



## wwPDB EM Map/Model Validation Report ⓘ

Jun 2, 2016 – 03:47 PM EDT

PDB ID : 4UJE  
EMDB ID: : EMD-2620  
Title : Regulation of the mammalian elongation cycle by 40S subunit rolling: a eukaryotic-specific ribosome rearrangement  
Authors : Budkevich, T.V.; Giesebrecht, J.; Behrmann, E.; Loerke, J.; Ramrath, D.J.F.; Mielke, T.; Ismer, J.; Hildebrand, P.; Tung, C.-S.; Nierhaus, K.H.; Sanbonmatsu, K.Y.; Spahn, C.M.T.  
Deposited on : 2014-04-05  
Resolution : 6.90 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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>

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MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027674

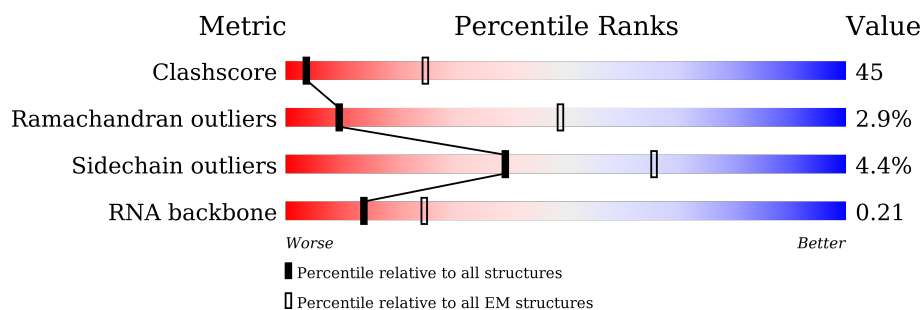
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 6.90 Å.

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






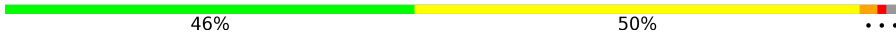


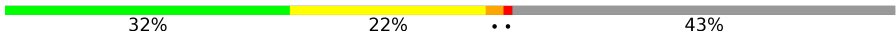




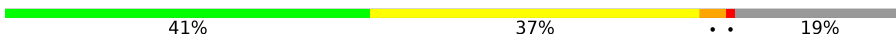

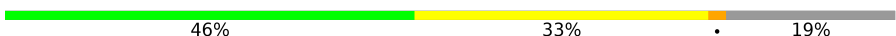











Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	AV	76	30% 41% 29%
2	AW	76	16% 47% 37%
3	AX	28	46% 50% .
4	B1	1869	6% 38% 48% . 7%
5	BA	295	41% 31% . 26%
6	BB	264	32% 41% 6% . 19%
7	BC	293	49% 23% . 24%
8	BD	243	52% 34% . 13%




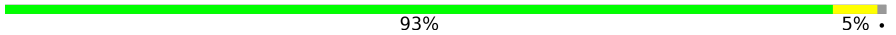


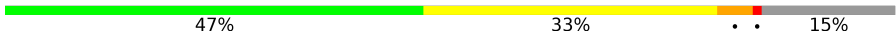






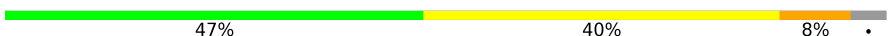

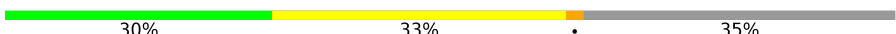









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Mol	Chain	Length	Quality of chain
9	BE	263	
10	BF	204	
11	BG	249	
12	BH	194	
13	BI	208	
14	BJ	194	
15	BK	165	
16	BL	158	
17	BM	132	
18	BN	151	
19	BO	151	
20	BP	145	
21	BQ	146	
22	BR	135	
23	BS	152	
24	BT	145	
25	BU	119	
26	BV	83	
27	BW	130	
28	BX	143	
29	BY	133	
30	BZ	125	
31	Ba	115	
32	Bb	84	
33	Bc	69	





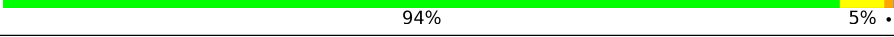



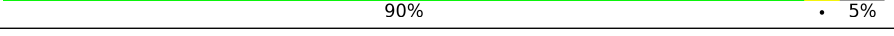

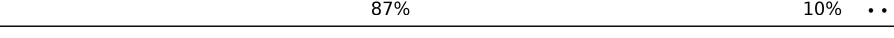
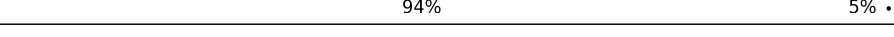

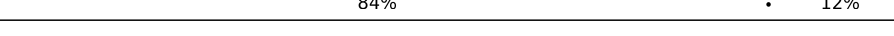
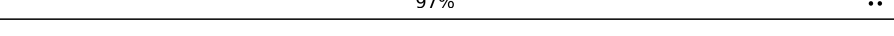
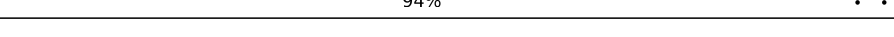
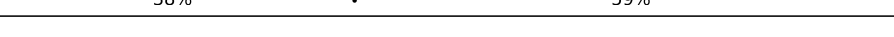
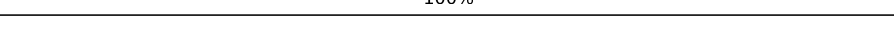
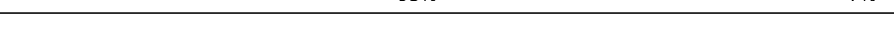






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Mol	Chain	Length	Quality of chain
34	Bd	56	
35	Be	59	
36	Bf	156	
37	Bg	317	
38	CA	257	
39	CB	403	
40	CC	427	
41	CD	297	
42	CE	288	
43	CF	248	
44	CG	266	
45	CH	192	
46	CI	214	
47	CJ	178	
48	CL	211	
49	CM	215	
50	CN	204	
51	CO	203	
52	CP	184	
53	CQ	188	
54	CR	196	
55	CS	176	
56	CT	160	
57	CU	128	
58	CV	140	

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Mol	Chain	Length	Quality of chain
59	CW	157	
60	CX	156	
61	CY	145	
62	CZ	136	
63	Ca	148	
64	Cb	159	
65	Cc	115	
66	Cd	125	
67	Ce	135	
68	Cf	110	
69	Cg	117	
70	Ch	123	
71	Ci	105	
72	Cj	97	
73	Ck	70	
74	Cl	51	
75	Cm	128	
76	Cn	25	
77	Co	106	
78	Cp	92	
79	Ct	137	
80	Cu	210	
81	A2	5025	
82	A3	194	
83	A4	121	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MIA	AW	37	-	-	X	-

## 2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 215620 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called TRNA-LYS.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AV	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 2 is a RNA chain called TRNA-PHE.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AW	76	Total	C	N	O	P	S	0	0
			1626	729	290	531	75	1		

- Molecule 3 is a RNA chain called MESSENGER RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AX	28	Total	C	N	O	P	0	0
			560	252	56	224	28		

- Molecule 4 is a RNA chain called 18S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B1	1742	Total	C	N	O	P	0	0
			37159	16589	6665	12164	1741		

- Molecule 5 is a protein called 40S RIBOSOMAL PROTEIN SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BA	218	Total	C	N	O	S	0	0
			1719	1091	301	319	8		

- Molecule 6 is a protein called 40S RIBOSOMAL PROTEIN S3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 7 is a protein called 40S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BC	222	Total	C	N	O	S	0	0
			1724	1114	296	304	10		

- Molecule 8 is a protein called 40S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BD	212	Total	C	N	O	S	0	0
			1646	1050	299	290	7		

- Molecule 9 is a protein called 40S RIBOSOMAL PROTEIN S4, Y ISOFORM 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BE	257	Total	C	N	O	S	0	0
			2031	1298	381	344	8		

- Molecule 10 is a protein called 40S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BF	188	Total	C	N	O	S	0	0
			1486	930	283	266	7		

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BG	232	Total	C	N	O	S	0	0
			1884	1176	379	322	7		

- Molecule 12 is a protein called 40S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BH	191	Total	C	N	O	S	0	0
			1535	978	282	274	1		

- Molecule 13 is a protein called 40S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BI	207	Total	C	N	O	S	0	0
			1695	1064	334	292	5		

- Molecule 14 is a protein called 40S RIBOSOMAL PROTEIN S9.



Mol	Chain	Residues	Atoms					AltConf	Trace
14	BJ	179	Total	C	N	O	S	0	0
			1495	953	299	241	2		

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BK	94	Total	C	N	O	S	0	0
			791	519	138	129	5		

- Molecule 16 is a protein called 40S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BL	146	Total	C	N	O	S	0	0
			1199	764	224	205	6		

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BM	120	Total	C	N	O	S	0	0
			931	584	164	174	9		

- Molecule 18 is a protein called 40S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BN	150	Total	C	N	O	S	0	0
			1207	773	229	204	1		

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BO	137	Total	C	N	O	S	0	0
			1023	627	200	190	6		

- Molecule 20 is a protein called 40S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BP	118	Total	C	N	O	S	0	0
			981	625	183	166	7		

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BQ	139	Total	C	N	O	S	0	0
			1108	704	210	191	3		

- Molecule 22 is a protein called 40S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BR	109	Total	C	N	O	S	0	0
			893	561	170	159	3		

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BS	142	Total	C	N	O	S	0	0
			1172	736	236	199	1		

- Molecule 24 is a protein called 40S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BT	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 25 is a protein called 40S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BU	101	Total	C	N	O	S	0	0
			803	502	153	144	4		

- Molecule 26 is a protein called 40S RIBOSOMAL PROTEIN S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 27 is a protein called 40S RIBOSOMAL PROTEIN S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BW	129	Total	C	N	O	S	0	0
			1033	659	193	175	6		

- Molecule 28 is a protein called 40S RIBOSOMAL PROTEIN S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BX	134	Total	C	N	O	S	0	0
			1046	663	205	176	2		

- Molecule 29 is a protein called 40S RIBOSOMAL PROTEIN S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BY	122	Total	C	N	O	S	0	0
			1002	635	196	166	5		

- Molecule 30 is a protein called 40S RIBOSOMAL PROTEIN S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BZ	76	Total	C	N	O	S	0	0
			605	387	112	105	1		

- Molecule 31 is a protein called 40S RIBOSOMAL PROTEIN S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ba	96	Total	C	N	O	S	0	0
			767	476	159	127	5		

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bb	80	Total	C	N	O	S	0	0
			625	391	116	111	7		

- Molecule 33 is a protein called 40S RIBOSOMAL PROTEIN S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Bc	62	Total	C	N	O	S	0	0
			490	298	99	91	2		

- Molecule 34 is a protein called 40S RIBOSOMAL PROTEIN S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bd	53	Total	C	N	O	S	0	0
			444	278	90	71	5		

- Molecule 35 is a protein called 40S RIBOSOMAL PROTEIN S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Be	51	Total	C	N	O	S	0	0
			412	258	90	63	1		

- Molecule 36 is a protein called UBIQUITIN-40S RIBOSOMAL PROTEIN S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Bf	61	Total	C	N	O	S	0	0
			497	312	94	84	7		

- Molecule 37 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Bg	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	CA	247	Total	C	N	O	S	0	1
			1888	1183	388	311	6		

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	CB	396	Total	C	N	O	S	0	1
			3190	2030	601	545	14		

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	CC	364	Total	C	N	O	S	0	1
			2889	1817	578	480	14		

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CD	290	Total	C	N	O	S	0	0
			2361	1489	431	427	14		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	CE	158	Total	C	N	O	0	0
			1286	834	238	214		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CF	234	Total	C	N	O	S	0	0
			1949	1252	376	312	9		

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CG	235	Total	C	N	O	S	0	1
			1881	1197	363	317	4		

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	CH	192	Total	C	N	O	S	0	0
			1535	965	286	278	6		

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CI	196	Total	C	N	O	S	0	0
			1604	1022	308	262	12		

- Molecule 47 is a protein called 60S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CJ	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 48 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CL	200	Total	C	N	O	S	0	1
			1617	1013	335	265	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CM	140	Total	C	N	O	S	0	1
			1139	730	219	183	7		

- Molecule 50 is a protein called 60S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CN	204	Total	C	N	O	S	0	0
			1708	1077	360	266	5		

- Molecule 51 is a protein called 60S RIBOSOMAL PROTEIN L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CO	196	Total	C	N	O	S	0	1
			1607	1034	316	252	5		

- Molecule 52 is a protein called 60S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CP	153	Total	C	N	O	S	0	1
			1234	771	241	213	9		

- Molecule 53 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CQ	184	Total	C	N	O	S	0	0
			1493	933	311	244	5		

- Molecule 54 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CR	183	Total	C	N	O	S	0	1
			1526	943	331	242	10		

- Molecule 55 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CS	173	Total	C	N	O	S	0	0
			1438	916	280	232	10		

- Molecule 56 is a protein called 60S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CT	159	Total	C	N	O	S	0	0
			1297	823	252	216	6		

- Molecule 57 is a protein called 60S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	CU	102	Total	C	N	O	S	0	1
			827	529	146	150	2		

- Molecule 58 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CV	128	Total	C	N	O	S	0	0
			963	610	181	167	5		

- Molecule 59 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CW	64	Total	C	N	O	S	0	1
			529	337	104	85	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	CX	119	Total	C	N	O	S	0	0
			975	624	183	167	1		

- Molecule 61 is a protein called 60S RIBOSOMAL PROTEIN L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	CY	128	Total	C	N	O	S	0	1
			1065	668	217	177	3		

- Molecule 62 is a protein called 60S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	CZ	136	Total	C	N	O	S	0	0
			1114	719	209	182	4		

- Molecule 63 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Ca	147	Total	C	N	O	S	0	0
			1161	736	237	185	3		

- Molecule 64 is a protein called 60S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Cb	69	Total	C	N	O	S	0	1
			560	344	123	90	3		

- Molecule 65 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Cc	104	Total	C	N	O	S	0	1
			802	508	142	145	7		

- Molecule 66 is a protein called 60S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cd	109	Total	C	N	O	S	0	0
			904	570	174	158	2		

- Molecule 67 is a protein called 60S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ce	128	Total	C	N	O	S	0	1
			1053	664	219	165	5		

- Molecule 68 is a protein called 60S RIBOSOMAL PROTEIN L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Cf	107	Total	C	N	O	S	0	0
			865	550	172	140	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Cg	115	Total	C	N	O	S	0	1
			907	566	188	147	6		

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



Mol	Chain	Residues	Atoms					AltConf	Trace
70	Ch	122	Total	C	N	O	S	0	0
			1014	641	205	167	1		

- Molecule 71 is a protein called 60S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ci	97	Total	C	N	O	S	0	1
			783	488	168	122	5		

- Molecule 72 is a protein called 60S RIBOSOMAL PROTEIN L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Cj	85	Total	C	N	O	S	0	1
			690	423	153	109	5		

- Molecule 73 is a protein called 60S RIBOSOMAL PROTEIN L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Ck	69	Total	C	N	O	S	0	0
			568	366	103	98	1		

