



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 01:09 pm GMT

PDB ID : 4V6X
EMDB ID: : EMD-5592
Title : Structure of the human 80S ribosome
Authors : Anger, A.M.; Armache, J.-P.; Berninghausen, O.; Habeck, M.; Subklewe, M.;
Wilson, D.N.; Beckmann, R.
Deposited on : 2013-02-27
Resolution : 5.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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) : recalc29047

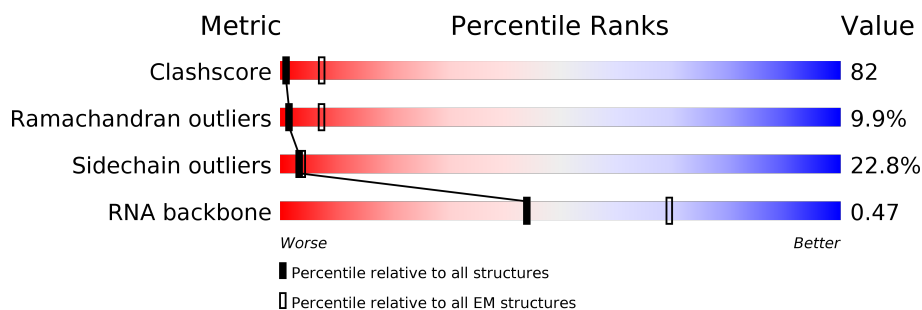
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.00 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.




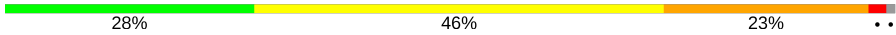
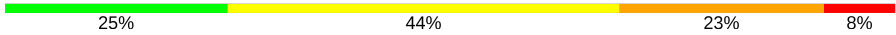
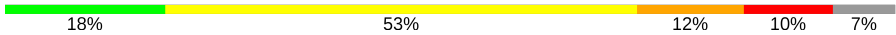
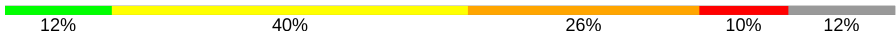

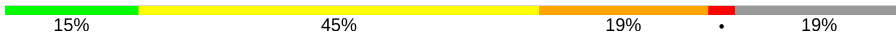

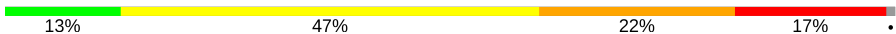
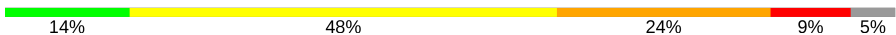
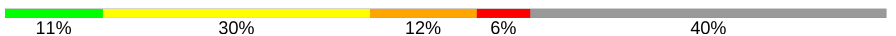





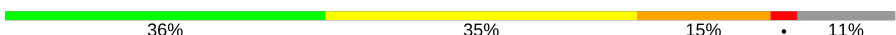







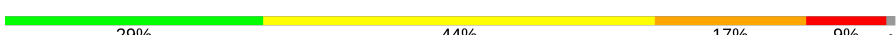
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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 ≥ 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	Az	858	74% 19% 5% •
2	Ag	317	74% 20% • •
3	AU	119	13% 39% 26% 9% 13%
4	AK	165	6% 27% 15% 12% 41%
5	AO	151	16% 48% 24% • 10%
6	AX	143	26% 49% 19% 6% •
7	AM	132	20% 45% 23% 6% 6%
8	AS	152	15% 47% 18% 11% 10%



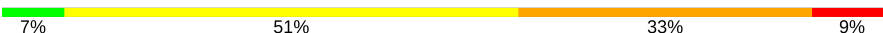



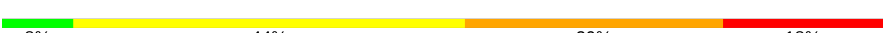







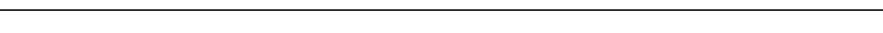
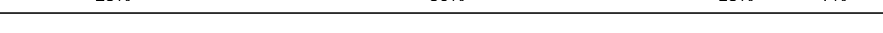

