



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jul 24, 2017 – 04:05 PM EDT

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 : unknown  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

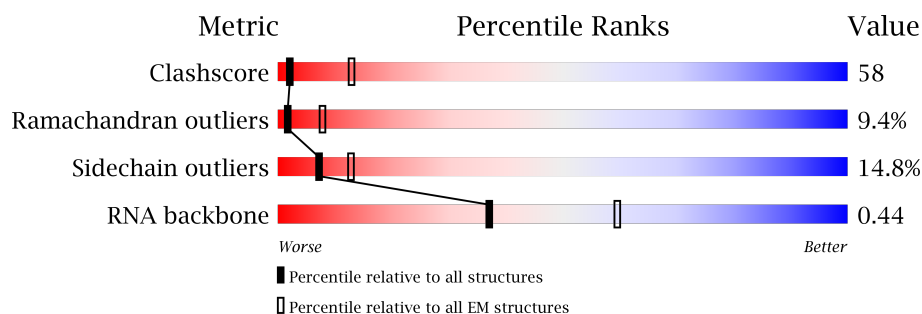
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.57 Å.

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




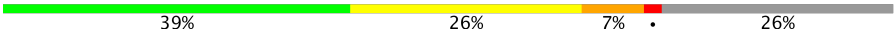

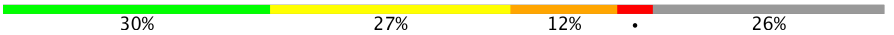

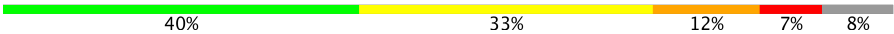

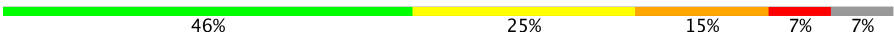
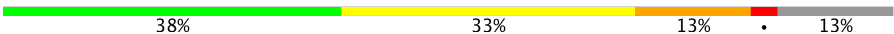

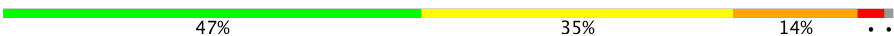

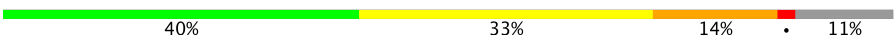






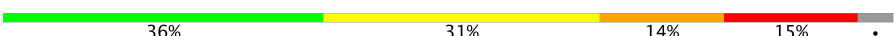





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	39% 30% 14% • 14%
2	A1	273	34% 40% 12% • 9%
3	A2	190	53% 27% 13% 5% •
4	A3	250	35% 42% 18% 5%
5	A4	202	35% 29% 22% 9% 5%
6	A5	220	40% 32% 12% 5% 11%
7	A6	190	41% 32% 15% 11% •












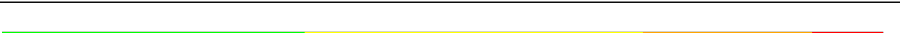





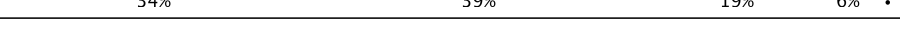

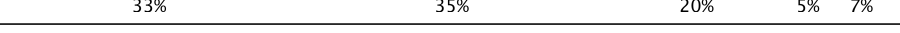
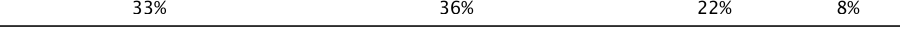




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Mol	Chain	Length	Quality of chain
8	A7	318	
9	A8	57	
10	A9	153	
11	AC	277	
12	AD	172	
13	AE	174	
14	AF	144	
15	AG	151	
16	AH	144	
17	AI	152	
18	AJ	130	
19	AK	149	
20	AL	142	
21	AM	153	
22	AO	167	
23	AP	266	
24	AQ	117	
25	AR	194	
26	AS	143	
27	AT	137	
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	?	-	T	DELETION	GB X14553
BA	?	-	T	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	?	-	T	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		

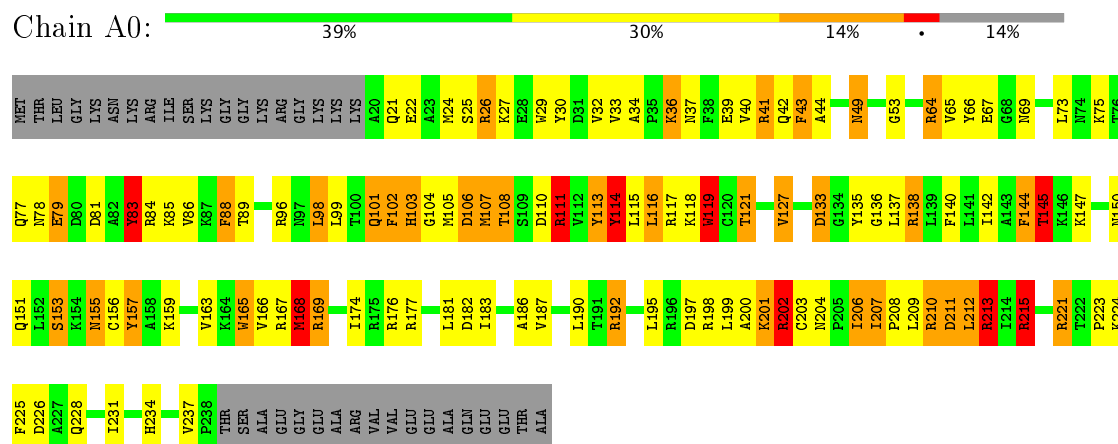
- Molecule 86 is a RNA chain called E-SITE TRNA.

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

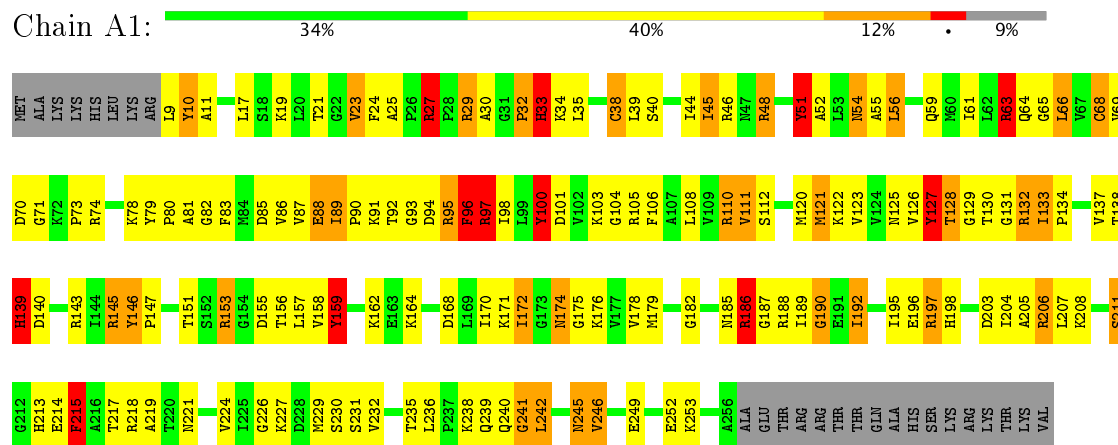
### 3 Residue-property plots

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.

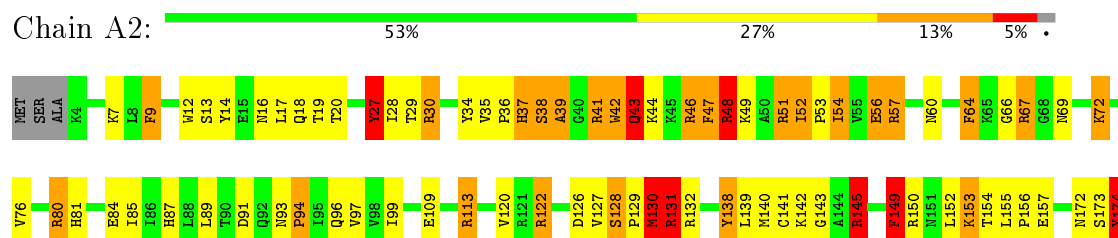
- Molecule 1: 40S RIBOSOMAL PROTEIN S3A, PUTATIVE

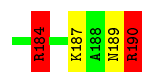


- Molecule 2: 40S RIBOSOMAL PROTEIN S4, PUTATIVE



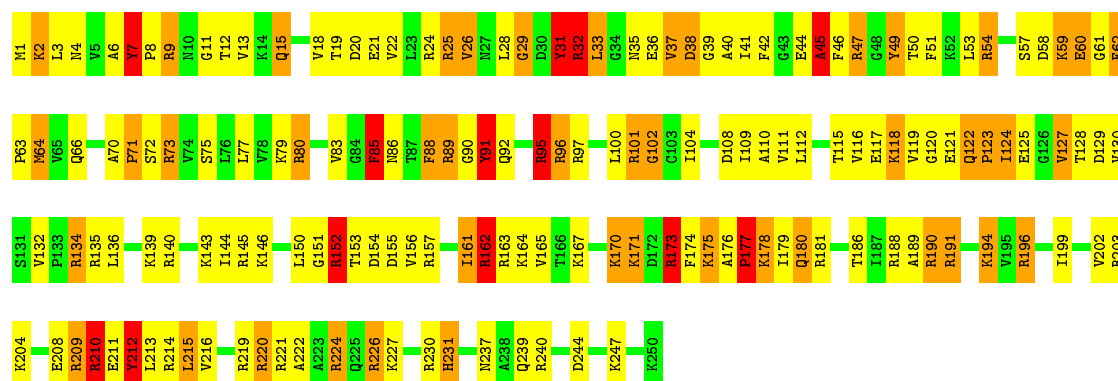
- Molecule 3: 40S RIBOSOMAL PROTEIN S5, PUTATIVE





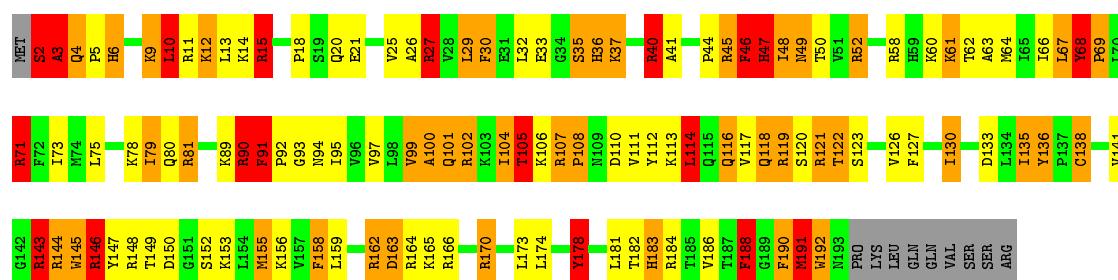
• Molecule 4: 40S RIBOSOMAL PROTEIN S6

Chain A3: 35% 42% 18% 5%



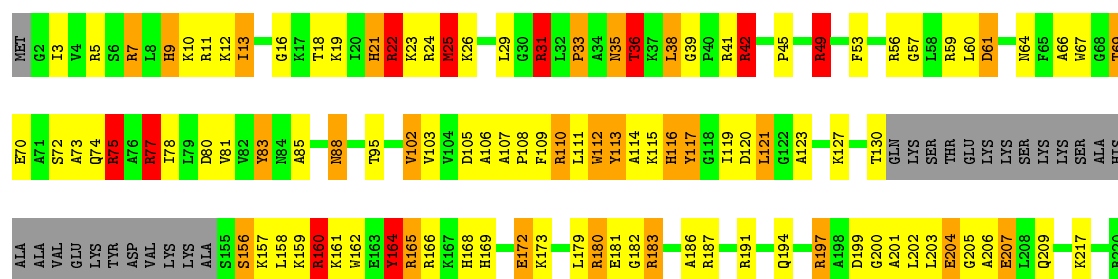
• Molecule 5: RIBOSOMAL PROTEIN S7, PUTATIVE

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



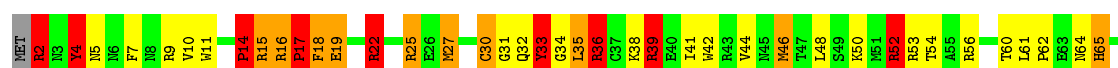
• Molecule 6: 40S RIBOSOMAL PROTEIN S8

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

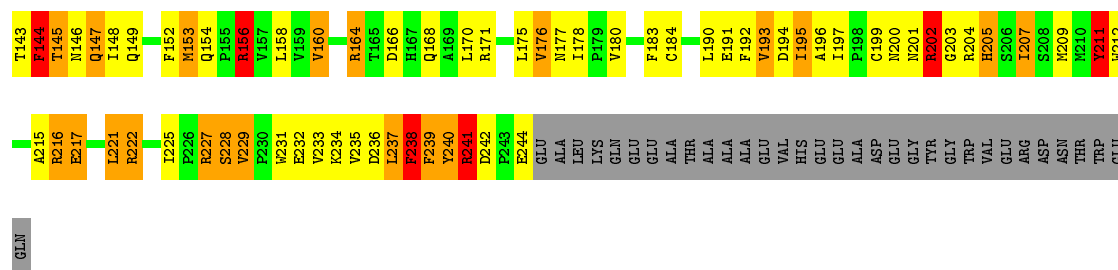


• Molecule 7: 40S RIBOSOMAL PROTEIN S9, PUTATIVE

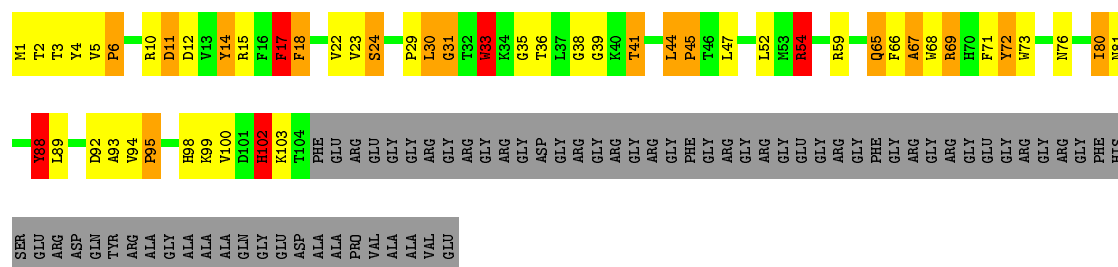
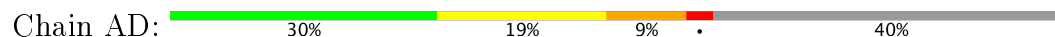
Chain A6: 41% 32% 15% 11%