- Molecule 74 is a protein called 60S RIBOSOMAL PROTEIN L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Cl	50	Total	C	N	O	S	0	0
			443	281	98	63	1		

- Molecule 75 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Cm	52	Total	C	N	O	S	0	0
			428	266	90	66	6		

- Molecule 76 is a protein called 60S RIBOSOMAL PROTEIN L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Cn	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 77 is a protein called 60S RIBOSOMAL PROTEIN L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Co	106	Total	C	N	O	S	0	0
			870	547	176	140	7		

- Molecule 78 is a protein called 60S RIBOSOMAL PROTEIN L37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Cp	91	Total	C	N	O	S	0	0
			707	445	136	119	7		

- Molecule 79 is a protein called 60S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Ct	130	Total	C	N	O	S	0	1
			1043	646	220	172	5		

- Molecule 80 is a protein called 60S RIBOSOMAL PROTEIN L10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cu	210	Total	C	N	O	S	0	0
			1621	990	278	347	6		

- Molecule 81 is a RNA chain called 28S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	A2	3616	Total	C	N	O	P	0	0
			77488	34508	14153	25212	3615		

- Molecule 82 is a RNA chain called 5.8S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	A3	157	Total	C	N	O	P	0	0
			3334	1489	587	1102	156		

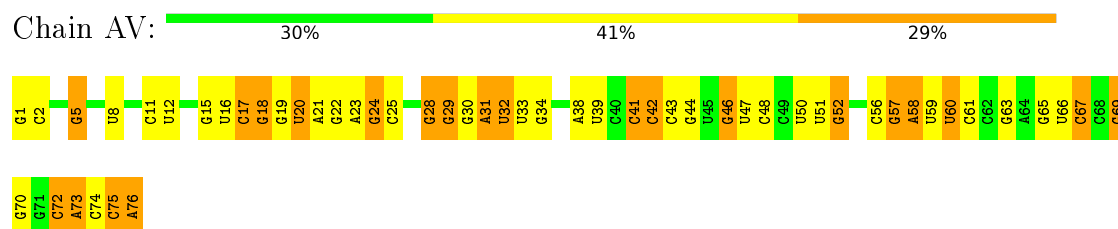
- Molecule 83 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	A4	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

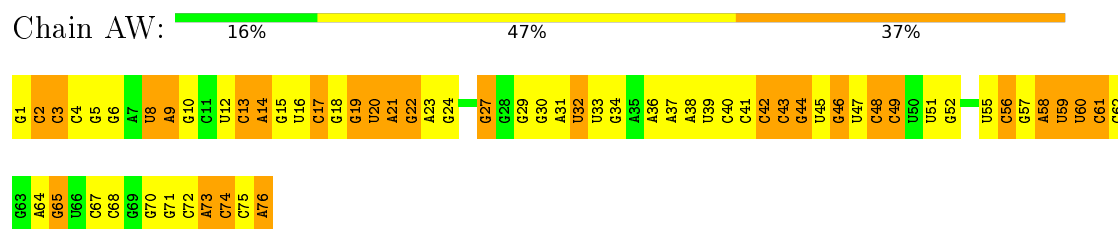
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

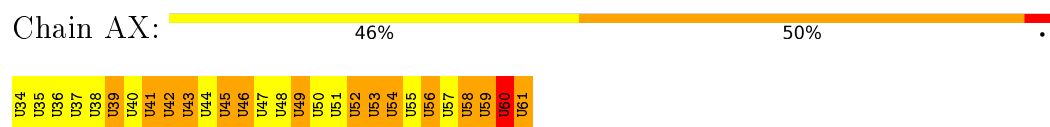
#### • Molecule 1: TRNA-LYS



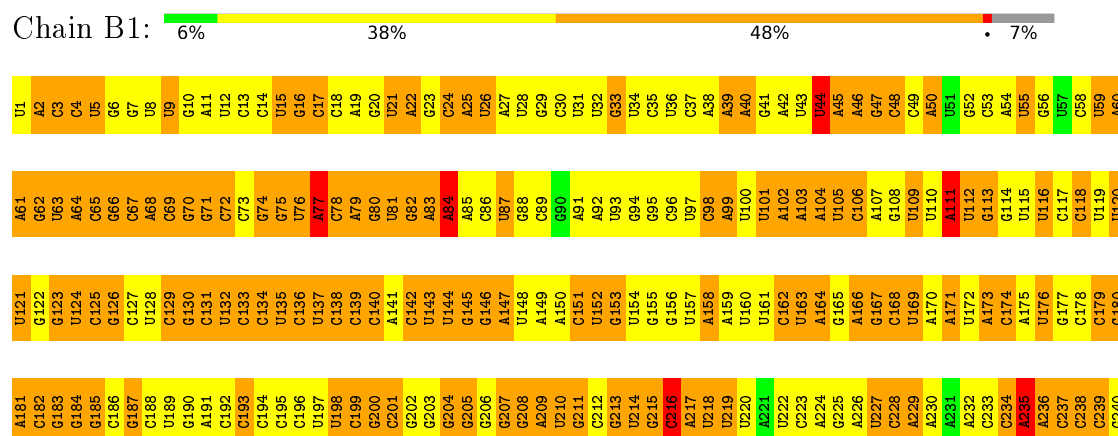
#### • Molecule 2: TRNA-PHE



#### • Molecule 3: MESSENGER RNA



#### • Molecule 4: 18S Ribosomal RNA



A1209	G1089	A1027	U965	C905	U944	G	A	A664	A604	G544	A484	C424	U361	A301	G
G1210	C1090	A1028	U966	U906	G845	C	C	G665	A605	A545	A485	G425	C362	A302	U
G1211	C1091	G1029	C967	G907	G846	G	C	U666	G606	G546	A486	A426	C363	C303	C
G1212	C1092	A1030	U968	A908	A847	G	G	U667	U607	G547	U487	U427	A364	C304	A
G1213	A1093	A1031	U969	G909	U948	G	C	A668	C508	C548	U488	U428	C365	U305	G
G1214	C1094	G1032	G970	G910	A849	C	C	A669	U609	C549	U489	C429	U366	C306	C
G1215	C1095	G1033	G971	C911	C950	C	C	A670	G610	C550	C490	G430	U367	G307	C
C1216	G1096	A1034	A972	C912	C851	G	G	A671	G611	U551	C491	G431	U368	G308	C
A1217	G1097	A1035	C973	C913	G852	C	C	A672	U612	U552	C492	G432	C369	G309	C
G1218	C1098	A1036	C974	U914	C853	C	C	G673	C613	U553	A493	A433	C370	C310	U
G1219	G1099	G1037	G975	G915	A854	C	C	G674	C614	A554	C494	G434	A371	C311	U
A1220	U1100	U1038	G976	A916	G855	C	C	U675	C615	A555	U495	A435	U372	G312	U
G1221	U1101	C1039	C977	U917	C856	C	C	G676	A616	U556	C496	G436	U373	G313	C
G1222	G1102	G1040	G978	U918	U857	C	C	G677	G617	U557	C497	G437	G374	U314	C
A1223	C1103	G1041	C979	A919	A858	C	C	U678	C618	G558	C498	G438	U375	C315	G
G1224	G1104	A1042	A980	A920	G859	C	C	A679	A619	G559	C499	A439	C376	G316	G
U1225	G1105	G1043	G981	G921	G860	C	C	G680	G620	A560	A500	A440	G377	C317	C
G1226	C1106	G1044	G982	A922	A861	C	C	U681	C621	A561	C501	C441	U378	A318	C
G1227	G1107	U1045	A983	G923	A862	C	C	U682	C622	U562	C502	U442	C379	C319	C
A1228	G1108	U1046	G984	G924	U863	C	C	G683	G623	G563	C503	U443	G380	G320	C
G1229	C1109	G1047	G985	G925	A864	C	C	A684	C624	A564	G504	G444	C381	C321	G
C1230	G1110	G1048	G986	A926	A865	C	C	U685	G625	G565	G505	A445	C382	C322	G
C1231	U1111	A1049	A987	C927	U866	C	C	U686	U626	U566	G506	G446	G383	C323	C
U1232	U1112	G1050	C988	G928	G867	C	C	G687	U627	C567	G507	A447	U384	C324	C
G1233	A1113	A1051	C989	G929	G868	C	C	U688	A628	C568	A508	A448	G385	C325	G
C1234	U1114	A1052	A990	C930	A869	C	C	U689	A629	A569	G509	A449	C386	C326	G
G1235	U1115	G1053	G991	C931	A870	C	C	G690	U630	C570	G510	C450	C387	G327	G
C1236	C1116	G1054	A992	G932	U871	C	C	U691	G631	U571	G511	G451	U388	U328	G
C1237	C1117	A1055	G993	G933	A872	C	C	G692	C632	U572	A512	G452	C389	G329	G
U1238	C1118	U1056	C994	G934	G873	C	C	A693	C633	U573	G513	C453	C390	G330	G
U1239	U1119	C1057	G995	G935	G874	C	C	G694	A634	A574	U514	U454	C391	C331	C
A1240	U1120	A1058	G999	G936	A875	C	C	G695	C635	A575	G515	A455	U393	G332	G
A1241	A1181	G1059	G1121	C937	C876	C	C	G696	C636	A576	A516	C456	G394	G333	G
U1242	A1182	A1060	C1000	A938	C877	C	C	G	U637	U577	G517	C457	C395	C334	G
U1243	C1123	U1061	A1001	U939	G878	C	C	G	C638	C578	G518	A458	U396	G335	C
U1244	C1124	A1062	U1002	U940	C879	C	C	G	C639	C579	A519	C459	G397	A336	G
G1245	C1125	G1063	U1003	C941	G880	C	C	G	A640	U580	A520	A460	A398	C337	C
A1246	G1126	C1064	U1004	G942	G881	C	C	G	A641	U581	A521	U461	C399	G338	C
C1247	C1127	G1065	G1005	U943	U883	C	C	G	C636	A576	G516	C462	C400	A339	G
U1248	C1128	U1066	C1006	A944	C884	C	C	G	A643	U577	A517	C463	A401	C340	G
C1249	G1129	C1067	C1007	U945	U885	C	C	G	C644	A584	U518	A464	C402	C341	C
A1250	G1130	G1068	A1008	U946	A886	C	C	G	C645	C585	A519	A465	C342	C342	C
C1251	G1131	U1069	A1009	G947	U887	C	C	U	U646	G586	A520	G466	U406	A343	G
C1252	C1132	A1070	G1010	C948	U888	C	C	U	U647	A587	C527	G467	G407	U344	C
A1253	A1133	G1071	A1011	G949	U889	C	C	C	A648	G588	A528	A468	A408	U345	U
C1254	G1134	G1072	A1012	C950	U890	C	C	C	U649	G589	A529	A469	C409	C346	U
G1255	C1135	C1073	U1013	C951	G891	C	C	G	A650	A590	U530	G470	G410	G347	U
C1256	U1136	C1074	G1014	G952	U892	C	C	G	U651	U591	A531	G471	G411	A348	G
G1257	U1137	G1075	U1015	G953	U893	C	C	G	U652	C592	C532	C472	G412	A349	G
A1258	C1138	G1076	U1016	U954	G894	C	C	C	A653	C593	A533	A473	G413	C350	U
A1259	C1139	C1079	U1017	A955	G895	C	C	C	A654	A594	G534	A474	A414	G351	G
A1260	G1140	A1080	U1018	G956	U896	C	C	A	A655	U595	G535	C475	A415	U352	A
C1261	U1201	U1081	C1019	A957	U897	C	C	G	A656	U596	A536	A476	U416	C353	C
C1262	G1142	A1082	A1020	G958	U898	C	C	G	U657	G597	C537	G477	C417	U354	U
G1263	A1143	G1203	U1021	G959	U899	C	C	C	G598	G598	U538	G478	A418	G355	G
C1264	A1144	U1022	U1022	U960	C900	C	C	G	U659	A599	C539	C479	G419	C356	C
A1265	C1205	C1085	A1023	G961	G901	C	C	G	C660	G600	U540	G480	G420	C357	G
C1266	G1206	G1086	A1024	A962	G902	C	C	G	U661	G601	U541	C481	G421	C358	G
C1267	C1147	U1087	U1025	A963	A903	C	C	G	C662	G602	U542	G482	U422	U359	G
C1268	A1208	U1088	C1026	A964	A904	C	C	C	C663	C603	C543	C483	U423	A360	G

U1269	U1270	U1271	U1272	U1273	U1274	U1275	U1276	U1277	U1278	U1279	U1280	U1281	U1282	U1283	U1284	U1285	U1286	U1287	U1288	U1289	U1290	U1291	U1292
C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354
U1392	U1393	U1394	U1395	U1396	U1397	U1398	U1399	U1400	U1401	U1402	U1403	U1404	U1405	U1406	U1407	U1408	U1409	U1410	U1411	U1412	U1413	U1414	U1415
A1452	A1453	A1454	A1455	A1456	A1457	A1458	A1459	A1460	A1461	A1462	A1463	A1464	A1465	A1466	A1467	A1468	A1469	A1470	A1471	A1472	A1473	A1474	A1475
C1513	C1514	C1515	C1516	C1517	C1518	C1519	C1520	C1521	C1522	C1523	C1524	C1525	C1526	C1527	C1528	C1529	C1530	C1531	C1532	C1533	C1534	C1535	C1536
G1575	G1576	G1577	G1578	G1579	G1580	G1581	G1582	G1583	G1584	G1585	G1586	G1587	G1588	G1589	G1590	G1591	G1592	G1593	G1594	G1595	G1596	G1597	G1598
C1636	C1637	C1638	C1639	C1640	C1641	C1642	C1643	C1644	C1645	C1646	C1647	C1648	C1649	C1650	C1651	C1652	C1653	C1654	C1655	C1656	C1657	C1658	C1659
A1695	A1696	A1697	A1698	A1699	A1700	A1701	A1702	A1703	A1704	A1705	A1706	A1707	A1708	A1709	A1710	A1711	A1712	A1713	A1714	A1715	A1716	A1717	A1718
G1760	G1761	G1762	G1763	G1764	G1765	G1766	G1767	G1768	G1769	G1770	G1771	G1772	G1773	G1774	G1775	G1776	G1777	G1778	G1779	G1780	G1781	G1782	G1783
A1824	A1825	A1826	A1827	A1828	A1829	A1830	A1831	A1832	A1833	A1834	A1835	A1836	A1837	A1838	A1839	A1840	A1841	A1842	A1843	A1844	A1845	A1846	A1847
G1865	G1866	G1867	G1868	G1869	G1870	G1871	G1872	G1873	G1874	G1875	G1876	G1877	G1878	G1879	G1880	G1881	G1882	G1883	G1884	G1885	G1886	G1887	G1888
A1859	A1860	A1861	A1862	A1863	A1864	A1865	A1866	A1867	A1868	A1869	A1870	A1871	A1872	A1873	A1874	A1875	A1876	A1877	A1878	A1879	A1880	A1881	A1882

