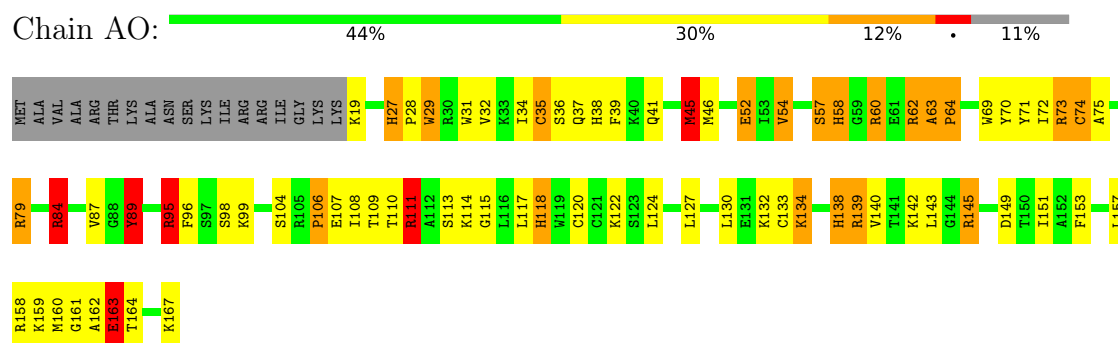
- Molecule 20: 40S RIBOSOMAL PROTEIN S17, PUTATIVE



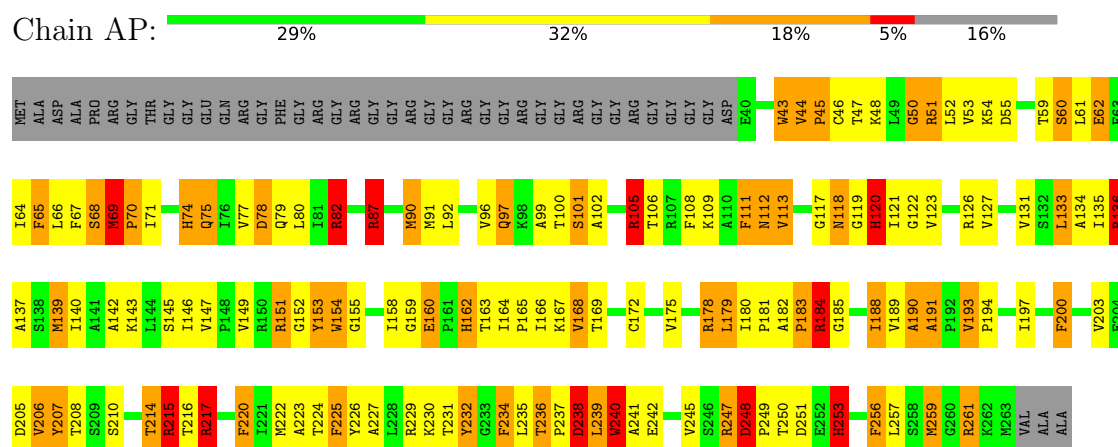
• Molecule 21: 40S RIBOSOMAL PROTEIN S18, PUTATIVE



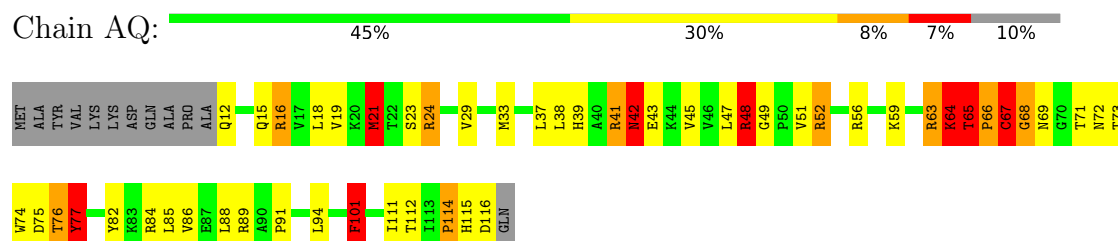
• Molecule 22: RIBOSOMAL PROTEIN S19, PUTATIVE



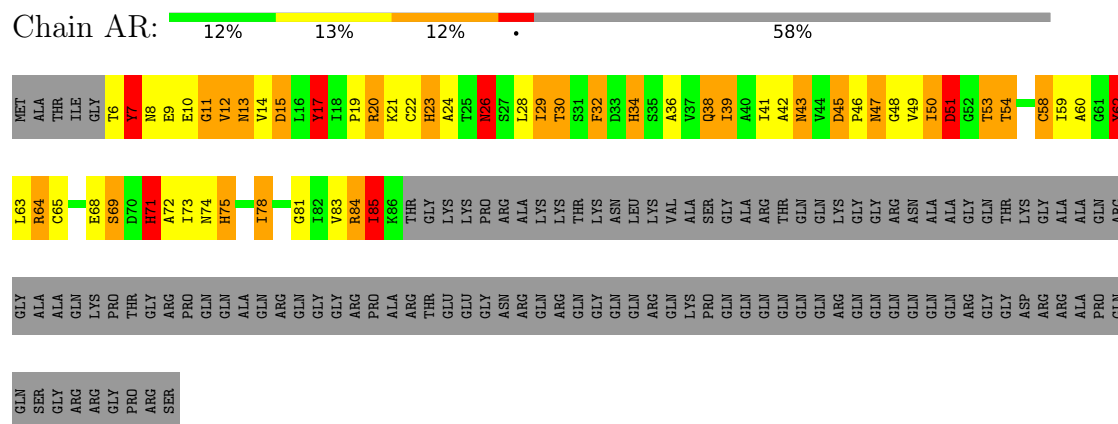
• Molecule 23: 40S RIBOSOMAL PROTEIN S2, PUTATIVE



• Molecule 24: RIBOSOMAL PROTEIN S20, PUTATIVE



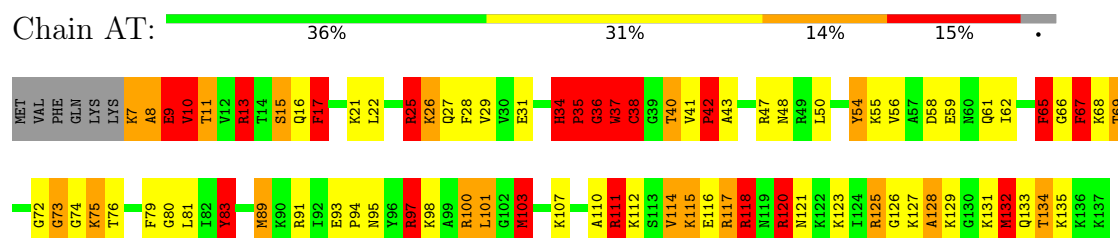
• Molecule 25: 40S RIBOSOMAL PROTEIN S21, PUTATIVE



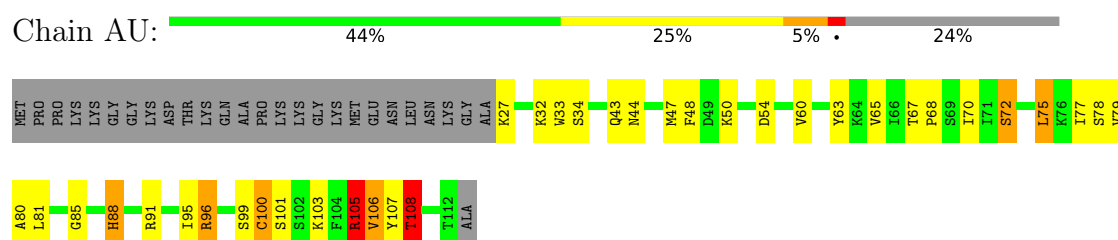
• Molecule 26: 40S RIBOSOMAL PROTEIN S23, PUTATIVE



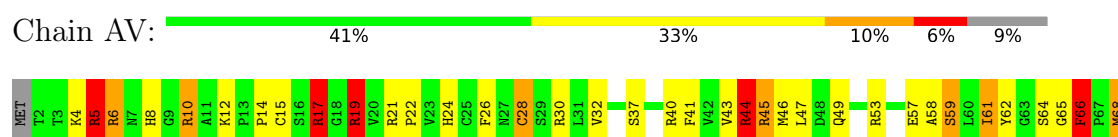
• Molecule 27: 40S RIBOSOMAL PROTEIN S24

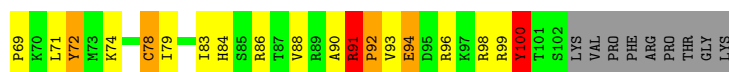


• Molecule 28: 40S RIBOSOMAL PROTEIN S25, PUTATIVE



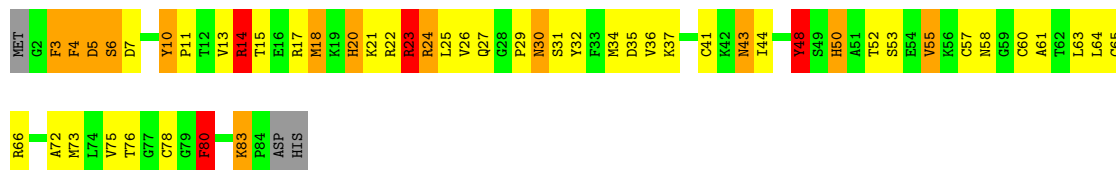
• Molecule 29: RIBOSOMAL PROTEIN S26, PUTATIVE





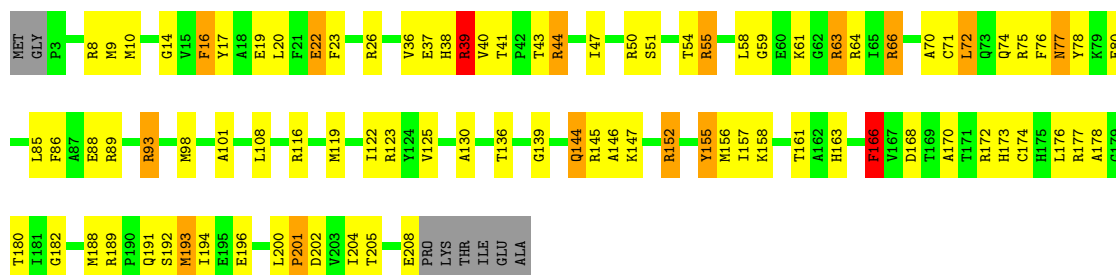
• Molecule 30: 40S RIBOSOMAL PROTEIN S27, PUTATIVE

Chain AW: 37% 40% 15% 5% .



• Molecule 31: 40S RIBOSOMAL PROTEIN S3, PUTATIVE

Chain AX: 54% 35% 7% . .



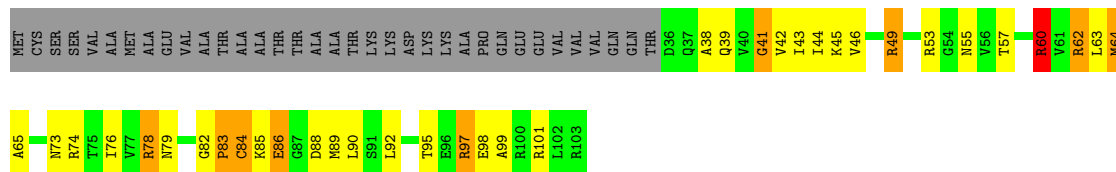
• Molecule 32: 40S RIBOSOMAL PROTEIN S30, PUTATIVE

Chain AY: 39% 30% 18% 11% .



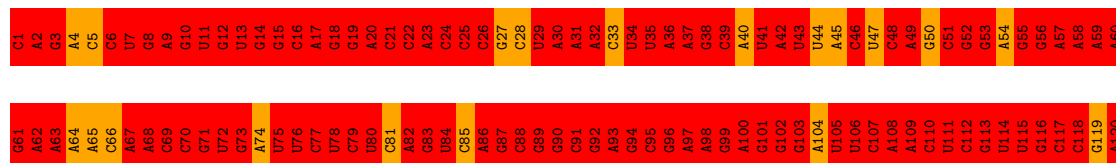
• Molecule 33: 40S RIBOSOMAL PROTEIN S33, PUTATIVE

Chain AZ: 31% 25% 9% . 34%



• Molecule 34: ALPHA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT 28S RRNA

Chain BA: 18% 80%



U1081	U1021	C981	C901	G841	U781	A721	C661	A601	C541	A481	G421	C361	U301	U241	G181	A121
U1082	C1022	U962	C902	U842	C762	A722	U662	G602	A542	C482	C422	G362	A302	U242	U182	U122
A1083	G1023	G963	C903	G843	C763	A723	U663	G603	A543	C483	C423	G363	C303	C243	C183	C123
A1084	A1024	U964	G904	U844	C764	A724	C664	G604	U544	C484	U424	C364	G304	G244	C184	G124
G1085	A1025	A965	A905	U845	G765	C725	C665	G605	U545	C485	G425	A365	C305	U245	A185	G125
A1086	C1026	G966	A906	U846	U766	G726	C666	G606	U546	C486	G426	G366	G306	G246	G186	G126
A1087	G1027	C967	A907	U847	C767	A727	U667	G607	C547	C487	G427	G367	C307	U247	U187	U127
G1088	A1028	G968	G908	U848	C768	A728	U668	G608	C548	C488	C428	U368	C308	G248	C188	C128
U1089	C1029	A969	G909	U849	U769	C729	U669	G609	C549	C489	G429	A369	U309	G249	U189	U129
A1090	U1030	U970	C1030	C850	G790	A730	U670	A610	U550	A490	A430	U370	C310	G250	U130	U130
U1091	U1031	G971	G911	C851	A791	A731	C871	A611	C552	U491	A431	U371	C311	U251	G191	A131
U1092	A1032	C972	G912	C852	A792	G732	U672	U612	C553	G492	A432	U372	U312	A252	G192	U132
G1093	G1033	U973	U913	A853	C793	A733	U673	A613	C554	G493	G433	U373	C313	U253	G193	A133
U1094	U1034	C974	G914	A854	G794	G734	C874	A614	A554	A494	U434	U374	A314	U254	G194	U134
G1095	A1035	G975	A915	C855	G795	A735	C875	A615	C555	A495	U435	C375	A315	G255	A195	G135
C1096	C1036	U976	A916	G856	G796	A736	C876	A616	A556	G496	U436	U376	G316	G256	A196	A136
G1097	U1037	C977	C917	C857	G797	U737	U677	U617	C557	U497	G437	G377	U317	U257	U197	C137
U1098	C1038	U978	U918	C858	G798	C738	C878	G618	C558	A498	A438	C378	U318	C258	U198	C138
U1099	G1039	C979	A919	G859	A799	A739	U679	U619	C559	C499	A439	C379	C319	C259	U199	U139
A1100	U1040	C980	U920	G860	C800	A740	C880	C620	U560	C500	A440	A380	C320	G260	C200	C140
U1101	U1041	G981	G921	C861	C801	A741	C881	G621	U561	U501	A441	A381	G321	A261	A201	G141
A1102	U1042	A982	C922	C862	C802	C742	A682	G622	C562	U502	G442	G382	U322	A262	A202	A142
G1103	A1043	U983	C923	G863	U803	A743	C883	U623	A563	C503	U443	C383	C323	G263	U203	A143
C1104	U1044	C984	U924	G864	C804	G744	C884	G624	C564	A504	A444	U384	C324	A264	U204	C144
A1105	A1045	C985	G925	C865	A805	A745	C885	U625	U565	U505	G445	U385	A325	G265	G205	U145
A1106	G1046	G986	A926	C866	U806	C746	U686	G626	C566	U506	U446	A386	A326	G266	C206	G146
U1107	U1047	C987	A927	C867	U807	G747	C887	U627	U567	U507	U447	A387	G327	G267	A207	U147
U1108	C1048	U988	C928	C868	C808	C748	C888	G628	C568	C508	U448	A388	A328	G268	G148	G148
G1109	G1049	C989	A929	G869	U809	A749	C889	U629	C569	U509	G449	U389	C329	G269	A209	G149
A1110	A1050	U990	A930	C870	A810	C750	C890	G630	U570	U510	G450	A390	A330	U270	G210	C150
U1111	U1051	G991	G931	C871	C811	A751	A691	G631	C571	U511	A451	U391	G331	C271	C211	A151
U1112	C1052	A992	C932	U872	A812	A752	C892	U632	C572	U512	A452	A392	U332	A272	A212	C152
A1113	U1053	G993	U933	C873	C813	G753	C893	G633	U573	U513	G453	A393	A333	G273	A213	C153
G1114	U1054	C994	G934	G874	C814	G754	C894	U634	U574	U514	G454	A394	G334	C274	A214	A154
A1115	U1055	A995	A935	C875	C815	G755	A695	G635	U575	U515	A455	C395	C335	C275	C215	U155
U1116	C1056	U996	C936	C876	C816	A756	A696	G636	C576	U516	G456	U396	A336	C276	C216	U156
G1117	U1057	G997	G937	U877	U817	G757	A697	G637	U577	A517	A457	A397	C337	A277	C217	U157
C1118	C1058	U998	C938	C878	C818	G758	U698	U638	C578	C518	G458	C398	U338	U278	G218	U158
A1119	U1059	C999	C939	C879	C819	A759	C899	U639	U579	G519	U459	C399	G339	U279	U219	U159
U1120	G1060	U999	A940	G880	C820	G760	C900	U640	U580	G520	G460	A400	U340	A280	U220	G160
U1121	A1061	G1001	G941	C881	C821	U761	G701	U641	U581	C521	A461	A401	U341	C281	G221	U161
G1122	G1062	U1002	C942	G882	U822	A762	G702	U642	U582	C522	C462	A402	U342	A282	C222	G162
A1123	C1063	A1003	G943	C883	C823	G763	U703	U643	U583	A523	A463	A403	G343	U283	U223	G163
U1124	U1064	U1004	G944	G884	C824	A764	G704	C544	A584	G524	U464	C404	G344	U284	G224	C164
G1125	U1065	A945	A945	A885	G825	U765	C705	U645	G585	A525	A465	C405	G345	C285	A225	C165
U1126	G1067	G1006	A946	G886	C826	A766	C706	C546	G586	C526	G466	A406	A346	U286	A226	G166
U1127	U1068	U1007	C947	U887	A827	U767	C707	U647	U587	C527	A467	A407	A347	U287	C227	U167
C1128	C1068	A1008	C948	G888	C828	G768	C708	C548	C588	C528	A468	U408	U348	U288	A228	C168
U1129	U1069	U1009	C949	U889	U829	U769	C709	A649	A589	A529	C469	A409	G349	A289	C229	C169
U1130	C1070	G990	U930	G890	U830	G770	A710	C650	U590	A530	C470	G410	C350	G290	A230	U170
G1131	G1071	C991	U931	C891	U831	A771	C711	U651	C591	C531	U471	C411	A351	C291	U231	U171
U1132	U1072	G992	C932	C892	C832	G772	C712	C652	G592	C532	G472	C412	C352	C292	U232	A172
A1133	C1073	A1013	G953	U893	U833	A773	C713	U653	G593	U533	A473	A413	U353	A293	U173	C173
A1134	C1074	G994	A954	G894	C834	A774	G714	C654	G594	C534	A474	A414	G354	C294	A234	A174
U1135	U1075	G1015	G955	U895	U835	C775	U715	U655	U595	G535	A475	C415	U355	G295	G235	G175
A1136	U1076	A1016	C956	U896	U836	U776	C716	U656	G596	C536	U476	A416	C356	G296	A236	G176
U1137	G1077	C1017	A957	U897	U837	C777	U717	C657	C597	C537	C477	A417	A357	A297	A237	G177
C1138	U1078	G998	G958	G898	U838	U778	U718	C658	G598	G538	G478	G418	A358	G298	C238	C178
G1139	U1079	C999	U959	G899	U839	U779	U719	C659	G599	C539	U479	U419	C359	G299	C239	U179
A1140	U1080	A1020	C960	A900	U840	U780	A720	C660	G600	G540	G480	A420	C360	C300	C240	G180