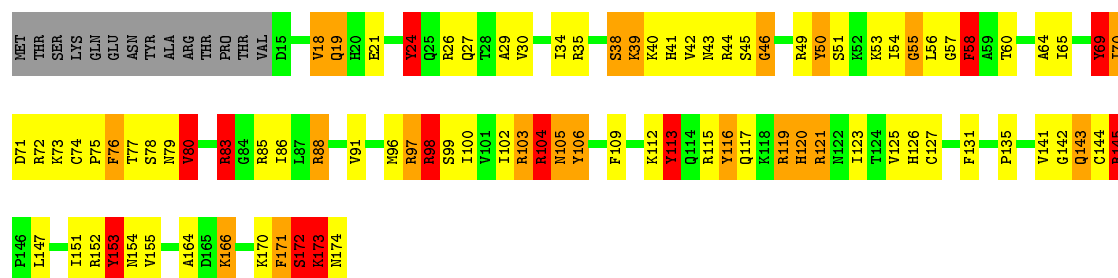




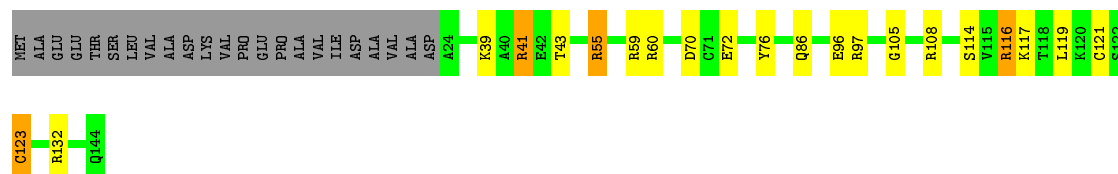
- Molecule 12: 40S RIBOSOMAL PROTEIN S10, PUTATIVE



- Molecule 13: 40S RIBOSOMAL PROTEINS S11, PUTATIVE



- Molecule 14: 40S RIBOSOMAL PROTEIN S12



- Molecule 15: 40S RIBOSOMAL PROTEIN S13, PUTATIVE

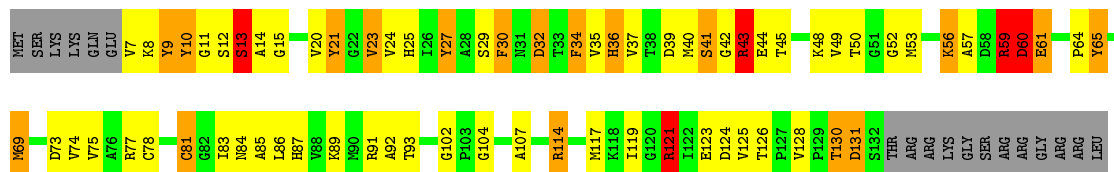






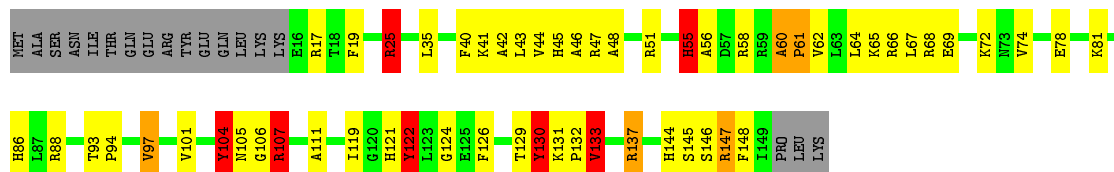
• Molecule 16: 40S RIBOSOMAL PROTEIN S14

Chain AH: 38% 33% 13% • 13%



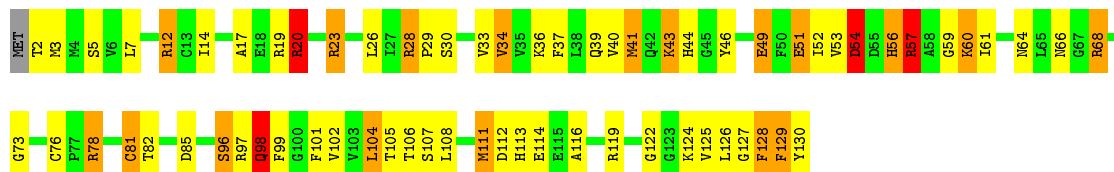
• Molecule 17: 40S RIBOSOMAL PROTEIN S15, PUTATIVE

Chain AI: 51% 30% • 5% 12%



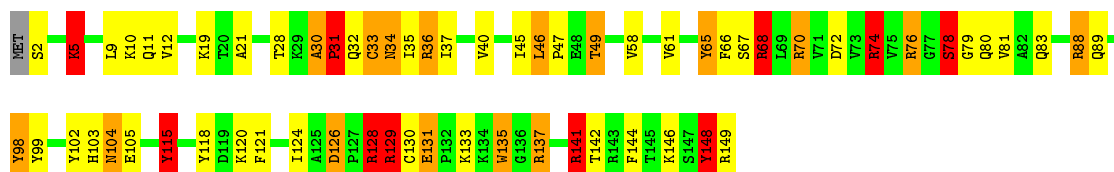
• Molecule 18: 40S RIBOSOMAL PROTEIN S15A, PUTATIVE

Chain AJ: 47% 35% 14% • •



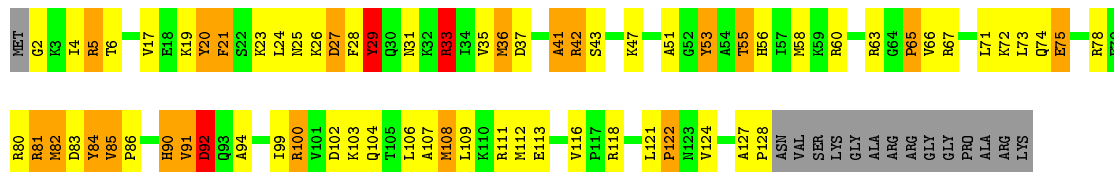
• Molecule 19: 40S RIBOSOMAL PROTEIN S16, PUTATIVE

Chain AK: 56% 26% 11% 7% •

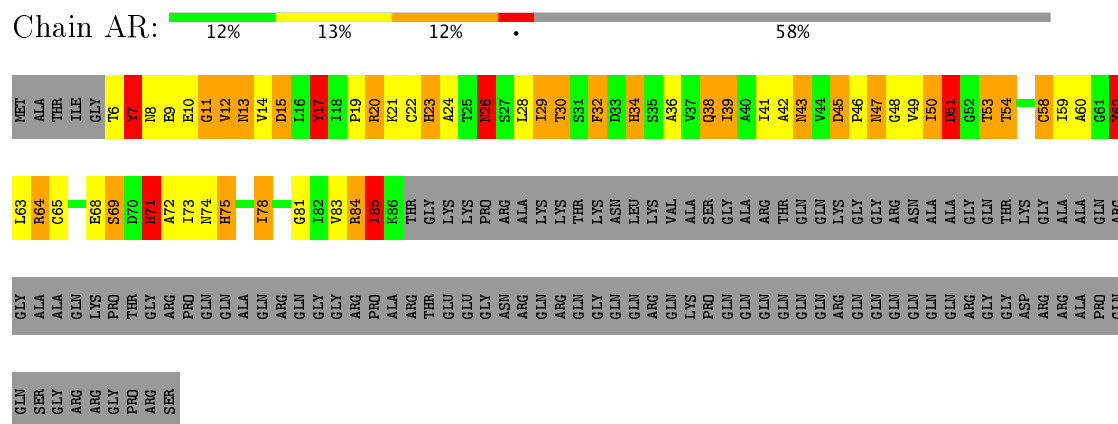


• Molecule 20: 40S RIBOSOMAL PROTEIN S17, PUTATIVE

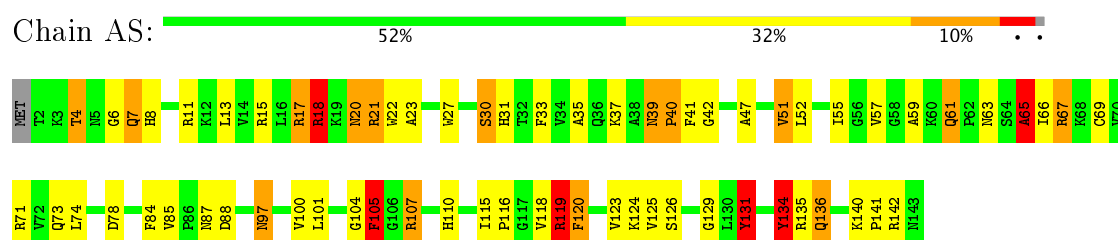
Chain AL: 40% 33% 14% • 11%



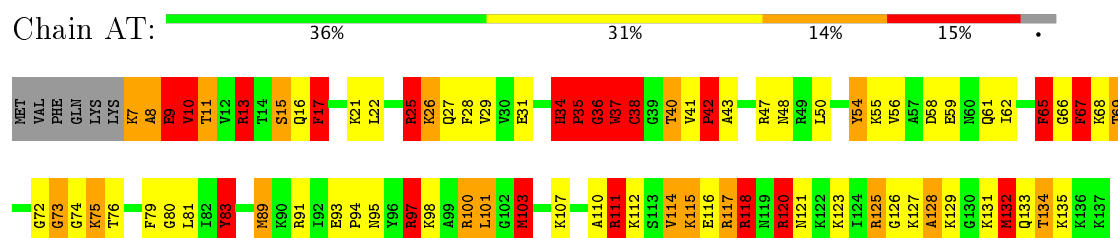
- Molecule 25: 40S RIBOSOMAL PROTEIN S21, PUTATIVE



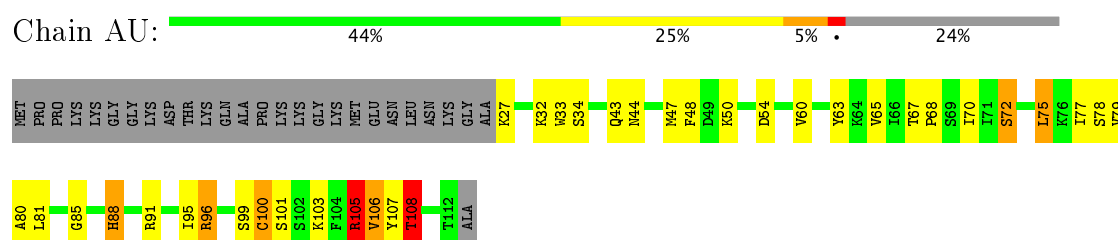
- Molecule 26: 40S RIBOSOMAL PROTEIN S23, PUTATIVE



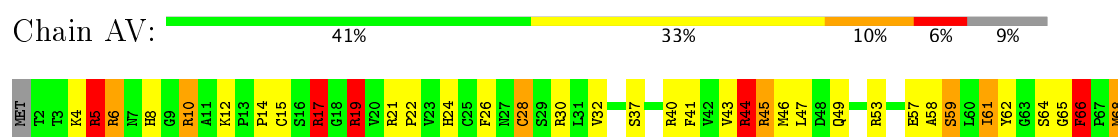
- Molecule 27: 40S RIBOSOMAL PROTEIN S24



- Molecule 28: 40S RIBOSOMAL PROTEIN S25, PUTATIVE

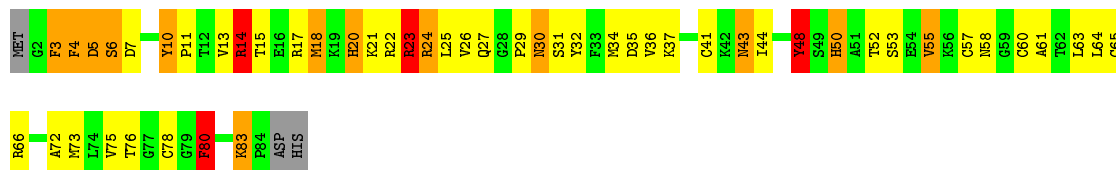


- Molecule 29: RIBOSOMAL PROTEIN S26, PUTATIVE



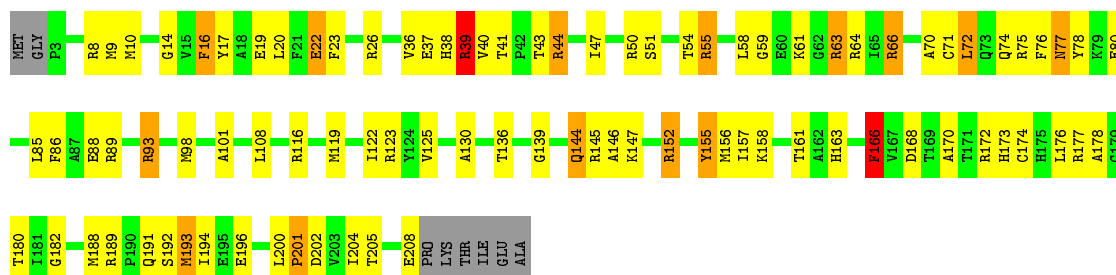
- Molecule 30: 40S RIBOSOMAL PROTEIN S27, PUTATIVE

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



- Molecule 31: 40S RIBOSOMAL PROTEIN S3, PUTATIVE

Chain AX:  54% 35% 7% . .

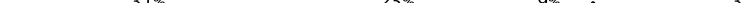


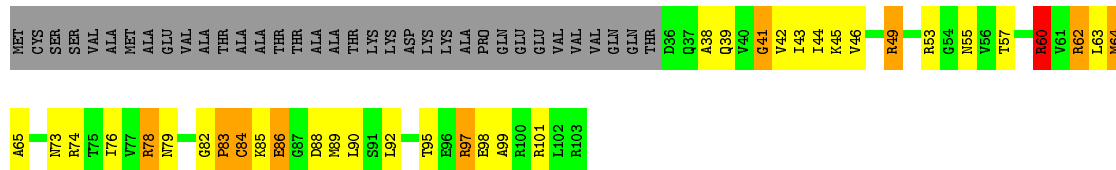
- Molecule 32: 40S RIBOSOMAL PROTEIN S30, PUTATIVE

Chain AY: 



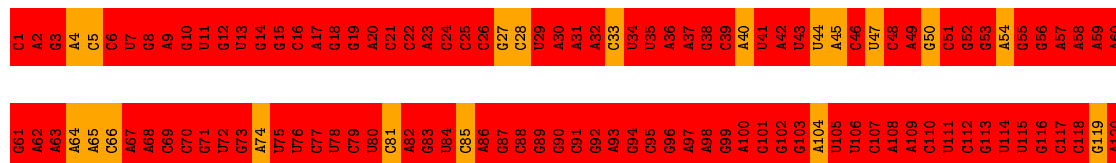
- Molecule 33: 40S RIBOSOMAL PROTEIN S33, PUTATIVE

Chain AZ: 