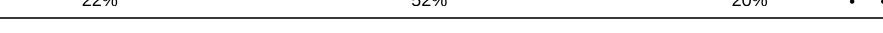

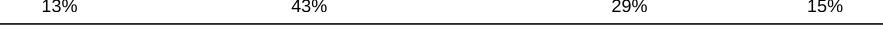

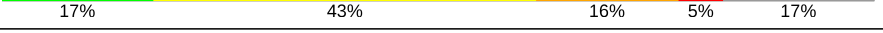



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Mol	Chain	Length	Quality of chain
9	Ad	56	
10	AN	151	
11	AL	158	
12	AR	135	
13	AP	145	
14	AT	145	
15	AB	264	
16	AA	295	
17	AV	83	
18	AY	133	
19	AZ	125	
20	Aa	115	
21	Ab	84	
22	Ac	69	
23	AD	243	
24	Ae	59	
25	Af	80	
26	AJ	194	
27	AE	263	
28	AC	293	
29	AG	249	
30	AF	204	
31	AH	194	
32	AW	130	
33	AI	208	





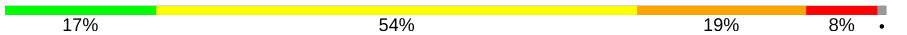
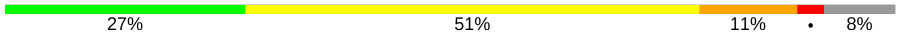















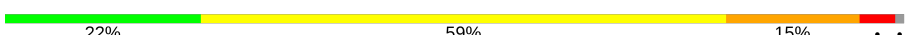



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Mol	Chain	Length	Quality of chain
34	AQ	146	
35	Ah	408	
36	B2	1869	
37	BC	75	
38	Cz	217	
39	Cq	317	
40	CK	165	
41	CO	203	
42	CL	211	
43	CV	140	
44	CM	215	
45	Ca	148	
46	CN	204	
47	CI	214	
48	CD	297	
49	CQ	188	
50	CR	196	
51	CA	257	
52	CS	176	
53	CT	160	
54	CP	184	
55	CU	128	
56	CX	156	
57	CY	145	
58	CW	157	

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Mol	Chain	Length	Quality of chain
59	CZ	136	
60	Cr	137	
61	Ch	123	
62	Cb	159	
63	CB	403	
64	CF	248	
65	Cc	115	
66	Cd	125	
67	Ce	135	
68	Cf	110	
69	Cg	117	
70	Ci	105	
71	Cj	97	
72	Ck	70	
73	Cl	51	
74	CC	427	
75	Cm	52	
76	Cn	25	
77	Cp	92	
78	Co	106	
79	CJ	178	
80	CH	192	
81	CE	288	
82	CG	266	
83	Cs	114	

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Mol	Chain	Length	Quality of chain
83	Ct	114	<div><div></div><div>45%5%50%</div></div>
84	Cu	115	<div><div></div><div>37%12%51%</div></div>
84	Cv	115	<div><div></div><div>39%8%51%</div></div>
85	A5	5070	<div><div></div><div>11%45%23%6%15%</div></div>
86	A7	121	<div><div></div><div>60%31%7%</div></div>
87	A8	157	<div><div></div><div>5%59%27%10%</div></div>

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 237685 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 Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Az	856	Total	C	N	O	S	0	0
			6673	4234	1148	1247	44		

- Molecule 2 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ag	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 3 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AU	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 4 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 5 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 6 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AX	142	Total	C	N	O	S	0	0
			1106	698	220	184	4		

- Molecule 7 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AM	124	Total	C	N	O	S	0	0
			960	600	171	181	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AM	52	GLN	LEU	CONFLICT	UNP P25398
AM	69	LEU	CYS	CONFLICT	UNP P25398
AM	99	ASN	LYS	CONFLICT	UNP P25398

- Molecule 8 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AS	137	Total	C	N	O	S	0	0
			1139	714	231	193	1		

- Molecule 9 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Ad	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 10 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 11 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	158	Total	C	N	O	S	0	0
			1296	827	241	221	7		

- Molecule 12 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AR	126	Total	C	N	O	S	0	0
			1019	639	188	187	5		

- Molecule 13 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AP	127	Total	C	N	O	S	0	0
			1062	674	202	179	7		

- Molecule 14 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AT	141	Total	C	N	O	S	0	0
			1101	690	212	196	3		

- Molecule 15 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AB	215	Total	C	N	O	S	0	0
			1747	1110	313	310	14		