● Molecule 35: BETA CHAIN OF THE LARGE RIBOSOMAL SUBUNIT 28S I																			
Chain BB: <div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div><div></div></div> 5%25%70%																			
A121	C62	A61	U1	C1801	G1741	C1681	U1621	C1561	U1501	C1441	A1381	A1321	G1261	G1201	C1141				
U122	C63	A62	C2	C1802	G1742	A1682	U1622	G1562	G1502	C1442	C1382	A1322	A1262	G1202	C1142				
C123	A63	C1803	C3	C1803	U1743	C1683	U1623	G1563	U1503	C1443	C1383	A1323	A1263	G1203	C1143				
G124	C64	A64	C4	C1804	G1744	A1684	U1624	C1564	G1504	C1444	C1384	G1324	U1264	U1204	A1144				
G125	A65	C1805	A5	C1805	G1745	C1685	U1625	U1565	G1505	C1445	C1385	G1325	U1265	A1205	U1145				
C126	G66	A66	A6	C1806	G1746	G1686	U1626	G1566	C1506	C1446	G1386	U1326	A1266	C1206	U1146				
U127	A67	C1807	C7	C1807	G1747	A1687	U1627	G1567	C1507	C1447	C1387	U1327	A1267	A1207	C1147				
C128	G68	A68	U8	C1808	G1748	G1688	A1628	C1568	C1508	C1448	C1388	U1328	C1268	U1208	U1148				
A129	C69	C1809	G9	C1809	G1749	U1689	A1629	C1569	U1509	C1449	C1389	U1329	C1269	A1209	C1149				
G130	A70	C1810	C10	C1810	U1750	U1690	A1630	C1570	C1510	C1450	C1390	C1330	G1270	U1210	A1150				
A131	C71	C1811	A11	C1811	C1751	G1691	U1631	C1571	C1511	C1451	A1391	G1331	C1271	G1211	A1151				
C132	G72	C1812	G12	C1812	U1752	U1692	G1632	G1572	C1512	U1452	C1392	U1332	U1272	A1212	A1152				
G133	C73	C1813	A13	C1813	U1753	U1693	C1633	C1573	C1513	U1453	C1393	C1333	U1273	A1213	C1153				
C134	U74	C1814	C14	C1814	G1754	G1694	A1634	C1574	A1514	C1454	C1394	G1334	A1274	U1214	U1154				
C135	A75	C1815	C15	C1815	U1755	C1695	A1635	U1575	C1515	C1455	C1395	A1335	G1275	U1215	U1155				
A136	C76	C1816	G16	C1816	G1756	G1696	C1636	C1576	G1516	C1456	A1396	U1336	G1276	G1216	U1156				
C137	A77	C1817	U17	C1817	C1757	U1697	G1637	U1577	U1517	C1457	C1397	G1337	G1277	A1217	U1157				
A138	C78	C1818	A18	C1818	C1758	C1698	U1638	A1578	C1518	C1458	C1398	G1338	A1278	G1218	A1158				
G139	U79	C1819	C19	C1819	U1759	A1699	U1639	G1579	C1519	C1459	A1399	C1339	U1279	G1219	A1159				
C140	C80	C1820	U20	C1820	U1760	C1700	G1640	U1580	A1520	U1460	C1400	G1340	A1280	C1220	U1160				
G141	A81	C1821	C21	C1821	U1761	U1701	G1641	G1581	C1521	C1461	C1401	A1341	U1281	A1221	G1161				
C142	G82	C1822	A22	C1822	U1762	G1702	A1642	C1582	G1522	U1462	C1402	C1342	G1282	C1222	U1162				
G143	C83	C1823	U23	C1823	U1763	A1703	U1643	A1583	U1523	C1463	C1403	A1343	U1283	C1223	G1163				
C144	G84	C1824	C24	C1824	U1764	G1704	A1644	G1584	G1524	C1464	A1404	G1344	G1284	A1224	C1164				
A145	A85	U1825	A25	U1825	U1765	C1705	C1645	A1585	C1525	C1465	A1405	U1345	G1285	A1225	A1165				
C146	C86	C1826	C26	C1826	G1766	A1706	U1646	U1586	C1526	U1466	C1406	G1346	G1286	G1226	A1166				
G147	A87	C1827	U27	C1827	G1767	C1707	G1647	C1587	G1527	C1467	C1407	U1347	G1287	U1227	A1167				
C148	U88	C1828	G28	C1828	U1768	A1708	G1648	U1588	U1528	U1468	C1408	G1348	U1288	G1228	C1168				
A149	C89	C1829	C29	C1829	U1769	A1709	A1649	U1589	G1529	C1469	A1409	U1349	C1289	G1229	A1169				
G150	G90	C1830	A30	C1830	U1770	C1710	U1650	G1590	C1530	G1470	C1410	C1350	A1290	G1230	A1170				
C151	C91	C1831	U31	C1831	U1771	C1711	G1651	G1591	G1531	C1471	C1411	G1351	A1291	C1231	C1171				
G152	C92	C1832	C32	C1832	U1772	U1712	G1652	U1592	G1532	G1472	C1412	G1352	A1292	C1232	C1172				
A154	A93	C1833	A33	C1833	U1773	C1713	G1653	C1593	C1533	C1473	C1413	U1353	A1293	U1233	C1173				
C155	C94	C1834	G34	C1834	G1774	A1714	G1654	G1594	U1534	G1474	C1414	G1354	C1294	U1234	A1174				
G156	A95	C1835	C35	C1835	U1775	C1715	G1655	G1595	C1535	G1475	C1415	G1355	U1295	C1235	C1175				
C157	U96	A1836	U36	C1836	G1776	A1716	A1656	C1596	A1536	C1476	C1416	C1356	U1296	C1236	C1176				
C158	U97	U1837	C37	C1837	U1777	C1717	A1657	C1597	G1537	C1477	C1417	C1357	G1297	U1237	C1177				
C159	A98	C1838	C38	C1838	U1778	C1718	G1658	U1598	C1538	G1478	C1418	A1358	U1298	C1238	U1178				
G160	C99	C1839	C39	C1839	U1779	G1719	C1659	A1599	A1539	G1479	C1419	U1359	C1299	G1239	C1179				
A100	C100	C1840	C40	C1840	U1780	U1720	A1660	G1600	C1540	C1480	C1420	G1360	G1300	G1240	A1180				
U101	A101	C1841	A41	C1841	U1781	U1721	U1661	C1601	G1541	U1481	A1421	C1361	G1301	U1241	C1181				
C162	C102	U1842	A42	U1842	C1782	U1722	U1662	A1602	A1542	A1482	A1422	C1362	C1302	U1242	U1182				
G163	C103	C1843	C43	C1843	C1783	U1723	U1663	A1603	C1543	U1483	C1423	G1363	C1303	G1243	C1183				
C164	C104	U1844	C44	U1844	G1784	G1724	C1664	A1604	C1544	A1484	C1424	G1364	C1304	A1244	A1184				
C165	A105	C1845	A45	C1845	G1785	U1725	G1665	G1605	C1545	U1485	G1425	U1365	A1305	C1245	U1185				
U167	A106	G1846	U46	C1846	C1786	U1726	U1666	A1606	C1546	U1486	A1426	C1366	G1306	G1246	U1186				
C168	A107	C1847	C47	C1847	U1787	A1727	G1667	U1607	G1547	U1487	U1427	G1367	U1307	G1247	U1187				
U169	G108	C1848	C48	C1848	U1788	G1728	C1668	C1608	U1548	C1488	G1428	C1368	C1308	U1248	U1188				
C253	C109	C1849	A49	C1849	A1789	G1729	C1669	U1609	U1549	U1489	A1429	C1369	U1309	G1249	A1189				
A254	U110	C1850	A50	C1850	U1790	A1730	A1670	C1610	G1550	U1490	C1430	A1370	C1310	C1250	A1190				
A255	C111	C1851	U51	C1851	C1791	A1731	A1671	A1611	G1551	U1491	C1431	U1371	C1311	A1251	C1191				
G256	C112	C1852	G52	C1852	U1792	A1732	C1672	C1612	C1552	G1492	C1432	C1372	C1312	G1252	A1192				
C113	C53	C1853	C53	C1853	C1793	U1733	C1673	C1613	G1553	U1493	C1433	C1373	U1313	G1253	A1193				
C258	A114	C1854	U54	C1854	A1794	U1734	G1674	G1614	C1554	G1494	C1434	G1374	A1314	C1254	G1194				
U259	C115	C1855	C55	C1855	A1795	A1735	C1675	A1615	G1555	A1495	A1435	C1375	C1315	G1255	G1195				
A260	G116	C1856	U56	C1856	U1796	A1736	A1676	A1616	C1556	G1496	A1436	U1376	G1316	A1256	C1196				
C261	A117	C1857	G57	C1857	A1797	U1737	C1677	U1617	G1557	A1497	G1437	A1377	U1317	U1257	C1197				
C262	A118	C1858	G58	C1858	G1798	G1738	U1678	A1618	C1558	A1498	C1438	A1378	G1318	G1258	U1198				
C263	G119	C1859	U59	C1859	C1799	U1739	C1679	U1619	C1559	A1499	C1439	G1379	A1319	C1259	U1199				

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

Chain BB: 5% 25% 70%

A121	U1	A61
U122	C2	C62
U123	C3	A63
G124	C4	U64
G125	A5	A65
C126	A6	G66
U127	C7	A67
C128	U8	G68
U129	G9	A69
G130	C10	A70
A131	A11	A71
G132	G12	G72
G133	A13	G73
G134	C14	U74
C135	C15	A75
A136	G16	G76
A137	U17	A77
A138	A18	C78
G139	C19	U79
U140	U20	C80
G141	C21	A81
G142	A22	G82
G143	U23	G83
G144	C24	G84
G145	A25	A85
U146	C26	A86
C147	C27	G87
A148	G28	U88
A149	C29	C89
	A30	G90
G152	U31	G91
G153	C32	C92
A154	A33	A93
G155	G34	A94
G156	G35	A95
G157	U36	A96
C158	C37	U97
C159	C38	A98
A160	C39	G99
U161	C40	A100
U162	A41	U101
G163	A42	G102
U164	G43	C103
C165	C44	G104
C166	A45	U105
U167	U46	A106
U168	C47	A107
U169	G48	G108
G253	A49	U109
A254	U50	U110
A255	U51	C111
G256	G52	G112
G257	C53	C113
C258	U54	A114
U259	C55	A115
A260	U56	G116
C261	G57	A117
C262	G58	A118
C263	U59	G119
		C120