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

Chain BA:  18% 80%



U1081	U1021	C981	C901	G841	U781	A721	C681	A601	C541	A481	G421	C361	U801	U241	G181	A121
U1082	C1022	U962	C902	U842	C782	A722	U682	G602	A542	C482	C422	G362	A302	U242	U182	U122
A1083	G1023	G983	G903	G843	U783	C723	U683	U603	A543	C483	G423	G363	C303	C243	C183	C123
A1084	A1024	U984	G904	U844	C784	A724	C684	G604	U544	A484	U424	C364	G304	C244	C184	G124
G1085	A1025	U985	A905	U845	U785	C725	C685	G605	U545	C485	G425	A365	C305	U245	A185	G125
A1086	C1026	G986	A906	U846	U786	C726	C686	G606	U546	C486	G426	G366	G306	G246	G186	G126
A1087	C1027	C987	A907	U847	U787	C727	U687	C607	C547	A487	G427	G367	C307	U247	G187	U127
G1088	A1028	U988	G908	U848	C788	A728	C688	G608	U548	C488	C428	U368	U308	C248	C188	C128
U1089	C1029	A989	G909	G849	U789	C729	U689	G609	G549	A489	G429	A369	U309	A249	G189	U129
U1090	U1030	U970	C910	C850	G790	A730	U670	A610	U550	A490	A430	U370	C310	G250	U130	U130
U1091	U1031	C971	G911	C851	A791	C731	C671	A611	C551	U491	A431	U371	C311	U251	U131	A131
U1092	A1032	G972	G912	C852	A792	A732	G672	U612	C552	G492	A432	U372	U312	A252	G192	U132
G1093	G1033	U973	U913	A853	A793	C733	U673	A613	C553	G493	A433	G373	C313	U253	G193	A133
U1094	U1034	G974	G914	A854	C794	A734	C674	A614	A554	A494	U434	U374	A314	U254	G194	U134
G1095	A1035	A975	A915	C855	U795	A735	C675	A615	C555	A495	U435	C375	U315	G255	G195	G135
C1096	C1036	G976	A916	G856	G796	A736	G676	G616	A556	A496	U436	U376	G316	A256	A196	A136
G1097	U1037	U977	C917	C857	A797	U737	U677	G617	U557	U497	G437	G377	U317	G257	A197	C137
U1098	U1038	G978	U918	C858	U798	C738	U678	G618	C558	A498	A438	G378	U318	C258	U198	C138
U1099	G1039	U979	A919	G859	A799	A739	U679	U619	C559	C499	A439	C379	C319	C259	U199	U139
A1100	U1040	G980	U920	G860	G800	A740	C680	C620	U560	C500	A440	A380	C320	A260	C200	C140
A1101	U1041	A981	G921	C861	U801	A741	C681	G621	U561	C501	A441	A381	G321	A261	A201	G141
A1102	U1042	U982	C922	C862	G802	C742	A682	G622	C562	U502	G442	G382	U322	A262	A202	A142
G1103	C1043	A983	G923	G863	U803	A743	C683	U623	A563	C503	U443	G383	C323	G263	U203	A143
C1104	A1044	U984	U924	G864	G804	C744	G684	G624	U564	A504	A444	U384	C324	A264	U204	C144
A1105	C1045	C985	G925	C865	A805	A745	G685	U625	U565	U505	U445	U385	A325	G265	U205	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	G687	U627	U567	U507	U447	A387	G327	G267	A207	U147
U1108	U1048	U988	C928	C868	U808	C748	C688	G628	U568	C508	U448	A388	A328	U268	G148	G148
G1109	G1049	G989	A929	C869	U809	A749	C689	G629	C569	U509	G449	U389	G329	G269	A209	G149
A1110	A1050	G990	A930	C870	A810	C750	G690	U630	G570	U510	G450	A390	A330	U270	G210	U150
U1111	U1051	U991	G931	G871	C811	A751	A691	G631	G571	U511	A451	U391	G331	C271	C211	A151
A1112	C1052	A992	C932	U872	A812	A752	C692	U632	U572	U512	A452	A392	U332	A272	A212	C152
U1113	U1053	G993	U933	G873	C813	C753	G693	G633	U573	U513	A453	G393	A333	G273	A213	C153
G1114	A1054	A994	G934	G874	C814	G754	C694	U634	U574	U514	A454	A394	G334	C274	A214	A154
A1115	U1055	G995	A935	G875	C815	C755	A695	G635	U575	U515	A455	G395	C335	C275	C215	U155
G1116	C1056	U996	A936	C876	G816	A756	A696	G636	C576	U516	G456	U396	A336	C276	C216	U156
U1117	U1057	G997	C937	U877	U817	G757	A697	G637	U577	U517	A457	A397	C337	A277	C217	U157
G1118	C1058	U998	C938	G878	C818	C758	U698	U638	C578	C518	G458	G398	U338	U278	G218	U158
A1119	U1059	G999	C939	C879	G819	A759	C699	U639	U579	G519	U459	G399	G339	U279	U219	U159
U1120	C1060	U999	C940	G880	C820	G760	G700	U640	U580	G520	G460	A400	U340	A280	G160	G160
U1121	A1061	G1001	G941	C881	G821	U761	G701	U641	U581	C521	A461	A401	U341	C281	G221	U161
G1122	G1062	U1002	G942	G882	U822	A762	G702	U642	U582	C522	A462	A402	U342	A282	C222	G162
A1123	C1063	A1003	G943	C883	G823	C763	U703	U643	U583	A523	A463	A403	G343	U283	G223	G163
U1124	A1064	U1004	G944	G884	C824	C764	C704	C644	A584	G524	U464	A404	G344	U284	G224	C164
G1125	U1065	A945	A945	A885	G825	U765	C705	U645	G585	A525	A465	C405	G345	C285	A225	C165
U1126	G1066	G946	A946	G886	C826	A766	C706	C546	G586	C526	G466	G406	A346	G286	A226	G166
U1127	U1067	U1007	A947	U887	A827	U767	C707	U647	U587	C527	A467	A407	U347	U287	C227	U167
C1128	C1068	A1008	C948	G888	A828	C768	C708	C548	C588	A528	A468	U408	G348	U288	U168	U168
U1129	U1069	U949	C949	U889	U829	U769	C709	A649	A589	A529	G469	A409	G349	A289	C229	C169
U1130	G1070	C950	G950	G890	U830	G770	A710	C650	U590	A530	C470	G410	C350	G290	A230	U170
G1131	C1071	C951	C951	C891	U831	A771	C711	U651	G591	C531	U471	G411	A351	C291	U231	U171
U1132	U1072	G952	G952	C892	C832	C772	C712	C652	G592	C532	U472	G412	C352	C292	U232	A172
A1133	G1073	U953	U953	U893	U833	A773	C713	U653	G593	U533	A473	A413	U353	C293	U233	U173
C1134	C1074	A1014	G954	G894	C834	A774	C714	C654	G594	C534	A474	A414	G354	C294	A234	A174
U1135	U1075	G955	G955	U895	U835	C775	U715	U655	U595	G535	U475	C415	U355	C295	G235	G175
A1136	U1076	U956	A956	U896	U836	U776	C716	U656	G596	C536	U476	A416	C356	G296	A236	G176
U1137	G1077	A957	A957	U897	U837	C777	U717	C657	C597	C537	C477	A417	A357	A297	A237	G177
C1138	U1078	G958	G958	G898	U838	U778	U718	C658	G598	G538	G478	G418	A358	G298	C238	C178
G1139	C1079	U959	U959	G899	U839	U779	U719	U659	U599	C539	U479	U419	C359	G299	C239	U179
A1140	U1080	A1020	C960	A900	U840	U780	A720	C660	G600	G540	G480	A420	C360	C240	C180	G120

C1441	G1201	G1261	A1321	A1381	C1441	U1501	C1561	U1621	U1681	G1741	G1801	U1	A61	A121
C1442	G1202	A1262	A1322	G1382	A1442	G1502	G1562	U1622	A1682	G1742	C1802	C2	C62	U122
U1143	G1203	A1263	G1323	G1383	U1443	U1503	G1563	U1623	A1683	C1743	A1803	C3	A63	U123
A1144	G1204	G1264	G1324	G1384	G1444	A1504	A1564	U1624	A1684	C1744	A1804	C4	U64	G124
U1145	G1205	G1265	G1325	U1385	U1445	G1505	G1565	U1625	G1685	G1745	C1805	A5	A65	G125
U1146	G1206	A1266	G1326	G1386	G1446	C1506	G1566	U1626	G1686	G1746	A1806	A6	G66	C126
C1147	A1207	A1267	G1327	U1387	C1447	C1507	G1567	U1627	A1687	C1747	A1807	C7	A67	U127
U1148	U1208	C1268	U1328	A1388	U1448	U1508	A1568	A1628	G1688	G1748	A1808	U8	G68	U128
C1149	U1209	C1269	U1329	A1389	U1449	U1509	C1569	A1629	G1689	C1749	G1809	G9	A69	C129
A1150	G1210	C1270	G1330	G1390	G1450	C1510	C1570	U1630	U1690	U1750	A1810	C10	A70	G130
A1151	G1211	G1271	G1331	A1391	A1451	C1511	C1571	U1631	G1691	C1751	A1811	C11	A71	A131
A1152	A1212	U1272	U1332	A1392	U1452	G1512	G1572	U1632	U1692	U1752	A1812	G12	G72	G132
C1153	A1213	U1273	G1333	C1393	U1453	C1513	C1573	C1633	U1693	U1753	C1813	A13	G73	G133
U1154	U1214	A1274	G1334	U1394	G1454	A1514	C1574	A1634	C1694	C1754	U1814	C14	U74	G134
U1155	G1215	G1275	A1335	C1395	C1455	U1515	G1575	A1635	G1695	U1755	G1815	C15	A75	C135
U1156	G1216	G1276	U1336	A1396	C1456	G1516	C1576	C1636	G1696	C1756	A1816	G16	C76	A136
A1157	A1217	G1277	A1337	C1397	C1457	U1517	A1577	G1637	U1697	C1757	G1817	U17	A77	A137
A1158	G1218	A1278	G1338	C1398	A1458	U1518	A1578	U1638	C1698	U1758	A1818	A18	C78	A138
U1159	U1219	U1279	G1339	A1399	U1459	G1519	G1579	U1639	A1699	U1759	U1819	C19	U79	G139
U1160	C1220	A1280	G1340	A1400	U1460	A1520	U1580	G1640	C1700	U1760	G1820	U20	C80	U140
G1161	A1221	U1281	A1341	A1401	A1461	G1521	G1581	G1641	U1701	U1761	A1821	C21	A81	G141
U1162	C1222	G1282	C1342	C1402	U1462	G1522	C1582	A1642	G1702	U1762	A1822	A22	G82	G142
G1163	C1223	U1283	G1343	G1403	U1463	U1523	A1583	A1643	U1703	U1763	A1823	U23	G83	G143
C1164	A1224	G1284	A1404	A1404	C1464	G1524	G1584	A1644	G1704	U1764	U1824	C24	G84	G144
A1165	A1225	G1285	U1345	A1405	C1465	G1525	A1585	C1645	C1705	G1765	U1825	A25	A85	G145
A1166	C1226	C1286	U1346	U1406	U1466	C1526	U1586	U1646	A1706	G1766	C1826	C26	A86	U146
C1167	U1227	G1287	G1347	C1407	U1467	G1527	C1587	G1647	C1707	G1767	C1827	C27	G87	C147
A1168	G1228	U1288	G1348	C1408	U1468	U1528	C1588	G1648	A1708	G1768	A1828	G28	U88	C148
A1169	G1229	C1289	A1349	A1409	U1469	G1529	U1589	A1649	U1709	U1769	A1829	C29	C89	A149
A1170	G1230	A1290	C1350	C1410	G1470	G1530	G1590	G1650	C1710	U1770	A1830	A30	G90	G150
C1171	C1231	G1291	G1351	U1411	U1471	G1531	G1591	C1651	G1711	U1771	A1831	U31	G91	G151
C1172	C1232	A1292	G1352	G1412	C1472	G1532	U1592	G1652	U1712	G1772	A1832	C32	C92	G152
C1173	U1233	A1293	U1353	G1413	A1473	G1533	U1593	G1653	U1713	U1773	A1833	A33	A93	G153
A1174	U1234	G1294	G1354	C1414	G1474	U1534	G1594	G1654	C1714	G1774	A1834	G34	A94	A154
G1175	C1235	U1295	G1355	C1415	G1475	G1535	C1595	G1655	C1715	U1775	A1835	G35	A95	G155
C1176	U1236	U1296	C1356	C1416	G1476	A1536	C1596	A1656	A1716	G1776	U1836	U36	A96	G156
C1177	U1237	G1297	C1357	G1417	C1477	G1537	G1597	A1657	C1717	U1777	U1837	C37	U97	G157
U1178	C1238	U1298	A1358	G1418	G1478	G1538	U1598	G1658	C1718	U1778	U1838	C38	A98	C158
U1179	G1239	G1299	U1359	A1419	G1479	A1539	A1599	G1659	G1719	U1779	G1839	C39	G99	C159
A1180	G1240	G1300	G1360	A1420	U1480	C1540	G1600	A1660	U1720	U1780	C1840	C40	A100	A160
G1181	U1241	G1301	G1361	A1421	U1481	G1541	A1601	U1661	U1721	U1781	A1841	A41	U101	G161
U1182	A1242	C1302	A1362	A1422	U1482	A1542	A1602	U1662	U1722	C1782	U1842	A42	G102	G162
U1183	A1243	U1303	G1363	U1423	U1483	A1543	A1603	C1663	G1723	C1783	U1843	G43	U103	U164
A1184	G1244	C1304	U1364	G1424	A1484	G1544	A1604	C1664	G1724	G1784	U1844	C44	C104	C165
U1185	C1245	A1305	U1365	G1425	U1485	C1545	C1605	G1665	U1725	G1785	G1845	A45	U105	C166
U1186	G1246	U1306	C1366	A1426	U1486	G1546	A1606	U1666	U1726	C1786	U1846	U46	A106	U167
U1187	G1247	U1307	G1367	U1427	U1487	C1547	C1607	G1667	U1727	U1787	U1847	C47	G107	U168
U1188	A1248	C1308	G1368	G1428	C1488	A1548	C1608	C1668	G1728	U1788	U1848	G48	U108	G253
A1189	G1249	U1309	C1369	A1429	U1489	U1549	G1609	C1669	U1729	A1789	U1849	A49	U109	G253
U1190	C1250	G1310	A1370	C1430	U1490	G1550	A1610	A1670	U1730	U1790	U1850	A50	U110	A254
C1191	A1251	G1311	U1371	G1431	U1491	G1551	A1611	A1671	U1731	C1791	G1851	U51	C111	A255
A1192	G1252	A1312	C1372	C1432	U1492	G1552	C1612	C1672	U1732	U1792	G1852	G52	G112	G256
A1193	C1253	U1313	C1373	U1433	U1493	G1553	G1613	C1673	G1733	G1793	U1853	C53	C113	G257
G1194	A1254	A1314	G1374	U1434	G1494	C1554	G1614	G1674	U1734	A1794	U1854	U54	A114	C258
G1195	G1255	C1315	U1375	A1435	A1495	G1555	A1615	C1675	G1735	A1795	U1855	C55	U115	U259
C1196	A1256	G1316	U1376	A1436	G1496	A1556	A1616	A1676	U1736	A1796	U1856	U56	G116	A260
U1197	U1257	U1317	A1377	G1437	A1497	G1557	U1617	C1677	U1737	A1797	G1857	G57	A117	C261
U1198	G1258	A1318	G1378	C1438	A1498	C1558	A1618	U1678	U1738	G1798	U1858	G58	A118	C262
U1199	C1259	G1319	C1379	C1439	A1499	G1559	U1619	C1679	G1739	G1799	G1859	U59	C119	C263
U1200	G1260	A1320	G1380	C1440	G1500	U1560	U1620	G1680	U1740	G1800	G1860	A60	C120	U264