• Molecule 5: 40S RIBOSOMAL PROTEIN SA

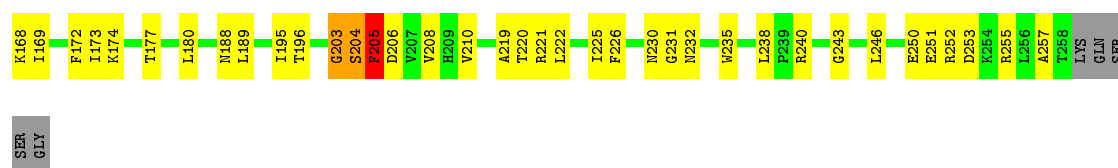
Chain BA:  41% 31% 26%

MET	S2	G3	G4	L5	D6	V7	L8	Q9	K11	E12	E13	D14	V15	L16	K17	F18	L19	L20	L21	L22	L23	L24	L25
T82	G83	R84	R85	A86	V87	L88	K89	F90	I99	R102	F103	T104	P105	G106	T107	F108	T109	M110	I111	I112	Q113	A114	A115
H175	M176	L177	L178	A179	E180	E181	V182	L183	M185	I188	S190	R191	P199	D200	T201	Y202	R203	Y204	R205	D206	T207	E208	E219
VAL	GLN	VAL	PRO	SER	VAL	PRO	TLE	GLN	GLN	PRO	THR	THR	GLU	ASP	TRP	SER	ALA	ALA	ALA	PRO	THR	ALA	ALA

• Molecule 6: 40S RIBOSOMAL PROTEIN S3A

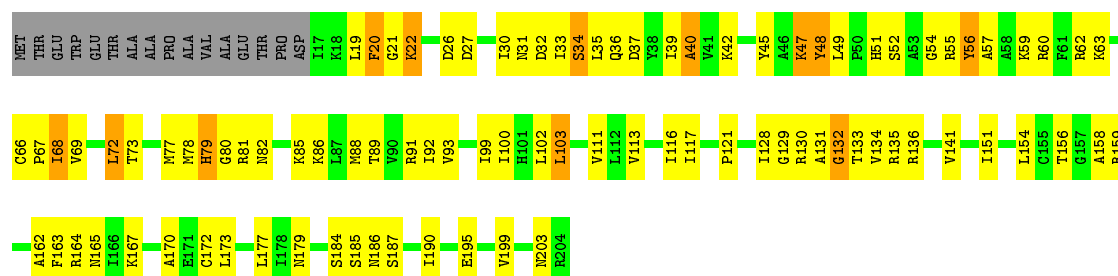
Chain BB:  32% 41% 6% 19%





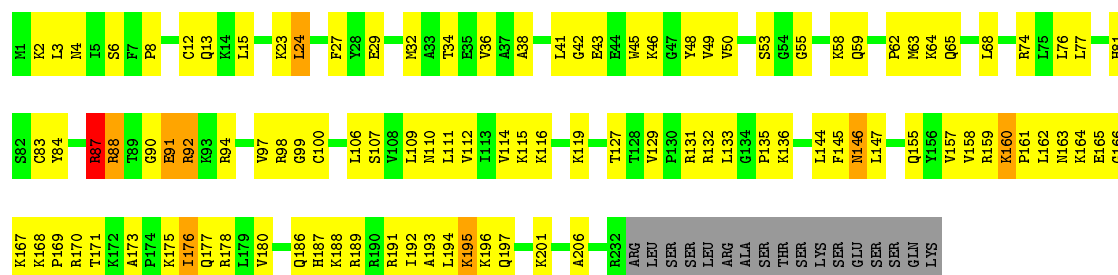
• Molecule 10: 40S RIBOSOMAL PROTEIN S5

Chain BF: 47% 39% 6% 8%



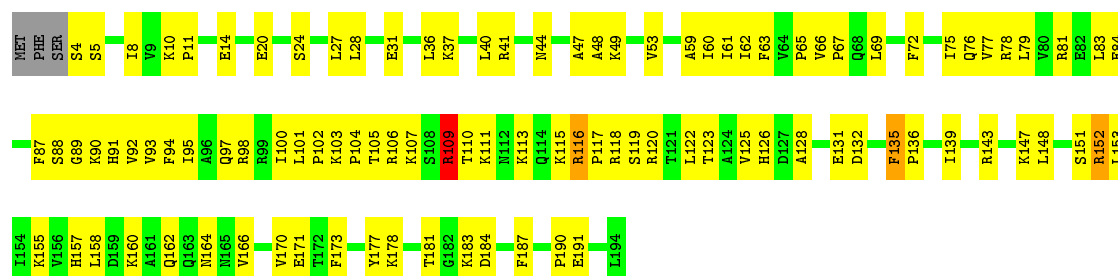
• Molecule 11: 40S RIBOSOMAL PROTEIN S6

Chain BG: 51% 39% 7%



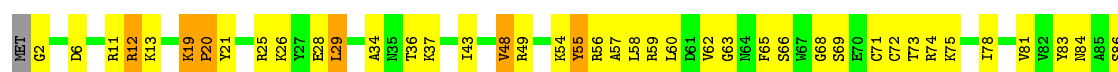
• Molecule 12: 40S RIBOSOMAL PROTEIN S7

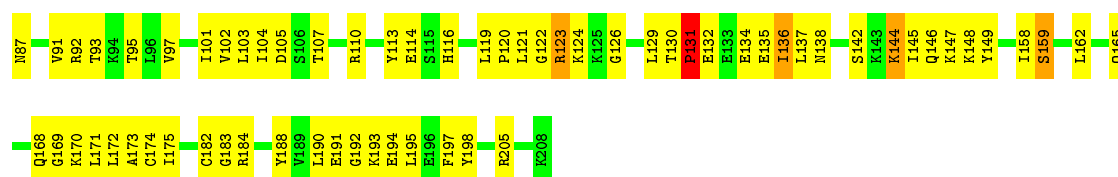
Chain BH: 46% 50% 4%



• Molecule 13: 40S RIBOSOMAL PROTEIN S8

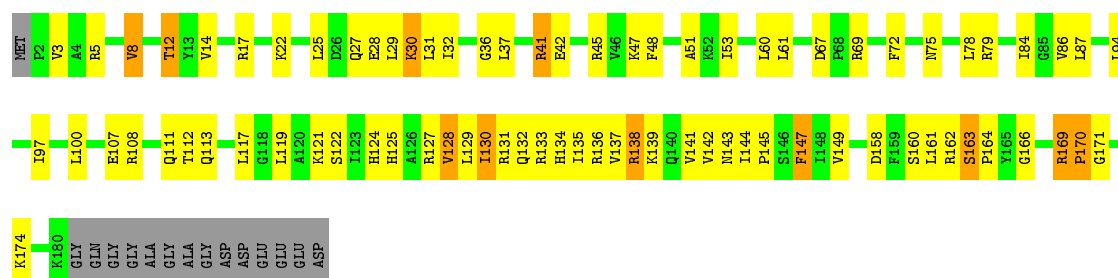
Chain BI: 49% 45% 5%





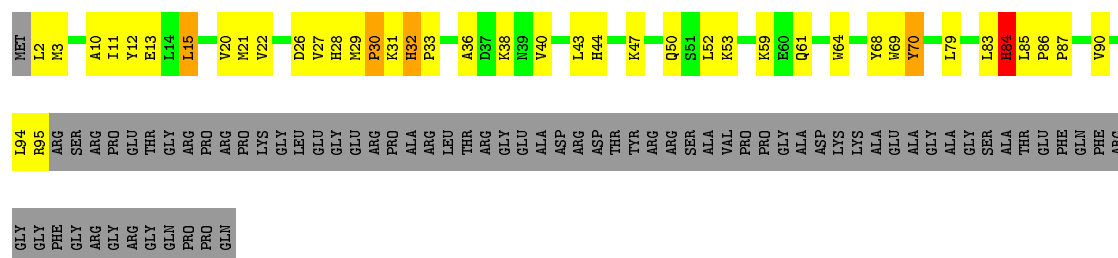
• Molecule 14: 40S RIBOSOMAL PROTEIN S9

Chain BJ: 52% 35% 6% 8%



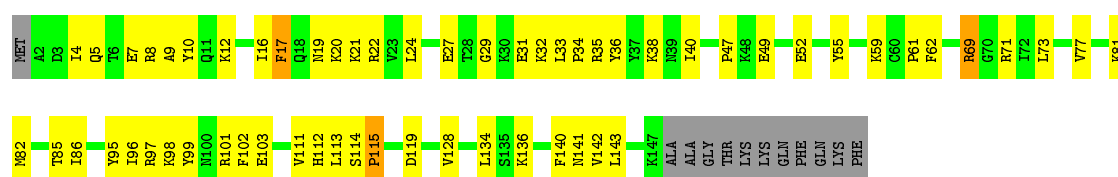
• Molecule 15: 40S RIBOSOMAL PROTEIN S10

Chain BK: 32% 22% 43%



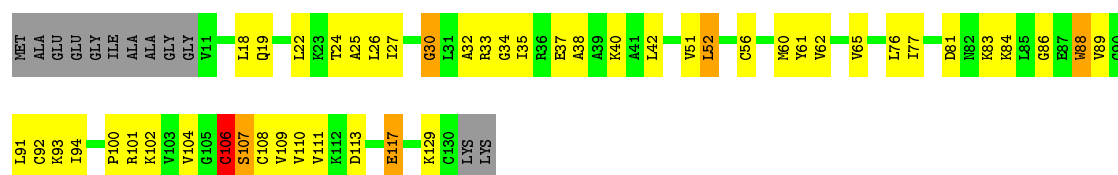
• Molecule 16: 40S RIBOSOMAL PROTEIN S11

Chain BL: 54% 36% 8%



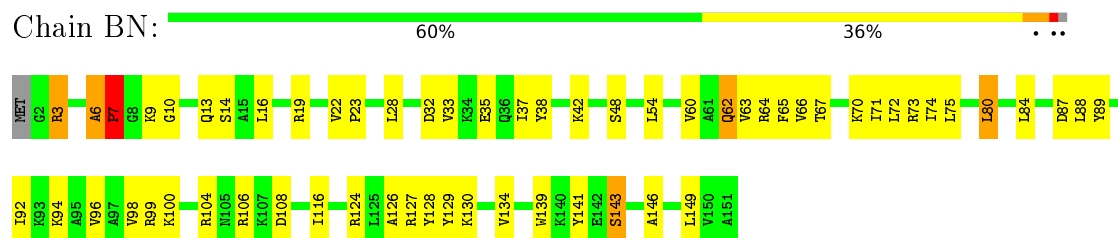
• Molecule 17: 40S RIBOSOMAL PROTEIN S12

Chain BM: 55% 32% 9%

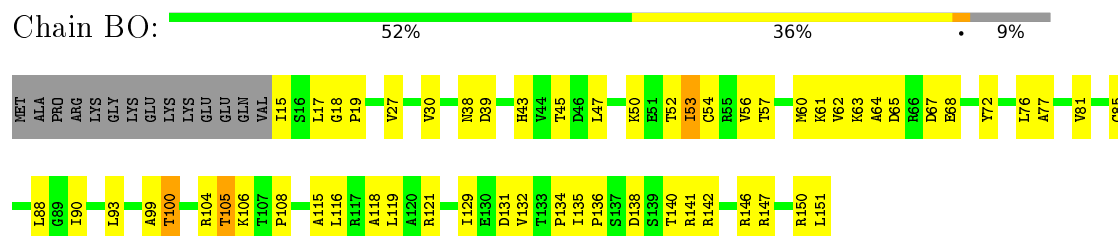


• Molecule 18: 40S RIBOSOMAL PROTEIN S13

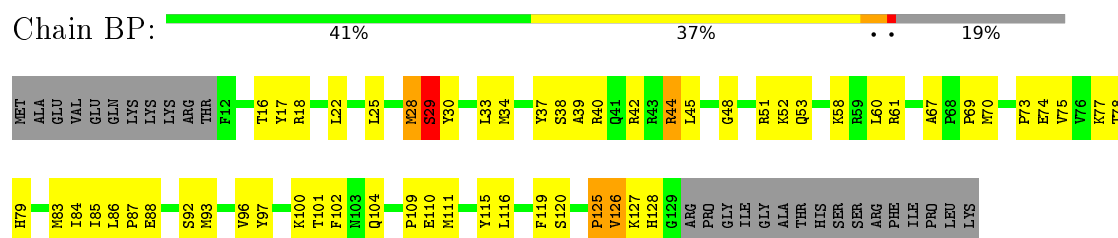




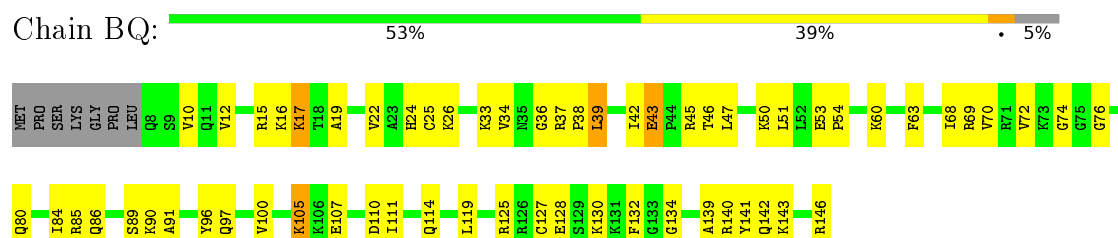
- Molecule 19: 40S RIBOSOMAL PROTEIN S14



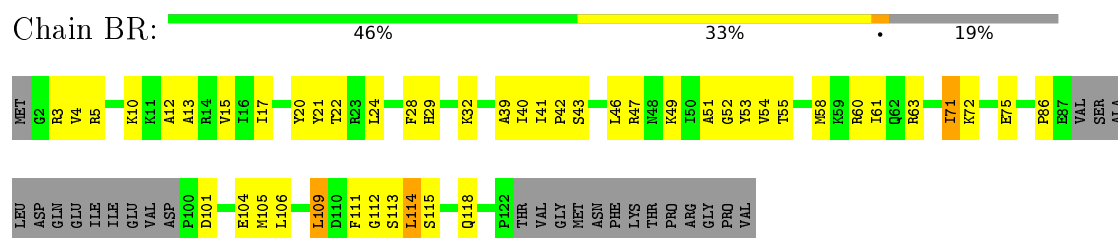
- Molecule 20: 40S RIBOSOMAL PROTEIN S15



- Molecule 21: 40S RIBOSOMAL PROTEIN S16

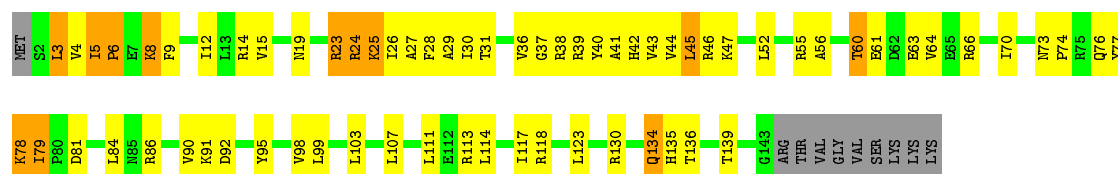


- Molecule 22: 40S RIBOSOMAL PROTEIN S17



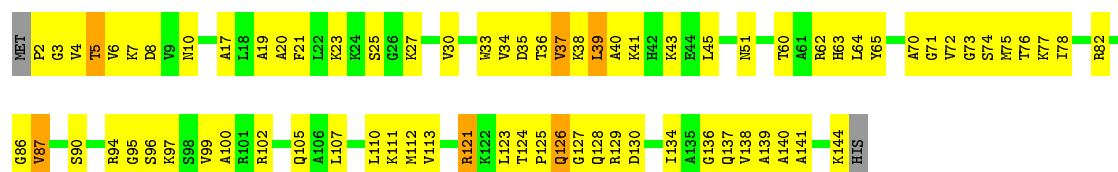
- Molecule 23: 40S RIBOSOMAL PROTEIN S18