G1226	A1166	G1106	C1046	C926	A866	U806	A746	A686	C626	A566	G506	U446	G386	G326	C266
G1227	C1167	C1107	C1047	U927	C867	U807	A747	C667	G627	G567	G507	C447	G387	U327	C267
A1228	G1168	G1108	A1048	C928	G868	U808	A748	U688	A628	A568	U508	A648	C388	U328	G268
A1229	A1229	A1109	G1049	C929	G869	U809	A749	C689	C629	G569	A509	A649	G389	U329	A269
A1230	U1170	G1110	A1050	C930	C870	G810	G750	C690	A630	A570	A510	A450	G390	U330	A270
U1231	U1051	C1111	U1051	U931	C871	C811	A751	A691	G631	G571	A511	A451	G391	U331	G270
A1232	G1052	U1112	G1052	U932	A872	G812	A752	G692	U632	G572	C512	A452	G392	U332	C271
U1233	G1053	C1113	G1053	U933	C873	C813	A753	U693	C633	C573	G513	C453	A393	C333	C272
G1234	C1174	A1114	G1054	U934	G874	A814	A754	G694	A634	G574	G514	U454	A394	G334	G273
A1235	A1175	G1115	G1055	U935	G875	G815	A755	G695	A635	C575	C515	A455	U395	C335	U274
A1236	G1176	U1116	A1056	U936	G876	U816	G756	G696	G636	A576	G516	A456	C396	U336	A275
G1237	U1177	G1117	G1057	U937	A877	C817	A757	G697	G637	U577	G517	U457	C397	U337	U276
A1238	G1058	C1118	U1058	G938	G878	U818	A758	G698	G638	G578	G518	U458	C398	C277	C277
A1239	C1179	G1119	U1059	G939	G879	U819	C759	U699	A639	A579	A519	U459	A399	C399	U278
A1240	G1180	A1120	G1060	G940	G880	G820	C760	G700	A640	A580	G520	C460	C400	U340	A279
U1241	A1181	A1121	U1061	C941	G881	C821	A761	U701	C541	U551	U521	U461	U401	U341	C280
C1242	C1182	C1122	G1062	G942	G882	G822	C762	G702	G642	G582	A522	A462	G402	U342	U281
A1243	U1183	A1123	C1063	U943	G883	G823	C763	G703	G643	G583	A523	C463	U403	U343	A282
U1244	C1184	C1124	U1064	U944	U884	C824	C764	G704	A644	A584	C524	A464	A404	U344	A283
A1245	G1185	A1125	G1065	U945	U885	U825	C765	C705	C545	U585	U525	C465	U405	U345	C284
C1246	A1186	A1126	G1066	U946	G886	G826	C766	G706	U646	U586	A526	A466	A406	U346	C285
U1247	G1187	A1127	G1067	A947	G887	U827	A767	G707	U647	A587	U527	A467	A407	G347	U286
A1248	A1188	U1128	U1068	G948	U888	G828	A768	G708	G648	A588	G528	U468	U408	G348	C287
G1249	C1189	C1129	C1069	G949	U889	C829	C769	G709	A649	U589	A529	A469	U409	U349	C288
U1250	U1190	U1130	G1070	G950	U890	G830	G770	A710	A650	G590	C530	C470	U410	U350	U289
G1251	G1191	C1131	G1071	U951	U891	C831	U771	C711	C651	A591	U531	U471	A411	G351	U290
G1252	C1192	A1132	C1072	U952	U892	G832	C772	U712	G652	G592	C532	C472	A412	C352	C291
U1253	G1193	C1133	A1073	G953	U893	G833	C773	U713	G653	A593	U533	U473	A413	G353	U292
G1254	A1194	U1134	U1074	G954	A894	U834	C774	U714	C654	U594	C534	A474	C414	C354	G293
U1255	A1195	U1135	A1075	U955	U895	C835	C775	U715	U655	U595	U535	A475	A415	A355	G294
G1256	A1196	C1136	U1076	G956	C896	U836	C776	U716	A656	C596	U536	A476	U416	C356	U295
A1257	G1197	G1137	U1077	A957	C897	A837	C777	A717	A657	G597	A537	U477	A417	C357	U296
G1258	C1198	A1138	U1078	G958	U898	G838	C778	U718	G658	C598	A538	A478	G418	U358	U297
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U1260	U1200	C1140	U1080	C960	C900	G840	U780	U720	G660	C600	G540	C480	U420	C360	U299
G1261	G1201	A1141	U1081	G961	U901	U841	A781	G721	G661	U601	A541	A481	U421	A361	U300
A1262	G1202	C1142	A1082	U962	C902	G842	A782	U722	G662	G602	A542	A482	U422	A362	G301
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U1265	A1205	G1145	C1085	G965	C905	C845	G785	U725	A665	C605	C545	U485	G425	U365	U305
A1266	G1206	G1146	G1086	C966	G906	A846	A786	A726	A666	C606	A546	A486	A426	U366	U306
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G1272	C1212	U1152	G1092	C972	C912	G852	G792	G732	C572	A612	C552	U492	C432	U372	U312
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U1280	U1280	U1160	C1100	G980	U920	U860	U800	A740	A680	G620	C560	C500	U440	G380	G320
G1281	C1221	C1161	A1101	A981	U921	C861	G801	A741	G681	G621	C561	G501	G441	C381	C321
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G1286	U1287	A1346	C1347	U1348	G1288	U1349	A1350	C1351	G1291	U1352	A1353	C1354	G1292	U1355	A1356	C1357	G1293	U1358	A1359	C1360	G1294	U1361	A1362	C1363	G1295	U1364	A1365	C1366	G1296	U1367	A1368	C1369	G1297	U1370	A1371	C1372	G1298	U1373	A1374	C1375	G1299	U1376	A1377	C1378	G1300	U1379	A1380	C1381	G1301	U1382	A1383	C1384	G1302	U1385	A1386	C1387	G1303	U1388	A1389	C1390	G1304	U1391	A1392	C1393	G1305	U1394	A1395	C1396	G1306	U1397	A1398	C1399	G1307	U1400	A1401	C1402	G1308	U1403	A1404	C1405	G1309	U1406	A1407	C1408	G1310	U1409	A1410	C1411	G1311	U1412	A1413	C1414	G1312	U1415	A1416	C1417	G1313	U1418	A1419	C1420	G1314	U1421	A1422	C1423	G1315	U1424	A1425	C1426	G1316	U1427	A1428	C1429	G1317	U1430	A1431	C1432	G1318	U1433	A1434	C1435	G1319	U1436	A1437	C1438	G1320	U1439	A1440	C1441	G1321	U1442	A1443	C1444	G1322	U1445	A1446	C1447	G1323	U1448	A1449	C1450	G1324	U1451	A1452	C1453	G1325	U1454	A1455	C1456	G1326	U1457	A1458	C1459	G1327	U1460	A1461	C1462	G1328	U1463	A1464	C1465	G1329	U1466	A1467	C1468	G1330	U1469	A1470	C1471	G1331	U1472	A1473	C1474	G1332	U1475	A1476	C1477	G1333	U1478	A1479	C1480	G1334	U1481	A1482	C1483	G1335	U1484	A1485	C1486	G1336	U1487	A1488	C1489	G1337	U1490	A1491	C1492	G1338	U1493	A1494	C1495	G1339	U1496	A1497	C1498	G1340	U1499	A1500	C1501	G1341	U1502	A1503	C1504	G1342	U1505	A1506	C1507	G1343	U1508	A1509	C1510	G1344	U1511	A1512	C1513	G1345	U1514	A1515	C1516	G1346	U1517	A1518	C1519	G1347	U1520	A1521	C1522	G1348	U1523	A1524	C1525	G1349	U1526	A1527	C1528	G1350	U1529	A1530	C1531	G1351	U1532	A1533	C1534	G1352	U1535	A1536	C1537	G1353	U1538	A1539	C1540	G1354	U1541	A1542	C1543	G1355	U1544	A1545	C1546	G1356	U1547	A1548	C1549	G1357	U1550	A1551	C1552	G1358	U1553	A1554	C1555	G1359	U1556	A1557	C1558	G1360	U1559	A1560	C1561	G1361	U1562	A1563	C1564	G1362	U1565	A1566	C1567	G1363	U1568	A1569	C1570	G1364	U1571	A1572	C1573	G1365	U1574	A1575	C1576	G1366	U1577	A1578	C1579	G1367	U1580	A1581	C1582	G1368	U1583	A1584	C1585	G1369	U1586	A1587	C1588	G1370	U1589	A1590	C1591	G1371	U1592	A1593	C1594	G1372	U1595	A1596	C1597	G1373	U1598	A1599	C1600	G1374	U1601	A1602	C1603	G1375	U1604	A1605	C1606	G1376	U1607	A1608	C1609	G1377	U1610	A1611	C1612	G1378	U1613	A1614	C1615	G1379	U1616	A1617	C1618	G1380	U1619	A1620	C1621	G1381	U1622	A1623	C1624	G1382	U1625	A1626	C1627	G1383	U1628	A1629	C1630	G1384	U1631	A1632	C1633	G1385	U1634	A1635	C1636	G1386	U1637	A1638	C1639	G1387	U1640	A1641	C1642	G1388	U1643	A1644	C1645	G1389	U1646	A1647	C1648	G1390	U1649	A1650	C1651	G1391	U1652	A1653	C1654	G1392	U1655	A1656	C1657	G1393	U1658	A1659	C1660	G1394	U1661	A1662	C1663	G1395	U1664	A1665	C1666	G1396	U1667	A1668	C1669	G1397	U1670	A1671	C1672	G1398	U1673	A1674	C1675	G1399	U1676	A1677	C1678	G1400	U1679	A1680	C1681	G1401	U1682	A1683	C1684	G1402	U1685	A1686	C1687	G1403	U1688	A1689	C1690	G1404	U1691	A1692	C1693	G1405	U1694	A1695	C1696	G1406	U1697	A1698	C1699	G1407	U1700	A1701	C1702	G1408	U1703	A1704	C1705	G1409	U1706	A1707	C1708	G1410	U1709	A1710	C1711	G1411	U1712	A1713	C1714	G1412	U1715	A1716	C1717	G1413	U1718	A1719	C1720	G1414	U1721	A1722	C1723	G1415	U1724	A1725	C1726	G1416	U1727	A1728	C1729	G1417	U1730	A1731	C1732	G1418	U1733	A1734	C1735	G1419	U1736	A1737	C1738	G1420	U1739	A1740	C1741	G1421	U1742	A1743	C1744	G1422	U1745	A1746	C1747	G1423	U1748	A1749	C1750	G1424	U1751	A1752	C1753	G1425	U1754	A1755	C1756	G1426	U1757	A1758	C1759	G1427	U1760	A1761	C1762	G1428	U1763	A1764	C1765	G1429	U1766	A1767	C1768	G1430	U1769	A1770	C1771	G1431	U1772	A1773	C1774	G1432	U1775	A1776	C1777	G1433	U1778	A1779	C1780	G1434	U1781	A1782	C1783	G1435	U1784	A1785	C1786	G1436	U1787	A1788	C1789	G1437	U1790	A1791	C1792	G1438	U1793	A1794	C1795	G1439	U1796	A1797	C1798	G1440	U1799	A1800	C1801	G1441	U1802	A1803	C1804	G1442	U1805	A1806	C1807	G1443	U1808	A1809	C1810	G1444	U1811	A1812	C1813	G1445	U1814	A1815	C1816	G1446	U1817	A1818	C1819	G1447	U1820	A1821	C1822	G1448	U1823	A1824	C1825	G1449	U1826	A1827	C1828	G1450	U1829	A1830	C1831	G1451	U1832	A1833	C1834	G1452	U1835	A1836	C1837	G1453	U1838	A1839	C1840	G1454	U1841	A1842	C1843	G1455	U1844	A1845	C1846	G1456	U1847	A1848	C1849	G1457	U1850	A1851	C1852	G1458	U1853	A1854	C1855	G1459	U1856	A1857	C1858	G1460	U1859	A1860	C1861	G1461	U1862	A1863	C1864	G1462	U1865	A1866	C1867	G1463	U1868	A1869	C1870	G1464	U1871	A1872	C1873	G1465	U1874	A1875	C1876	G1466	U1877	A1878	C1879	G1467	U1880	A1881	C1882	G1468	U1883	A1884	C1885	G1469	U1886	A1887	C1888	G1470	U1889	A1890	C1891	G1471	U1892	A1893	C1894	G1472	U1895	A1896	C1897	G1473	U1898	A1899	C1900	G1474	U1901	A1902	C1903	G1475	U1904	A1905	C1906	G1476	U1907	A1908	C1909	G1477	U1910	A1911	C1912	G1478	U1913	A1914	C1915	G1479	U1916	A1917	C1918	G1480	U1919	A1920	C1921	G1481	U1922	A1923	C1924	G1482	U1925	A1926	C1927	G1483	U1928	A1929	C1930	G1484	U1931	A1932	C1933	G1485	U1934	A1935	C1936	G1486	U1937	A1938	C1939	G1487	U1940	A1941	C1942	G1488	U1943	A1944	C1945	G1489	U1946	A1947	C1948	G1490	U1949	A1950	C1951	G1491	U1952	A1953	C1954	G1492	U1955	A1956	C1957	G1493	U1958	A1959	C1960	G1494	U1961	A1962	C1963	G1495	U1964	A1965	C1966	G1496	U1967	A1968	C1969	G1497	U1970	A1971	C1972	G1498	U1973	A1974	C1975	G1499	U1976	A1980	C1981	G1500	U1982	A1983	C1984	G1501	U1985	A1986	C1987	G1502	U1988	A1989	C1990	G1503	U1991	A1992	C1993	G1504	U1994	A1995	C1996	G1505	U1997	A1998	C1999	G1506	U2000	A2001	C2002	G1507	U2003	A2004	C2005	G1508	U2006	A2007	C2008	G1509	U2010	A2011	C2012	G1510	U2013	A2014	C2015	G1511	U2016	A2017	C2018	G1512	U2019	A2020	C2021	G1513	U2022	A2023	C2024	G1514	U2025	A2026	C2027	G1515	U2028	A2029	C2030	G1516	U2031	A2032	C2033	G1517	U2034	A2035	C2036	G1518	U2037	A2038	C2039	G1519	U2040	A2041	C2042	G1520	U2043	A2044	C2045	G1521	U2046	A2047	C2048	G1522	U2049	A2050	C2051	G1523	U2052	A2053	C2054	G1524	U2055	A2056	C2057	G1525	U2058	A2059	C2060	G1526	U2061	A2062	C2063	G1527	U2064	A2065	C2066	G1528	U2067	A2068	C2069	G1529	U2070	A2071	C2072	G1530	U2073	A2074	C2075	G1531	U2076	A2077	C2078	G1532	U2079	A2080	C2081	G1533	U2082	A2083	C2084	G1534	U2085	A2086	C2087	G1535	U2088	A2089	C2090	G1536	U2091	A2092	C2093	G1537	U2094	A2095	C2096	G1538	U2097	A2098	C2099	G1539	U2100	A2101	C2102	G1540	U2103	A2104	C2105	G1541	U2106	A2107	C2108	G1542	U2109	A2110	C2111	G1543	U2112	A2113	C2114	G1544	U2115	A2116	C2117	G1545	U2118	A2119	C2120	G1546	U2121	A2122	C2123	G1547	U2124	A2125	C2126	G1548	U2127	A2128	C2129	G1549	U2130	A2131	C2132	G1550	U2133	A2134	C2135	G1551	U2136	A2137	C2138	G1552	U2139	A2138	C2139	G1553	U2140	A2139	C2141	G1554	U2142	A2143	C2144	G1555	U2145	A2146	C2146	G1556	U2147	A2148	C2149	G1557	U2150	A2151	C2152	G1558	U2153	A2154	C2155	G1559	U2156	A2157	C2158	G1560	U2159	A2160	C2161	G1561	U2162	A2163	C2164	G1562	U2165	A2166	C2167	G1563	U2168	A2169	C2170	G1564	U2171	A2172	C2173	G1565	U2174	A2175	C2176	G1566	U2177	A2178	C2179	G1567	U2180	A2181	C2182	G1568	U2183	A2184	C2185	G1569	U2186	A2187	C2188	G1570	U2189	A2190	C2191	G1571	U2192	A2193	C2194	G1572	U2195	A2196	C2197	G1573	U2198	A2199	C2200	G1574	U2201	A2202	C2203	G1575	U2204	A2205	C2206	G1576	U2207	A2208	C2209	G1577	U2210	A2211	C2212	G1578	U2213	A2214	C2215	G1579	U2216	A2217	C2218	G1580	U2219	A2220	C2221	G1581	U2222	A2223	C2224	G1582	U2225	A2226	C2227	G1583	U2228	A2229	C2230	G1584	U2231	A2232	C2233	G1585	U2234	A2235	C2236	G1586	U2237	A2238	C2239	G1587	U2240	A2241	C2242	G1588	U2243	A2244	C2245	G1589	U2246	A2247	C2248	G1590	U2249	A2250	C2251	G1591	U2252	A2253	C2254	G1592	U2255	A2256	C2257	G1593	U2258	A2259	C2260	G1594	U2261	A2262	C2263	G1595	U2264	A2265	C2266	G1596	U2267	A2268	C2269	G1597	U2270	A2271	C2272	G1598	U2273	A2274	C2275	G1599	U2276	A2300	C2301	G1600	U2302	A2303	C2304	G1601	U2305	A2306	C2307	G1602	U2308	A2309	C2310	G1603	U2311	A2312	C2313	G1604	U2314	A2315	C2316	G1605	U2317	A2318	C2319	G1606	U2320	A2321	C2322	G1607	U2323	A2324	C2325	G1608	U2326	A2327	C2328	G1609	U2329	A2330	C2331	G1610	U2332	A2333	C2334	G1611	U2335	A2336	C2337	G1612	U2338	A2339	C2340	G1613	U2341	A2342	C2343	G1614	U2344	A2345	C2346	G1615	U2347	A2348	C2349	G1616	U2350	A2351	C2352	G1617	U2353	A2354	C2355	G1618	U2356	A2357	C2358	G1619	U2359	A2360
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U181
U182
C183
G184
G185
C186
G187
C188
A189
U190
U191
A192
A193
A194
G195
C196
A197
A198
A199
A200
C201
C202
C203
C204
G205
G206
G207
G208
U209
G210

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

Chain BF: 8% 92%

C1
G2
A3
U4
U5
C6
G7
C8
C9
A10
C11
U12
U13
C14
U15
C16
U17
U18
A19
U20
C21
U22
G23
G24
G25
U26
G27
C28
U29
C30
U31
G32
C33
C34
C35
G36
C37
C38
C39
U40
U41
U42
U43
U44
G45
G46
G47
G48
C49
G50
C51
G52
G53
U54
A55
C56
C57
U58
U59
C60

A61
U62
U63
U64
U65
U66
U67
A68
C69
A70
G71
A72
U73

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

Chain BG: 17% 83%

G1
U2
G3
U4
A5
U6
U7
U8
C9
U10
C11
U12
U13
C14
U15
G16
U17
U18
C19
U20
C21
G22
C23
A24
G25
C26
C27
A28
U29
C30
U31
U32
G33
A34
G35
G36
G37
A38
A39
G40
U41
U42
U43
U44
G45
G46
G47
U48
A49
G50
U51
A52
C53
G54
A55
G56
A57
G58
U59
A60

A61
C62
U63
C64
C65
C66
A67
U68
G69
C70
C71
G72
U73
G74
C75
G76
U77
C78
U79
G80
G81
U82
U83
U84
C85
U86
G87
G88
A89
U90
U91
U92
U93
G94
U95
C96
G97
A98
A99
G100
U101
G102
U103
A104
A105
G106
U107
G108
C109
U110
C111
C112
G113
A114
G115
G116
C117
U118
A119
U120

C121
G122
C123
U124
C125
G126
U127
U128
G129
C130
U131
U132
C133
U134
C135
G136
U137
C138
U139
G140
A141
A142
U143
G144
C145
C146
U147
G148
U149
A150
C151
U152
C153
A154
U155
G156
U157
A158
A159
C160
C161
A162
G163
U164
C165
C166
U167
A168
A169
G170
U171
C172
G173
U174
G175
G176
U177
G178
C179
C180

C181
G182

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

Chain BH: 28% 69%

U1
U2
U3
U4
U5
U6
C7
C8
C9
U10
C11
U12
C13
C14
A15
U16
C17
U18
G19
A20
G21
U22
G23
U24
A25
C26
U27
C28
G29
C30
A31
U32
G33
G34
C35
C36
U37
C38
G39
A40
U41
U42
C43
A44
G45
U46
G47
C48
U49
C50
U51
U52
G53
C54
A55
U56
C57
U58
A59
G60
U61
U62
G63
U64
G65
G66
G67
G68
U69
C70
U71
G72
U73
G74
G75
G76
U77
C78
A79
C80
U81
U82
U83
A84
C85
G86
U87
C88
U89
C90
G91
A92
G93
G94
C95
G96
C97
U98
G99
A100
U101
C102
C103
U104
U105
G106
U107
U108
C109
U110
U111
U112
G113
C114
A115
U116
U117
U118
U119
C120