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

Chain BB: 5% 25% 70%

U1	A61	A121
C2	C62	U122
C3	A63	U123
C4	U64	G124
A5	G65	G125
A6	G66	C126
C7	A67	U127
U8	G68	U128
G9	A69	C129
C10	A70	G130
A11	A71	A131
G12	G72	G132
A13	G73	G133
C14	U74	G134
C15	A75	C135
G16	C76	A136
U17	A77	A137
A18	C78	A138
C19	U79	G139
U20	C80	U140
C21	A81	G141
U22	G82	G142
G23	G83	G143
C24	G84	G144
A25	A85	G145
C26	A86	U146
C27	G87	C147
G28	U88	C148
C29	C89	A149
A30	G90	G150
U31	G91	C151
C32	C92	G152
A33	A93	A153
G34	A94	C154
C35	A95	G155
U36	A96	G156
C37	U97	C157
C38	A98	C158
C39	G99	C159
C40	A100	A160
A41	U101	G161
A42	G102	U162
G43	C103	G163
C44	U104	U164
A45	U105	C165
U46	A106	C166
C47	G107	U167
G48	U108	U168
A49	G109	C169
U50	U110	A254
C111	C111	A255
G52	G112	G256
C53	C113	G257
U54	A114	C258
C55	U115	U259
U56	G116	A260
G57	A117	C261
G58	C118	C262
U59	C119	G1799
A60	C120	U264

G1226	A1166	G1106	C1046	C926	A866	U806	A746	A686	C626	A566	G506	U446	G386	G326	C286
G1227	C1167	C1107	C1047	U927	C867	U807	A747	C687	G627	G567	G507	C447	G387	U327	C287
A1228	G1168	G1108	A1048	C928	C868	U808	U748	U688	A628	A568	U508	A648	C388	G328	C288
A1229	A1169	A1109	G1049	C929	C869	U809	U749	C689	A629	A569	A509	G449	G389	U329	C289
A1230	U1170	G1110	A1050	C930	C870	G810	G750	C690	A630	A570	A510	A450	G390	U330	A269
U1231	U1171	U1051	U1051	U931	C871	C811	A751	A691	G631	C571	A511	A451	G391	U331	G270
A1232	U1172	U1112	G1052	U932	A872	G812	A752	G692	U832	G572	C512	A452	G392	U332	C271
U1233	C1173	C1113	G1053	U933	C873	C813	A753	U693	C633	C573	G513	C453	A393	C333	C272
G1234	C1174	A1114	G1054	U934	G874	A814	U754	C694	A634	G574	G514	U454	G394	G334	G273
A1235	A1175	G1115	G1055	U935	G875	U815	A755	G695	A635	C575	C515	G455	U395	C335	U274
A1236	U1176	U1116	A1056	U936	G876	U816	C756	G696	A636	A576	G516	A456	U396	U336	A275
G1237	U1177	G1117	G1057	U937	A877	C817	A757	G697	G637	U577	G517	U457	C397	U337	U276
A1238	G1118	U1058	G938	G938	G878	U818	A758	C698	A638	U578	G518	U458	A398	C338	C277
A1239	C1179	G1119	G939	G939	G879	U819	C759	U699	A639	A579	A519	U459	A399	C339	U278
A1240	G1180	A1120	U1060	G940	G880	C820	A760	C700	A640	A580	G520	C460	C400	U340	A279
U1241	A1181	A1121	G1061	G941	G881	G821	A761	C701	C641	U581	U521	U461	U401	U341	C280
C1242	A1182	C1122	G1062	G942	U882	G822	G762	G702	G642	G582	A522	G462	G402	U342	U281
A1243	U1183	G1123	G1063	U943	G883	G823	U763	G703	G643	G583	A523	C463	U403	U343	A282
U1244	C1184	A1124	U1064	U944	U884	C824	G764	G704	G644	A584	C524	A464	A404	U344	A283
A1245	G1185	A1125	G1065	U945	U885	U825	G765	C705	C645	U585	U525	A465	U405	U345	C284
C1246	A1186	A1126	G1066	G946	G886	G826	G766	G706	U646	U586	A526	A466	A406	U346	C285
G1247	G1187	U1127	G1067	A947	G887	U827	A767	C707	U647	A587	U527	G467	A407	G347	U286
A1248	A1188	U1128	G1068	G948	U888	G828	A768	C708	G648	A588	G528	U468	U408	G348	C287
G1249	C1189	C1129	G1069	G949	U889	C829	G769	G709	A649	U589	A529	G469	U409	U349	C288
U1250	U1190	U1130	G1070	G950	U890	G830	G770	C710	A650	G590	C530	C470	A410	U350	U289
G1251	G1191	C1131	G1071	U951	U891	C831	U771	C711	G651	A591	U531	U471	A411	G351	U290
G1252	C1192	A1132	C1072	U952	U892	C832	G772	C712	G652	G592	C532	C472	A412	C352	C291
U1253	G1193	C1133	U1013	G953	U893	G833	G773	C713	G653	A593	U533	U473	A413	G353	U292
G1254	A1194	U1134	U1014	G954	A894	U834	C774	C714	C654	U594	C534	C474	C414	C354	G293
U1255	A1195	U1135	U1015	U955	U895	C835	C775	C715	U655	A595	U535	A475	A415	A355	G294
G1256	U1196	G1136	C1016	G956	C896	U836	U776	C716	A656	C596	U536	A476	U416	C356	U295
A1257	G1197	G1137	C1077	A957	C897	A837	C777	C717	G657	U597	A537	U477	A417	C357	G296
G1258	C1198	U1138	U1078	C958	U898	G838	A778	C718	G658	C598	A538	G478	G418	U358	U297
A1259	A1199	A1139	G1079	C959	C899	G839	C779	C719	C659	U599	G539	U479	G419	A359	G298
U1260	U1200	C1140	U1080	C960	C900	C840	U780	U720	G660	G600	G540	C480	U420	C360	U299
U1261	G1201	A1141	C1021	G961	U901	G841	A781	G721	G661	U601	U541	A481	U421	A361	U300
A1262	C1202	C1142	C1022	U962	C902	G842	A782	U722	G662	G602	A542	A482	U422	A362	G301
G1263	C1203	A1143	G1023	G963	U903	C843	U783	C723	G663	U603	C543	C483	G423	A363	
U1264	C1204	A1084	G1024	G964	C904	G844	C784	G724	A664	C604	C544	G484	G424	U364	U304
U1265	A1205	G1145	C1085	G965	C905	C845	G785	U725	A665	C605	C545	U485	G425	U365	U305
G1266	G1206	C1146	G1086	C966	G906	A846	A786	C726	G666	C606	A546	A486	A426	G366	U306
U1267	U1207	G1147	U1027	G967	U907	U847	A787	G727	G667	G607	A547	A487	U427	C367	A307
G1268	C1208	U1148	C1028	C968	U908	A848	U788	C728	A668	A608	U548	G488	G428	C368	C308
A1269	A1209	A1149	U1029	C969	U909	A849	G789	G729	A669	G609	U549	A489	C429	A369	C309
C1270	U1210	A1150	U1030	C970	C910	U850	A790	G730	G670	U610	G550	G490	A430	A370	U310
A1271	C1211	A1151	G1031	U911	U911	U851	A791	U731	A671	U611	C551	A491	U431	C371	C311
G1272	C1212	U1152	U1032	C972	C912	G852	G792	G732	C672	A612	C552	U492	C432	U372	U312
G1273	U1213	G1153	U1033	G973	C913	U853	A793	G733	C673	C613	U553	U493	C433	C373	C313
G1274	U1214	C1154	U1034	C974	U914	G854	G794	A734	G674	U614	C554	C494	A434	A374	A314
A1275	U1215	U1155	C1035	G975	U915	G855	A795	A735	U675	A615	G555	A495	A435	G375	C315
U1276	G1216	U1156	G1036	U976	U916	U856	C796	G736	G676	U616	U556	C496	G436	A376	U316
A1277	U1217	G1157	A1037	G977	U917	G857	C797	C737	U677	C617	C557	A497	U437	A377	C317
A1278	C1218	C1158	G1038	C978	C918	U858	A798	G738	U678	U618	U558	G498	G438	C378	C318
C1279	A1219	U1159	A1039	G979	U919	U859	A799	C739	G679	A619	U559	A499	G439	U379	C319
U1280	U1220	U1160	C1040	G980	C920	U860	U800	A740	A680	G620	C560	C500	U440	G380	G320
G1281	G1221	G1161	A1041	A981	U921	C861	G801	A741	G681	C621	C561	G501	G441	C381	C321
G1282	A1222	A1162	U1042	A982	C922	U862	G802	G742	U682	G622	A562	C502	U442	U382	G322
G1283	A1223	U1163	C1043	G983	U923	U863	U803	C743	U683	A623	A563	G503	A443	U383	G323
U1284	U1224	U1164	U1044	U984	U924	U864	U804	C744	U684	A624	U564	C504	U444	A384	A324
U1285	A1225	G1105	G1045	A985	U925	C865	G805	C745	G685	A625	U565	G505	G445	C385	G325

A1286	A1346	C1406	A1466	C1526
U1287	C1347	U1407	A1467	A1527
G1288	C1348	G1408	A1468	U1528
G1289	U1349	G1409	A1469	G1529
C1290	A1350	G1410	A1470	U1530
G1291	C1351	U1411	A1471	G1531
C1292	C1352	U1412	U1472	G1532
G1293	G1353	U1413	U1473	U1533
C1294	C1354	A1414	A1474	U1534
A1295	C1355	G1415	A1475	G1535
A1296	G1356	A1416	C1476	G1536
G1297	C1357	C1417	C1477	C1537
C1298	A1358	G1418	G1478	G1538
G1299	G1359	G1419	C1479	C1539
U1300	A1360	U1420	G1480	U1540
U1301	A1361	C1421	C1481	G1541
C1302	G1362	G1422	A1482	C1542
A1303	A1363	U1423	A1483	C1543
U1304	G1364	G1424	A1484	A1544
A1305	C1365	A1425	C1485	U1545
G1306	G1366	G1426	C1486	C1546
C1307	U1367	A1427	G1487	U1547
G1308	A1368	C1428	G1488	C1548
A1309	A1369	A1429	A1489	
C1310	G1370	G1430	G1490	
G1311	C1371	G1431	G1491	
U1312	G1372	U1432	C1492	
C1313	U1373	U1433	A1493	
G1314	G1374	G1434	G1494	
C1315	U1375	G1435	U1495	
U1316	G1376	U1436	C1496	
G1317	A1377	U1437	C1497	
U1318	U1378	U1438	G1498	
U1319	U1379	U1439	U1499	
U1320	G1380	A1440	U1500	
G1321	U1381	C1441	U1501	
U1322	U1382	C1442	U1502	
C1323	C1383	C1443	U1503	
C1324	A1384	U1444	U1504	
G1325	C1385	A1445	U1505	
U1326	C1386	C1446	C1506	
U1327	C1387	U1447	U1507	
C1328	A1388	U1448	G1508	
G1329	C1389	G1449	G1509	
A1330	U1390	G1450	U1510	
U1331	G1391	C1451	U1511	
G1332	A1392	U1452	C1512	
C1333	C1393	G1453	U1513	
U1334	A1394	G1454	G1514	
G1335	G1395	A1455	C1515	
G1336	C1396	G1456	C1516	
U1337	G1397	A1457	G1517	
U1338	A1398	U1458	U1518	
C1339	A1399	U1459	U1519	
U1340	C1400	G1460	G1520	
U1341	G1401	C1461	G1521	
C1342	U1402	G1462	G1522	
C1343	A1403	A1463	U1523	
U1344	G1404	G1464	G1524	
A1345	G1405	U1465	G1525	

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

Chain BC: . 21% 78%

A1	A61	G121
A2	A62	A122
C3	G63	G123
G4	U64	A124
U5	G65	A125
G6	G66	G126
U7	U67	C127
C8	A68	U128
G9	U69	C129
C10	C70	U130
G11	A71	C131
A12	A72	U132
U13	U73	C133
G14	U74	G134
G15	G75	A135
U16	G76	G136
C17	A77	C137
G18	G78	C138
A19	A79	A139
C20	A80	U140
U21	U81	C141
G22	C82	C142
C23	A83	C143
G24	U84	C144
C25	U85	G145
U26	U86	U146
C27	C87	G147
A28	A88	C148
C29	U89	A149
U30	U90	U150
A31	G91	G151
U32	C92	C152
G33	C93	C153
U34	C94	A154
C35	A95	C155
G36	A96	A156
U37	U97	U157
C38	C98	U158
G39	U99	U159
A40	U100	C160
U41	A101	U161
G42	C102	C162
A43	A103	A163
U44	A104	G164
C45	C105	U165
G46	G106	G166
C47	U107	U167
A48	A108	C168
G49	A109	U169
C50	U110	
A51	C111	
A52	G112	
A53	G113	
G54	C114	
U55	G115	
C56	C116	
G57	A117	
U58	U118	
A59	G119	
U60	G120	

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

Chain BD: . 21% 79%

G1	C61	G121
G2	A62	A122
C3	C63	G123
U4	A64	A124
A5	G65	A125
C6	G66	G126
U7	C67	C127
A8	C68	U128
C9	U69	C129
G10	C70	U130
A11	G71	C131
U12	U72	U132
A13	U73	C133
C14	A74	G134
U15	G75	A135
G16	U76	G136
C17	A77	C137
G18	G78	C138
A19	G79	A139
C20	G80	U140
G21	C81	C141
A22	G82	C142
C23	A83	C143
G24	U84	C144
C25	G85	G145
G26	A86	U146
U27	G87	G147
C28	U88	C148
G29	A89	A149
C30	G90	U150
A31	G91	G151
U32	C92	C152
C33	G93	C153
G34	C94	A154
A35	G95	C155
U36	C96	A156
C37	U97	U157
G38	G98	U158
U39	G99	U159
C40	U100	C160
A41	C101	U161
G42	C102	C162
A43	C103	A163
U44	C104	G164
C45	G105	U165
G46	G106	G166
U47	U107	U167
C48	G108	C168
A49	U109	U169
G50	G110	
C51	U111	
U52	U112	
C53	G113	
U54	U114	
G55	A115	
C56	C116	
U57	U117	
G58	C118	
C59	U119	
G60	C120	

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

Chain BE: . 14% 85%

U1	A61	G121
G2	C62	G122
A3	C63	A123
G4	A64	G124
U5	U65	C125
A6	A66	G126
U7	A67	G127
G8	U68	G128
C9	C69	G129
U10	C70	U130
A11	A71	C131
U12	G72	U132
A13	A73	C133
C14	U74	A134
A15	C75	A135
C16	U76	G136
U17	C77	A137
G18	C78	U138
A19	G79	U139
C20	G80	G140
G21	C81	A141
A22	C82	A142
C23	U83	A143
G24	U84	A144
U25	G85	A145
C26	C86	U146
A27	U87	G147
G28	C88	C148
C29	G89	A149
G30	G90	U150
A31	G91	C151
U32	C92	U152
C33	G93	C153
G34	U94	A154
A35	G95	C155
U36	C96	C156
C37	G97	U157
G38	C98	U158
U39	G99	A159
C40	U100	C160
A41	C101	G161
G42	C102	U162
A43	C103	A163
U44	G104	C164
C45	A105	U165
G46	C106	G166
U47	U107	U167
C48	U108	C168
A49	C109	C169
G50	U110	U170
C51	C111	U171
U52	U112	U172
C53	G113	C173
U54	U114	U174
G55	U115	U175
C56	U116	G176
U57	A117	U177
G58	C118	G178
C59	U119	A179
G60	C120	U180



U181  
U182  
C183  
G184  
G185  
C186  
G187  
C188  
A189  
U190  
U191  
A192  
A193  
A194  
G195  
C196  
A197  
A198  
A199  
A200  
A201  
C202  
C203  
U204  
G205  
G206  
G207  
U208  
U209  
G210