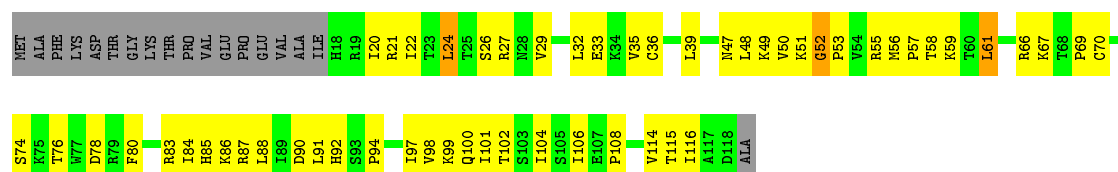
• Molecule 24: 40S RIBOSOMAL PROTEIN S19

Chain BT: 46% 48%



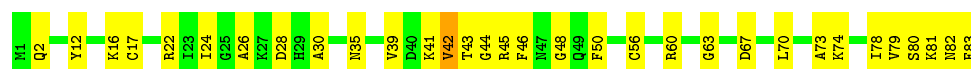
• Molecule 25: 40S RIBOSOMAL PROTEIN S20

Chain BU: 39% 44% 15%



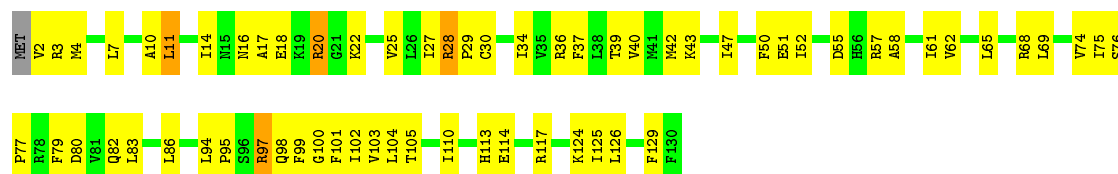
• Molecule 26: 40S RIBOSOMAL PROTEIN S21

Chain BV: 61% 37%



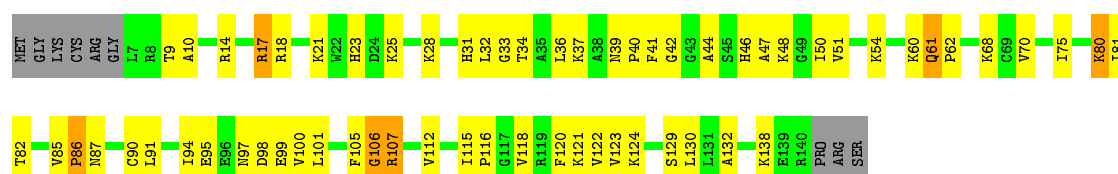
• Molecule 27: 40S RIBOSOMAL PROTEIN S15A

Chain BW: 50% 46%

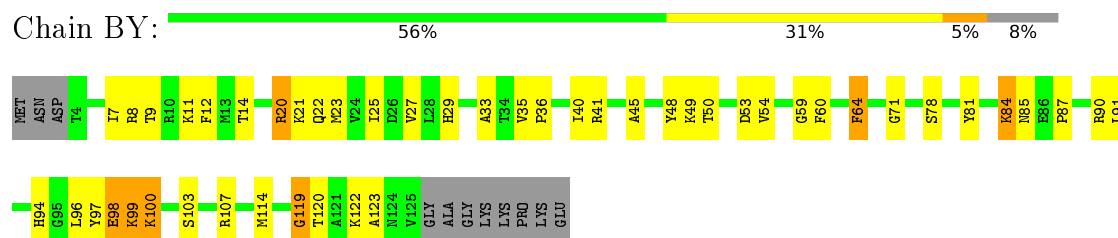


• Molecule 28: 40S RIBOSOMAL PROTEIN S23

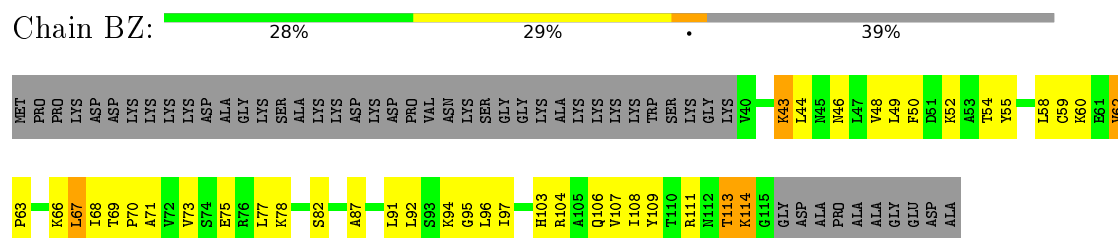
Chain BX: 50% 40% 6%



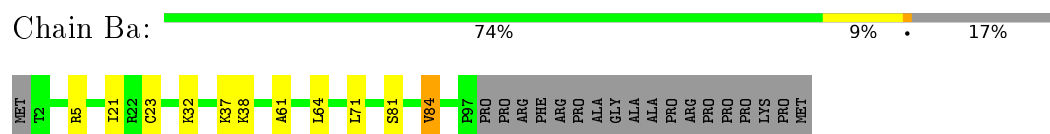
- Molecule 29: 40S RIBOSOMAL PROTEIN S24



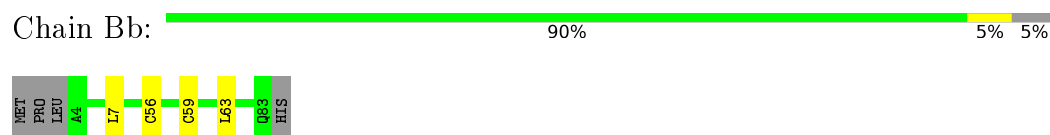
- Molecule 30: 40S RIBOSOMAL PROTEIN S25



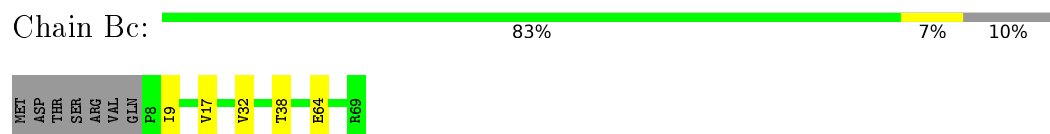
- Molecule 31: 40S RIBOSOMAL PROTEIN S26



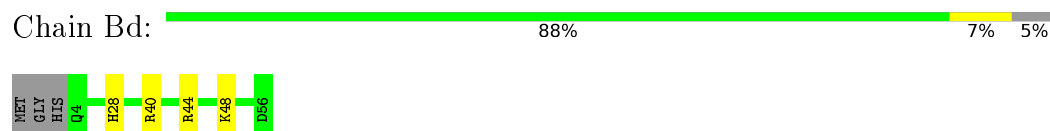
- Molecule 32: 40S RIBOSOMAL PROTEIN S27



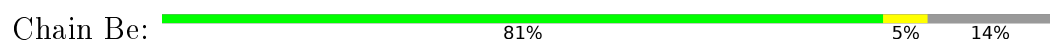
- Molecule 33: 40S RIBOSOMAL PROTEIN S28



- Molecule 34: 40S RIBOSOMAL PROTEIN S29

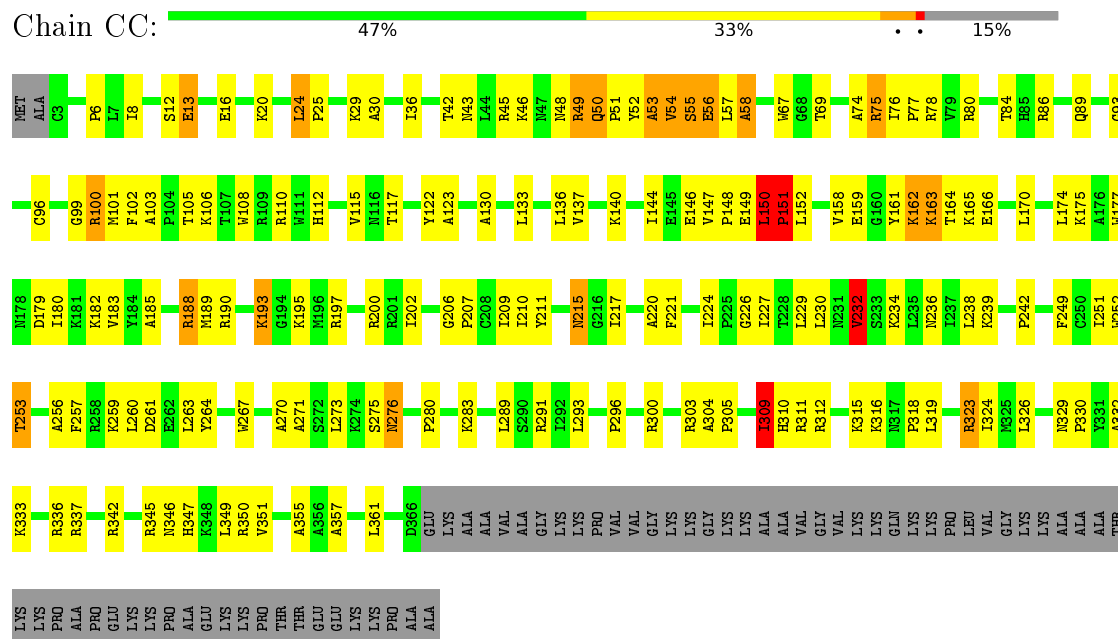


- Molecule 35: 40S RIBOSOMAL PROTEIN S30

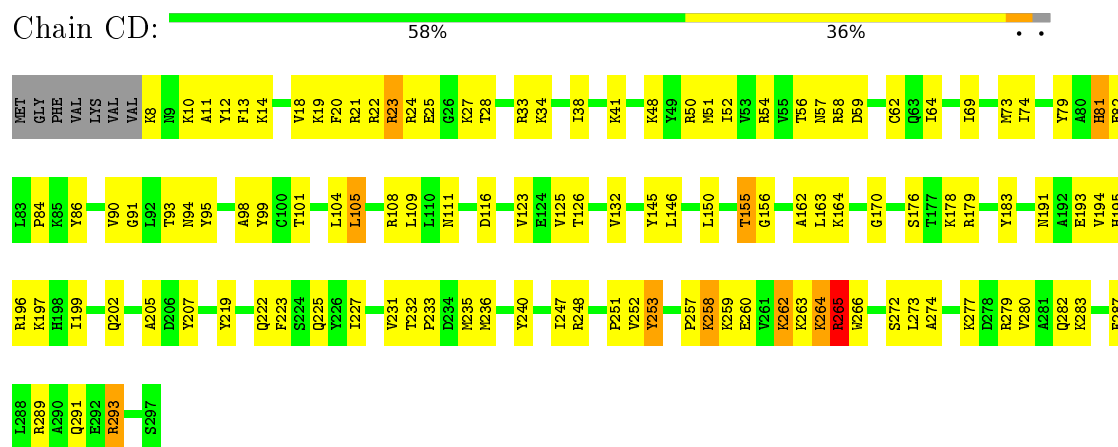




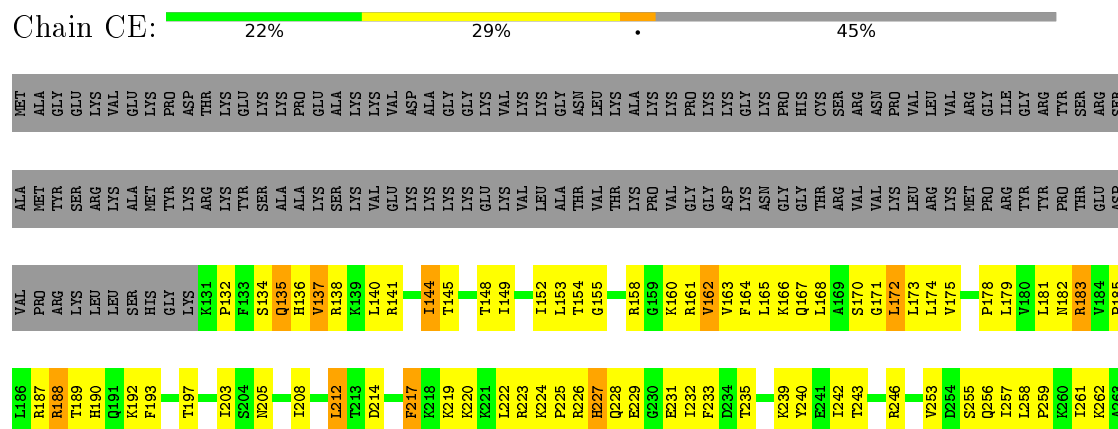
- Molecule 40: 60S RIBOSOMAL PROTEIN L4



- Molecule 41: 60S RIBOSOMAL PROTEIN L5



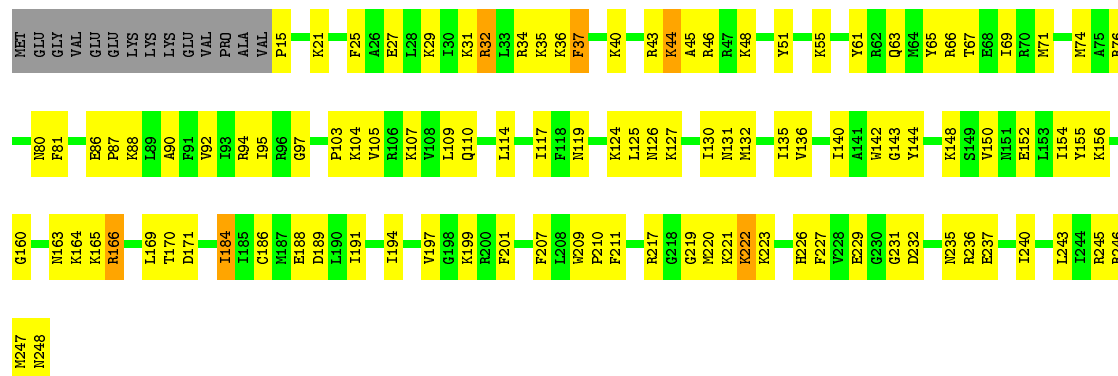
- Molecule 42: 60S RIBOSOMAL PROTEIN L6





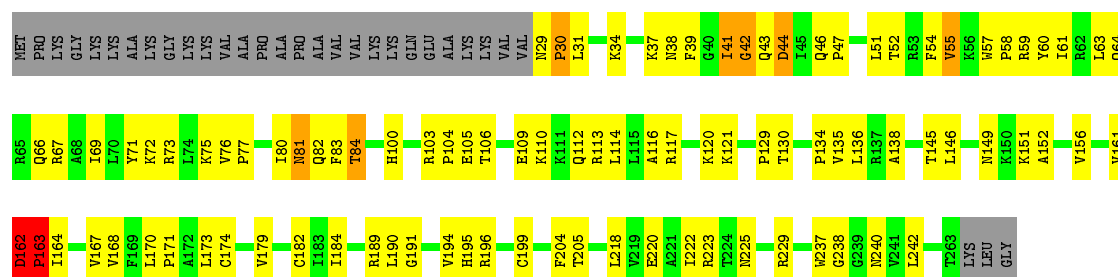
• Molecule 43: 60S RIBOSOMAL PROTEIN L7

Chain CF: 51% 41% 6%



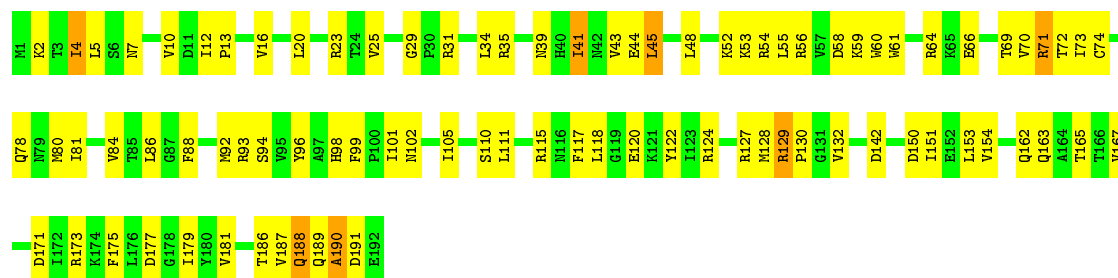
• Molecule 44: 60S RIBOSOMAL PROTEIN L7A