A121
U122
G123
C124
U125
G126
U127
A128
G129
U130
A131
C132
U133
U134
U135

• Molecule 42: 60S RIBOSOMAL PROTEIN L18


Chain BI: 39% 35% 19% 7%

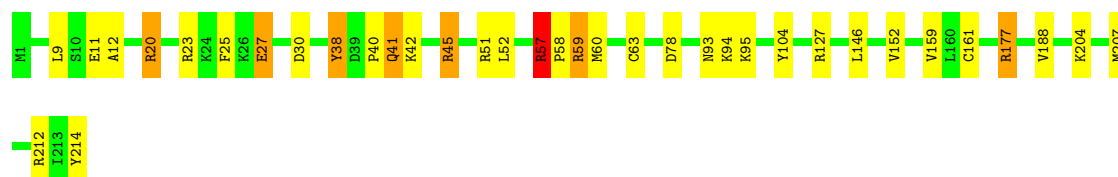
MET
G2
V3
D4
L5
V8
Q9
K10
K11
K12
K13
V14
V15
R16
A17
H18
T19
Y20
S21
P24
Y25
L26
K27
L28
L29
I30
K31
L32
K33
Y34
F35
L36
G37
K38
R39
T40
N41
F44
N45
I48
H49
K50
R51
R56
N57
N58
R59
A60
P61
L64
S65
R66
F138
T139

G70
K71
R72
R73
R74
T75
V76
W77
L78
K79
K80
S84
P85
R86
A87
H88
I89
Y90
G91
D92
Y93
L94
D95
D96
V97
R98
M99
T100
R101
I102
P103
A104
L105
R106
I107
C108
A109
L110
R111
F112
S113
K114
S115
A116
R117
E118
R119
I120
G125
E126
C127
A134
M135
W136
A137
F138
T139



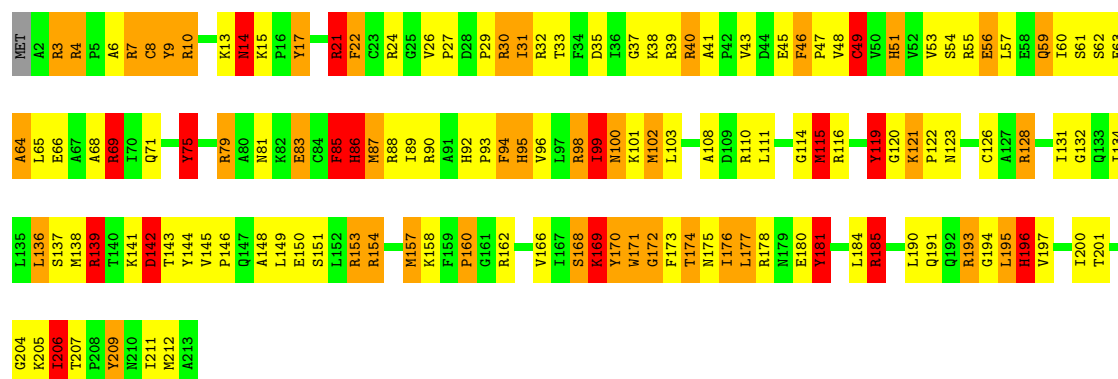
● Molecule 43: RIBOSOMAL PROTEIN

Chain B.J:  83% 13% 4%



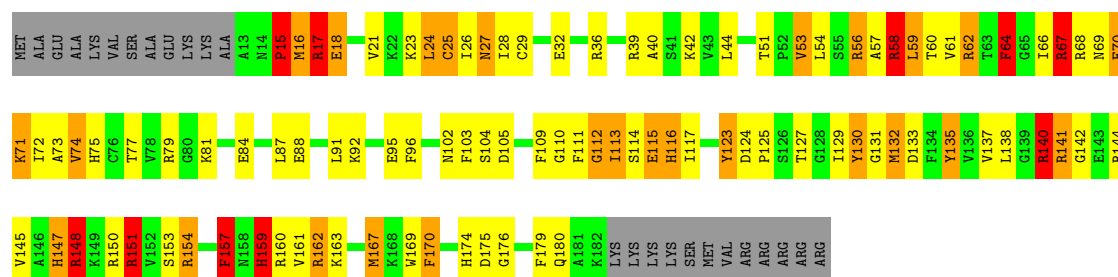
- Molecule 44: 60S RIBOSOMAL PROTEIN L10, PUTATIVE

Chain BK:

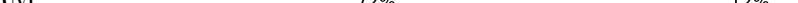


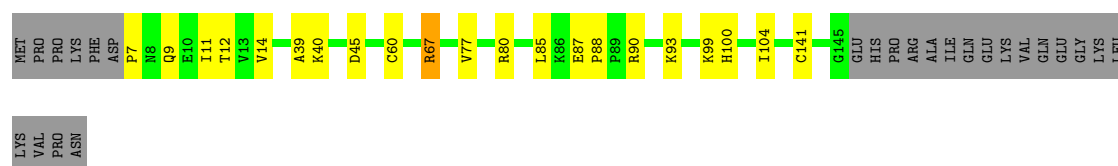
- Molecule 45: 60S RIBOSOMAL PROTEIN L11, PUTATIVE

Chain BL: 



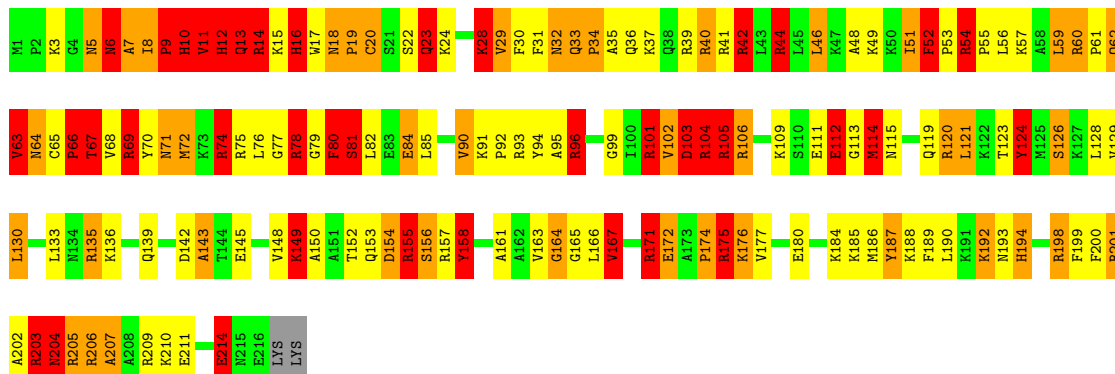
- Molecule 46: 60S RIBOSOMAL PROTEIN L12, PUTATIVE

Chain BM:  72% 12% 15%



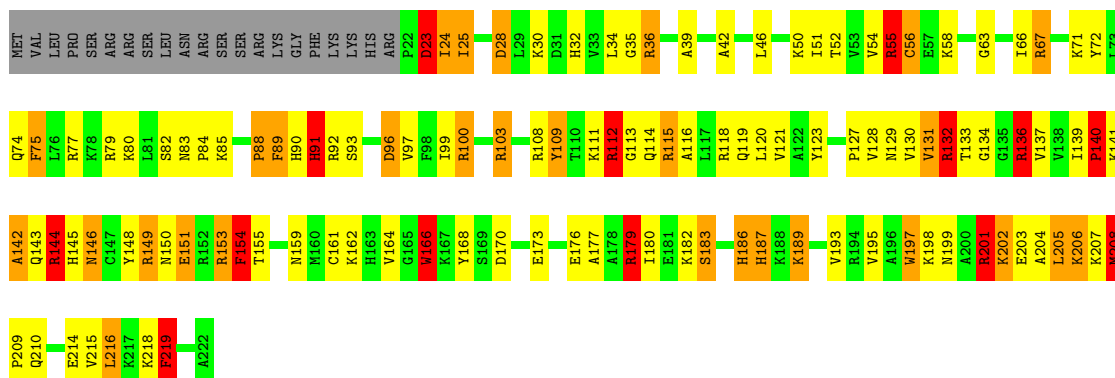
● Molecule 47: 60S RIBOSOMAL PROTEIN L13

Chain BN: 



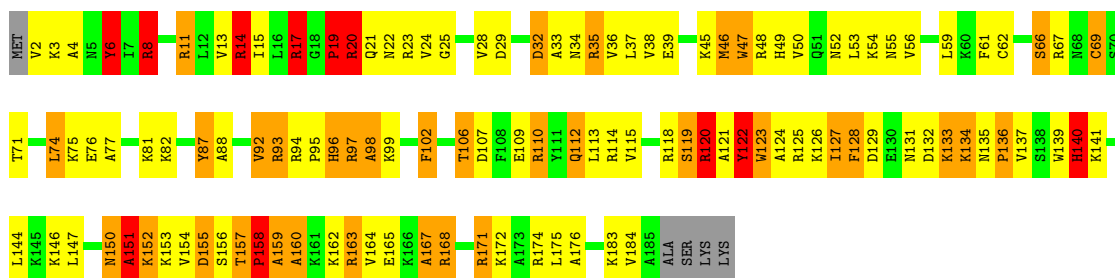
- Molecule 48: 60S RIBOSOMAL PROTEIN L13A, PUTATIVE

Chain BO: 



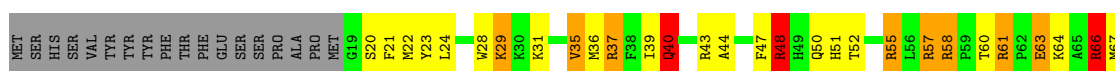
- Molecule 49: PROBABLE 60S RIBOSOMAL PROTEIN L14

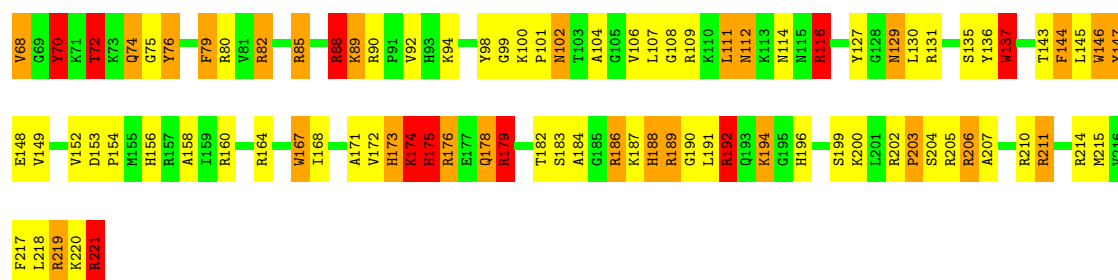
Chain BP: 



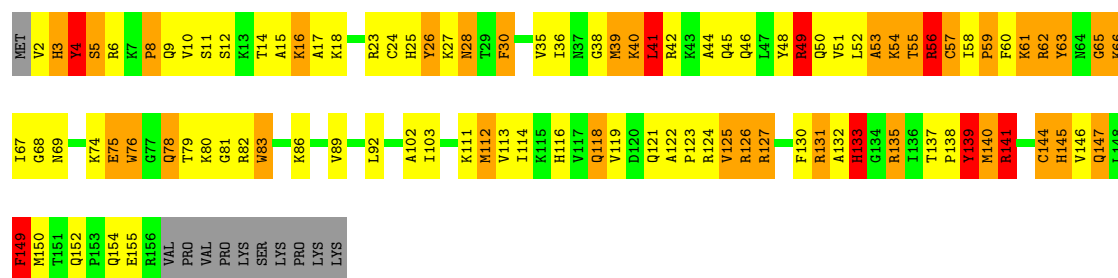
- Molecule 50: RIBOSOMAL PROTEIN L15

Chain BQ: 

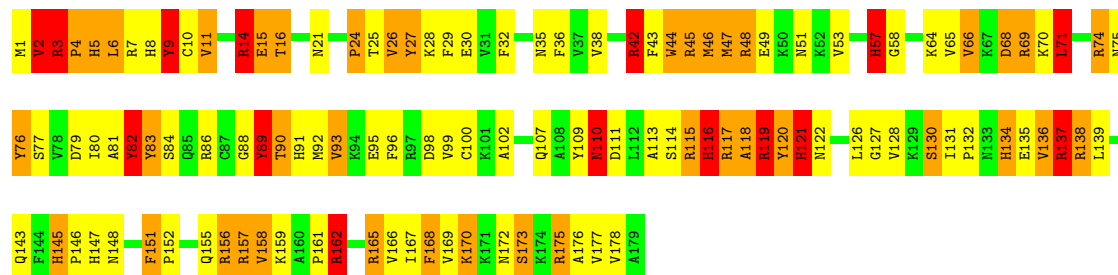




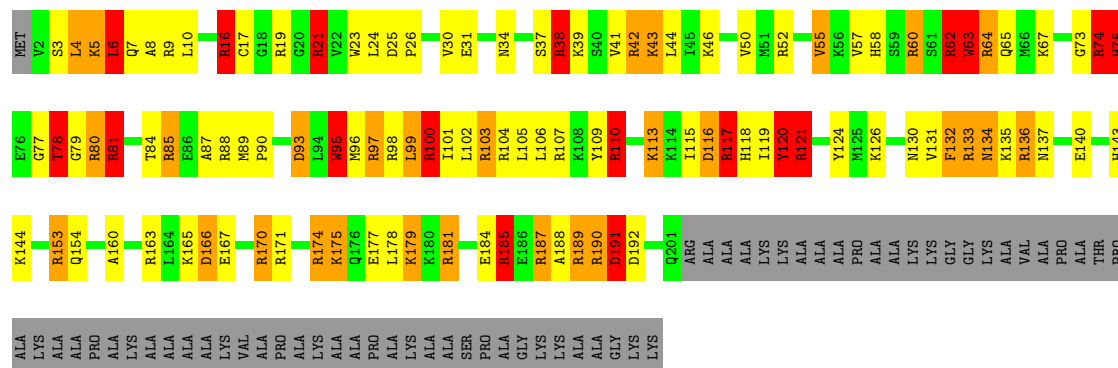
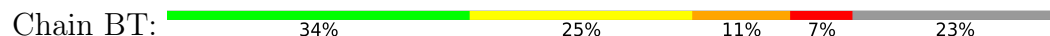
- Molecule 51: 60S RIBOSOMAL PROTEIN L17, PUTATIVE



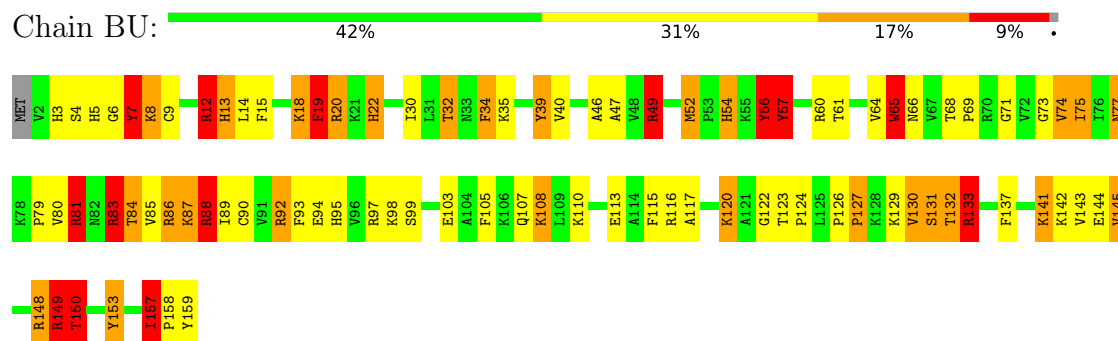
- Molecule 52: 60S RIBOSOMAL PROTEIN L18A



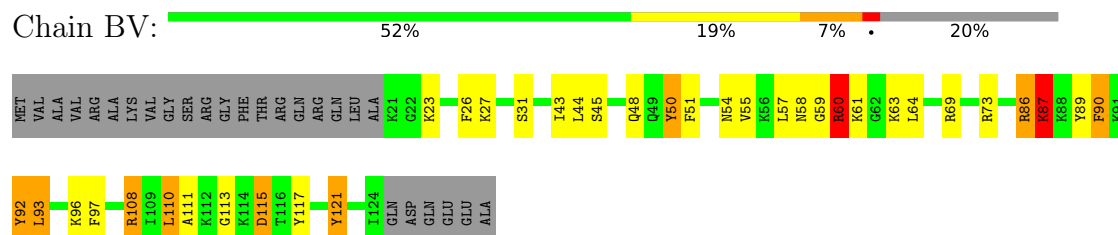
- Molecule 53: 60S RIBOSOMAL PROTEIN L19, PUTATIVE