- Molecule 16 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 17 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AV	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 18 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AY	126	Total	C	N	O	S	0	0
			1023	646	200	172	5		

- Molecule 19 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 20 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Aa	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 21 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Ab	84	Total	C	N	O	S	0	0
			659	413	122	116	8		

- Molecule 22 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ac	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 23 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 24 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ae	59	Total	C	N	O	S	0	0
			468	290	102	75	1		

- Molecule 25 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Af	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 26 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AJ	182	Total	C	N	O	S	0	0
			1498	952	300	244	2		

- Molecule 27 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AE	263	Total	C	N	O	S	0	0
			2084	1329	387	359	9		

- Molecule 28 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AC	226	Total	C	N	O	S	0	0
			1751	1130	301	310	10		

- Molecule 29 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 30 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 31 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AH	190	Total	C	N	O	S	0	0
			1530	975	281	273	1		

- Molecule 32 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 33 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 34 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 35 is a protein called Plasminogen activator inhibitor 1 RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ah	73	Total	C	N	O	S	0	0
			566	340	116	108	2		

- Molecule 36 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B2	1861	Total	C	N	O	P	0	0
			38377	17073	6745	12699	1860		

- Molecule 37 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 38 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Cz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 39 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Cq	280	Total	C	N	O	S	0	0
			2138	1367	366	395	10		

- Molecule 40 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	CK	163	Total	C	N	O	S	0	0
			1238	773	230	230	5		

- Molecule 41 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CO	202	Total	C	N	O	S	0	0
			1655	1066	322	262	5		

- Molecule 42 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	CL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 43 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CV	133	Total	C	N	O	S	0	0
			989	623	186	175	5		

- Molecule 44 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CM	139	Total	C	N	O	S	0	0
			1139	730	218	183	8		

- Molecule 45 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ca	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 46 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 47 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 48 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CD	289	Total	C	N	O	S	0	0
			2353	1483	429	427	14		

- Molecule 49 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CQ	188	Total	C	N	O	S	0	0
			1521	949	315	251	6		

- Molecule 50 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CR	189	Total	C	N	O	S	0	0
			1580	979	338	253	10		

- Molecule 51 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CA	255	Total	C	N	O	S	0	0
			1957	1225	399	327	6		

- Molecule 52 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 53 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 54 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CP	152	Total	C	N	O	S	0	0
			1233	771	240	213	9		

- Molecule 55 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CU	112	Total	C	N	O	S	0	0
			921	583	159	177	2		

- Molecule 56 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CX	121	Total	C	N	O	S	0	0
			994	636	187	170	1		

- Molecule 57 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	CY	133	Total	C	N	O	S	0	0
			1107	695	225	185	2		

- Molecule 58 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 59 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 60 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Cr	137	Total	C	N	O	S	0	0
			1104	682	231	185	6		

- Molecule 61 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Ch	123	Total	C	N	O	S	0	0
			1023	646	206	169	2		

- Molecule 62 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Cb	78	Total	C	N	O	S	0	0
			635	395	135	102	3		

- Molecule 63 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CB	397	Total	C	N	O	S	0	0
			3202	2039	602	547	14		

- Molecule 64 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	CF	229	Total	C	N	O	S	0	0
			1910	1226	370	305	9		

- Molecule 65 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Cc	100	Total	C	N	O	S	0	0
			776	492	136	141	7		

- Molecule 66 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cd	113	Total	C	N	O	S	0	0
			931	586	181	162	2		

- Molecule 67 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ce	133	Total	C	N	O	S	0	0
			1096	691	224	175	6		

- Molecule 68 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Cf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 69 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Cg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Ci	103	Total	C	N	O	S	0	0
			840	526	178	130	6		

- Molecule 71 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Cj	90	Total	C	N	O	S	0	0
			733	451	162	115	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Ck	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Cl	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 74 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	CC	368	Total	C	N	O	S	0	0
			2925	1840	583	489	13		

- Molecule 75 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Cm	52	Total	C	N	O	S	0	0
			429	266	90	67	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
			240	145	64	28	3		

- Molecule 77 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cp	90	Total	C	N	O	S	0	0
			703	442	135	119	7		

- Molecule 78 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Co	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 79 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CJ	168	Total	C	N	O	S	0	0
			1349	853	251	239	6		