Chain CG: 52% 33% 12%



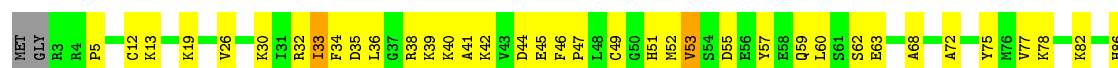
• Molecule 45: 60S RIBOSOMAL PROTEIN L9

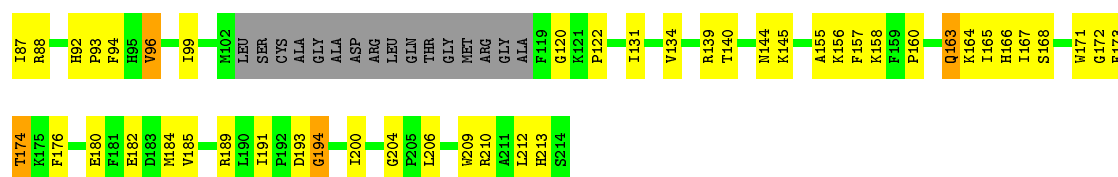
Chain CH: 55% 42%



• Molecule 46: 60S RIBOSOMAL PROTEIN L10

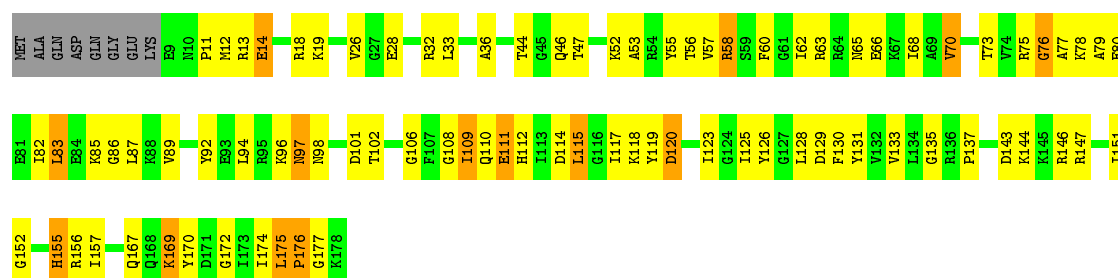
Chain CI: 53% 36% 8%





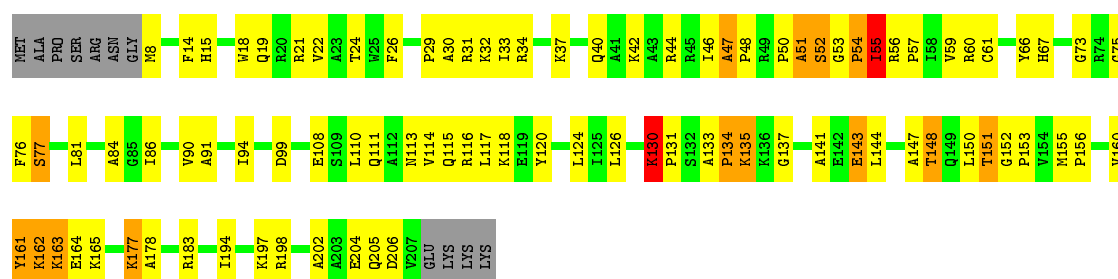
• Molecule 47: 60S RIBOSOMAL PROTEIN L11

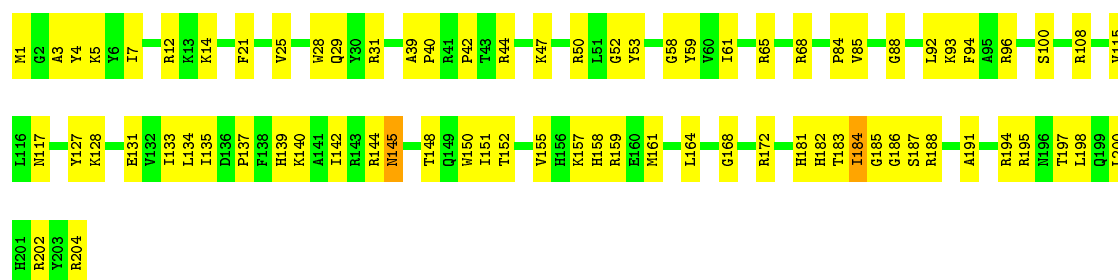
Chain CJ: 47% 40% 8%



• Molecule 48: 60S RIBOSOMAL PROTEIN L13

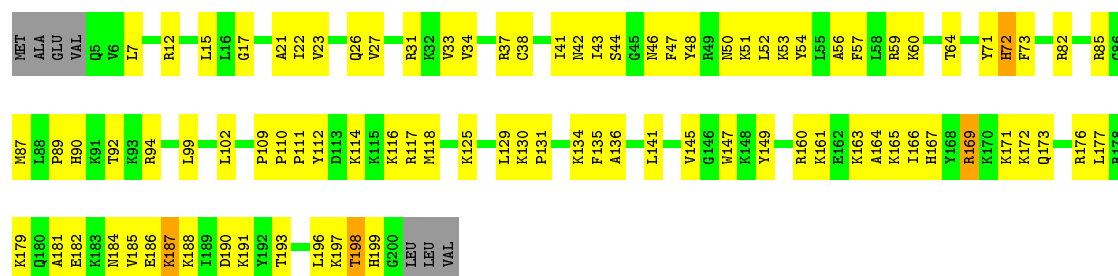
Chain CL: 52% 36% 7% 5%





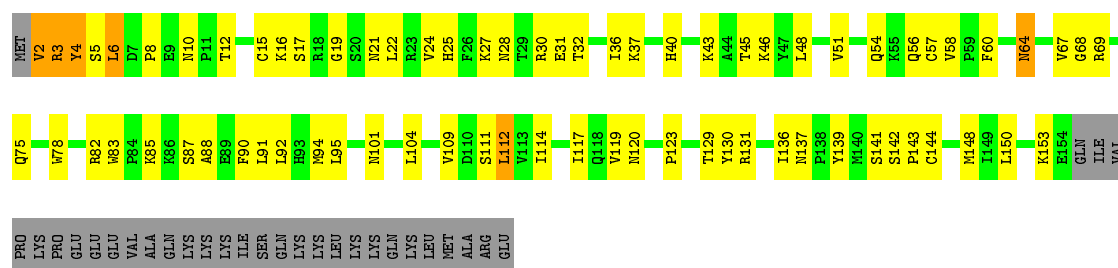
• Molecule 51: 60S RIBOSOMAL PROTEIN L13A

Chain CO: 52% 42% . .



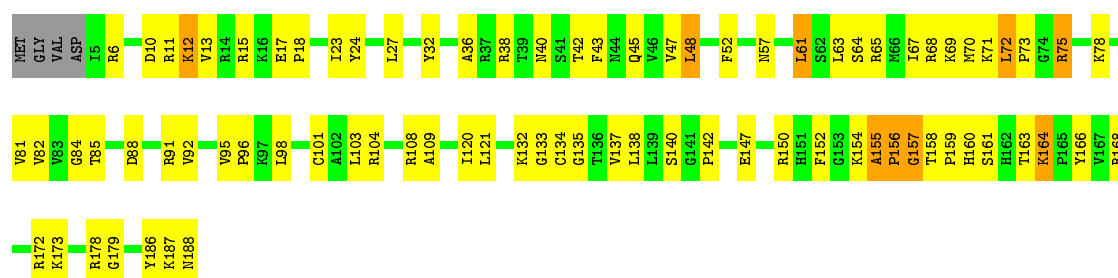
• Molecule 52: 60S RIBOSOMAL PROTEIN L17

Chain CP: 43% 36% 17%



• Molecule 53: 60S RIBOSOMAL PROTEIN L18

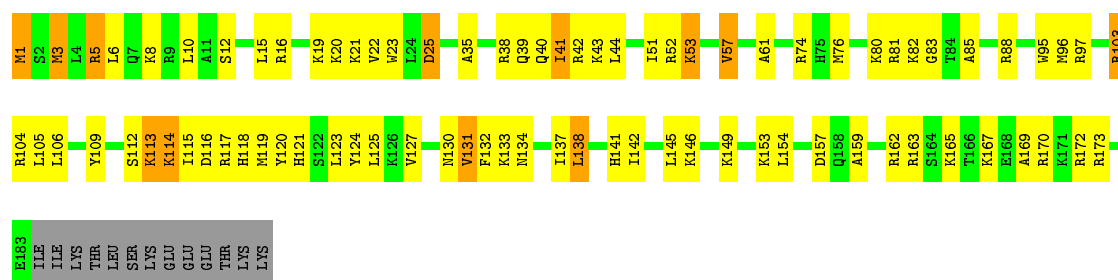
Chain CQ: 54% 39% 5%



• Molecule 54: 60S RIBOSOMAL PROTEIN L19

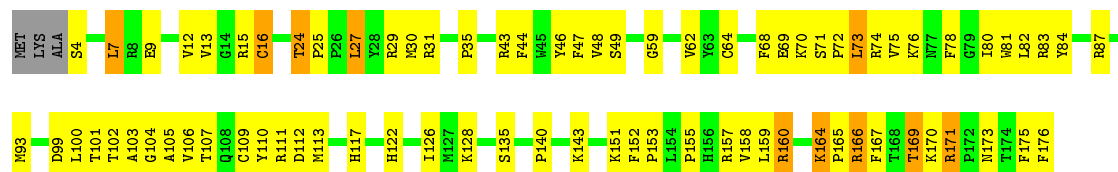
Chain CR: 52% 36% 6% 7%





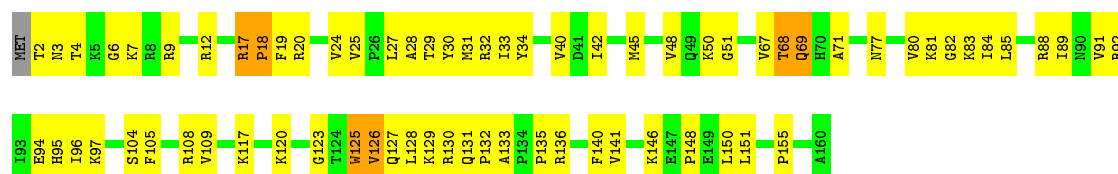
• Molecule 55: 60S RIBOSOMAL PROTEIN L18A

Chain CS: 53% 39% 6%



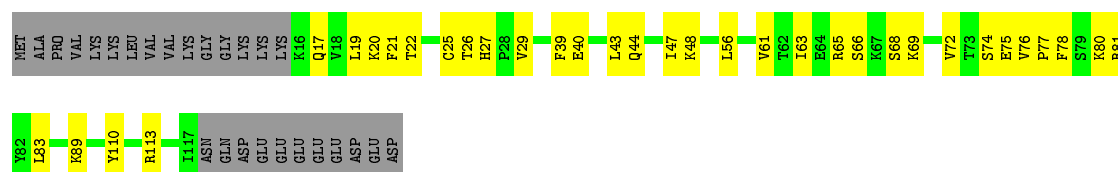
• Molecule 56: 60S RIBOSOMAL PROTEIN L21

Chain CT: 55% 41% 4%



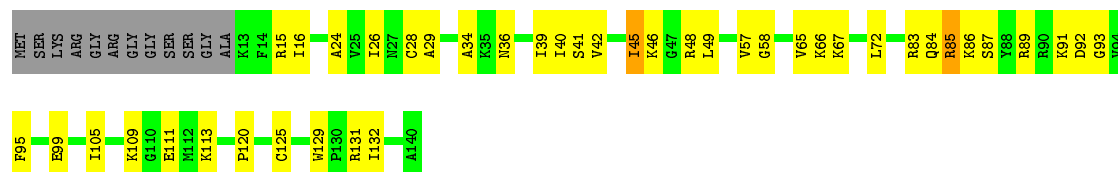
• Molecule 57: 60S RIBOSOMAL PROTEIN L22

Chain CU: 53% 27% 20%



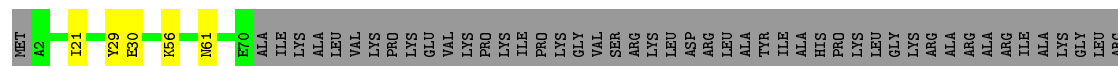
• Molecule 58: 60S RIBOSOMAL PROTEIN L23

Chain CV: 61% 29% 9%



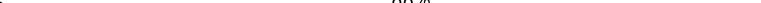
• Molecule 59: 60S RIBOSOMAL PROTEIN L24

Chain CW: 27% 13% 59%




LEU	CYS	ARG	PRO	LYS	ALA	LYS	ALA	LYS	ALA	LYS	ALA	LYS	ASP	GLN	THR	LYS	ALA	GLN	ALA	ALA	ALA	PRO	ALA	SER	VAL	PRO	ALA	GLN	ALA	PRO	LYS	ARG	THR	GLN	ALA	PRO	THR	LYS	ALA	SER	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

• Molecule 65: 60S RIBOSOMAL PROTEIN L30

Chain Cc:  88% . 10%

MET VAL ALA ALA LYS LYS T7 R17 P53 S107 E110 GLN THR GLY GLU LYS

• Molecule 66: 60S RIBOSOMAL PROTEIN L31

Chain Cd:  83% . 13%

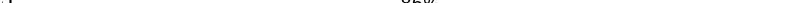
MET	ALA	PRO	ALA	LYS	LYS	GLY	GLY	GLU	LYS	LYS	GLY	ARG	SER	ALA	I17	V20	K39	R92	K115	T119	N125
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------

• Molecule 67: 60S RIBOSOMAL PROTEIN L32

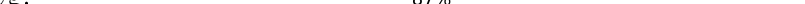
Chain Ce:  90% • 5%

MET ALA ALA LEU R5 P6 V13 K19 F20 L70 L88 E132 GLU ASN GLU

• Molecule 68: 60S RIBOSOMAL PROTEIN L35A

Chain Cf:  86% 10% ..