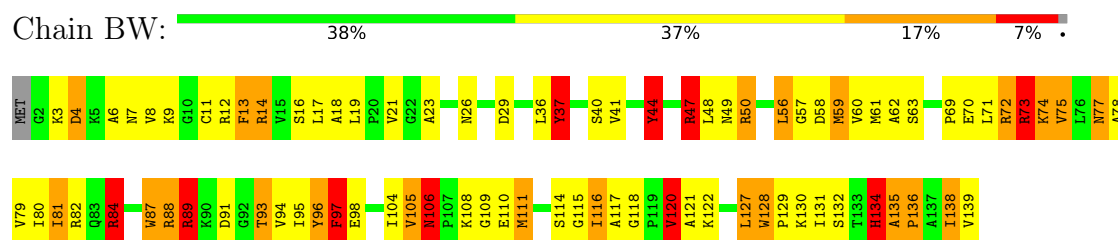
- Molecule 54: 60S RIBOSOMAL PROTEIN L21E, PUTATIVE



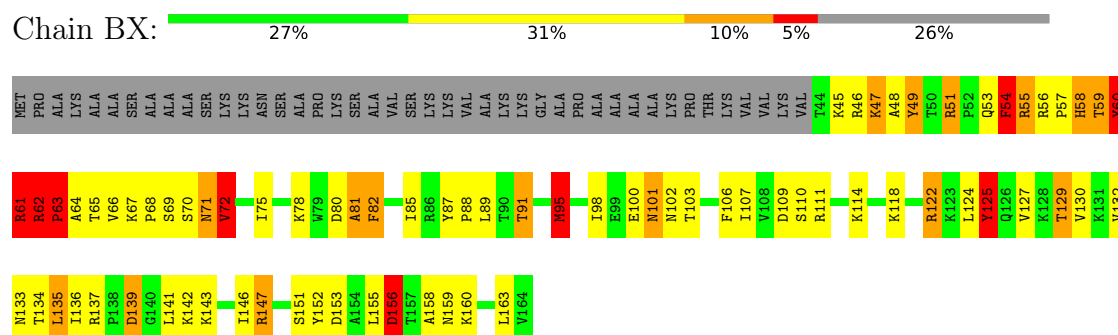
• Molecule 55: 60S RIBOSOMAL PROTEIN L22, PUTATIVE



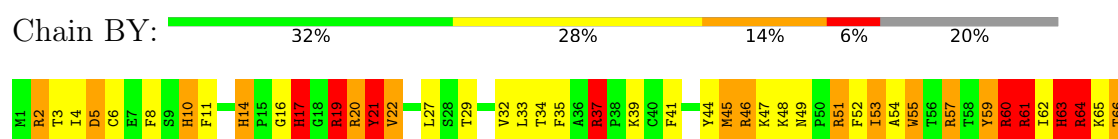
• Molecule 56: 60S RIBOSOMAL PROTEIN L23, PUTATIVE



• Molecule 57: 60S RIBOSOMAL PROTEIN L23A



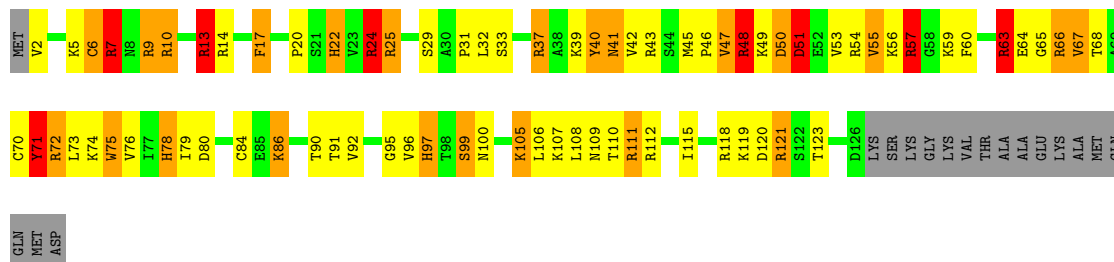
• Molecule 58: 60S RIBOSOMAL PROTEIN L24, PUTATIVE





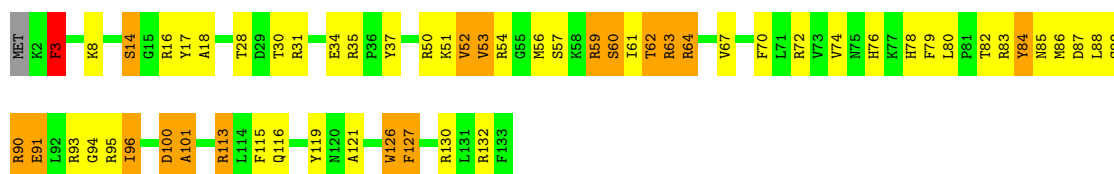
• Molecule 59: 60S RIBOSOMAL PROTEIN L26, PUTATIVE

Chain BZ: 34% 32% 16% 6% 13%



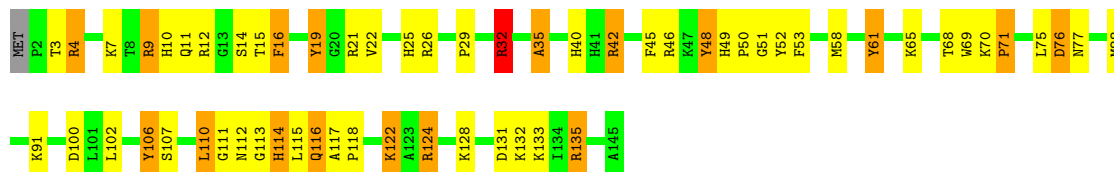
• Molecule 60: 60S RIBOSOMAL PROTEIN L27, PUTATIVE

Chain Ba: 56% 30% 13% ..



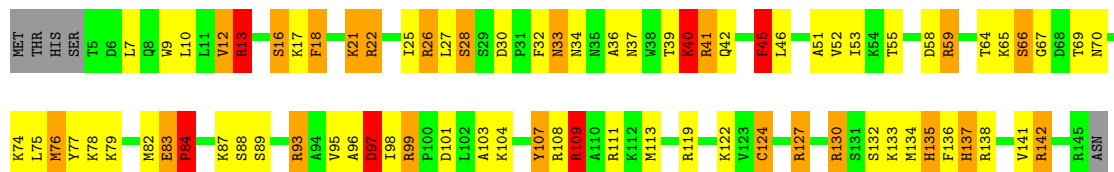
• Molecule 61: 60S RIBOSOMAL PROTEIN L27A

Chain Bb: 58% 29% 12% ..



• Molecule 62: 60S RIBOSOMAL PROTEIN L28, PUTATIVE

Chain Bc: 43% 34% 15% ..

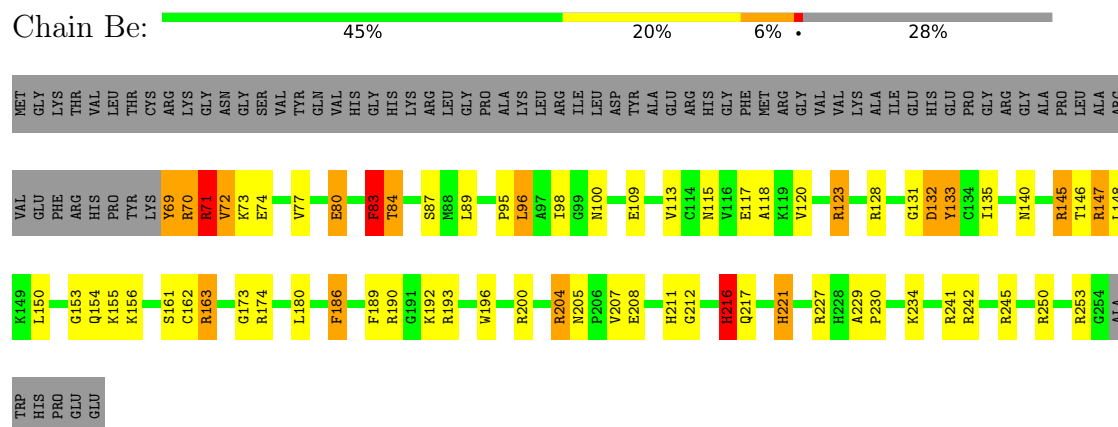


• Molecule 63: 60S RIBOSOMAL PROTEIN L29, PUTATIVE

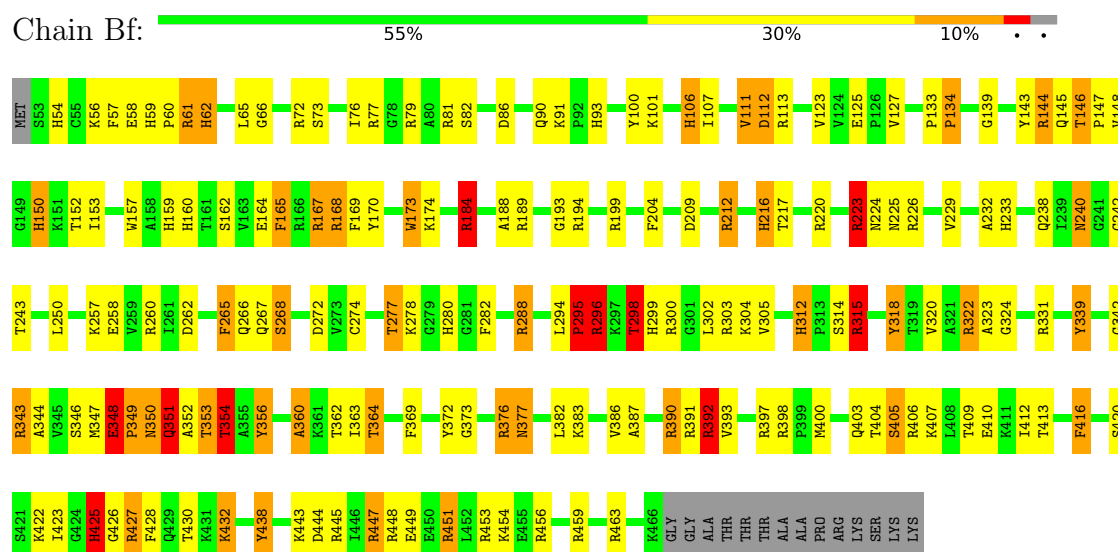
Chain Bd: 59% 27% 11% ..



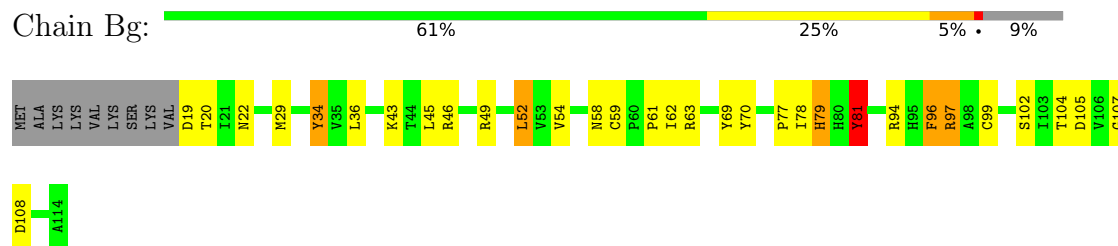
• Molecule 64: 60S RIBOSOMAL PROTEIN L2, PUTATIVE



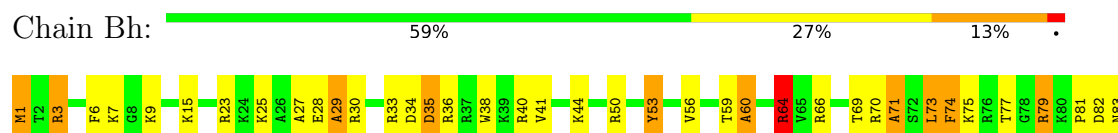
• Molecule 65: RIBOSOMAL PROTEIN L3, MITOCHONDRIAL, PUTATIVE

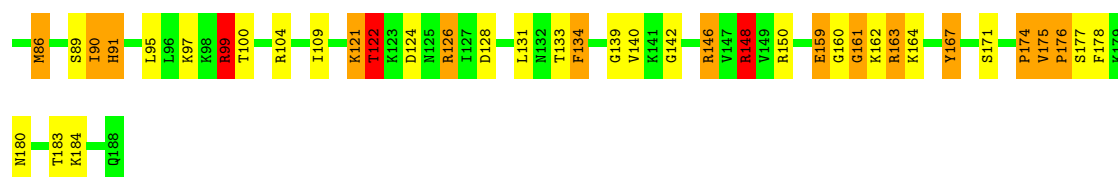


• Molecule 66: 60S RIBOSOMAL PROTEIN L30



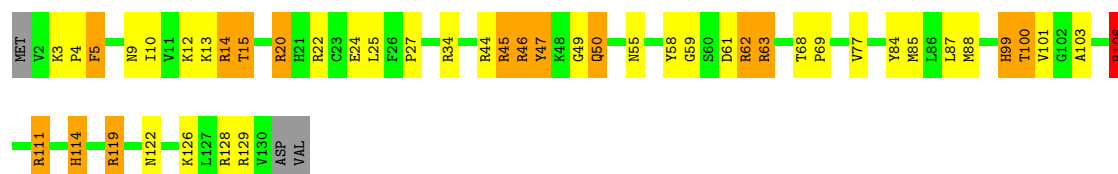
• Molecule 67: 60S RIBOSOMAL SUBUNIT PROTEIN L31, PUTATIVE





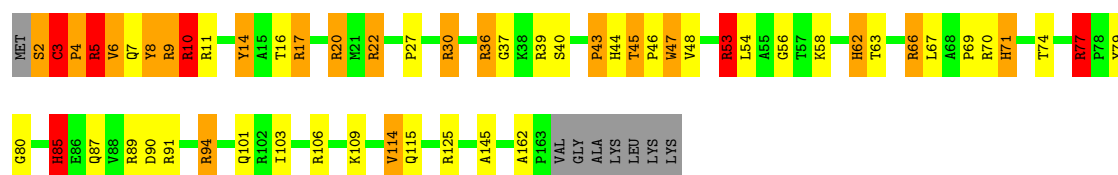
- Molecule 68: 60S RIBOSOMAL PROTEIN L32, PUTATIVE

Chain Bi: 63% 23% 11% ..



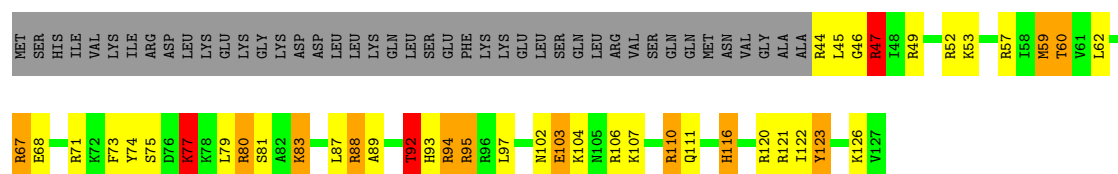
- Molecule 69: 60S RIBOSOMAL PROTEIN L34, PUTATIVE

Chain Bj: 62% 19% 11% • 5%



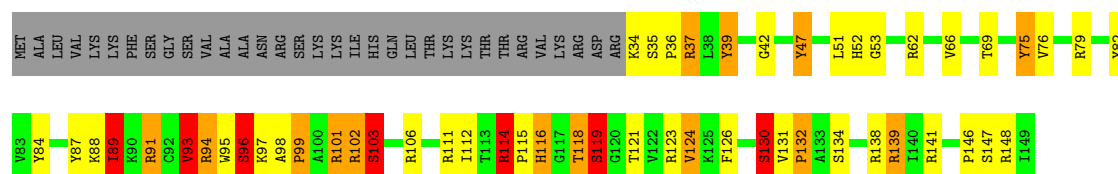
- Molecule 70: 60S RIBOSOMAL PROTEIN L35, PUTATIVE

Chain Bk: 32% 22% 9% • 34%



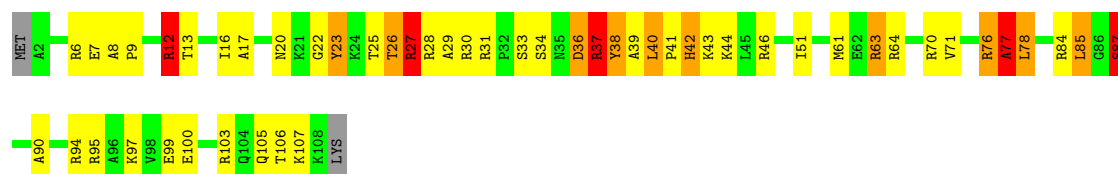
- Molecule 71: 60S RIBOSOMAL PROTEIN L35A, PUTATIVE

Chain Bl: 42% 22% 9% 5% 22%



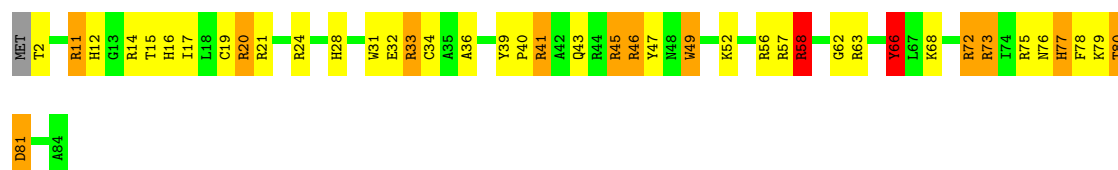
- Molecule 72: RIBOSOMAL PROTEIN L36, PUTATIVE

Chain Bm: 50% 34% 9% 5% •



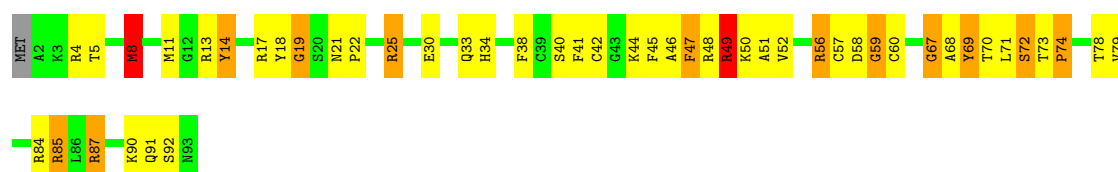
• Molecule 73: RIBOSOMAL PROTEIN L37

Chain Bn: 49% 33% 14% ..