- Molecule 80 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CH	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 81 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CE	262	Total	C	N	O	S	0	0
			2113	1357	403	349	4		

- Molecule 82 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CG	246	Total	C	N	O	S	0	0
			1973	1256	379	334	4		

- Molecule 83 is a protein called 60S acidic ribosomal protein P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cs	57	Total	C	N	O	S	0	0
			426	277	68	79	2		
83	Ct	57	Total	C	N	O	S	0	0
			426	277	68	79	2		

- Molecule 84 is a protein called 60S acidic ribosomal protein P2.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Cu	56	Total	C	N	O	S	0	0
			419	261	71	86	1		
84	Cv	56	Total	C	N	O	S	0	0
			419	261	71	86	1		

- Molecule 85 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	A5	4298	Total	C	N	O	P	0	0
			84946	37522	14767	28360	4297		

- Molecule 86 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	A7	121	Total	C	N	O	P	0	0
			2578	1150	458	850	120		

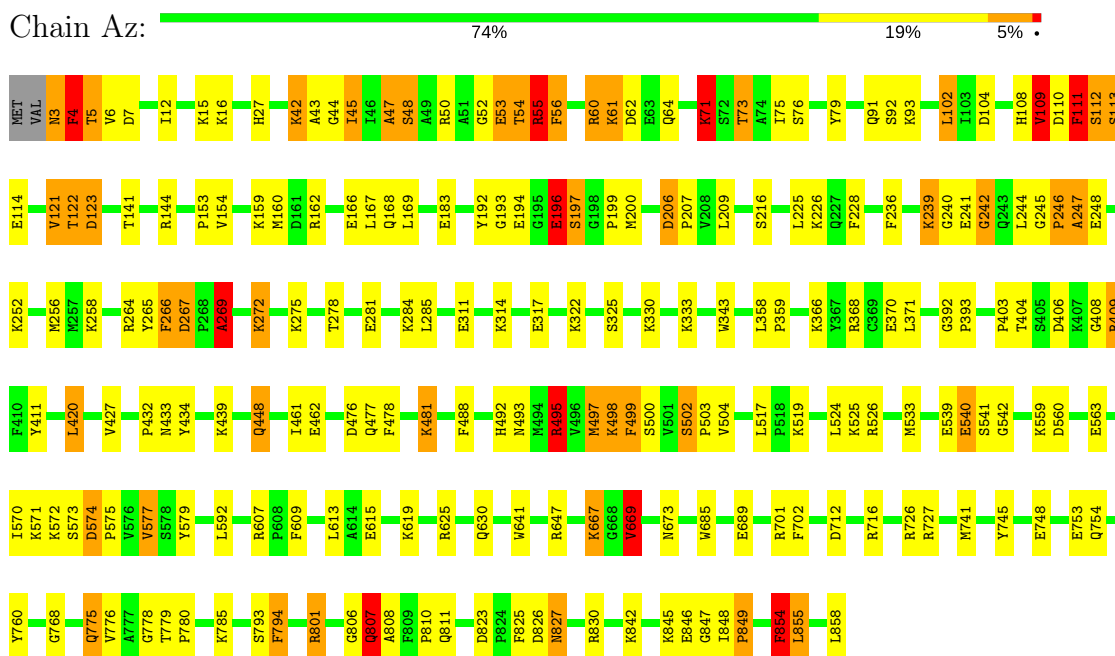
- Molecule 87 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	A8	157	Total	C	N	O	P	0	0
			3334	1489	587	1102	156		