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

Chain BF: 8% 92%

C1  
G2  
A3  
A4  
U5  
C6  
G7  
C8  
C9  
A10  
U11  
C11  
U12  
U13  
C14  
U15  
C16  
U17  
U18  
A19  
U20  
C21  
U22  
G23  
G24  
G25  
U26  
G27  
C28  
U29  
U30  
U31  
C32  
C33  
C34  
C35  
G36  
C37  
C38  
C39  
U40  
U41  
G42  
U43  
C44  
G45  
G46  
G47  
G48  
C49  
C50  
C51  
A52  
G53  
U54  
A55  
C56  
C57  
U58  
U59  
C60

A61  
U62  
U63  
U64  
U65  
C66  
A67  
C68  
A69  
U70  
G71  
A72  
U73

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

Chain BG: 17% 83%

C1  
U2  
G3  
A4  
G5  
U6  
U7  
U8  
C9  
U10  
C11  
U12  
A13  
G14  
U15  
G16  
A17  
U18  
C19  
U20  
C21  
U22  
G23  
A24  
G25  
C26  
C27  
A28  
U29  
C30  
U31  
U32  
C33  
A34  
G35  
G36  
G37  
A38  
A39  
G40  
U41  
A42  
U43  
G44  
G45  
G46  
G47  
U48  
A49  
G50  
U51  
A52  
C53  
G54  
A55  
G56  
A57  
G58  
U59  
A60

A61  
C62  
U63  
C64  
G65  
C66  
A67  
U68  
G69  
C70  
U71  
G72  
U73  
G74  
C75  
G76  
U77  
C78  
U79  
G80  
A81  
U82  
C83  
U84  
C85  
U86  
G87  
C88  
A89  
U90  
U91  
U92  
G93  
G94  
U95  
C96  
G97  
A98  
A99  
G100  
U101  
G102  
C103  
U104  
A105  
G106  
U107  
G108  
C109  
U110  
C111  
G112  
C113  
A114  
G115  
G116  
C117  
U118  
A119  
U120

C121  
G122  
C123  
A124  
G125  
U126  
G127  
U128  
G129  
U130  
C131  
U132  
C133  
U134  
C135  
G136  
U137  
C138  
U139  
G140  
A141  
U142  
C143  
U144  
C145  
C146  
U147  
C148  
U149  
A150  
U151  
C152  
C153  
A154  
U155  
G156  
U157  
A158  
A159  
C160  
U161  
A162  
G163  
U164  
C165  
G166  
U167  
A168  
C169  
G170  
U171  
C172  
G173  
U174  
G175  
G176  
U177  
C178  
U179  
C180

C181  
G182

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

Chain BH: 28% 69%

U1  
U2  
U3  
U4  
G5  
U6  
C7  
C8  
C9  
U10  
C11  
U12  
C13  
C14  
A15  
G16  
U17  
C18  
G19  
A20  
U21  
G22  
C23  
U24  
A25  
C26  
A27  
C28  
U29  
C30  
A31  
U32  
G33  
G34  
C35  
C36  
U37  
C38  
G39  
A40  
U41  
A42  
C43  
A44  
G45  
U46  
G47  
C48  
A49  
U50  
C51  
G52  
C53  
U54  
C55  
G56  
A57  
C58  
U59  
A60

C61  
C62  
G63  
U64  
G65  
G66  
G67  
C68  
C69  
U70  
C71  
G72  
A73  
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  
G114  
A115  
C116  
U117  
U118  
U119  
C120

A121  
U122  
G123  
C124  
U125  
C126  
U127  
G128  
U129  
G130  
A131  
C132  
U133  
U134  
U135

• Molecule 42: 60S RIBOSOMAL PROTEIN L18

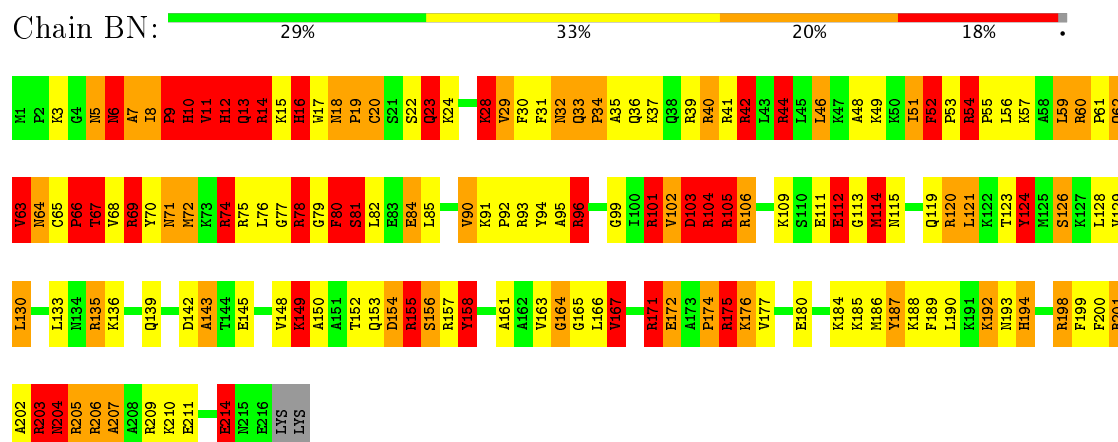
Chain BI: 39% 35% 19% 7%

MET  
G2  
V3  
D4  
L5  
V8  
Q9  
K10  
K11  
K12  
K13  
V14  
V15  
R16  
H17  
H18  
T19  
Y20  
S21  
P24  
Y25  
L26  
K27  
L28  
L29  
L30  
M99  
K101  
L32  
Y33  
K34  
F35  
L36  
G37  
I107  
K38  
R39  
T40  
N41  
F44  
N45  
I48  
R49  
K50  
R51  
R56  
N57  
N58  
R59  
A60  
P61  
L64  
S65  
R66  
F138  
T139

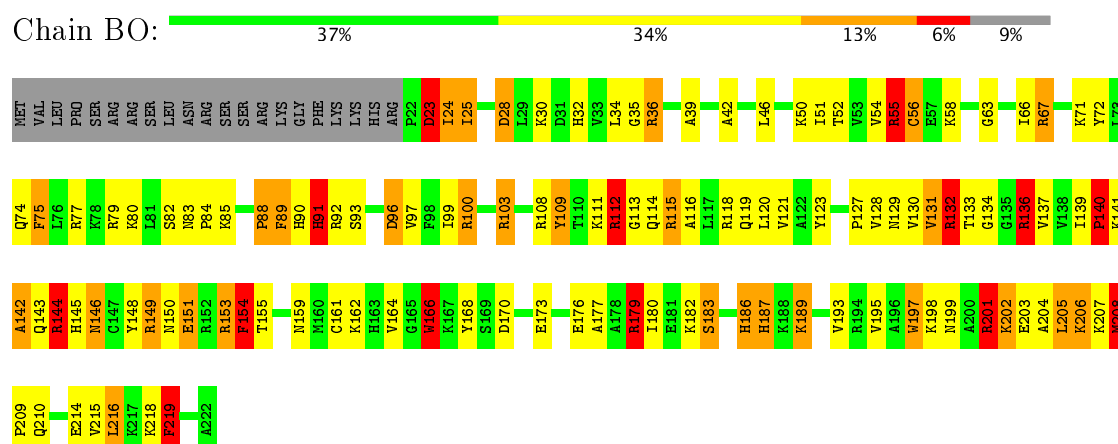
C70  
M71  
R72  
R73  
R74  
T75  
V76  
W77  
L78  
K79  
K80  
K81  
S84  
P85  
R86  
A87  
H88  
L89  
Y90  
G91  
D92  
Y93  
L94  
D95  
D96  
K97  
V97  
R98  
M99  
T100  
R101  
L102  
P103  
A104  
L105  
R106  
I107  
G108  
A109  
L110  
R111  
F112  
S113  
K114  
S115  
A116  
R117  
E118  
R119  
I120  
G125  
E126  
C127  
A134  
M135  
M136  
A137  
F138  
T139



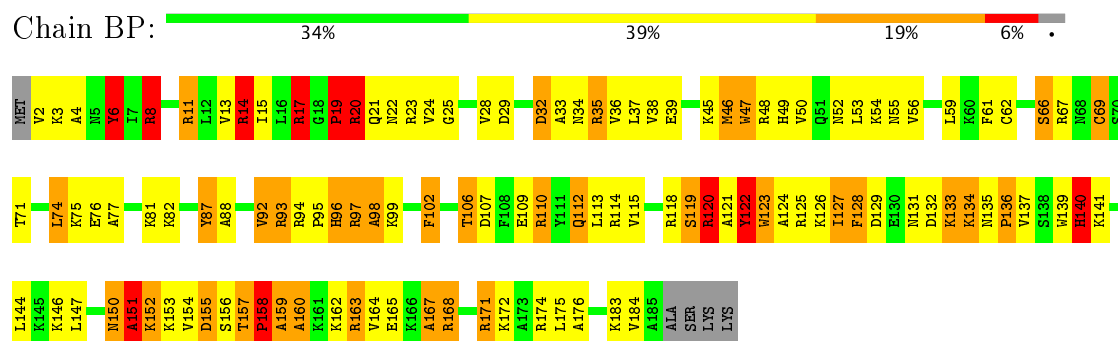
- Molecule 47: 60S RIBOSOMAL PROTEIN L13



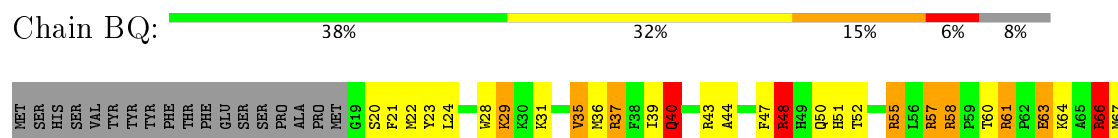
- Molecule 48: 60S RIBOSOMAL PROTEIN L13A, PUTATIVE



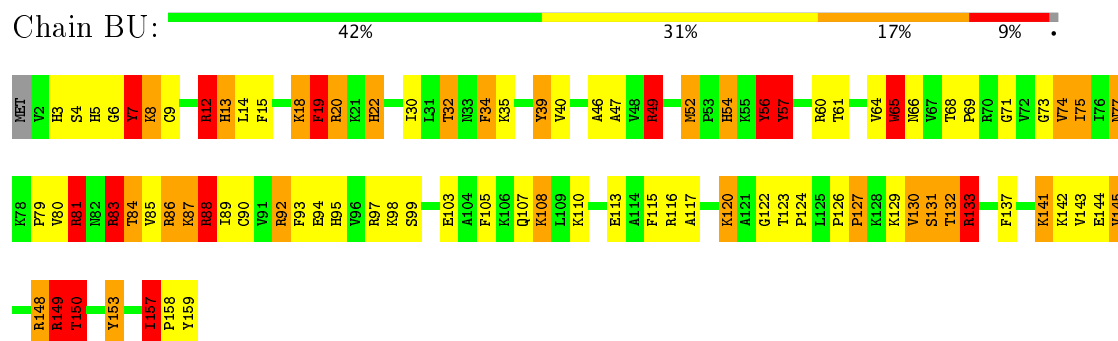
- Molecule 49: PROBABLE 60S RIBOSOMAL PROTEIN L14



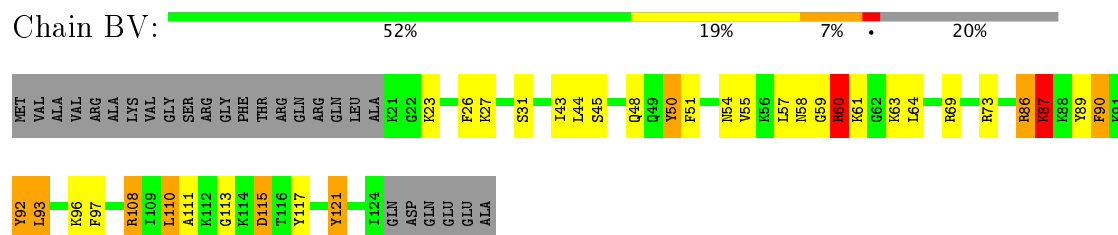
- Molecule 50: RIBOSOMAL PROTEIN L15



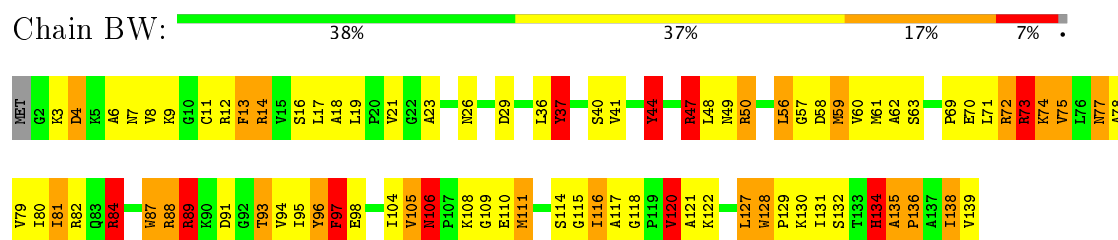




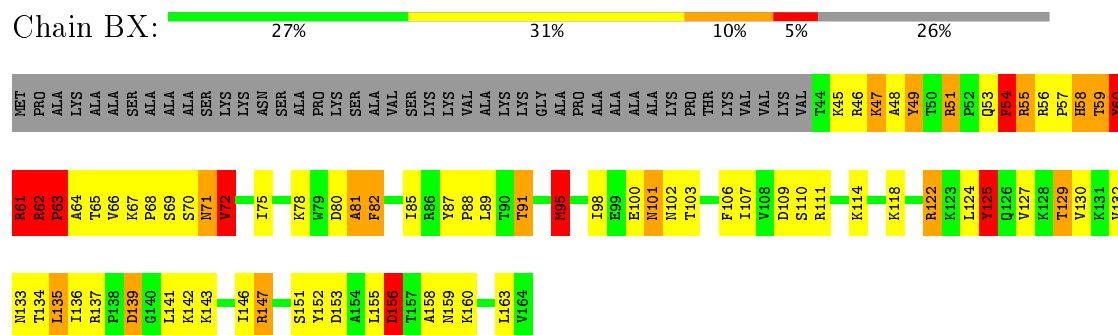
• Molecule 55: 60S RIBOSOMAL PROTEIN L22, PUTATIVE



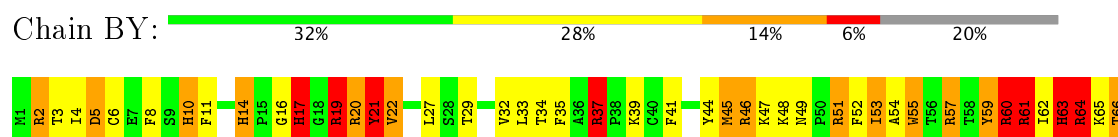
• Molecule 56: 60S RIBOSOMAL PROTEIN L23, PUTATIVE