• Molecule 74: 60S RIBOSOMAL PROTEIN L37A, PUTATIVE

Chain Bo: 46% 38% 13% ..



• Molecule 75: 60S RIBOSOMAL PROTEIN L38, PUTATIVE

Chain Bp: 59% 34% 5% ..



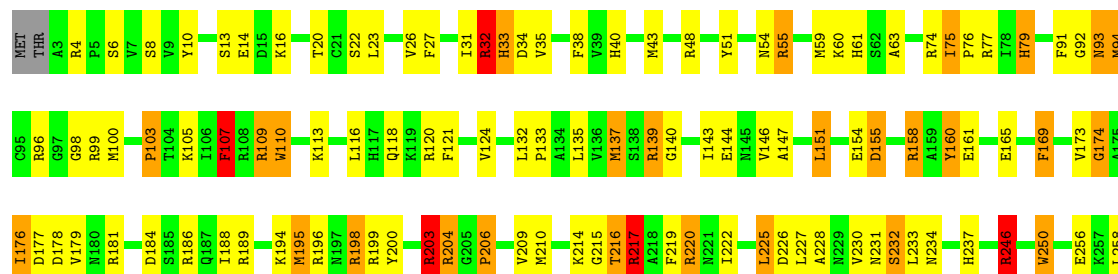
• Molecule 76: 60S RIBOSOMAL PROTEIN L39, PUTATIVE

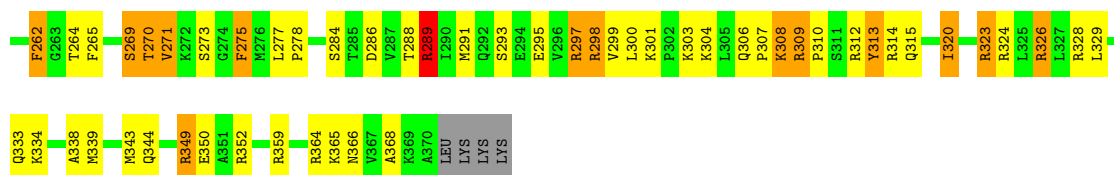
Chain Bq: 53% 27% 14% ..



• Molecule 77: 60S RIBOSOMAL PROTEIN L4

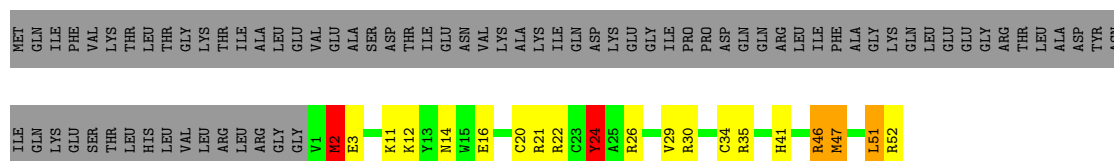
Chain Br: 54% 32% 11% ..





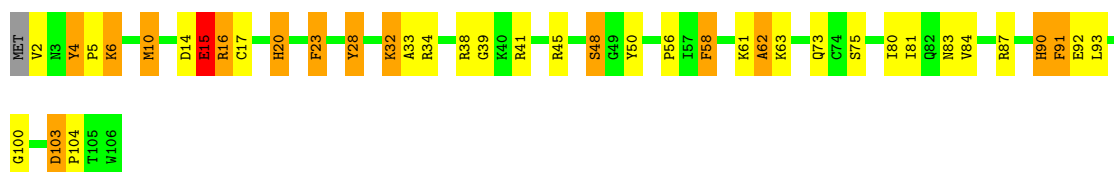
• Molecule 78: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain Bs: 25% 12% 59%



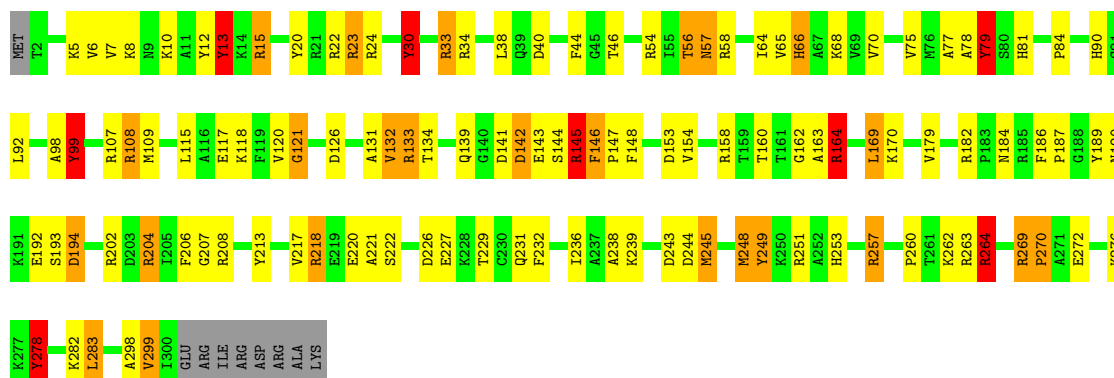
• Molecule 79: 60S RIBOSOMAL PROTEIN L44

Chain Bt: 61% 24% 13%



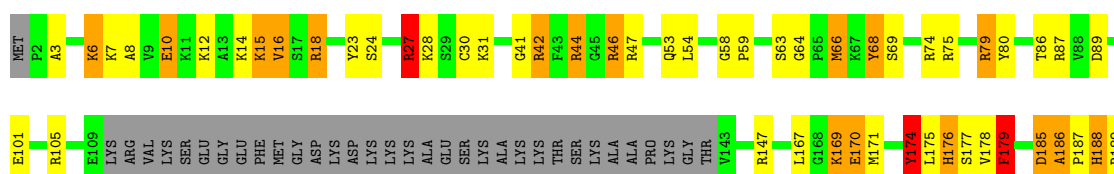
• Molecule 80: 60S RIBOSOMAL PROTEIN L5, PUTATIVE

Chain Bu: 58% 28% 8%



• Molecule 81: 60S RIBOSOMAL PROTEIN L6, PUTATIVE

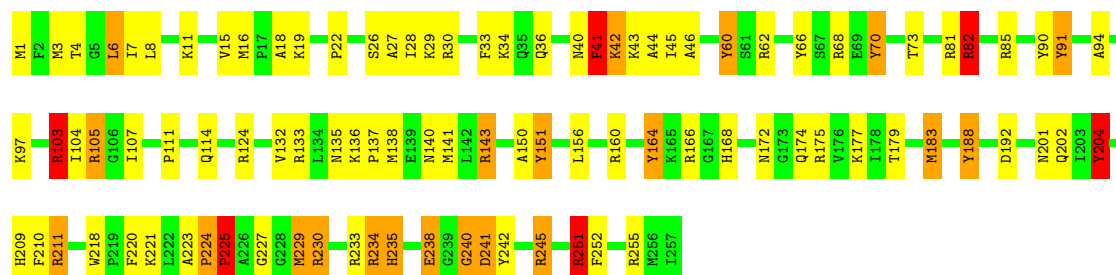
Chain Bv: 53% 19% 9% 18%





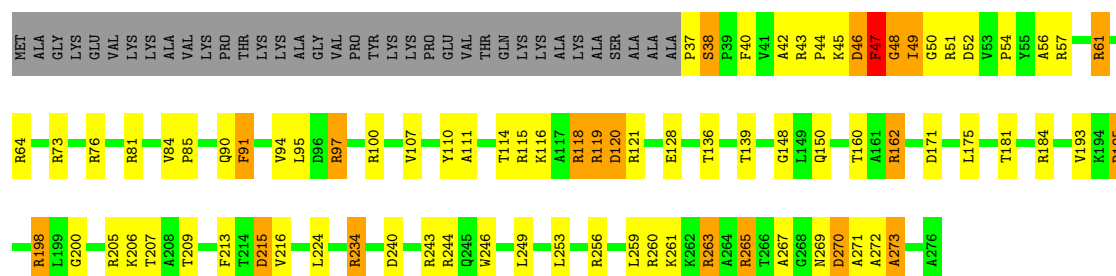
• Molecule 82: 60S RIBOSOMAL PROTEIN L7, PUTATIVE

Chain Bw: 62% 27% 8%



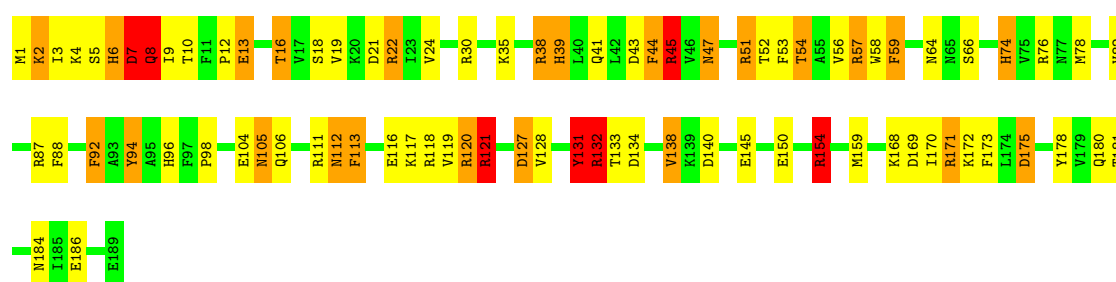
• Molecule 83: 60S RIBOSOMAL PROTEIN L7A, PUTATIVE

Chain Bx: 57% 22% 7% 13%



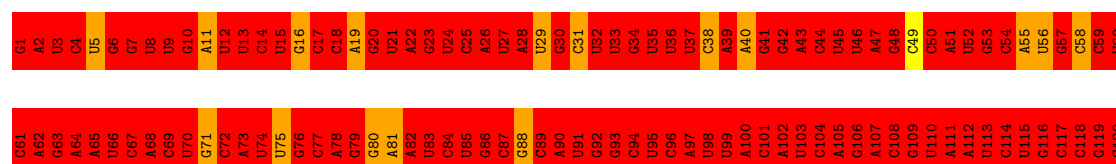
• Molecule 84: 60S RIBOSOMAL PROTEIN L9, PUTATIVE

Chain By: 56% 28% 13%



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

Chain AA: 19% 75%



U1082	C1082	U1022	U952	A902	G842	G782	G722	U602	G542	C482	G422	G362	C302	G242	A181	C121
C1083	C1083	U1023	U963	G903	U943	C783	U723	C603	A543	G483	G423	A362	A303	A242	C181	A122
A1084	G1024	C964	C964	U904	C964	C784	A724	C504	A544	G484	A424	G364	G304	G244	C183	A123
U1085	U1025	C965	C965	C905	A845	C785	G725	A605	A545	A545	G425	G365	A305	A245	A184	A124
U1086	U1026	C966	C966	U906	U946	C786	U726	U606	A546	A486	G426	A366	C306	C246	A185	A125
G1087	U1027	C967	C967	U907	G847	C787	U727	U607	A547	G487	G427	A367	G307	G247	U186	U126
C1088	C1028	U968	U968	C908	C948	C788	U728	A608	G548	G488	G428	C368	U308	U248	C187	U127
G1089	G1029	U969	U969	C909	A849	C789	U729	U609	A549	G489	G429	A369	C309	C249	G188	U128
A1090	U1030	U970	U970	G910	U850	C790	U730	C510	G550	A490	G429	A370	U310	C250	G189	U129
C1091	G1031	U971	U971	A911	G851	C791	U731	G611	C551	G491	G431	C371	U311	C251	A190	G130
G1092	U1032	C972	C972	C912	C852	A792	G732	A612	C552	G492	A432	U372	G312	G252	C191	G131
C1093	G1033	U973	U973	U913	G853	C793	C733	G613	G553	A493	U433	G373	A313	G253	G192	G132
G1094	U1034	U974	U974	U914	A854	A794	G734	U614	A554	G494	U434	C374	C314	G254	G193	G133
C1095	C1035	C975	C975	G915	G855	C795	G735	A615	C555	G495	A435	C375	U315	A255	U194	U134
U1096	A1036	G976	G976	A916	G856	C796	U736	A616	C556	G496	A436	C376	C316	A256	C195	C135
G1097	G1037	U977	U977	A917	G857	C797	G737	C517	G557	G497	G437	U377	A317	U257	U196	U136
C1098	U1038	U978	U978	U918	G858	A798	C738	A618	U558	G498	G438	A378	A318	A258	C197	C137
U1099	U1039	G979	G979	U919	G859	C799	C739	A619	G559	G499	U439	U379	U319	A259	U198	C138
A1100	U1040	U980	U980	A920	C860	A800	A740	U620	C560	C500	U440	C380	U320	A260	U199	G139
C1101	U1041	A981	A981	C921	G861	U801	G741	U621	C561	A501	C441	A381	C321	U261	U200	C140
G1102	C1042	C982	C982	A922	G862	A802	U742	G622	C562	A502	G442	A382	A322	G262	U201	A141
A1103	U1043	A983	A983	A923	C863	C803	C743	G623	U563	A503	A443	C383	U323	A263	C202	U142
G1104	G1044	A984	A984	A924	C864	A804	C744	A624	A564	U504	U444	C384	U324	A264	U203	U143
G1105	G1045	G985	G985	G925	G865	A805	G745	G625	G565	U505	U445	A385	C325	A265	U204	A144
A1106	C1046	U986	U986	C926	U866	G806	G746	G626	U566	G506	C446	G386	C326	U266	A205	C145
U1107	G1047	C987	C987	A927	G867	A807	U747	A627	C567	C507	C447	U387	C327	U267	U206	U146
G1108	C1048	C988	C988	U928	C868	C808	C748	C628	C568	C508	G448	G388	U328	A268	G147	G148
U1109	G1049	U989	U989	G929	A869	A809	C749	A629	A569	C509	U449	A389	G329	G269	U208	
A1110	C1050	U990	U990	G930	U870	A810	A750	A630	U570	A510	A450	U390	G330	A270	C210	U150
C1111	A1051	C991	C991	A931	U871	A811	G751	A631	G571	A511	G451	G391	G331	A271	G211	A151
G1112	C1052	G992	G992	U932	U872	C812	G752	U632	U572	A512	A452	G392	A332	C272	G212	
C1113	A1053	C993	C993	A933	U873	G813	U753	C633	U573	G513	G453	C393	A333	C273	G213	A152
A1114	U1054	A994	A994	A934	A874	G814	C754	U634	U574	C514	G454	C394	A334	A274	C214	C153
G1115	U1055	C995	C995	A935	A875	G815	G755	G635	G575	C515	G455	G395	G335	A275	C215	U154
U1116	C1056	U996	U996	C936	C876	A816	G756	A636	U576	G516	A456	U396	C336	C276	U216	U155
G1117	G1057	C997	C997	U937	G877	C817	A757	U637	U577	A517	G457	G397	G337	G277	G217	G156
U1118	G1058	U998	U998	A938	U878	C818	C758	G638	U578	A518	C458	U398	G338	C278	G218	G157
A1119	C1059	C999	C999	A939	G879	C819	G759	C639	U579	A519	C459	A399	A339	C279	U219	C158
G1120	U1060	U1000	U1000	G940	A880	G820	U760	C640	C580	A520	U460	G400	G340	U280	G159	
U1121	C1061	C1001	C1001	C941	C881	U821	G761	A641	A581	A521	G461	U401	C341	C281	A160	A160
U1122	U1062	G1002	G1002	A942	C882	U822	U762	G642	A582	A522	A462	G402	C342	C282	A161	
C1123	U1063	G1003	G1003	U943	C883	C823	U763	C643	U583	U523	G463	G403	U343	A283	A162	A162
G1124	C1064	A1004	G1004	C944	A884	U824	U764	A644	G584	A524	A464	A404	U344	C284	G163	
U1125	G1065	U1005	U1005	A945	A885	U825	G765	C645	G585	C525	A465	C405	U345	C285	G164	
G1126	U1066	C1006	C1006	G	A886	C826	G766	C646	G586	G526	A466	U406	U346	C286	C165	
U1127	G1067	G1007	G1007	C	A887	C827	A767	C647	G587	A527	U467	G407	U347	G287	A227	U222
G1128	A1068	C1008	C1008	C	A888	U828	C768	G648	G588	U528	A468	C408	G348	G288	A167	
A1129	U1069	G1009	G1009	C	G889	C829	C769	C649	A589	G529	G469	C409	C349	G289	U229	
G1130	U1070	U1010	U1010	U	U890	A830	C770	G650	U590	A530	C470	A410	U350	G290	U230	G169
A1131	U1071	C1011	C1011	G	G891	C831	A771	G651	A591	G531	U471	U411	C351	G291	G231	C170
C1132	U1072	G1012	G1012	G	C892	U832	C772	U652	C592	G532	A472	G412	G352	C292	U232	U171
G1133	U1073	C1013	C1013	G	G893	C833	G773	A653	U593	C533	C473	G413	G353	A293	C233	A172
U1134	G1074	U1014	U1014	G	A894	U834	C774	G654	C594	A534	C474	C414	C354	G294	G234	A173
U1135	U1075	U1015	U1015	C	C895	C835	C775	U655	A595	G535	A475	G415	G355	U295	U235	U174
A1136	U1076	C1016	G1016	C956	C896	A836	C776	U656	A596	C536	C476	U416	U356	A296	G236	A175
C1137	U1077	G1017	G1017	A957	A897	C837	U777	C657	A597	G537	U477	U417	C357	A297	G237	C176
U1138	A1078	G1018	G1018	C958	A898	C838	C778	C658	C598	A538	U478	G418	U358	C298	C238	A177
G1139	C1079	U1019	U1019	C959	A899	C839	G779	A659	C599	A539	C479	A419	A359	A299	G239	U178
G1140	A1080	C1020	C1020	G960	A900	A840	U780	G660	C600	A540	U480	C420	C360	C300	G240	G179
U1141	U1081	G1021	G1021	U961	C901	U841	G781	C661	A601	A541	A481	G421	U361	U301	U241	A180