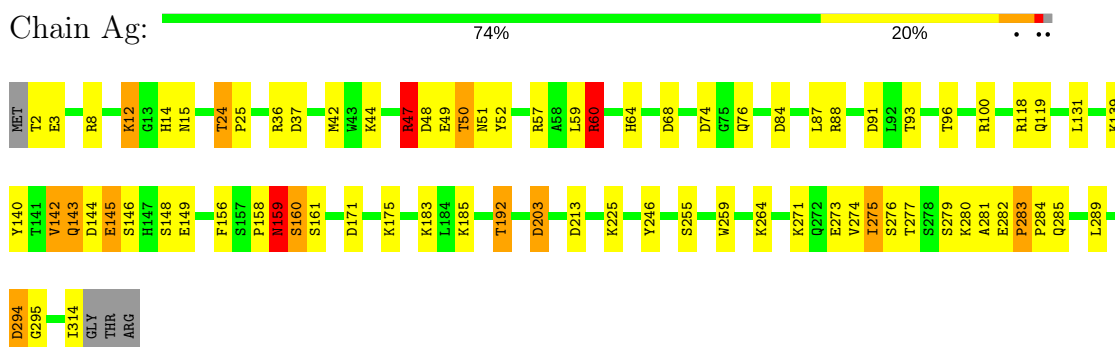
3 Residue-property plots

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: Elongation factor 2



• Molecule 2: Guanine nucleotide-binding protein subunit beta-2-like 1

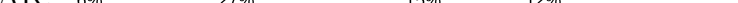


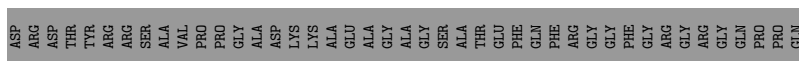
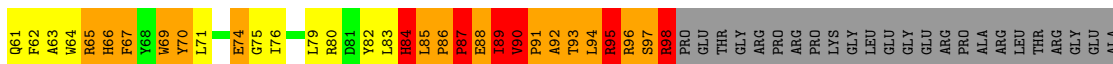
• Molecule 3: 40S ribosomal protein S20





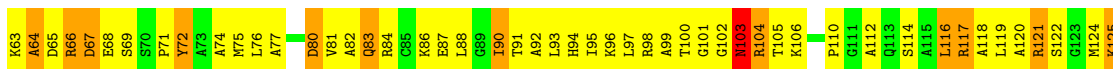
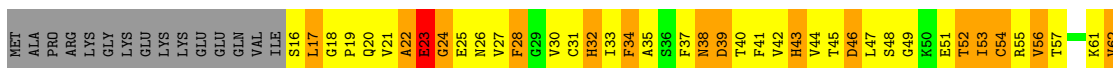
- Molecule 4: 40S ribosomal protein S10

Chain AK: 

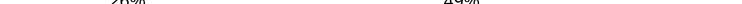


- Molecule 5: 40S ribosomal protein S14

Chain AO:



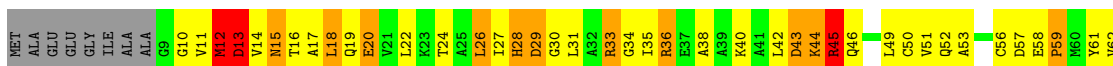
- Molecule 6: 40S ribosomal protein S23

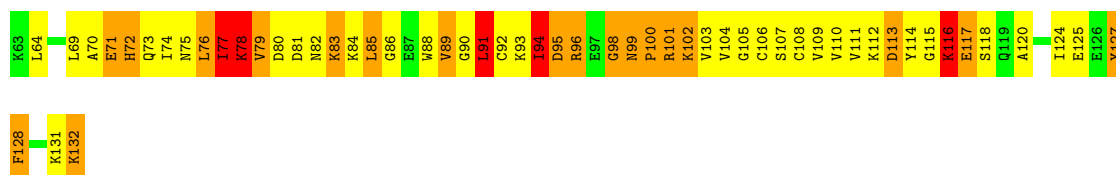
Chain AX: 



- Molecule 7: 40S ribosomal protein S12

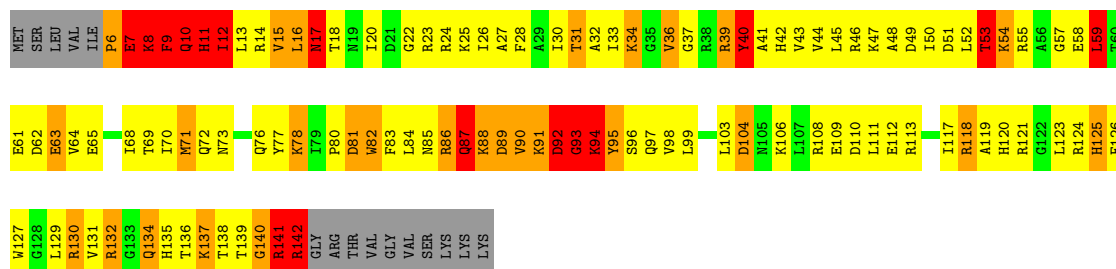
Chain AM:





• Molecule 8: 40S ribosomal protein S18

Chain AS: 15% 47% 18% 11% 10%



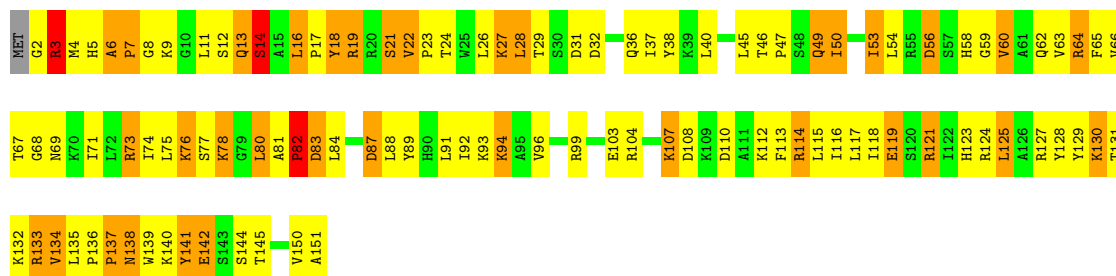
• Molecule 9: 40S ribosomal protein S29

Chain Ad: 66% 27% 5%



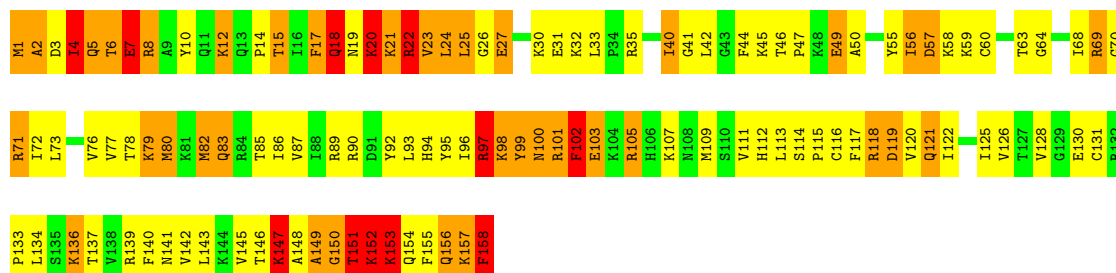
• Molecule 10: 40S ribosomal protein S13

Chain AN: 28% 46% 23%



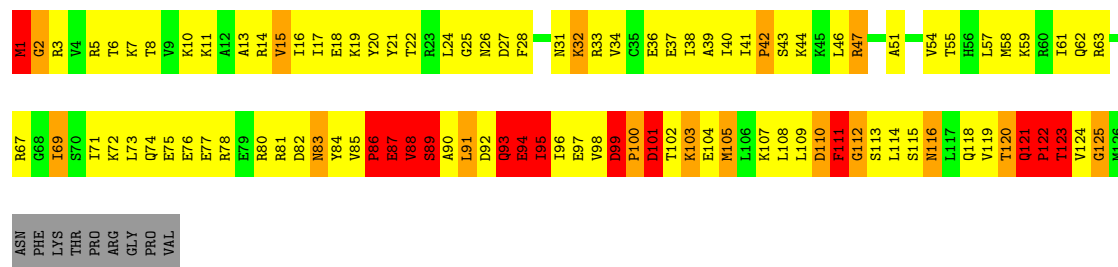
• Molecule 11: 40S ribosomal protein S11

Chain AL: 25% 44% 23% 8%



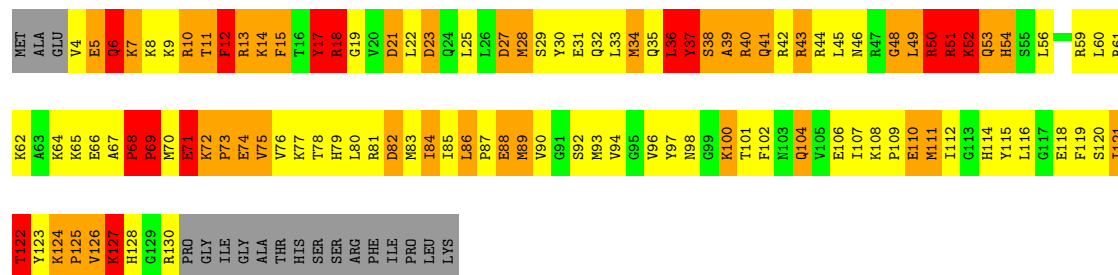
- Molecule 12: 40S ribosomal protein S17