• Molecule 69: 60S RIBOSOMAL PROTEIN L34


Chain Cg:  87% 10% ...

MTF
V2
Q3
R4
L5
L22
K36
S44
A45
R54
R60
L67
S68
K69
G79
G80
S81
A84
A116
LVS

• Molecule 70: 60S RIBOSOMAL PROTEIN L35


Chain Ch:  94% 5%

• Molecule 71: 60S RIBOSOMAL PROTEIN L36

Chain Ci:  83% 8% • 8%

Amino Acid	Percentage (%)
MET	~12
ALA	~10
LEU	~8
ARG	~7
TVR	~6
P6	~5
V21	~4
R28	~3
L33	~2
T34	~2
K65	~1
T79	~1
L90	~1
M97	~1
R98	~1
A101	~1
A102	~1
LYS	~1
LYS	~1
ASP	~1

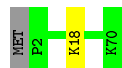
• Molecule 72: 60S RIBOSOMAL PROTEIN L37

Chain Cj:  84% 12%



- Molecule 73: 60S RIBOSOMAL PROTEIN L38

Chain Ck:  97%



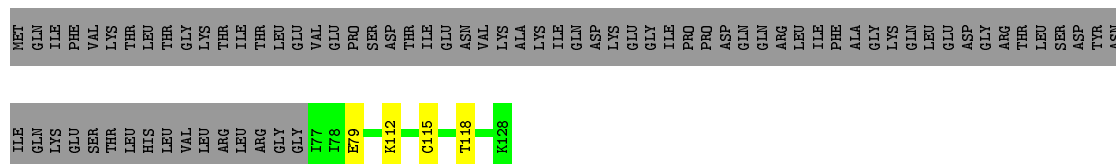
- Molecule 74: 60S RIBOSOMAL PROTEIN L39

Chain Cl:  94%



- Molecule 75: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain Cm:  38% 59%



- Molecule 76: 60S RIBOSOMAL PROTEIN L41

Chain Cn:  100%

There are no outlier residues recorded for this chain.

- Molecule 77: 60S RIBOSOMAL PROTEIN L36A

Chain Co:  93% 7%




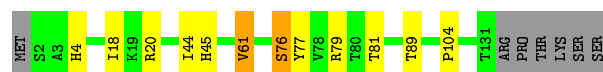
- Molecule 78: 60S RIBOSOMAL PROTEIN L37A

Chain Cp:  93% 5%



- Molecule 79: 60S RIBOSOMAL PROTEIN L28

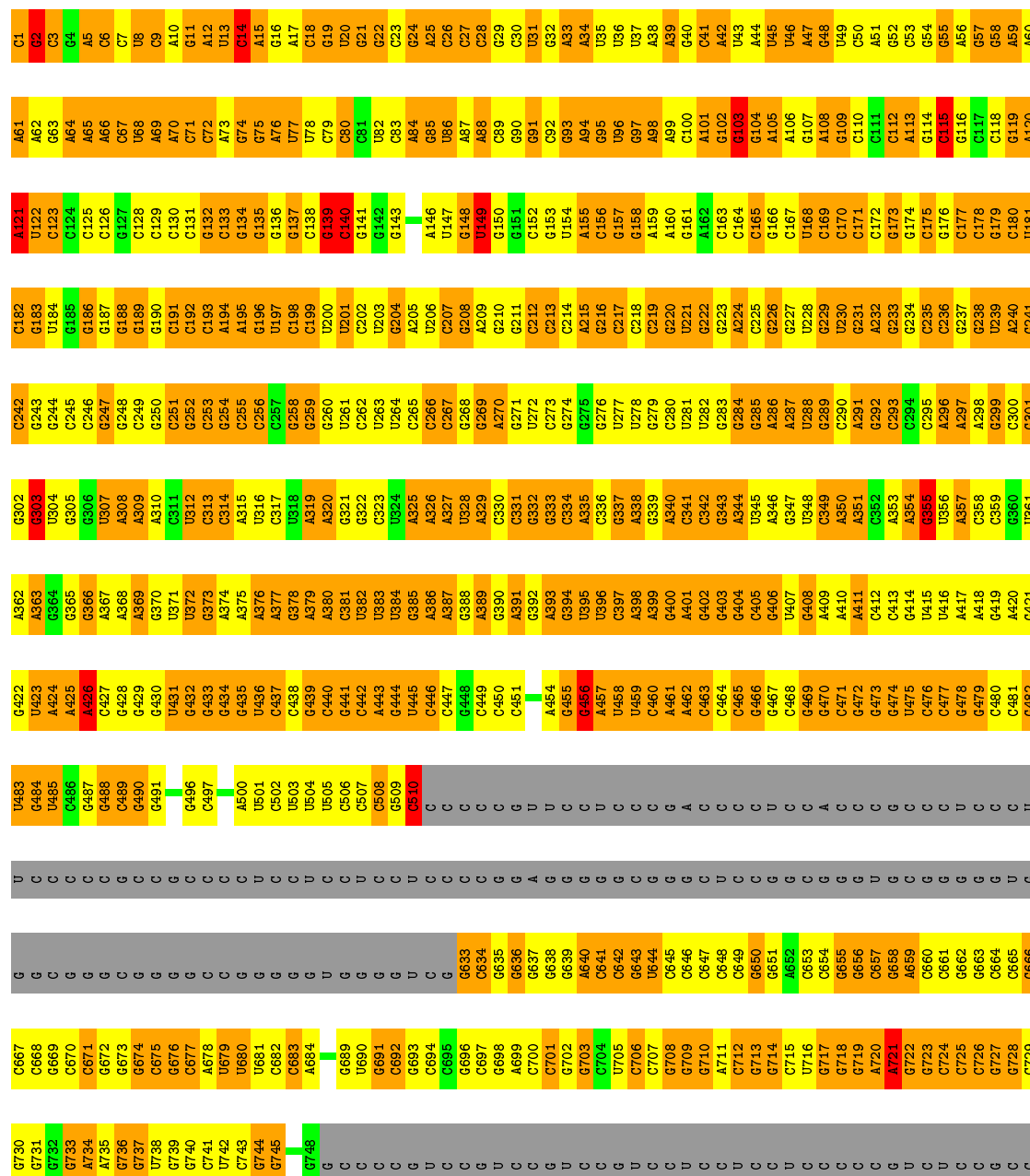
Chain Ct:  86% 7% 5%



• Molecule 80: 60S RIBOSOMAL PROTEIN L10A



• Molecule 81: 28S Ribosomal RNA



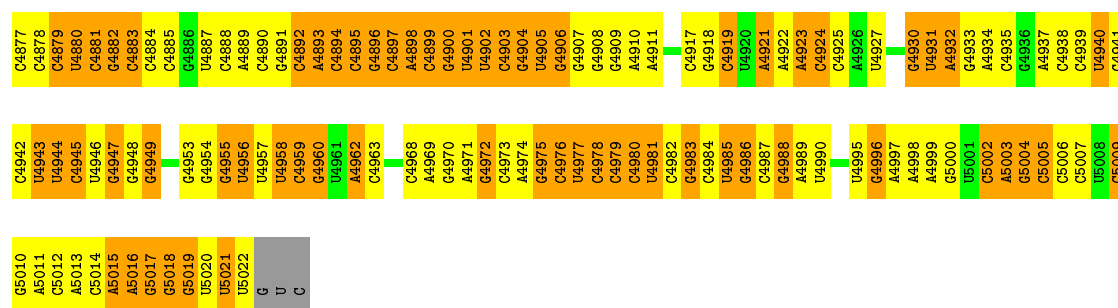
U1707	A1647	C1586	G1524	C1462	G1401	G1340	U1277	G1217	C1156	U1094	C	C	A913	U973	G	C
A1708	A1648	G1587	C1525	G1463	G1402	G1341	C1278	A1218	U1157	C1095	G	C	G914	C974	U	C
U1709	G1649	U1588	A1526	C1464	U1403	G1342	G1279	G1219	G1158	C1096	U	C	C915	C975	G	C
C1710	U1650	C1589	G	C1465	U1404	C1343	G1280	G1220	U1159	C1097	C	C	A916	C976	G	C
U1711	U1651	C1590	G1529	G1466	G1405	U1344	U1281	G1221	C1160	C	U	C	G917	G977	C	G
G1712	U1652	G1591	C1530	G1467	G1406	G	U1282	G1222	C1161	G	C	C	C918	G978	G	G
C1713	C1653	A1592	G1531	A1468	U1407	C1347	A1283	G1223	C1162	C	C	C	A919	C979	G	C
U1714	C1654	A1532	A1532	G1471	U1408	A1348	C1284	G1224	C1163	G	U	C	C920	G	C	C
A1715	C1655	A1533	A1533	G1472	U1409	C1349	C1285	G1225	A1164	C	C	C	U921	G	C	C
U1716	U1656	U1595	G1534	U1473	C1410	C1350	C1286	G1226	G1165	C	G	C	C922	C	C	C
A1717	C1657	C1535	U1473	A1473	C1411	A1351	A1287	U1227	U1166	C	U	C	G923	C	C	C
G1718	A1658	G1597	G1474	G1475	G1412	A1352	C1288	C1228	G1167	C	C	A	C924	C	C	C
C1719	G1659	A1537	A1537	G1475	A1353	A1353	G1288	C1229	G	C	C	G1044	C925	G	C	C
G1720	G1660	U1599	G1538	A1476	G1415	G1354	C1290	C1230	C1170	G	C	G1045	C926	G	C	C
A1721	A1661	A1600	A1539	G1477	C1416	G1355	G1291	C1231	C1171	C	C	G1046	C927	C	U	U
G	U1662	G1540	G1540	C1478	C1417	C1356	A1292	C1232	C1172	C	C	G1047	A927	G	C	C
A1724	G1663	G1603	G1541	A1479	U1418	C1357	C1293	G	C1173	C	C	G1048	A928	G	C	C
A1725	G1664	G1604	A1542	A1480	C1419	C1358	C1294	A	G1174	C	C	G1049	U929	G	U	U
U1726	C1665	G1605	A1543	G1481	U1420	C1359	C1295	A	C1175	C	C	G1050	C930	G	C	C
U1727	U1666	G1606	A1544	A1482	C1421	G1360	G1296	G	G1176	G	C	C1051	C931	G	C	C
A1728	C1667	C1607	C1545	A1483	C1422	U1361	G1297	A	G1177	C	C	C1052	C932	G	C	C
G1729	G1668	G1608	U1546	G1484	A1423	G1362	C1298	G1238	G1178	G	C	G1053	G933	G	C	C
A1730	C1669	A1609	C1547	G1485	G1424	G1363	U1299	G1239	G1179	A	C	G1054	G934	G	C	C
G1731	G1670	U1548	U1548	A1486	U1425	C1364	U1300	G1240	G1180	C	C	C1056	G935	C	C	C
C1732	A1671	A1611	G1549	U1487	U1426	G1365	G1301	G1241	U1181	G	C	C1057	G936	G	C	C
U1733	U1672	G1612	G1550	C1488	C1427	C1366	A1302	G1242	C1182	G	C	A1058	C937	G	C	C
C1734	C1673	A1613	U1551	A1489	G1428	A1367	A1303	G1243	G1183	G	C	C1059	C938	G	A	A
U1735	G	C1614	G1552	U1490	C1429	A1368	A1304	A1243	C1184	G	C	C1060	G939	A	C	C
U1736	C	U1615	G1553	G1491	C1430	U1369	C1305	G1245	G1185	G	C	C1061	G941	C	C	C
G1737	C	A1616	A1554	U1492	G1431	G1370	A1306	G1246	C1186	G	C	C1062	G942	C	C	C
C1738	C	A1617	G1555	U1493	A1432	A1371	C1307	C1247	C1187	G	C	C1063	G943	A	C	C
G1739	A	U1618	G1556	A1494	A1433	A1372	G1308	G1248	C1188	G	C	C1064	A944	A	C	C
G1740	G	C1619	U1557	G1495	G1434	G1373	G	G1249	U1189	U	C	C1065	G945	A	C	C
C1741	A	C1620	C1558	G1496	G1435	G1374	C1312	A1250	C1190	G	C	C1066	G946	C	C	C
C1742	C	A1621	C1559	A1497	A1436	U1375	A1313	G1251	G1191	C	C	C1067	G947	C	C	C
G1743	C	A1622	G1560	C1498	C1437	G1376	A1314	C1252	G1192	C	C	C1068	A948	C	C	C
A1744	C	G1623	U1561	C1499	A1438	A1377	G1315	G1253	G1193	G	C	G1069	G949	G	C	C
A1745	G	C1624	A1562	C1500	C1439	A1378	G1316	A1254	C1194	C	C	G1070	A950	C	U	U
A1746	A	A1625	G1563	G1501	A1440	G1379	A1317	G1255	C1195	G	C	C1071	C951	C	C	C
C1747	C	U1626	G1564	A1502	A1441	G1380	G1318	C1256	C1196	C	C	G	C952	C	C	C
G1748	G	C1627	G1565	A1503	C1442	C1381	U1319	G1257	G1197	G	C	C1074	C953	C	C	C
A1749	C	U1628	G1566	A1504	C1443	C1382	G	C1258	G1198	C	C	A1075	C954	G	C	C
U1750	A	A1629	U1567	G1505	G1444	G1383	A1322	A1259	G1199	C	C	C1076	G955	G	C	C
C1751	C	G1630	C1568	A1506	G1445	G1384	A1323	C1260	G1200	G1136	C	C1077	A893	G	C	C
U1752	C	U1631	C1569	U1507	C1446	C1385	C1324	G1261	G1201	G1137	C	G1078	G956	C	C	C
C1753	C	A1632	G1570	G1508	C1447	G1386	A1325	G1262	C1202	G1138	C	C1079	G957	C	C	C
A1754	C	G1633	U1571	G1509	C1448	C1387	C1326	G1263	G1203	C1139	C	U1080	C958	C	C	C
A1755	C	C1634	A1572	U1510	G1449	C1388	G1327	G1264	G1204	G1140	C	C1081	U897	C	C	C
C1756	G	U1635	G1573	G1509	U1450	G1389	U1328	U1265	G1205	G1141	C	U1082	G960	C	C	C
C1757	C	G1636	G1574	A1513	C1451	U1390	G1329	C1266	U1206	G1142	C	C1083	C961	G	C	C
U1758	C	G1637	U1575	C1514	U1452	C1391	C1330	G1267	G1207	G1143	C	C1084	G962	C	C	C
A1759	A	U1638	G1576	U1515	U1453	G1392	G1331	G1268	U1208	G1144	C	C1085	C963	C	C	C
U1760	C	U1639	C1577	A1516	G1454	C1393	C1332	C1269	G1209	G1145	C	A1086	U964	C	C	C
U1761	G	C1640	U1517	U1517	C1455	C1394	G1333	G1270	U1210	C1146	C	C1087	U898	C	C	C
C1762	C	G1641	G1580	G1518	C1456	G1395	A1334	G1271	C1211	G1147	C	C1088	G965	C	C	C
U1763	C	U1581	U1581	C1519	C1457	G1396	G1335	C1272	G1212	G1148	C	C1089	C966	C	C	C
A1766	C	C1582	U1581	C1520	G1458	C1397	U1336	G1273	G1213	G1150	C	C1090	C967	C	C	C
A1767	C	G1583	U1521	C1521	C1459	C1398	C1337	A1274	G1214	G	C	U1091	C968	C	C	C
U1705	C	G1584	G1522	G1522	C1460	C1399	C1338	C1275	G1215	G1154	C	U1092	C970	C	C	C
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															C912	C