U2045	G1985	A1805	A	G1685	G1565	C1445	C1322	G1262	G1202	G1142
G2046	G1986	C1806	G	G1686	A1566	U1446	G1323	G1263	G1203	C1143
G2047	G1987	A1807	G	G1687	C1567	U1447	G1324	G1264	A1204	G1144
C2048	G1988	G1808	A	G1688	U1568	C1448	C1325	C1265	U1145	U1145
U2049	G1989	G1809	C	G1689	C1569	U1449		C1266	A1206	G1146
C2050	G1990	C1810	A	A1690	A1570	U1450	U1328	A1267	G1207	A1147
G2051	C1991	C1811	G1751	U1691	A1571	U1451	U1329	C1268	U1208	G1148
U2052	C1992	C1812	C1752	U1692	C1572	U1452	U1330	A1269	U1209	G1149
C2053	G1993	C1813	A1753	C1693	A1573	U1453	G1331	U1270	U1210	G1150
A2054	G1994	C1814	G1754	C1694	A1574	U1454		U1271	C1211	U1151
G2055	G1995	C1815	U1755	C1695	A1575	C1455	C1334	G1272	C1212	U1152
C2056	G1996	C1816	G1756	C1696	A1576	U1456	C1335	C1273	U1213	G1153
G2057	G1997	U1817	C1757	C1697	G1577	U1457	G1336	A1274	C1214	A1154
C2058	A1998	C1818	C1758	A1698	G1578	U1458	A1337	A1275	A1215	A1155
A2059	G1999	U1819	U1759	A1699	A1579	U1459		A1276	A1216	A1156
G2060	C2000	G1820	G1760	C1700	A1580	U1460	C1339	G1277	U1217	U1157
C2061	C2001	C1821	G1761	C1701	C1581	A1461	U1400	C1278	C1218	U1158
U2062	A2002	G1822	G1762	G1702	U1582	A1462	U1341	A1279	A1219	C1159
C2063	C2003	C1823	G1763	A1703	C1583	A1463	C1342	U1280	U1220	U1160
A2064	U2004	A1824	C1764	C1704	U1584	G1464	G1403	G1281	G1221	U1161
U2065	U2005	A1825	G1765	G1705	A1585	C1465	G1343	A1282	A1222	A1162
G2066	G2006	U1826	G1766	A1706	C1586	U1466	U1406	C1283	A1223	G1163
A2067	G2007	G1827	G1767	G1707	C1587	U1467	C1346	A1284	C1224	A1164
A2068	C2008	A1948	G1768	A1708	A1588	G1468	C1347	C1285	C1225	G1165
A2069	U2009	C1828	A1769	U1709	A1589	G1469	U1409	A1226	G1226	C1166
C2070	C2010	U1830	U1770	C1710	A1590	U1470	C1410	C1287	A1227	G1167
U2071	C2011	U1831	U1771	C1711	C1591	U1471	A1349	U1288	A1228	C1168
G2072	G2012	G1832	U1772	A1712	U1592	G1472	U1351	A1289	G1229	A1169
C2073	A2013	C1833	U1773	A1713	C1593	U1473	U1352	G1290	U1230	C1170
G2074	G2014	U1834	U1774	G1714	A1594	U1474	U1353	A1291	G1231	C1171
C2075	U2015	U1835	U1775	C1715	G1595	A1475	A1354	A1292	U1232	A1172
G2076	A2016	U1836	C1776	U1716	A1596	C1476	U1416	U1293	A1173	A1173
C2077	U2017	G1837	G1777	G1717	C1597	U1477	U1355	U1294	G1233	G1174
A2078	U2018	C1838	C1778	C1718	A1598	U1478	U1357	G1295	G1235	A1175
U2079	G2019	G1839	C1779	A1719	C1599	U1479	U1358	G1296	C1176	C1176
C2080	C2020	C1840	A1780	C1720	A1540	C1480	U1359	G1297	A1237	G1177
A2081	A2021	G1841	A1781	A1721	G1601	U1481	U1420	G1298	U1238	A1178
C2082	A2022	C1842	C1782	G1722	U1602	C1482	A1421	A1299	C1239	A1179
G2083	U2023	A1843	G1783	U1723	G1603	C1483	A1422	A1300	G1240	C1180
U2084	C2024	C1844	G1784	A1724	A1604	U1484	G1424	C1301	A1241	U1181
C2085	A2025	G1845	U1785	G1725	G1605	U1485	U1364	A1302	A1242	A1182
G2086	C2026	G1846	G1786	U1726	G1606	G1486	G1425	U1303	G1243	C1183
C2087	U2027	U1847	G1787	G1727	A1607	G1487	A1427	C1304	A1244	A1184
U2088	G2028	G1848	U1788	G1728	U1608	G1488	C1367	A1305	U1245	G1185
C2089	A2029	A1849	C1789	C1729	U1609	G1489	U1428	U1306	G1246	C1186
U2090	U2030	G1850	G1790	G1730	C1550	A1490	U1369	U1307	A1247	G1187
C2091	C2031	A1851	U1791	G1731	G1551	U1491	G1370	G1308	U1248	A1188
A2092	G2032	U1852	C1792	G1732	C1612	U1492	C1371	G1309	U1249	A1189
C2093	C2033	U1853	A1793	G1733	A1613	A1493	C1372	G1310	A1250	G1190
G2094	G2034	C1854	U1794	A1734	G1614	C1494	U1373	U1311	G1251	G1191
U2095	C2035	U1855	C1795	U1735	A1615	G1555	A1374	G1312	A1252	C1192
C2096	A2036	G1856	G1796	U1736	U1616	G1556	U1375	C1313	G1253	A1193
U2097	G2037	G1857	U1797	G	A1617	U1497	U1376	C1314	A1254	U1194
A2098	C2038	G1858	U1798	U	G1618	C1498	C1377	C1315	U1255	U1195
C2099	G2039	A1859	C1799	C	A1619	U1559	U1378	G1316	C1256	G1196
A2100	A2040	U1860	U1800	C	G1620	A1560	A1379	U1317	U1257	U1197
C2101	G2041	A1861	U1801	A	G1681	A1561	U1380	G1318	U1258	U1198
A2102	C2042	C1862	U1802	C	U1682	G1562	C1381	U1319	U1259	C1199
G2103	A2043	A1863	U1803	A	U1683	U1563	A1382	G1320	U1260	A1200
C2104	G1864	C1864	U1804	C	U1684	A1564	A1383	G1321	U1261	A1201

G2105	G2106	C2107	C2108	G2109	U2110	C2111	G2112	U2113	U2114	G2115	U2116	U2117	U2118	C2119	C2120	G2121	A2122	U2123	G2124	A2125	U2126	G2127	G2128	U2129	G2130	C2131	A2132	A2133	U2134	A2135	C2136	A2137	G2138	G2139	U2140	G2141	A2142	U2143	C2144	G2145	G2146	A2147	C2148	U2149	G2150	U2151	C2152	G2153	C2154	U2155	G2156	U2157	U2158	C2159	U2160	C2161	G2162	C2163	G2164
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C2165	G2166	A2167	C2168	G2169	U2170	A2171	A2172	A2173	U2174	U2175	U2176	C2177	A2178	C2179	C2180	G2181	A2182	U2183	A2184	U2185	U2186	G2187	C2188	U2189	U2190	C2191	A2192	A2193	U2194	A2195	G2196	A2197	G2198	G2199	A2200	A2201	G2202	C2203	A2204	A2205	A2206	A2207	G2208	U2209	C2210	G2211	U2212	A2213	A2214	C2215	A2216	A2217	G2218	G2219	U2220	A2221	G2222	C2223	U2224
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G2225	U2226	A2227	G2228	G2229	U2230	G2231	A2232	A2233	C2234	C2235	U2236	G2237	C2238	A2239	G2240	C2241	U2242	G2243	G2244	A2245	U2246	C2247	A2248	U2249	U2250	U2251
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● Molecule 86: E-SITE TRNA



G1	C2	C3	C4	G5	G6	A7	U8	A9	G10	C11	U12	C13	A14	G15	U16	C17	G18	G19	U20	A21	G22	A23	G24	C25	A26	G27	G28	G29	G30	A31	U32	U33	G34	A35	A36	A37	A38	U39	C40	C41	C42	C43	G44	U45	G46	U47	C48	C49	U50	U51	G52	G53	U54	U55	C56	G57	A58	U59	U60
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C61	C62	G63	A64	G65	U66	C67	C68	G69	G70	G71	C72	A73
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4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	164000	Depositor
Resolution determination method	Not provided	Depositor
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

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 >2	RMSZ	# Z >2
1	A0	1.19	2/1808 (0.1%)	1.83	45/2432 (1.9%)
10	A9	0.91	0/542	1.55	8/722 (1.1%)
11	AC	1.41	1/1655 (0.1%)	1.76	29/2240 (1.3%)
12	AD	1.02	0/877	1.60	13/1182 (1.1%)
13	AE	1.32	4/1324 (0.3%)	1.83	29/1771 (1.6%)
14	AF	0.76	0/946	1.36	11/1270 (0.9%)
15	AG	1.45	2/1170 (0.2%)	1.93	41/1567 (2.6%)
16	AH	1.24	0/937	1.77	21/1263 (1.7%)
17	AI	0.92	0/1098	1.64	15/1473 (1.0%)
18	AJ	1.29	0/1035	1.78	13/1386 (0.9%)
19	AK	1.06	0/1211	1.77	24/1625 (1.5%)
2	A1	1.37	5/1973 (0.3%)	1.90	53/2657 (2.0%)
20	AL	1.24	1/1033 (0.1%)	1.91	27/1380 (2.0%)
21	AM	1.05	0/1247	1.76	29/1666 (1.7%)
22	AO	1.08	0/1206	1.81	23/1613 (1.4%)
23	AP	1.40	1/1766 (0.1%)	1.83	37/2383 (1.6%)
24	AQ	1.11	0/839	1.77	23/1139 (2.0%)
25	AR	1.52	3/612 (0.5%)	1.96	26/835 (3.1%)
26	AS	1.22	0/1137	1.73	27/1520 (1.8%)
27	AT	1.17	2/1065 (0.2%)	1.99	30/1411 (2.1%)
28	AU	1.00	0/681	1.54	6/907 (0.7%)
29	AV	1.17	0/825	1.95	19/1105 (1.7%)
3	A2	1.08	0/1507	1.76	36/2027 (1.8%)
30	AW	1.37	1/648 (0.2%)	1.84	14/868 (1.6%)
31	AX	1.11	2/1649 (0.1%)	1.71	35/2203 (1.6%)
32	AY	1.22	0/521	1.83	9/685 (1.3%)
33	AZ	1.20	1/527 (0.2%)	1.77	13/702 (1.9%)
34	BA	4.08	8852/44057 (20.1%)	3.34	8033/68678 (11.7%)
35	BB	3.66	5797/34826 (16.6%)	2.99	5090/54269 (9.4%)
36	BC	4.32	938/4004 (23.4%)	3.24	674/6235 (10.8%)
37	BD	4.09	601/2830 (21.2%)	3.33	521/4410 (11.8%)
38	BE	3.90	902/4956 (18.2%)	3.64	1067/7716 (13.8%)
39	BF	3.69	277/1691 (16.4%)	3.64	354/2627 (13.5%)
4	A3	1.32	1/2026 (0.0%)	1.92	53/2699 (2.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	BG	4.34	1057/4358 (24.3%)	3.41	840/6797 (12.4%)
41	BH	3.79	548/3201 (17.1%)	3.52	652/4987 (13.1%)
42	BI	1.47	4/1553 (0.3%)	2.04	64/2070 (3.1%)
43	BJ	0.72	0/1743	1.28	12/2339 (0.5%)
44	BK	1.40	3/1760 (0.2%)	1.89	45/2359 (1.9%)
45	BL	1.33	1/1385 (0.1%)	1.80	33/1851 (1.8%)
46	BM	0.67	0/1033	1.21	1/1394 (0.1%)
47	BN	2.40	4/1793 (0.2%)	2.18	80/2392 (3.3%)
48	BO	1.46	2/1655 (0.1%)	1.84	44/2214 (2.0%)
49	BP	1.48	3/1506 (0.2%)	1.97	45/2014 (2.2%)
5	A4	1.33	2/1623 (0.1%)	2.04	60/2185 (2.7%)
50	BQ	1.52	1/1755 (0.1%)	1.84	42/2346 (1.8%)
51	BR	1.39	1/1270 (0.1%)	1.99	39/1705 (2.3%)
52	BS	1.36	3/1508 (0.2%)	2.06	54/2028 (2.7%)
53	BT	1.45	1/1689 (0.1%)	1.97	65/2232 (2.9%)
54	BU	1.35	1/1290 (0.1%)	1.89	39/1734 (2.2%)
55	BV	0.96	0/878	1.57	13/1169 (1.1%)
56	BW	1.44	5/1059 (0.5%)	2.00	32/1424 (2.2%)
57	BX	1.56	4/1007 (0.4%)	1.97	35/1353 (2.6%)
58	BY	1.28	1/857 (0.1%)	1.82	26/1150 (2.3%)
59	BZ	1.44	3/1021 (0.3%)	2.07	43/1362 (3.2%)
6	A5	1.42	6/1574 (0.4%)	1.83	36/2100 (1.7%)
60	Ba	1.40	0/1111	1.95	31/1479 (2.1%)
61	Bb	1.35	4/1165 (0.3%)	1.92	34/1554 (2.2%)
62	Bc	2.50	3/1145 (0.3%)	2.20	62/1528 (4.1%)
63	Bd	1.21	2/582 (0.3%)	1.98	22/777 (2.8%)
64	Be	1.50	7/1416 (0.5%)	1.91	38/1905 (2.0%)
65	Bf	1.43	8/3387 (0.2%)	1.99	129/4548 (2.8%)
66	Bg	1.75	3/745 (0.4%)	2.09	23/1005 (2.3%)
67	Bh	1.27	4/1551 (0.3%)	2.00	56/2059 (2.7%)
68	Bi	1.39	2/1076 (0.2%)	1.91	30/1439 (2.1%)
69	Bj	1.24	3/1312 (0.2%)	1.85	34/1743 (2.0%)
7	A6	1.38	3/1548 (0.2%)	1.95	44/2076 (2.1%)
70	Bk	1.46	0/726	2.06	31/957 (3.2%)
71	Bl	1.44	4/958 (0.4%)	2.05	35/1290 (2.7%)
72	Bm	1.54	1/859 (0.1%)	1.97	29/1141 (2.5%)
73	Bn	1.60	1/713 (0.1%)	2.01	28/949 (3.0%)
74	Bo	1.70	8/727 (1.1%)	1.88	26/968 (2.7%)
75	Bp	1.50	1/666 (0.2%)	1.87	15/885 (1.7%)
76	Bq	1.31	1/471 (0.2%)	1.71	9/626 (1.4%)
77	Br	1.46	5/2937 (0.2%)	1.98	106/3943 (2.7%)
78	Bs	1.40	1/433 (0.2%)	1.86	12/572 (2.1%)
79	Bt	1.36	1/883 (0.1%)	1.87	24/1170 (2.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
8	A7	1.06	0/2471	1.64	33/3368 (1.0%)
80	Bu	1.30	1/2397 (0.0%)	1.88	65/3219 (2.0%)
81	Bv	1.30	1/1242 (0.1%)	1.84	29/1667 (1.7%)
82	Bw	1.44	2/2105 (0.1%)	1.91	49/2823 (1.7%)
83	Bx	1.48	5/1936 (0.3%)	1.85	38/2603 (1.5%)
84	By	1.32	1/1561 (0.1%)	1.95	62/2098 (3.0%)
85	AA	3.42	7237/52940 (13.7%)	3.10	8226/82489 (10.0%)
86	AB	2.36	80/1740 (4.6%)	2.66	188/2712 (6.9%)
9	A8	1.09	0/337	1.68	4/445 (0.9%)
All	All	3.06	26432/250887 (10.5%)	2.80	28260/369909 (7.6%)