• Molecule 57: 60S RIBOSOMAL PROTEIN L23A



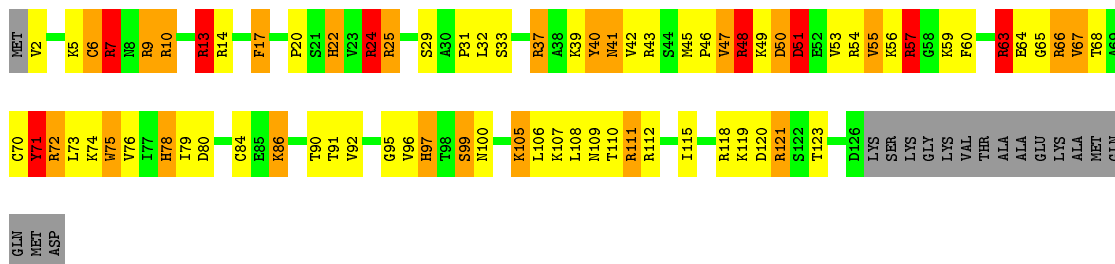
• Molecule 58: 60S RIBOSOMAL PROTEIN L24, PUTATIVE





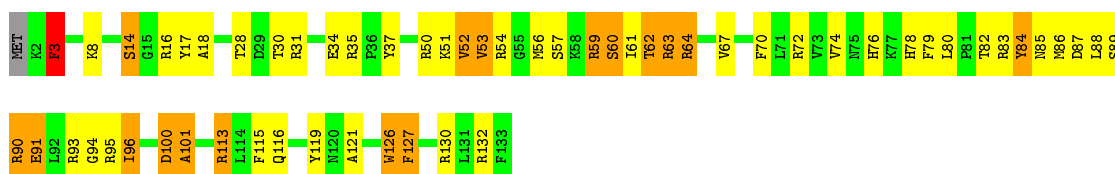
• Molecule 59: 60S RIBOSOMAL PROTEIN L26, PUTATIVE

Chain BZ:



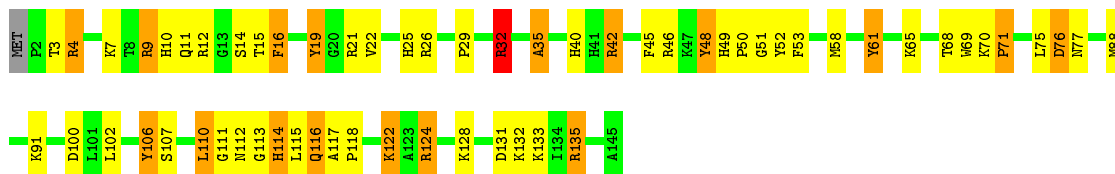
• Molecule 60: 60S RIBOSOMAL PROTEIN L27, PUTATIVE

Chain Ba:



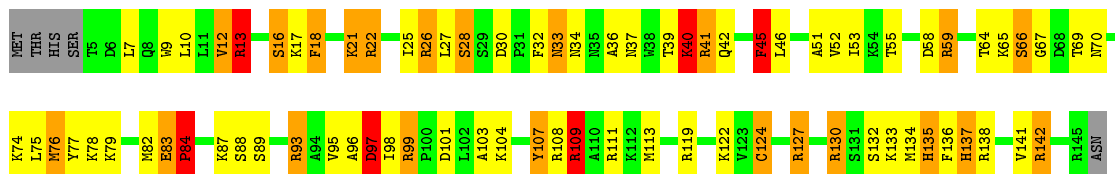
• Molecule 61: 60S RIBOSOMAL PROTEIN L27A

Chain Bb:



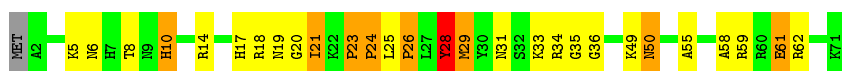
• Molecule 62: 60S RIBOSOMAL PROTEIN L28, PUTATIVE

Chain Bc:

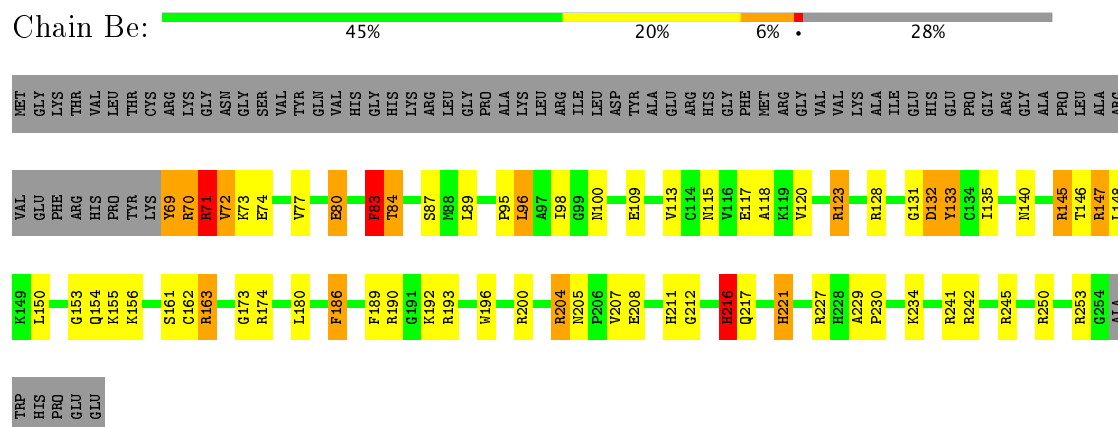


• Molecule 63: 60S RIBOSOMAL PROTEIN L29, PUTATIVE

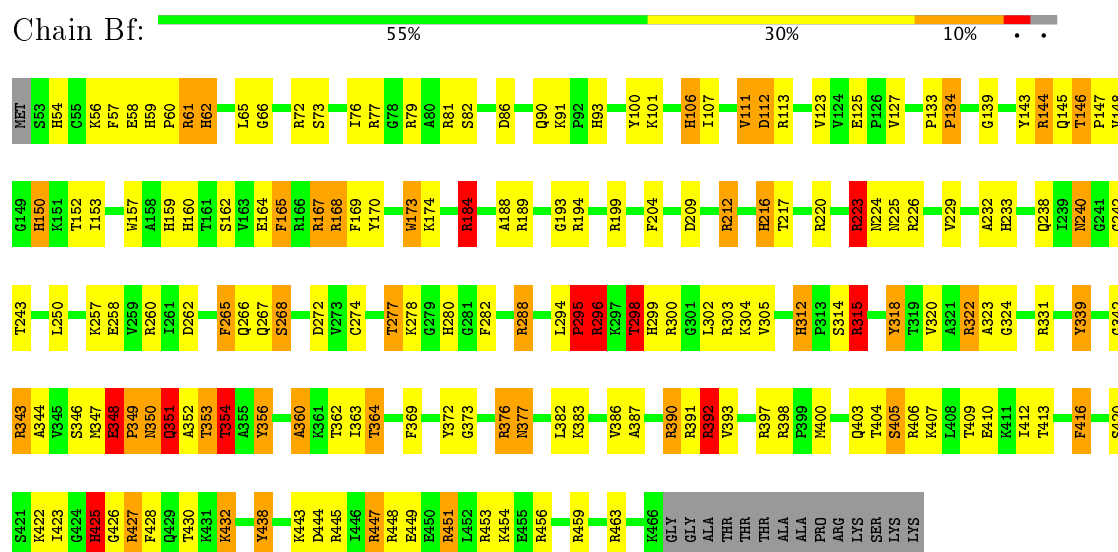
Chain Bd:



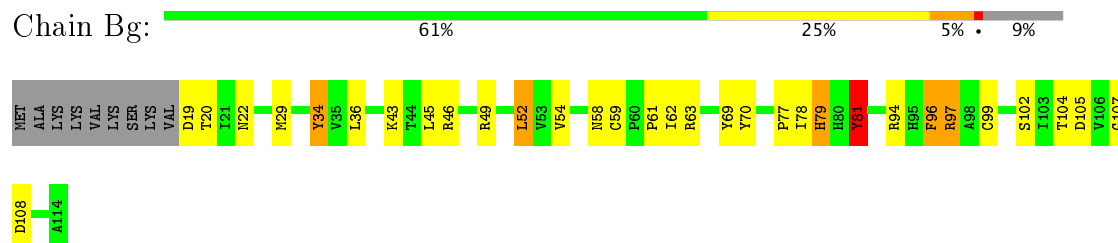
- Molecule 64: 60S RIBOSOMAL PROTEIN L2, PUTATIVE



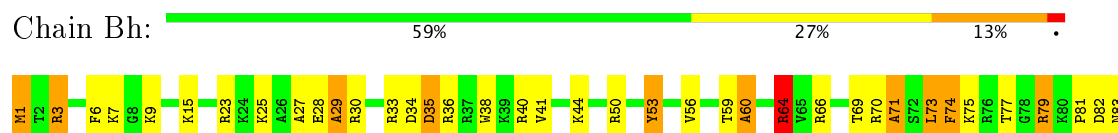
- Molecule 65: RIBOSOMAL PROTEIN L3, MITOCHONDRIAL, PUTATIVE

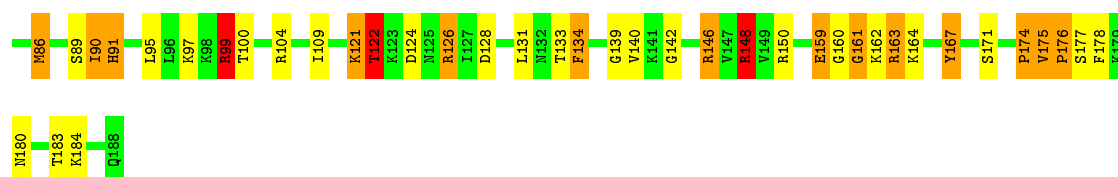


- Molecule 66: 60S RIBOSOMAL PROTEIN L30



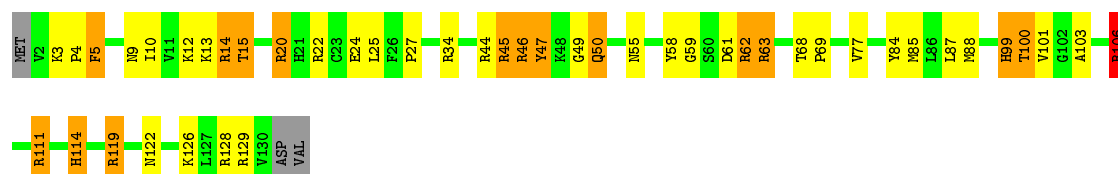
- Molecule 67: 60S RIBOSOMAL SUBUNIT PROTEIN L31, PUTATIVE





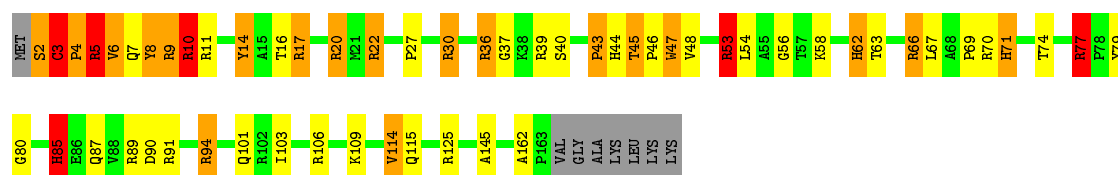
- Molecule 68: 60S RIBOSOMAL PROTEIN L32, PUTATIVE

Chain Bi: 63% 23% 11% ..



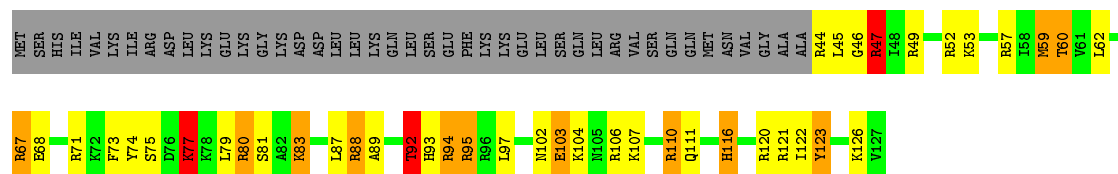
- Molecule 69: 60S RIBOSOMAL PROTEIN L34, PUTATIVE

Chain Bj: 62% 19% 11% • 5%



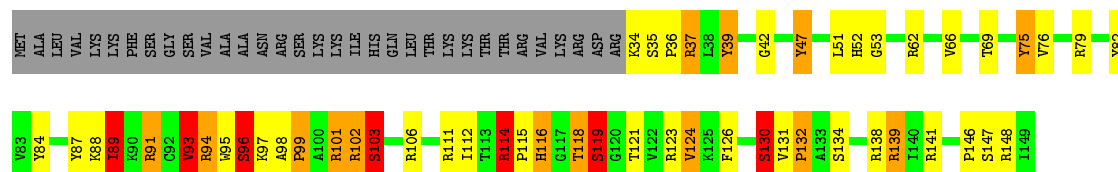
- Molecule 70: 60S RIBOSOMAL PROTEIN L35, PUTATIVE

Chain Bk: 32% 22% 9% • 34%



- Molecule 71: 60S RIBOSOMAL PROTEIN L35A, PUTATIVE

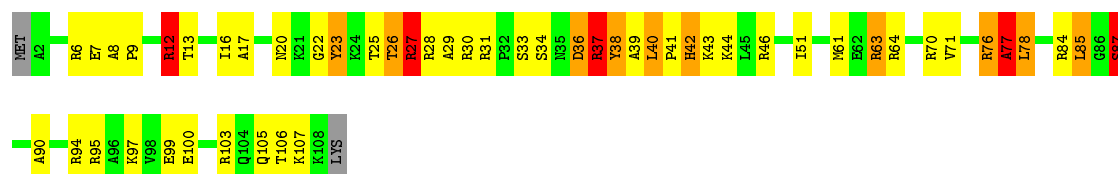
Chain Bl: 42% 22% 9% 5% 22%



- Molecule 72: RIBOSOMAL PROTEIN L36, PUTATIVE

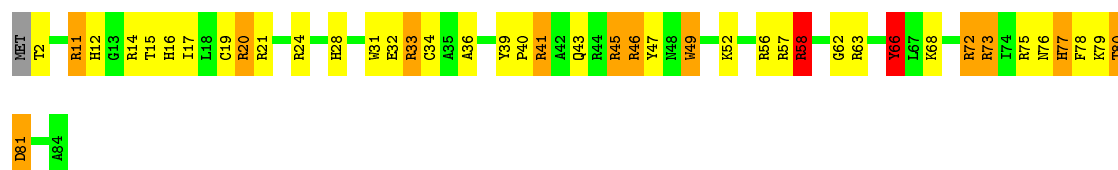
Chain Bm: 50% 34% 9% 5% •





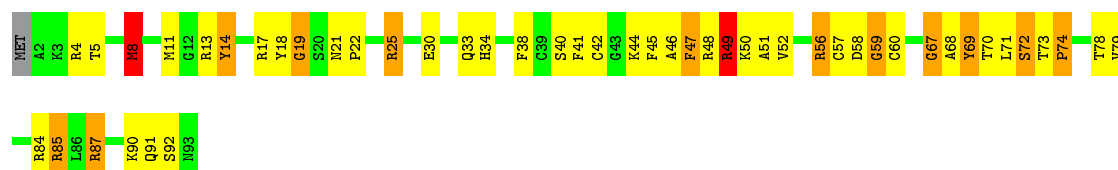
• Molecule 73: RIBOSOMAL PROTEIN L37

Chain Bn: 49% 33% 14% ..



• Molecule 74: 60S RIBOSOMAL PROTEIN L37A, PUTATIVE

Chain Bo: 46% 38% 13% ..