U2684	G2438	G2378	G2316	G2254	G2014	G	G	C1893	G1829	U1769
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G2628	G2442	G2382	U2321	A2258	A2018	C	A	G1897	G1833	A1773
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C2508	C2446	U2386	G2325	G2262	U2022	C	A	C1837	G1777	G1777
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G2517	A2454	A2395	G2334	G2271	C2031	C	U	C1910	G1847	G1785
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C2525	G2464	U2403	C2342	C2279	U2039	C	G	G1918	G1856	G1794
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G2527	C2466	A2405	A2344	U2281	G2041	C	A	G1920	U1796	U1796
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A2530	C2468	U2408	A2347	A2284	C2044	C	C	G1923	C1799	C1799
U2531	C2469	U2409	U2348	G2285	C2045	C	U	G1924	G1800	G1800
G2532	G2470	G2410	U2349	G2286	C2046	C	G	U1925	U1801	U1801
U2533	U2471	G2411	C2350	U2288	A2047	C	U	G1926	G1802	G1802
G2536	U2472	G2412	A2351	A2289	U2048	C	A	U1927	A1866	G1803
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C2538	C2476	C2414	A2353	G2291	C2050	C	C	G1929	G1867	G1805
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G2540	C2478	G2416	G2355	G2293	C2052	C	A	U1931	A1869	C1807
A2541	G2479	U2417	A2356	G2294	G2053	C	C	U1932	G1870	G1808
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G2544	C2482	G2420	A2359	G2297	C2056	C	C	U1935	G1873	G1811
C2545	G2483	U2421	C2360	G2298	G2057	C	U	A1936	A1874	G1812
G2546	A2484	C2422	U2361	G2299	U2058	C	G	U1937	A1875	U1812
U2547	U2485	C2423	U2362	G2301	C2059	C	U	A1938	C1876	G1813
C2548	C2486	U2424	U2363	G2302	G2060	C	G	G1939	G1877	G1814
C2549	G2487	G2425	G2364	G2303	C2061	C	C	A1940	C1878	A1815
A2550	A2488	A2426	G2365	G2304	G2062	C	C	C1941	G1879	A1816
U2551	A2489	G2427	G2366	U2305	G2063	C	U	A1942	G1880	U1817
U2552	A2490	A2428	G2367	U2306	G2064	C	A	G1943	G1881	G1818
G2553	G2491	G2429	G2368	G2307	G2065	C	C	C1944	G1882	C1819
C2554	G2492	A2430	C2370	A2308	A	C	G	U1945	U1883	G1820
C2555	G2493	U2431	G2371	G2309	G	C	A	G	U1884	A1821
G2556	A2494	G2432	A2372	G2310	C2247	C	A	A2007	A1885	G1822
U2557	G2495	G2433	A2373	G2311	G2248	C	U	G	U1886	U1823
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G2561	G2499	A2437	G2377	G2315	C2252	C	U	G	C1891	U1827
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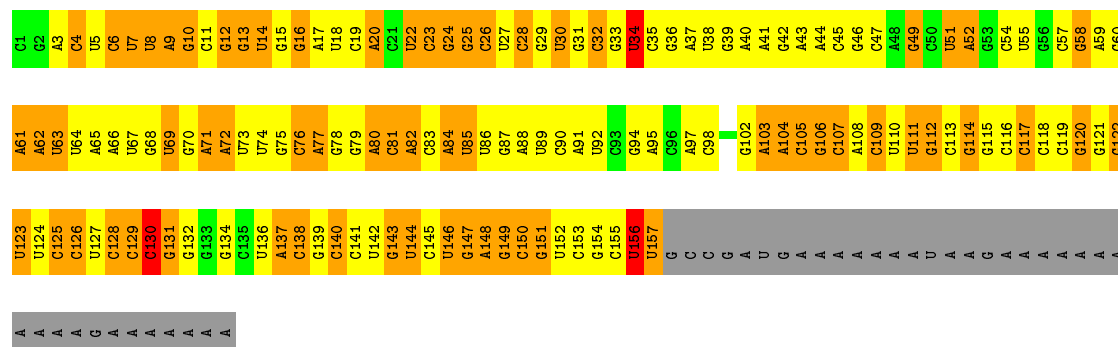



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C4820	C4700	G4639	U4578	U4516	G4454	G4394	G4333	U4272	G4212	G4147	U4084	U4023	C3900
G4821	C4701	G4640	U4579	U4517	G4455	U4395	G4334	A4273	C4213	U4148	U4085	A4024	G3903
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U4824	C4704	U4643	A4582	C4520	U4458	U4398	G4337	A4278	A4216	G4151	G4088	C4027	C3906
G4825	U4705	A4644	G4583	C4521	U4459	U4399	A4338	C4278	G4217	G4152	G4089	U4028	C3907
C4826	C4706	U4645	A4584	U4522	U4460	A4401	A4339	C4279	A4217	C4153	G4090	G4029	G3908
G4827	C4707	G4646	C4585	U4523	U4461	A4402	A4340	G4280	G4218	U4154	G4091	A4030	G3909
G4828	G4708	A4647	A4586	A4524	G4462	U4403	A4341	U4281	U4219	G4155	C4092	U4031	U3909
A4829	C4709	U4648	U4587	C4525	C4463	G4403	G4342	G4282	U4220	G4156	C4093	C4032	G3910
G4830	U4710	U4649	U4588	U4526	C4464	C4404	U4343	A4283	C4221	G4157	A4094	G4033	A3911
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G4832	U4712	A4651	G4590	A4528	C4468	U4406	A4345	A4285	C4223	C4159	G4096	U4035	A3913
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G4837	C4717	U4656	A4595	G4533	A4473	G4411	A4350	G4290	A4228	C4164	G4102	C4040	G3920
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G4846	G4726	G4666	G4604	C4542	G4482	U4420	A4359	A4299	G4237	C4175	A3929	A4051	G3930
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G4850	C4730	C4670	G4608	G4546	U4486	A4424	G4364	U4303	A4241	U4178	A4117	G4054	U3934
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G4855	G4735	C4675	C4613	U4551	U4491	U4429	C4369	A4308	G4247	C4183	C4122	G4059	G3939
C4856	C4736	U4676	G4614	C4552	U4492	G4430	G4370	C4309	C4248	A4184	U4123	G4060	G3940
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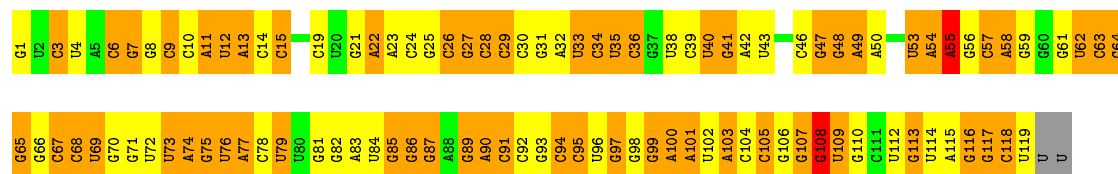
- Molecule 82: 5.8S Ribosomal RNA

Chain A3: 7% 38% 34% 19%



- Molecule 83: 5S Ribosomal RNA

Chain A4: 12% 36% 49%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	DEFOCUS GROUP	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO-163 FILM	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MIA

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	AV	0.29	0/1809	0.75	0/2819
10	BF	0.43	0/1507	0.74	0/2026
11	BG	0.47	0/1907	0.74	0/2538
12	BH	0.46	0/1558	0.74	1/2087 (0.0%)
13	BI	0.47	0/1724	0.72	0/2298
14	BJ	0.45	0/1520	0.77	0/2030
15	BK	0.48	0/815	0.68	0/1101
16	BL	0.45	0/1220	0.72	0/1633
17	BM	0.48	0/941	0.72	0/1264
18	BN	0.43	0/1231	0.73	1/1656 (0.1%)
19	BO	0.46	0/1036	0.71	0/1391
2	AW	0.31	0/1783	0.76	0/2776
20	BP	0.43	0/1000	0.67	0/1335
21	BQ	0.43	0/1125	0.66	0/1506
22	BR	0.42	0/904	0.67	0/1208
23	BS	0.42	0/1190	0.68	0/1594
24	BT	0.44	0/1131	0.69	0/1515
25	BU	0.50	0/813	0.70	0/1092
26	BV	0.47	0/643	0.71	0/860
27	BW	0.44	0/1050	0.69	0/1406
28	BX	0.46	0/1063	0.70	0/1421
29	BY	0.45	0/1019	0.70	0/1354
3	AX	0.42	1/615 (0.2%)	1.25	11/948 (1.2%)
30	BZ	0.46	0/611	0.71	0/820
31	Ba	0.48	0/778	0.75	1/1041 (0.1%)
32	Bb	0.48	0/637	0.68	0/854
33	Bc	0.46	0/492	0.74	0/657
34	Bd	0.51	0/454	0.76	0/603
35	Be	0.45	0/417	0.69	0/548
36	Bf	0.53	0/507	0.84	1/673 (0.1%)
37	Bg	0.45	0/2497	0.67	0/3399
38	CA	0.44	0/1926	0.67	0/2583

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	CB	0.45	0/3258	0.73	2/4361 (0.0%)
4	B1	0.37	2/41550 (0.0%)	0.79	6/64763 (0.0%)
40	CC	0.47	0/2943	0.73	0/3953
41	CD	0.49	1/2406 (0.0%)	0.70	1/3221 (0.0%)
42	CE	0.52	0/1311	0.73	0/1763
43	CF	0.45	0/1985	0.68	0/2644
44	CG	0.46	0/1914	0.72	0/2578
45	CH	0.43	0/1554	0.69	0/2089
46	CI	0.42	0/1642	0.67	0/2194
47	CJ	0.49	0/1385	0.71	0/1852
48	CL	0.53	2/1647 (0.1%)	0.73	3/2205 (0.1%)
49	CM	0.49	0/1162	0.70	0/1556
5	BA	0.51	0/1756	0.68	0/2386
50	CN	0.43	0/1753	0.65	0/2348
51	CO	0.44	0/1639	0.69	0/2193
52	CP	0.44	0/1260	0.70	0/1691
53	CQ	0.45	0/1517	0.74	0/2026
54	CR	0.40	0/1542	0.64	0/2037
55	CS	0.44	0/1478	0.73	0/1985
56	CT	0.46	0/1325	0.71	0/1770
57	CU	0.47	0/841	0.71	0/1128
58	CV	0.43	0/977	0.63	0/1312
59	CW	0.43	0/542	0.59	0/722
6	BB	0.51	0/1756	0.75	1/2350 (0.0%)
60	CX	0.41	0/992	0.67	0/1334
61	CY	0.47	0/1082	0.72	1/1441 (0.1%)
62	CZ	0.47	0/1137	0.79	0/1517
63	Ca	0.44	0/1190	0.71	0/1591
64	Cb	0.45	0/570	0.72	0/752
65	Cc	0.46	0/813	0.70	0/1091
66	Cd	0.44	0/919	0.67	0/1238
67	Ce	0.45	0/1071	0.68	0/1428
68	Cf	0.50	0/884	0.81	0/1185
69	Cg	0.48	0/917	0.74	0/1222
7	BC	0.42	0/1761	0.65	0/2379
70	Ch	0.38	0/1022	0.64	0/1351
71	Ci	0.43	0/793	0.75	0/1048
72	Cj	0.49	0/704	0.76	0/931
73	Ck	0.43	0/574	0.73	0/761
74	Cl	0.41	0/453	0.61	0/599
75	Cm	0.42	0/434	0.70	0/575
76	Cn	0.39	0/240	0.50	0/305
77	Co	0.45	0/884	0.74	0/1166

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
78	Cp	0.40	0/717	0.61	0/953
79	Ct	0.48	0/1058	0.75	0/1416
8	BD	0.40	0/1672	0.66	0/2250
80	Cu	0.45	0/1638	0.69	1/2222 (0.0%)
81	A2	0.41	23/86672 (0.0%)	0.80	40/135198 (0.0%)
82	A3	0.35	0/3723	0.79	1/5800 (0.0%)
83	A4	0.37	0/2836	0.81	3/4421 (0.1%)
9	BE	0.47	0/2072	0.70	0/2793
All	All	0.42	29/231894 (0.0%)	0.77	74/341130 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	AX	1	0
4	B1	0	23
81	A2	0	35
82	A3	0	2
All	All	1	60

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	A2	1701	C	C5'-C4'	18.39	1.73	1.51
81	A2	1673	C	C3'-O3'	15.36	1.63	1.42
81	A2	1701	C	O5'-C5'	14.45	1.67	1.44
81	A2	1673	C	O3'-P	14.13	1.78	1.61
81	A2	1701	C	P-O5'	13.52	1.73	1.59

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	A2	1701	C	O4'-C4'-C3'	-15.19	88.81	104.00
39	CB	258	HIS	C-N-CD	-13.96	89.88	120.60
3	AX	58	U	P-O5'-C5'	12.68	141.18	120.90
81	A2	1701	C	O4'-C1'-N1	12.30	118.04	108.20
81	A2	1701	C	C4'-C3'-O3'	12.16	137.32	113.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	AX	58	U	C3'

5 of 60 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	B1	111	A	Sidechain
4	B1	216	C	Sidechain
4	B1	44	U	Sidechain
4	B1	77	A	Sidechain
4	B1	84	A	Sidechain

## 5.2 Too-close contacts

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	AV	1619	0	820	128	0
2	AW	1626	0	826	188	0
3	AX	560	0	281	141	0
4	B1	37159	0	18778	3865	0
5	BA	1719	0	1717	132	0
6	BB	1729	0	1803	139	0
7	BC	1724	0	1808	73	0
8	BD	1646	0	1737	91	0
9	BE	2031	0	2138	118	0
10	BF	1486	0	1540	146	0
11	BG	1884	0	2044	152	0
12	BH	1535	0	1632	132	0
13	BI	1695	0	1785	163	0
14	BJ	1495	0	1615	90	0
15	BK	791	0	811	46	0
16	BL	1199	0	1269	68	0
17	BM	931	0	961	41	0
18	BN	1207	0	1292	66	0
19	BO	1023	0	1049	62	0
20	BP	981	0	1026	56	0
21	BQ	1108	0	1172	92	0
22	BR	893	0	946	57	0
23	BS	1172	0	1229	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	BT	1112	0	1146	114	0
25	BU	803	0	866	69	0
26	BV	636	0	637	44	0
27	BW	1033	0	1080	64	0
28	BX	1046	0	1110	67	0
29	BY	1002	0	1075	64	0
30	BZ	605	0	665	55	0
31	Ba	767	0	816	0	0
32	Bb	625	0	642	0	0
33	Bc	490	0	520	0	0
34	Bd	444	0	442	0	0
35	Be	412	0	463	0	0
36	Bf	497	0	497	0	0
37	Bg	2440	0	2396	0	0
38	CA	1888	0	1983	137	0
39	CB	3190	0	3327	185	0
40	CC	2889	0	3064	240	0
41	CD	2361	0	2385	137	0
42	CE	1286	0	1398	151	0
43	CF	1949	0	2093	140	0
44	CG	1881	0	2018	119	0
45	CH	1535	0	1611	104	0
46	CI	1604	0	1652	62	0
47	CJ	1362	0	1399	100	0
48	CL	1617	0	1725	98	0
49	CM	1139	0	1204	136	0
50	CN	1708	0	1761	86	0
51	CO	1607	0	1745	123	0
52	CP	1234	0	1263	73	0
53	CQ	1493	0	1612	93	0
54	CR	1526	0	1682	116	0
55	CS	1438	0	1472	87	0
56	CT	1297	0	1366	104	0
57	CU	827	0	852	26	0
58	CV	963	0	1026	40	0
59	CW	529	0	541	32	0
60	CX	975	0	1053	44	0
61	CY	1065	0	1145	86	0
62	CZ	1114	0	1194	74	0
63	Ca	1161	0	1213	0	0
64	Cb	560	0	590	0	0
65	Cc	802	0	844	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
66	Cd	904	0	947	0	0
67	Ce	1053	0	1144	0	0
68	Cf	865	0	904	0	0
69	Cg	907	0	1002	0	0
70	Ch	1014	0	1148	0	0
71	Ci	783	0	862	0	0
72	Cj	690	0	719	0	0
73	Ck	568	0	637	0	0
74	Cl	443	0	483	0	0
75	Cm	428	0	466	0	0
76	Cn	239	0	285	0	0
77	Co	870	0	943	0	0
78	Cp	707	0	760	0	0
79	Ct	1043	0	1120	0	0
80	Cu	1621	0	1563	0	0
81	A2	77488	0	39155	7537	0
82	A3	3334	0	1693	288	0
83	A4	2538	0	1286	248	0
All	All	215620	0	158969	15128	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 45.