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
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
2	A1	0	18
20	AL	0	6
21	AM	0	18
22	AO	0	17
23	AP	0	14
24	AQ	0	7
25	AR	0	12
26	AS	0	7
27	AT	0	27
28	AU	0	7
29	AV	0	13
3	A2	0	11
30	AW	0	13
31	AX	0	10

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Mol	Chain	#Chirality outliers	#Planarity outliers
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
4	A3	0	23
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
5	A4	0	27
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
6	A5	0	23
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
69	Bj	1	23
7	A6	0	26
70	Bk	0	12

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Mol	Chain	#Chirality outliers	#Planarity outliers
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
8	A7	0	17
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
9	A8	0	4
All	All	3	5934

The worst 5 of 26432 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	AA	469	G	C5-C4	80.15	1.94	1.38
47	BN	7	ALA	CA-C	79.39	3.59	1.52
34	BA	743	A	N9-C4	74.20	1.82	1.37
62	Bc	78	LYS	CD-CE	69.91	3.26	1.51
34	BA	214	A	C6-N1	57.25	1.75	1.35

The worst 5 of 28260 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	AA	469	G	N9-C4-C5	-49.23	85.71	105.40
39	BF	32	G	P-O3'-C3'	41.15	169.07	119.70
35	BB	1212	C	C6-N1-C2	-40.14	104.24	120.30
85	AA	769	C	C6-N1-C2	-39.18	104.63	120.30
34	BA	692	U	P-O3'-C3'	38.13	165.46	119.70

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	78	0
2	A1	1940	0	2043	92	0
3	A2	1484	0	1547	84	0
4	A3	2003	0	2138	152	0
5	A4	1592	0	1688	137	0
6	A5	1551	0	1660	81	0
7	A6	1518	0	1571	97	0
8	A7	2412	0	2334	76	0
9	A8	334	0	343	13	0
10	A9	530	0	527	17	0
11	AC	1620	0	1660	81	0
12	AD	853	0	857	36	0
13	AE	1300	0	1359	72	0
14	AF	940	0	962	6	0
15	AG	1148	0	1226	84	0
16	AH	922	0	923	49	0
17	AI	1074	0	1097	48	0
18	AJ	1018	0	1050	60	0
19	AK	1190	0	1254	34	0
20	AL	1021	0	1096	45	0
21	AM	1229	0	1291	92	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	AO	1181	0	1240	51	0
23	AP	1731	0	1782	133	0
24	AQ	827	0	883	40	0
25	AR	603	0	592	53	0
26	AS	1116	0	1170	41	0
27	AT	1050	0	1141	96	0
28	AU	673	0	735	25	0
29	AV	809	0	841	36	0
30	AW	636	0	648	34	0
31	AX	1628	0	1695	43	0
32	AY	514	0	571	53	0
33	AZ	526	0	550	22	0
34	BA	39395	0	19108	6136	0
35	BB	31164	0	15283	3844	0
36	BC	3584	0	1759	705	0
37	BD	2533	0	1235	393	0
38	BE	4441	0	2194	693	0
39	BF	1521	0	773	229	0
40	BG	3896	0	1874	617	0
41	BH	2867	0	1408	474	0
42	BI	1527	0	1646	76	0
43	BJ	1717	0	1815	12	0
44	BK	1725	0	1797	129	0
45	BL	1363	0	1402	82	0
46	BM	1022	0	1109	4	0
47	BN	1762	0	1869	216	0
48	BO	1627	0	1761	95	0
49	BP	1484	0	1601	135	0
50	BQ	1716	0	1796	87	0
51	BR	1245	0	1300	79	0
52	BS	1473	0	1512	83	0
53	BT	1672	0	1799	138	0
54	BU	1260	0	1315	66	0
55	BV	863	0	908	52	0
56	BW	1042	0	1106	55	0
57	BX	990	0	1059	76	0
58	BY	836	0	863	136	0
59	BZ	1008	0	1088	55	0
60	Ba	1091	0	1162	0	0
61	Bb	1137	0	1174	0	0
62	Bc	1129	0	1213	0	0
63	Bd	571	0	595	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	Be	1390	0	1444	0	0
65	Bf	3317	0	3451	0	0
66	Bg	735	0	754	0	0
67	Bh	1526	0	1654	0	0
68	Bi	1054	0	1112	0	0
69	Bj	1293	0	1420	0	0
70	Bk	719	0	811	0	0
71	Bl	936	0	968	0	0
72	Bm	849	0	934	0	0
73	Bn	699	0	718	0	0
74	Bo	715	0	743	0	0
75	Bp	656	0	717	0	0
76	Bq	457	0	495	0	0
77	Br	2883	0	3011	0	0
78	Bs	427	0	465	0	0
79	Bt	866	0	922	0	0
80	Bu	2354	0	2425	0	0
81	Bv	1222	0	1318	0	0
82	Bw	2066	0	2180	0	0
83	Bx	1908	0	2047	0	0
84	By	1540	0	1608	0	0
85	AA	47370	0	23451	5915	0
86	AB	1557	0	775	109	0
All	All	232955	0	167276	20891	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 58.

The worst 5 of 20891 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	19
2	A1	246/273 (90%)	189 (77%)	38 (15%)	19 (8%)	1	17
3	A2	185/190 (97%)	159 (86%)	17 (9%)	9 (5%)	2	26
4	A3	248/250 (99%)	204 (82%)	24 (10%)	20 (8%)	1	15
5	A4	190/202 (94%)	148 (78%)	24 (13%)	18 (10%)	1	13
6	A5	191/220 (87%)	158 (83%)	18 (9%)	15 (8%)	1	16
7	A6	185/190 (97%)	135 (73%)	30 (16%)	20 (11%)	0	9
8	A7	313/318 (98%)	256 (82%)	39 (12%)	18 (6%)	2	23
9	A8	40/57 (70%)	34 (85%)	3 (8%)	3 (8%)	1	17
10	A9	64/153 (42%)	50 (78%)	9 (14%)	5 (8%)	1	17
11	AC	202/277 (73%)	162 (80%)	25 (12%)	15 (7%)	1	17
12	AD	102/172 (59%)	79 (78%)	9 (9%)	14 (14%)	0	5
13	AE	158/174 (91%)	126 (80%)	12 (8%)	20 (13%)	0	6
14	AF	119/144 (83%)	105 (88%)	11 (9%)	3 (2%)	6	39
15	AG	139/151 (92%)	120 (86%)	12 (9%)	7 (5%)	2	25
16	AH	124/144 (86%)	99 (80%)	14 (11%)	11 (9%)	1	14
17	AI	132/152 (87%)	100 (76%)	21 (16%)	11 (8%)	1	15
18	AJ	127/130 (98%)	114 (90%)	7 (6%)	6 (5%)	2	27
19	AK	146/149 (98%)	118 (81%)	18 (12%)	10 (7%)	1	19
20	AL	125/142 (88%)	94 (75%)	19 (15%)	12 (10%)	1	12
21	AM	151/153 (99%)	114 (76%)	16 (11%)	21 (14%)	0	5
22	AO	147/167 (88%)	128 (87%)	10 (7%)	9 (6%)	1	21
23	AP	222/266 (84%)	171 (77%)	29 (13%)	22 (10%)	1	12
24	AQ	103/117 (88%)	86 (84%)	10 (10%)	7 (7%)	1	19
25	AR	79/194 (41%)	59 (75%)	12 (15%)	8 (10%)	0	11

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	Bf	412/429 (96%)	296 (72%)	66 (16%)	50 (12%)	0	7
66	Bg	94/105 (90%)	88 (94%)	5 (5%)	1 (1%)	16	58
67	Bh	186/188 (99%)	155 (83%)	13 (7%)	18 (10%)	1	12
68	Bi	127/132 (96%)	98 (77%)	18 (14%)	11 (9%)	1	14
69	Bj	160/170 (94%)	123 (77%)	22 (14%)	15 (9%)	1	13
70	Bk	82/127 (65%)	56 (68%)	14 (17%)	12 (15%)	0	5
71	Bl	114/149 (76%)	84 (74%)	10 (9%)	20 (18%)	0	3
72	Bm	105/109 (96%)	79 (75%)	8 (8%)	18 (17%)	0	4
73	Bn	81/84 (96%)	56 (69%)	15 (18%)	10 (12%)	0	6
74	Bo	90/93 (97%)	71 (79%)	6 (7%)	13 (14%)	0	5
75	Bp	79/82 (96%)	59 (75%)	10 (13%)	10 (13%)	0	6
76	Bq	48/51 (94%)	34 (71%)	6 (12%)	8 (17%)	0	4
77	Br	366/374 (98%)	274 (75%)	56 (15%)	36 (10%)	1	12
78	Bs	50/128 (39%)	44 (88%)	4 (8%)	2 (4%)	3	29
79	Bt	103/106 (97%)	75 (73%)	16 (16%)	12 (12%)	0	7
80	Bu	297/308 (96%)	216 (73%)	46 (16%)	35 (12%)	0	7
81	Bv	154/192 (80%)	114 (74%)	25 (16%)	15 (10%)	1	12
82	Bw	255/257 (99%)	200 (78%)	33 (13%)	22 (9%)	1	14
83	Bx	238/276 (86%)	188 (79%)	26 (11%)	24 (10%)	0	11
84	By	187/189 (99%)	155 (83%)	15 (8%)	17 (9%)	1	14
All	All	11687/13211 (88%)	9172 (78%)	1415 (12%)	1100 (9%)	1	13

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%)	159 (84%)	30 (16%)	3	17
2	A1	209/231 (90%)	172 (82%)	37 (18%)	2	13
3	A2	158/160 (99%)	132 (84%)	26 (16%)	2	15
4	A3	207/207 (100%)	174 (84%)	33 (16%)	3	17
5	A4	176/187 (94%)	144 (82%)	32 (18%)	2	12
6	A5	158/180 (88%)	140 (89%)	18 (11%)	6	26
7	A6	162/166 (98%)	137 (85%)	25 (15%)	3	17
8	A7	264/267 (99%)	232 (88%)	32 (12%)	5	24
9	A8	36/49 (74%)	32 (89%)	4 (11%)	7	27
10	A9	57/126 (45%)	52 (91%)	5 (9%)	11	37
11	AC	179/243 (74%)	143 (80%)	36 (20%)	1	9
12	AD	92/131 (70%)	81 (88%)	11 (12%)	5	25
13	AE	143/156 (92%)	126 (88%)	17 (12%)	6	25
14	AF	102/120 (85%)	99 (97%)	3 (3%)	45	70
15	AG	124/131 (95%)	110 (89%)	14 (11%)	6	26
16	AH	95/112 (85%)	83 (87%)	12 (13%)	5	23
17	AI	110/128 (86%)	102 (93%)	8 (7%)	15	46
18	AJ	108/109 (99%)	90 (83%)	18 (17%)	2	15
19	AK	123/124 (99%)	105 (85%)	18 (15%)	3	19
20	AL	111/122 (91%)	101 (91%)	10 (9%)	10	36
21	AM	133/133 (100%)	121 (91%)	12 (9%)	10	36
22	AO	123/137 (90%)	107 (87%)	16 (13%)	4	22
23	AP	185/204 (91%)	154 (83%)	31 (17%)	2	15
24	AQ	94/104 (90%)	84 (89%)	10 (11%)	7	29
25	AR	66/150 (44%)	55 (83%)	11 (17%)	2	15
26	AS	117/118 (99%)	105 (90%)	12 (10%)	8	30
27	AT	110/116 (95%)	82 (74%)	28 (26%)	0	4
28	AU	73/94 (78%)	67 (92%)	6 (8%)	12	41
29	AV	87/97 (90%)	74 (85%)	13 (15%)	3	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	AW	71/75 (95%)	58 (82%)	13 (18%)	2	12
31	AX	173/180 (96%)	155 (90%)	18 (10%)	8	30
32	AY	52/53 (98%)	41 (79%)	11 (21%)	1	7
33	AZ	57/84 (68%)	52 (91%)	5 (9%)	11	37
42	BI	164/165 (99%)	140 (85%)	24 (15%)	3	19
43	BJ	201/201 (100%)	189 (94%)	12 (6%)	21	52
44	BK	184/185 (100%)	154 (84%)	30 (16%)	2	16
45	BL	146/167 (87%)	120 (82%)	26 (18%)	2	13
46	BM	114/137 (83%)	106 (93%)	8 (7%)	16	47
47	BN	185/188 (98%)	142 (77%)	43 (23%)	1	6
48	BO	175/195 (90%)	150 (86%)	25 (14%)	3	20
49	BP	156/160 (98%)	139 (89%)	17 (11%)	7	28
50	BQ	176/193 (91%)	147 (84%)	29 (16%)	2	15
51	BR	132/144 (92%)	106 (80%)	26 (20%)	1	10
52	BS	160/160 (100%)	130 (81%)	30 (19%)	1	11
53	BT	170/198 (86%)	144 (85%)	26 (15%)	3	18
54	BU	133/134 (99%)	115 (86%)	18 (14%)	4	22
55	BV	95/116 (82%)	85 (90%)	10 (10%)	7	29
56	BW	107/108 (99%)	86 (80%)	21 (20%)	1	10
57	BX	108/136 (79%)	97 (90%)	11 (10%)	8	30
58	BY	85/102 (83%)	78 (92%)	7 (8%)	12	41
59	BZ	110/125 (88%)	98 (89%)	12 (11%)	7	28
60	Ba	116/117 (99%)	100 (86%)	16 (14%)	4	21
61	Bb	115/116 (99%)	95 (83%)	20 (17%)	2	13
62	Bc	124/130 (95%)	95 (77%)	29 (23%)	1	5
63	Bd	58/59 (98%)	54 (93%)	4 (7%)	17	48
64	Be	145/204 (71%)	122 (84%)	23 (16%)	3	17
65	Bf	349/360 (97%)	305 (87%)	44 (13%)	5	23
66	Bg	84/92 (91%)	72 (86%)	12 (14%)	3	20
67	Bh	162/162 (100%)	136 (84%)	26 (16%)	2	17
68	Bi	113/117 (97%)	96 (85%)	17 (15%)	3	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Bj	130/137 (95%)	105 (81%)	25 (19%)	1	10
70	Bk	75/114 (66%)	60 (80%)	15 (20%)	1	9
71	Bl	97/126 (77%)	81 (84%)	16 (16%)	2	15
72	Bm	87/90 (97%)	72 (83%)	15 (17%)	2	14
73	Bn	70/71 (99%)	55 (79%)	15 (21%)	1	7
74	Bo	74/76 (97%)	59 (80%)	15 (20%)	1	8
75	Bp	76/77 (99%)	68 (90%)	8 (10%)	7	29
76	Bq	46/47 (98%)	35 (76%)	11 (24%)	1	5
77	Br	304/310 (98%)	251 (83%)	53 (17%)	2	13
78	Bs	46/111 (41%)	38 (83%)	8 (17%)	2	13
79	Bt	94/95 (99%)	83 (88%)	11 (12%)	6	25
80	Bu	238/247 (96%)	199 (84%)	39 (16%)	2	15
81	Bv	132/160 (82%)	112 (85%)	20 (15%)	3	18
82	Bw	213/213 (100%)	176 (83%)	37 (17%)	2	13
83	Bx	203/229 (89%)	173 (85%)	30 (15%)	3	19
84	By	172/172 (100%)	138 (80%)	34 (20%)	1	9
All	All	10068/11158 (90%)	8575 (85%)	1493 (15%)	7	19

5 of 1493 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	BN	6	ASN
52	BS	92	MET
81	Bv	27	ARG
47	BN	93	ARG
49	BP	140	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 164 such sidechains are listed below:

Mol	Chain	Res	Type
47	BN	10	HIS
51	BR	121	GLN
80	Bu	57	ASN
48	BO	91	HIS
50	BQ	156	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	BA	1846/1847 (99%)	616 (33%)	225 (12%)
35	BB	1464/1465 (99%)	460 (31%)	143 (9%)
36	BC	169/169 (100%)	46 (27%)	20 (11%)
37	BD	118/119 (99%)	31 (26%)	9 (7%)
38	BE	209/210 (99%)	78 (37%)	27 (12%)
39	BF	73/73 (100%)	48 (65%)	23 (31%)
40	BG	181/182 (99%)	40 (22%)	8 (4%)
41	BH	134/135 (99%)	49 (36%)	16 (11%)
85	AA	2226/2251 (98%)	767 (34%)	312 (14%)
86	AB	72/73 (98%)	30 (41%)	7 (9%)
All	All	6492/6524 (99%)	2165 (33%)	790 (12%)

5 of 2165 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
35	BB	1482	A
39	BF	60	C
85	AA	1787	G
35	BB	1535	G
38	BE	26	G

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 carbohydrates 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