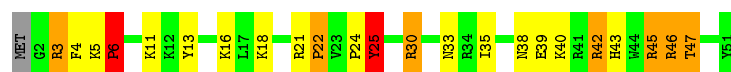
• Molecule 75: 60S RIBOSOMAL PROTEIN L38, PUTATIVE

Chain Bp: 59% 34% 5% ..



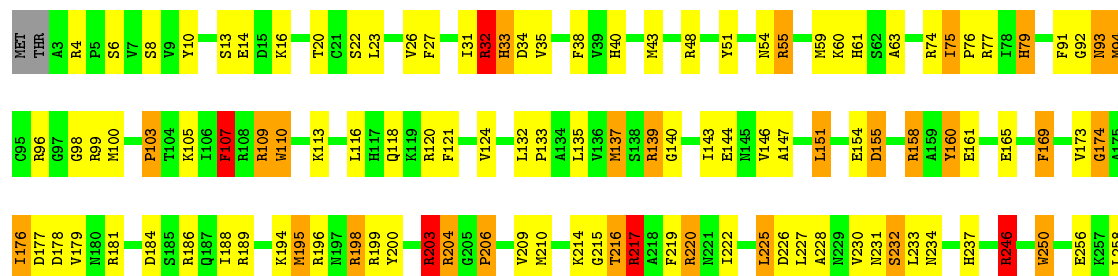
• Molecule 76: 60S RIBOSOMAL PROTEIN L39, PUTATIVE

Chain Bq: 53% 27% 14% ..



• Molecule 77: 60S RIBOSOMAL PROTEIN L4

Chain Br: 54% 32% 11% ..

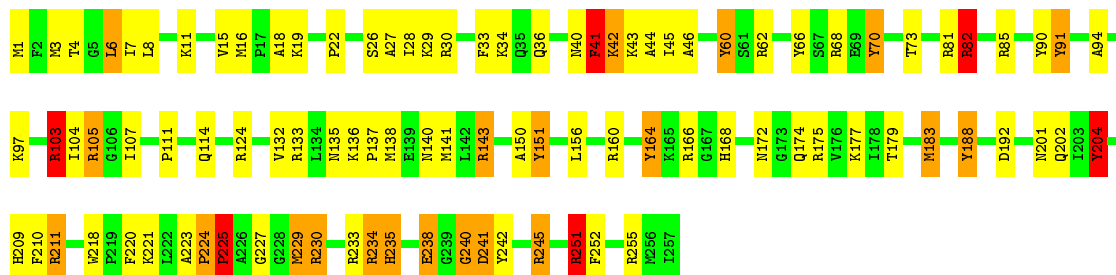






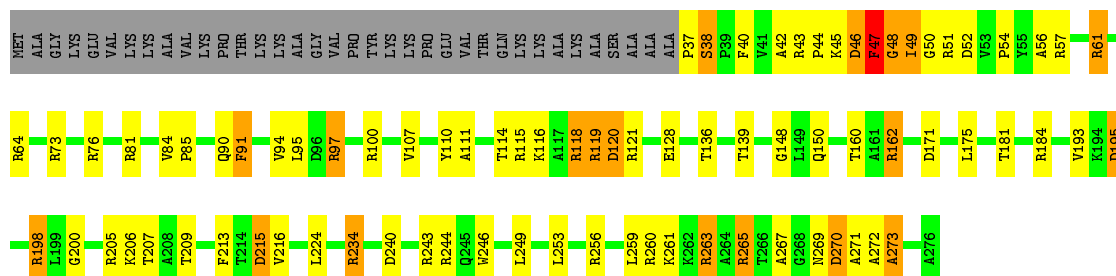
- Molecule 82: 60S RIBOSOMAL PROTEIN L7, PUTATIVE

Chain Bw: 62% 27% 8% .



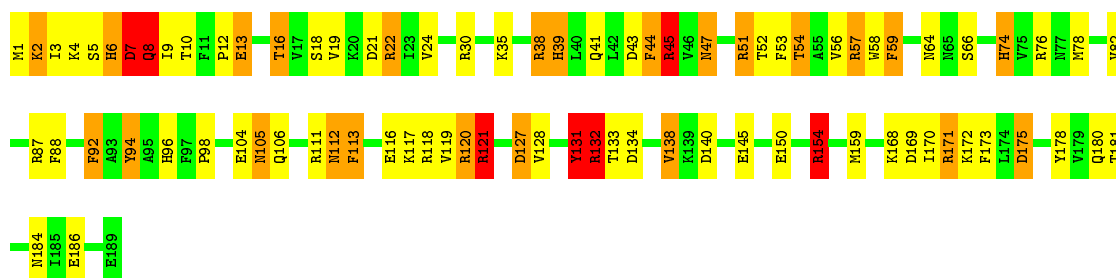
- Molecule 83: 60S RIBOSOMAL PROTEIN L7A, PUTATIVE

Chain Bx: 57% 22% 7% 13%



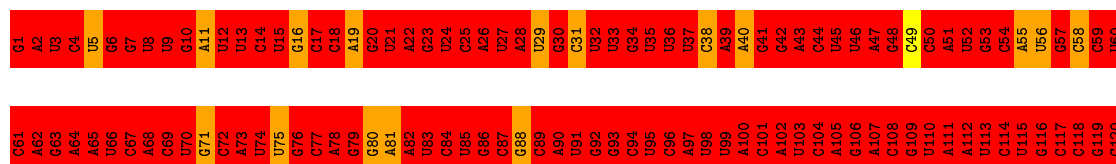
- Molecule 84: 60S RIBOSOMAL PROTEIN L9, PUTATIVE

Chain By: 56% 28% 13% .



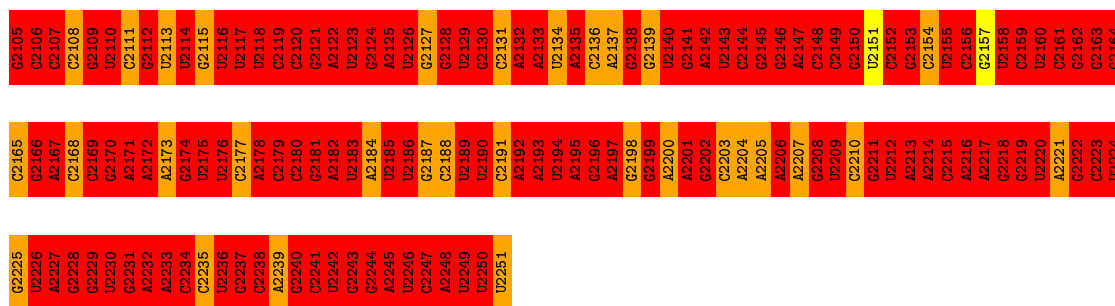
- Molecule 85: 18S RRNA OF THE SMALL RIBOSOMAL SUBUNIT

Chain AA: 19% 75%

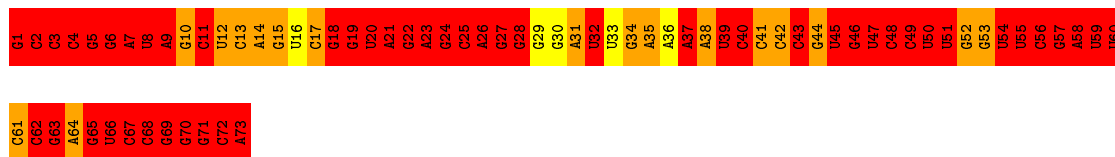


U1082	G1022	U952	A902	G842	G782	G722	U602	G542	C482	G422	G362	C302	G242	A181	G121
G1083	U1023	U953	G903	U943	C783	U723	C503	A543	G483	G423	A363	A303	A243	A182	A122
A1084	G1024	C954	U904	C844	C684	A724	C504	A544	A484	G424	C364	G304	G244	C183	A123
U1085	U1025	U955	C905	A845	A685	G725	A605	A545	A485	G425	G365	A305	A245	A184	A124
U1086	U1026	G956	U906	U946	A686	U726	U606	U546	G486	G426	A366	G306	C246	A185	A125
U1087	U1027	C957	G907	G847	U787	U727	U607	G547	G487	G427	A367	G307	G247	U186	U126
U1088	C1028	U958	C908	C848	G788	U728	A608	G548	G488	G428	C368	U308	U248	C187	U127
G1089	G1029	U959	C909	A849	A789	U729	U609	A549	C489	G429	C369	G309	C249	G188	U128
U1090	U1030	U970	G910	U950	C790	U730	C510	G550	A490	G430	A370	U310	C250	G189	U129
C1091	G1031	U971	U911	G851	U791	U731	G611	C551	G491	A431	C371	U311	G251	A190	G130
U1092	U1032	C972	C912	C852	A792	G732	A612	C552	C492	A432	U372	G312	G252	C191	C131
G1093	G1033	U973	U913	G853	G793	G733	G613	G553	A493	U433	G373	A313	C253	G192	G132
C1094	U1034	U974	U914	A854	A794	C734	U614	A554	G494	U434	C374	A314	G254	G193	G133
C1095	C1035	G975	G915	G855	C795	G735	A615	C555	G495	A435	C375	U315	A255	U194	U134
U1096	A1036	G976	A916	G856	C796	U736	A616	C556	C496	G436	C376	A316	A256	C195	C135
G1097	U1037	U977	A917	G857	C797	U737	C517	G557	G497	A437	U377	U317	U257	U196	U136
C1098	U1038	U978	U918	G858	A798	C738	A618	U558	C498	A438	A378	A318	G258	C197	C137
U1099	U1039	U979	U919	G859	G799	G739	A619	G559	G499	U439	U379	U319	A259	U198	C138
U1100	U1040	U980	A920	C860	A800	A740	U620	C560	C500	U440	C380	U320	A260	U199	G139
C1101	U1041	A981	C921	G861	U801	G741	U621	C561	A501	C441	A381	C321	U261	U200	C140
C1102	U1042	G982	A922	G862	A802	U742	G622	C562	A502	A442	A382	A322	G262	U201	A141
A1103	U1043	A983	A923	C863	C803	C743	G623	U563	A503	A443	C383	U323	A263	U202	U142
G1104	G1044	A984	A924	C864	A804	C744	A624	A564	U504	U444	C384	U324	A264	C203	U143
G1105	G1045	G985	G925	G865	A805	C745	G625	G565	U505	U445	A385	G325	A265	U204	A144
C1106	C1046	U986	C926	U866	G806	G746	G626	U566	G506	C446	G386	C327	U267	A205	C145
A1107	G1047	C987	A927	G867	C807	U747	A627	C567	C507	C447	U387	G327	U267	U206	U146
U1108	U1048	C988	U928	A868	C808	C748	C528	C568	C508	G448	G388	U328	A268	G207	G147
U1109	G1049	U989	G929	A869	A809	C749	A629	A569	C509	G449	A389	G329	G269	U208	G148
U1110	U1050	U990	G930	U870	C810	A750	A630	U570	A510	A450	U390	G330	A270	C209	A149
A1111	A1051	G991	G931	U871	A811	C751	G631	G571	A511	G451	G391	A331	A271	G210	U150
G1112	C1052	G992	U932	U872	C812	C752	U632	U572	U512	A452	G392	A332	C272	C211	A151
C1113	A1053	G993	U933	C873	G813	U753	U633	U573	G513	G453	C393	A333	C273	G212	A152
A1114	U1054	A994	A934	A874	G814	C754	U634	U574	C514	G454	C394	A334	A274	G213	C153
G1115	U1055	G995	A935	C875	G815	G755	G635	G575	C515	G455	G395	A335	A275	C214	U154
U1116	C1056	A996	C936	U876	A816	G756	G636	U576	G516	A456	U396	G336	C276	U215	U155
G1117	G1057	U997	G937	G877	G817	A757	U637	G577	A517	G457	G397	G337	G277	G216	G156
U1118	U1058	U998	A938	U878	C818	C758	G638	U578	A518	C458	U398	G338	C278	G157	C157
A1119	C1059	A999	A939	G879	G819	C759	C539	U579	A519	C459	A399	A339	C279	U218	C158
G1120	U1060	U1000	G940	A880	G820	U760	C540	C580	A520	U460	G400	G340	U280	G219	G159
U1121	C1061	G1001	C941	C881	U821	G761	A641	A581	A521	G461	U401	C341	C281	U222	A160
U1122	U1062	G1002	A942	C882	U822	U762	G642	A582	A522	A462	G402	C342	C282	A223	A161
C1123	U1063	G1003	U943	C883	C823	U763	C543	U583	U523	G463	G403	U343	A283	C224	A162
G1124	C1064	A1004	C944	A884	G824	U764	A644	G584	A524	A464	A404	U344	C284	G225	C163
U1125	U1065	U1005	A945	A885	U825	U765	C545	G585	C525	A465	U405	U345	C285	G226	G164
G1126	U1066	C1006	G	A886	C826	G766	C546	G586	G526	A466	U406	U346	C286	C165	C165
U1127	G1067	G1007	C	A887	C827	A767	C547	G587	G527	U467	G407	U347	G287	A227	C166
G1128	A1068	C1008	C	A888	U828	C768	G648	G588	U528	A468	C408	G348	G288	A167	C167
A1129	U1069	G1009	C	G889	A709	C769	C549	A589	G529	G469	C409	C349	G289	U229	A168
G1130	G1070	U1010	U	U890	A830	C770	G650	U590	A530	C470	A410	U350	G290	U230	G169
A1131	U1071	G1011	G	G891	C831	A771	G651	A591	G531	U471	U411	G351	C291	G231	C170
A1132	U1072	C1012	G	C892	U832	C772	U652	C592	G532	A472	G412	G352	C292	U232	U171
C1133	U1073	C1013	G	G893	G773	G773	A653	U593	C533	C473	G413	G353	A293	C233	A172
G1134	U1074	U1014	G	A894	U834	C774	A654	C594	A534	C474	C414	C354	G294	G234	A173
U1135	U1075	U1015	C	C895	C775	C775	U655	A595	G535	A475	G415	G355	U295	U235	A174
A1136	U1076	G1016	C956	C896	G776	C776	U656	A596	G536	C476	U416	U356	A296	G236	A175
C1137	U1077	U1017	A957	A897	C837	U777	C557	A597	G537	U477	U417	C357	A297	G237	C176
U1138	A1078	G1018	C958	A898	C838	C778	C558	U598	A538	U478	G418	U358	C298	C238	A177
G1139	C1079	U1019	C959	A899	C839	G779	C559	C599	A539	C479	A419	A359	G299	G239	U178
G1140	A1080	G1020	G960	G900	A840	U780	G660	C600	A540	U480	C420	A360	C300	U179	G179
U1141	U1081	G1021	U961	C901	U841	G781	C661	A601	A541	A481	G421	U361	U301	U241	A180