The worst 5 of 15128 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)
3:AX:45:U:C2	4:B1:1207:G:C2	1.88	1.61
2:AW:19:G:C8	81:A2:3927:G:H1'	1.13	1.59
3:AX:45:U:C2	4:B1:1207:G:N2	1.69	1.58
13:BI:123:ARG:CZ	81:A2:4979:C:H5''	1.25	1.58
3:AX:43:U:H5'	4:B1:961:G:C1'	1.21	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	
5	BA	216/295 (73%)	209 (97%)	5 (2%)	2 (1%)	21	67
6	BB	211/264 (80%)	176 (83%)	18 (8%)	17 (8%)	1	19
7	BC	220/293 (75%)	213 (97%)	2 (1%)	5 (2%)	8	48
8	BD	210/243 (86%)	201 (96%)	4 (2%)	5 (2%)	7	47
9	BE	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	9	51
10	BF	186/204 (91%)	163 (88%)	13 (7%)	10 (5%)	2	29
11	BG	230/249 (92%)	216 (94%)	5 (2%)	9 (4%)	4	36
12	BH	189/194 (97%)	178 (94%)	7 (4%)	4 (2%)	9	50
13	BI	205/208 (99%)	184 (90%)	14 (7%)	7 (3%)	5	40
14	BJ	177/194 (91%)	169 (96%)	5 (3%)	3 (2%)	11	55
15	BK	92/165 (56%)	84 (91%)	1 (1%)	7 (8%)	1	20
16	BL	144/158 (91%)	133 (92%)	5 (4%)	6 (4%)	3	34
17	BM	118/132 (89%)	111 (94%)	1 (1%)	6 (5%)	2	30
18	BN	148/151 (98%)	138 (93%)	5 (3%)	5 (3%)	5	40
19	BO	135/151 (89%)	129 (96%)	3 (2%)	3 (2%)	8	49
20	BP	116/145 (80%)	106 (91%)	5 (4%)	5 (4%)	3	34
21	BQ	137/146 (94%)	129 (94%)	6 (4%)	2 (2%)	13	57
22	BR	105/135 (78%)	99 (94%)	4 (4%)	2 (2%)	10	52
23	BS	140/152 (92%)	125 (89%)	7 (5%)	8 (6%)	2	27
24	BT	141/145 (97%)	135 (96%)	4 (3%)	2 (1%)	14	58
25	BU	99/119 (83%)	95 (96%)	3 (3%)	1 (1%)	19	65
26	BV	81/83 (98%)	78 (96%)	1 (1%)	2 (2%)	7	46
27	BW	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	12	56
28	BX	132/143 (92%)	120 (91%)	5 (4%)	7 (5%)	2	29
29	BY	120/133 (90%)	114 (95%)	2 (2%)	4 (3%)	5	40
30	BZ	74/125 (59%)	71 (96%)	0	3 (4%)	3	35
31	Ba	94/115 (82%)	85 (90%)	5 (5%)	4 (4%)	3	34
32	Bb	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
33	Bc	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	5	40
34	Bd	51/56 (91%)	44 (86%)	7 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	Be	49/59 (83%)	43 (88%)	5 (10%)	1 (2%)	9	51
36	Bf	59/156 (38%)	53 (90%)	6 (10%)	0	100	100
37	Bg	312/317 (98%)	291 (93%)	14 (4%)	7 (2%)	8	49
38	CA	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	16	61
39	CB	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	4	38
40	CC	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	3	35
41	CD	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	11	55
42	CE	156/288 (54%)	141 (90%)	8 (5%)	7 (4%)	3	33
43	CF	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	11	55
44	CG	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	4	36
45	CH	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	12	56
46	CI	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	12	56
47	CJ	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	22
48	CL	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	2	28
49	CM	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	14	58
50	CN	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	13	57
51	CO	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	13	57
52	CP	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	9	51
53	CQ	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	5	40
54	CR	181/196 (92%)	175 (97%)	3 (2%)	3 (2%)	11	55
55	CS	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	4	39
56	CT	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	10	52
57	CU	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
58	CV	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	12	56
59	CW	62/157 (40%)	61 (98%)	1 (2%)	0	100	100
60	CX	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
61	CY	126/145 (87%)	119 (94%)	4 (3%)	3 (2%)	7	47
62	CZ	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	5	42
63	Ca	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	5	40
64	Cb	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	2	26
65	Cc	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	9	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	Cd	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	21	67
67	Ce	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	7	47
68	Cf	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	3	32
69	Cg	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	4	39
70	Ch	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	7	46
71	Ci	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	2	25
72	Cj	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	7	47
73	Ck	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	13	57
74	Cl	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	9	50
75	Cm	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	9	51
76	Cn	23/25 (92%)	23 (100%)	0	0	100	100
77	Co	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	10	52
78	Cp	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	5	40
79	Ct	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	2	29
80	Cu	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	14	58
All	All	11190/12898 (87%)	10477 (94%)	390 (4%)	323 (3%)	9	43

5 of 323 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	BB	76	ASN
6	BB	132	GLY
6	BB	148	ASN
6	BB	154	SER
6	BB	176	VAL

### 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	
5	BA	181/243 (74%)	176 (97%)	5 (3%)	51	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	BB	194/231 (84%)	183 (94%)	11 (6%)	25	62
7	BC	188/225 (84%)	181 (96%)	7 (4%)	41	73
8	BD	175/202 (87%)	166 (95%)	9 (5%)	29	66
9	BE	220/225 (98%)	208 (94%)	12 (6%)	27	63
10	BF	158/170 (93%)	151 (96%)	7 (4%)	35	69
11	BG	202/218 (93%)	195 (96%)	7 (4%)	43	74
12	BH	171/174 (98%)	167 (98%)	4 (2%)	58	82
13	BI	179/180 (99%)	167 (93%)	12 (7%)	20	57
14	BJ	160/168 (95%)	150 (94%)	10 (6%)	22	59
15	BK	85/136 (62%)	82 (96%)	3 (4%)	43	74
16	BL	133/142 (94%)	131 (98%)	2 (2%)	72	88
17	BM	102/108 (94%)	97 (95%)	5 (5%)	31	66
18	BN	130/131 (99%)	128 (98%)	2 (2%)	72	88
19	BO	107/119 (90%)	100 (94%)	7 (6%)	21	58
20	BP	107/130 (82%)	102 (95%)	5 (5%)	32	68
21	BQ	115/121 (95%)	111 (96%)	4 (4%)	43	74
22	BR	99/122 (81%)	94 (95%)	5 (5%)	29	66
23	BS	123/132 (93%)	114 (93%)	9 (7%)	17	54
24	BT	113/115 (98%)	106 (94%)	7 (6%)	23	60
25	BU	93/107 (87%)	89 (96%)	4 (4%)	35	70
26	BV	67/67 (100%)	66 (98%)	1 (2%)	72	88
27	BW	112/113 (99%)	107 (96%)	5 (4%)	34	69
28	BX	108/115 (94%)	103 (95%)	5 (5%)	33	68
29	BY	107/115 (93%)	101 (94%)	6 (6%)	26	62
30	BZ	67/103 (65%)	63 (94%)	4 (6%)	24	60
31	Ba	83/98 (85%)	76 (92%)	7 (8%)	14	48
32	Bb	72/76 (95%)	68 (94%)	4 (6%)	26	62
33	Bc	55/62 (89%)	52 (94%)	3 (6%)	27	63
34	Bd	47/49 (96%)	43 (92%)	4 (8%)	13	48
35	Be	42/48 (88%)	40 (95%)	2 (5%)	31	67
36	Bf	54/140 (39%)	51 (94%)	3 (6%)	26	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	Bg	272/275 (99%)	260 (96%)	12 (4%)	35	69
38	CA	189/199 (95%)	185 (98%)	4 (2%)	61	84
39	CB	344/349 (99%)	326 (95%)	18 (5%)	29	65
40	CC	302/348 (87%)	284 (94%)	18 (6%)	24	60
41	CD	244/250 (98%)	237 (97%)	7 (3%)	50	78
42	CE	143/252 (57%)	135 (94%)	8 (6%)	26	62
43	CF	203/215 (94%)	196 (97%)	7 (3%)	44	75
44	CG	199/223 (89%)	192 (96%)	7 (4%)	43	74
45	CH	171/171 (100%)	164 (96%)	7 (4%)	37	71
46	CI	170/181 (94%)	161 (95%)	9 (5%)	28	64
47	CJ	143/149 (96%)	137 (96%)	6 (4%)	36	70
48	CL	167/177 (94%)	156 (93%)	11 (7%)	21	57
49	CM	118/161 (73%)	114 (97%)	4 (3%)	44	75
50	CN	172/172 (100%)	170 (99%)	2 (1%)	78	90
51	CO	168/174 (97%)	166 (99%)	2 (1%)	78	90
52	CP	133/163 (82%)	126 (95%)	7 (5%)	28	64
53	CQ	162/165 (98%)	157 (97%)	5 (3%)	47	77
54	CR	161/175 (92%)	150 (93%)	11 (7%)	20	57
55	CS	155/157 (99%)	148 (96%)	7 (4%)	34	69
56	CT	139/140 (99%)	134 (96%)	5 (4%)	42	74
57	CU	91/115 (79%)	88 (97%)	3 (3%)	45	76
58	CV	100/107 (94%)	99 (99%)	1 (1%)	82	92
59	CW	55/126 (44%)	52 (94%)	3 (6%)	27	63
60	CX	107/133 (80%)	105 (98%)	2 (2%)	65	86
61	CY	119/135 (88%)	115 (97%)	4 (3%)	44	75
62	CZ	118/118 (100%)	112 (95%)	6 (5%)	29	66
63	Ca	120/121 (99%)	116 (97%)	4 (3%)	45	76
64	Cb	58/126 (46%)	57 (98%)	1 (2%)	68	87
65	Cc	88/97 (91%)	87 (99%)	1 (1%)	80	91
66	Cd	100/110 (91%)	96 (96%)	4 (4%)	38	71
67	Ce	115/121 (95%)	112 (97%)	3 (3%)	54	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	Cf	87/89 (98%)	79 (91%)	8 (9%)	11	43
69	Cg	98/100 (98%)	88 (90%)	10 (10%)	9	37
70	Ch	109/110 (99%)	106 (97%)	3 (3%)	51	78
71	Ci	82/89 (92%)	76 (93%)	6 (7%)	17	54
72	Cj	71/80 (89%)	69 (97%)	2 (3%)	51	78
73	Ck	64/65 (98%)	64 (100%)	0	100	100
74	Cl	47/48 (98%)	46 (98%)	1 (2%)	61	84
75	Cm	48/116 (41%)	45 (94%)	3 (6%)	22	59
76	Cn	24/24 (100%)	24 (100%)	0	100	100
77	Co	94/94 (100%)	89 (95%)	5 (5%)	28	64
78	Cp	74/75 (99%)	72 (97%)	2 (3%)	52	79
79	Ct	113/121 (93%)	106 (94%)	7 (6%)	23	60
80	Cu	177/177 (100%)	163 (92%)	14 (8%)	15	51
All	All	9763/10978 (89%)	9332 (96%)	431 (4%)	39	69

5 of 431 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	CA	116	LEU
42	CE	172	LEU
72	Cj	83	THR
39	CB	101	THR
40	CC	78	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 210 such sidechains are listed below:

Mol	Chain	Res	Type
39	CB	271	GLN
43	CF	151	ASN
70	Ch	101	ASN
40	CC	43	ASN
41	CD	291	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AV	75/76 (98%)	37 (49%)	2 (2%)
2	AW	74/76 (97%)	33 (44%)	5 (6%)
3	AX	27/28 (96%)	15 (55%)	4 (14%)
4	B1	1738/1869 (92%)	1038 (59%)	152 (8%)
81	A2	3605/5025 (71%)	2042 (56%)	325 (9%)
82	A3	156/194 (80%)	81 (51%)	6 (3%)
83	A4	118/121 (97%)	68 (57%)	9 (7%)
All	All	5793/7389 (78%)	3314 (57%)	503 (8%)

5 of 3314 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AV	2	C
1	AV	5	G
1	AV	8	U
1	AV	11	C
1	AV	17	C

5 of 503 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
81	A2	939	G
81	A2	1532	A
81	A2	4740	U
81	A2	967	C
81	A2	1282	U

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	MIA	AW	37	2	22,31,32	1.74	4 (18%)	26,44,47	3.43	7 (26%)



In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MIA	AW	37	2	-	0/11/33/34	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AW	37	MIA	C13-C12	-4.41	1.33	1.52
2	AW	37	MIA	C4-N3	-2.52	1.31	1.35
2	AW	37	MIA	C6-N1	2.59	1.36	1.33
2	AW	37	MIA	C2-S10	4.24	1.79	1.75

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AW	37	MIA	C12-N6-C6	-8.49	113.64	123.46
2	AW	37	MIA	C5-C6-N1	-4.67	115.84	120.58
2	AW	37	MIA	N6-C6-N1	-2.84	115.16	118.55
2	AW	37	MIA	C1'-N9-C4	2.23	129.29	126.81
2	AW	37	MIA	C2-N1-C6	2.75	120.69	113.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AW	37	MIA	44	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.