U2045	C1985	A1805	G1685	C1625	G1565	C1445	C1322	A1262	G1202	G1142
G2046	G1986	C1806	G1686	U1626	A1566	U1446	G1385	G1263	G1203	C1143
U2047	G1987	A1807	G1687	U1627	A1567	U1447	C1386	G1264	A1204	G1144
U2049	A1988	G1808	U1688	U1628	U1568	A1448	C1387	C1265	U1145	U1145
C2050	G1989	C1809	G1689	U1629	C1569	C1449	A1388	C1266	A1206	C1146
G2051	U1990	G1810	A1690	U1630	A1570	U1450	G1389	C1267	C1207	A1147
U2052	C1991	C1811	U1691	C1631	A1571	U1451	U1390	C1268	C1208	G1148
A2053	G1992	G1812	G1692	G1632	C1572	U1452	U1391	A1269	U1209	A1149
C2054	C1993	C1813	G1693	A1633	U1573	U1453	C1392	C1270	G1150	G1150
G2054	A1994	G1814	G1694	U1634	C1574	U1454	C1393	U1271	G1211	G1151
G2055	G1995	U1815	G1695	C1635	A1575	C1455	C1394	G1272	C1212	U1152
C2056	U1996	C1816	U1696	G1636	G1576	A1456	U1395	C1273	G1213	G1153
G2057	G1997	U1817	C1697	C1637	G1577	C1457	G1396	A1274	C1214	A1154
A2058	U1998	C1818	A1698	C1638	G1578	G1458	A1397	U1275	A1215	A1155
C2059	G1999	U1819	A1699	U1639	A1579	C1459	U1398	A1276	A1216	A1156
G2060	C2000	G1820	C1700	G1640	A1580	G1460	C1399	G1277	U1217	U1157
C2061	C2001	C1821	G1701	A1641	C1581	A1461	U1400	C1340	C1218	U1158
U2062	A2002	G1822	G1702	A1642	U1582	A1462	U1341	A1278	A1219	C1159
C2063	C1983	G1823	A1703	U1643	U1583	A1463	G1403	U1280	C1220	U1160
A2064	U1944	G1824	C1704	G1644	A1584	G1464	G1404	G1281	G1221	U1161
U2065	A1885	A1825	G1705	U1645	C1585	C1465	U1405	A1282	A1222	A1162
C2066	G1946	U1826	A1706	U1646	U1586	U1466	U1406	C1283	C1223	G1163
A2067	G1947	U1827	G1707	G1647	C1587	U1467	C1407	A1284	C1224	A1164
C2068	A1948	C1828	A1708	G1648	A1588	G1468	U1408	C1285	G1225	C1165
A2069	U1949	G1829	U1709	U1649	G1589	G1469	U1409	C1286	A1226	G1166
C2070	C1890	U1830	C1710	G1650	A1590	A1470	C1410	C1287	A1227	G1167
U2071	C2011	G1831	C1711	G1651	U1591	G1471	C1411	U1288	A1228	C1168
G2072	G2012	G1832	A1712	A1652	G1592	G1472	U1351	U1289	G1229	A1169
U2073	A2013	C1833	A1713	U1653	C1593	U1473	G1413	G1290	U1230	C1170
C2074	G2014	U1834	G1714	G1654	A1594	U1474	U1353	A1291	G1231	C1171
G2075	U2015	G1835	C1715	G1655	G1595	A1475	G1415	A1292	U1232	A1172
C2076	A2016	U1836	C1716	C1656	C1596	C1476	U1416	U1293	G1233	A1173
U2077	G1957	U1837	G1717	G1657	U1597	U1477	U1417	U1294	G1234	G1174
A2078	C1958	C1838	C1718	G1658	A1598	G1478	U1418	G1295	G1235	A1175
U2079	G1959	G1839	G1719	C1659	C1599	U1479	U1419	G1296	G1236	C1176
C2080	C2020	G1840	C1720	U1660	G1600	C1480	U1420	G1297	A1237	G1177
A2081	U1961	G1841	A1721	U1661	U1601	U1481	U1421	G1298	U1238	A1178
C2082	U1962	C1842	G1722	U1662	U1602	C1482	A1422	A1299	C1239	A1179
U2083	G1963	A1843	U1723	U1663	G1603	A1483	A1362	A1300	A1240	C1180
C2084	C1964	G1844	A1724	G1664	A1604	G1484	G1423	C1301	A1241	U1181
A2085	A1905	G1845	G1725	G1665	G1605	G1485	G1425	U1364	A1242	A1182
C2086	C1906	U1846	G1726	U1666	G1606	G1486	G1426	U1303	G1243	C1183
U2087	U1907	U1847	G1727	C1667	A1607	G1487	A1427	C1304	A1244	A1184
C2088	A1908	G1848	G1728	G1668	U1608	G1488	A1428	A1305	U1245	G1185
G2089	C1909	U1849	C1729	G1669	U1609	G1489	U1429	U1306	G1246	C1186
U2090	G1910	G1850	C1730	U1670	G1610	A1490	A1430	U1307	A1247	G1187
C2091	A1911	C1851	G1731	U1671	A1611	G1491	G1370	G1308	U1248	A1188
A2092	U1912	U1852	C1732	G1672	C1612	U1492	C1431	U1249	A1189	C1189
C2093	G1913	U1853	G1733	A1673	A1613	A1493	C1433	G1310	A1250	G1190
G2094	U1914	U1854	A1734	G1674	C1614	C1494	U1434	U1311	G1251	G1191
U2095	C1915	U1855	U1735	U1675	G1615	G1495	C1435	G1312	A1252	C1192
C2096	A1916	G1856	U1736	G1676	U1616	U1496	A1436	C1313	G1253	A1193
U2097	G1917	C1857	G1737	A1677	G1617	U1497	U1376	C1314	A1254	U1194
C2098	U1918	G1858	U1738	U1678	G1618	U1498	C1437	C1315	C1255	U1195
G2099	A1919	C1859	G1739	U1679	U1619	A1499	A1439	G1316	C1256	C1196
A2100	U1920	U1860	C1740	U1680	A1620	C1500	A1440	U1317	A1257	U1197
C2101	A1981	G1861	A1801	G1681	U1621	A1501	G1441	G1318	U1258	U1198
U2102	C1982	C1862	U1802	G1682	G1622	A1502	U1442	G1319	U1259	C1199
C2103	A1923	A1863	C1741	U1683	U1623	U1503	U1443	G1320	G1260	A1200
C2104	A2044	G1864	C1742	U1684	U1624	A1504	U1444	C1321	U1261	A1201



- Molecule 86: E-SITE tRNA



## 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	20
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	27
4	A3	248/250 (99%)	204 (82%)	24 (10%)	20 (8%)	1	16
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	17
7	A6	185/190 (97%)	135 (73%)	30 (16%)	20 (11%)	0	10
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	18
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	18
12	AD	102/172 (59%)	79 (78%)	9 (9%)	14 (14%)	0	6
13	AE	158/174 (91%)	126 (80%)	12 (8%)	20 (13%)	0	7
14	AF	119/144 (83%)	105 (88%)	11 (9%)	3 (2%)	6	41
15	AG	139/151 (92%)	120 (86%)	12 (9%)	7 (5%)	2	27
16	AH	124/144 (86%)	99 (80%)	14 (11%)	11 (9%)	1	15
17	AI	132/152 (87%)	100 (76%)	21 (16%)	11 (8%)	1	16
18	AJ	127/130 (98%)	114 (90%)	7 (6%)	6 (5%)	3	28
19	AK	146/149 (98%)	118 (81%)	18 (12%)	10 (7%)	1	20
20	AL	125/142 (88%)	94 (75%)	19 (15%)	12 (10%)	1	13
21	AM	151/153 (99%)	114 (76%)	16 (11%)	21 (14%)	0	5
22	AO	147/167 (88%)	128 (87%)	10 (7%)	9 (6%)	2	22
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	20
25	AR	79/194 (41%)	59 (75%)	12 (15%)	8 (10%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	AS	140/143 (98%)	111 (79%)	18 (13%)	11 (8%)	1	17
27	AT	129/137 (94%)	100 (78%)	15 (12%)	14 (11%)	0	10
28	AU	84/113 (74%)	66 (79%)	12 (14%)	6 (7%)	1	19
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	25
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	29
42	BI	190/193 (98%)	126 (66%)	37 (20%)	27 (14%)	0	5
43	BJ	212/214 (99%)	186 (88%)	20 (9%)	6 (3%)	6	40
44	BK	210/213 (99%)	161 (77%)	26 (12%)	23 (11%)	0	10
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	21
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	19
49	BP	182/189 (96%)	149 (82%)	19 (10%)	14 (8%)	1	17
50	BQ	201/221 (91%)	160 (80%)	21 (10%)	20 (10%)	1	12
51	BR	153/166 (92%)	121 (79%)	21 (14%)	11 (7%)	1	19
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	26
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	27
56	BW	136/139 (98%)	103 (76%)	18 (13%)	15 (11%)	0	10
57	BX	119/164 (73%)	97 (82%)	9 (8%)	13 (11%)	0	10
58	BY	98/125 (78%)	81 (83%)	9 (9%)	8 (8%)	1	16
59	BZ	123/143 (86%)	104 (85%)	12 (10%)	7 (6%)	2	24
60	Ba	130/133 (98%)	93 (72%)	21 (16%)	16 (12%)	0	7
61	Bb	142/145 (98%)	108 (76%)	19 (13%)	15 (11%)	0	10
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%)	17	60
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	15
69	Bj	160/170 (94%)	123 (77%)	22 (14%)	15 (9%)	1	14
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	7
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	7
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	31
79	Bt	103/106 (97%)	75 (73%)	16 (16%)	12 (12%)	0	8
80	Bu	297/308 (96%)	216 (73%)	46 (16%)	35 (12%)	0	8
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	15
83	Bx	238/276 (86%)	188 (79%)	26 (11%)	24 (10%)	1	12
84	By	187/189 (99%)	155 (83%)	15 (8%)	17 (9%)	1	15
All	All	11687/13211 (88%)	9172 (78%)	1415 (12%)	1100 (9%)	2	14

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	18
2	A1	209/231 (90%)	172 (82%)	37 (18%)	2	14
3	A2	158/160 (99%)	132 (84%)	26 (16%)	2	17
4	A3	207/207 (100%)	174 (84%)	33 (16%)	3	18
5	A4	176/187 (94%)	144 (82%)	32 (18%)	2	13
6	A5	158/180 (88%)	140 (89%)	18 (11%)	7	29
7	A6	162/166 (98%)	137 (85%)	25 (15%)	3	19
8	A7	264/267 (99%)	232 (88%)	32 (12%)	6	27
9	A8	36/49 (74%)	32 (89%)	4 (11%)	7	30
10	A9	57/126 (45%)	52 (91%)	5 (9%)	12	40
11	AC	179/243 (74%)	143 (80%)	36 (20%)	1	9
12	AD	92/131 (70%)	81 (88%)	11 (12%)	6	27
13	AE	143/156 (92%)	126 (88%)	17 (12%)	6	27
14	AF	102/120 (85%)	99 (97%)	3 (3%)	48	73
15	AG	124/131 (95%)	110 (89%)	14 (11%)	7	29
16	AH	95/112 (85%)	83 (87%)	12 (13%)	5	26
17	AI	110/128 (86%)	102 (93%)	8 (7%)	16	49
18	AJ	108/109 (99%)	90 (83%)	18 (17%)	2	16
19	AK	123/124 (99%)	105 (85%)	18 (15%)	3	21
20	AL	111/122 (91%)	101 (91%)	10 (9%)	11	39
21	AM	133/133 (100%)	121 (91%)	12 (9%)	11	39
22	AO	123/137 (90%)	107 (87%)	16 (13%)	5	25
23	AP	185/204 (91%)	154 (83%)	31 (17%)	2	16
24	AQ	94/104 (90%)	84 (89%)	10 (11%)	8	32
25	AR	66/150 (44%)	55 (83%)	11 (17%)	2	16
26	AS	117/118 (99%)	105 (90%)	12 (10%)	8	33
27	AT	110/116 (95%)	82 (74%)	28 (26%)	0	5
28	AU	73/94 (78%)	67 (92%)	6 (8%)	13	44
29	AV	87/97 (90%)	74 (85%)	13 (15%)	3	20

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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	32
32	AY	52/53 (98%)	41 (79%)	11 (21%)	1	8
33	AZ	57/84 (68%)	52 (91%)	5 (9%)	12	40
42	BI	164/165 (99%)	140 (85%)	24 (15%)	3	21
43	BJ	201/201 (100%)	189 (94%)	12 (6%)	22	56
44	BK	184/185 (100%)	154 (84%)	30 (16%)	3	17
45	BL	146/167 (87%)	120 (82%)	26 (18%)	2	14
46	BM	114/137 (83%)	106 (93%)	8 (7%)	18	50
47	BN	185/188 (98%)	142 (77%)	43 (23%)	1	6
48	BO	175/195 (90%)	150 (86%)	25 (14%)	4	22
49	BP	156/160 (98%)	139 (89%)	17 (11%)	7	31
50	BQ	176/193 (91%)	147 (84%)	29 (16%)	2	17
51	BR	132/144 (92%)	106 (80%)	26 (20%)	1	10
52	BS	160/160 (100%)	130 (81%)	30 (19%)	2	12
53	BT	170/198 (86%)	144 (85%)	26 (15%)	3	19
54	BU	133/134 (99%)	115 (86%)	18 (14%)	4	24
55	BV	95/116 (82%)	85 (90%)	10 (10%)	8	32
56	BW	107/108 (99%)	86 (80%)	21 (20%)	1	10
57	BX	108/136 (79%)	97 (90%)	11 (10%)	8	33
58	BY	85/102 (83%)	78 (92%)	7 (8%)	13	44
59	BZ	110/125 (88%)	98 (89%)	12 (11%)	7	31
60	Ba	116/117 (99%)	100 (86%)	16 (14%)	4	23
61	Bb	115/116 (99%)	95 (83%)	20 (17%)	2	14
62	Bc	124/130 (95%)	95 (77%)	29 (23%)	1	6
63	Bd	58/59 (98%)	54 (93%)	4 (7%)	18	51
64	Be	145/204 (71%)	122 (84%)	23 (16%)	3	18
65	Bf	349/360 (97%)	305 (87%)	44 (13%)	5	26
66	Bg	84/92 (91%)	72 (86%)	12 (14%)	4	22
67	Bh	162/162 (100%)	136 (84%)	26 (16%)	3	18
68	Bi	113/117 (97%)	96 (85%)	17 (15%)	3	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Bj	130/137 (95%)	105 (81%)	25 (19%)	1	11
70	Bk	75/114 (66%)	60 (80%)	15 (20%)	1	9
71	Bl	97/126 (77%)	81 (84%)	16 (16%)	2	17
72	Bm	87/90 (97%)	72 (83%)	15 (17%)	2	15
73	Bn	70/71 (99%)	55 (79%)	15 (21%)	1	8
74	Bo	74/76 (97%)	59 (80%)	15 (20%)	1	9
75	Bp	76/77 (99%)	68 (90%)	8 (10%)	8	32
76	Bq	46/47 (98%)	35 (76%)	11 (24%)	1	5
77	Br	304/310 (98%)	251 (83%)	53 (17%)	2	14
78	Bs	46/111 (41%)	38 (83%)	8 (17%)	2	14
79	Bt	94/95 (99%)	83 (88%)	11 (12%)	6	28
80	Bu	238/247 (96%)	199 (84%)	39 (16%)	2	17
81	Bv	132/160 (82%)	112 (85%)	20 (15%)	3	20
82	Bw	213/213 (100%)	176 (83%)	37 (17%)	2	14
83	Bx	203/229 (89%)	173 (85%)	30 (15%)	3	20
84	By	172/172 (100%)	138 (80%)	34 (20%)	1	10
All	All	10068/11158 (90%)	8575 (85%)	1493 (15%)	7	20

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