Chain AR:



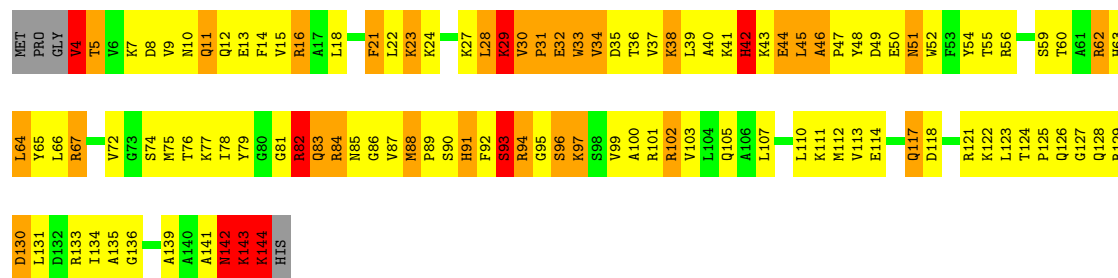
- Molecule 13: 40S ribosomal protein S15

Chain AP: 

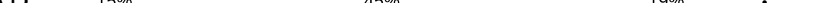


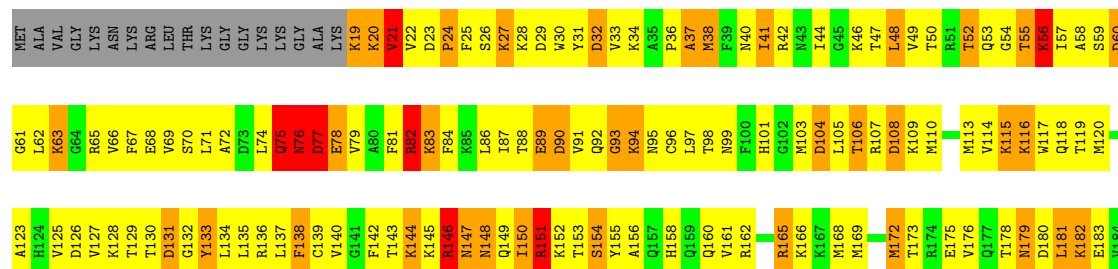
- Molecule 14: 40S ribosomal protein S19

Chain AT:  20% 52% 20% 6% .



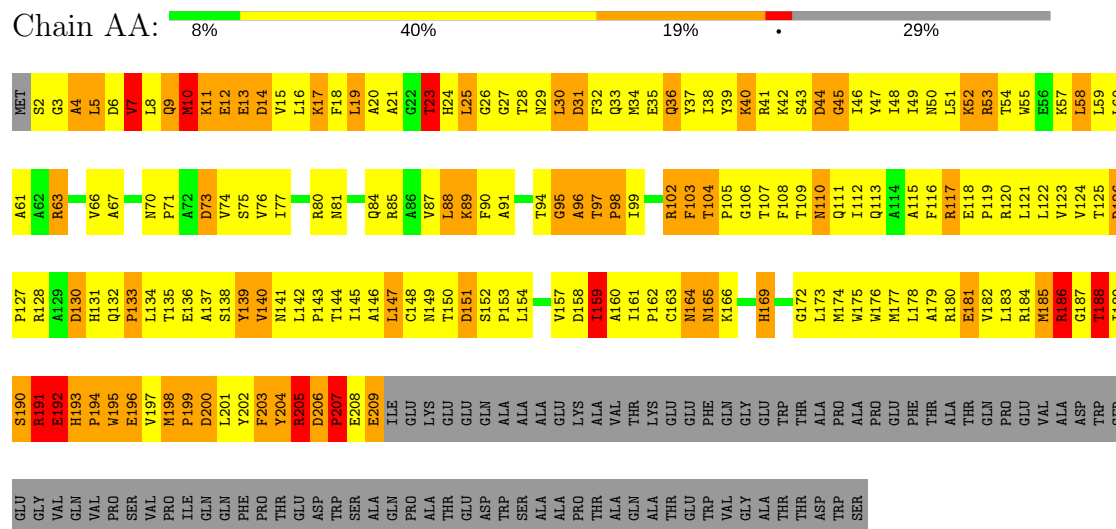
- Molecule 15: 40S ribosomal protein S3a

Chain AB: 

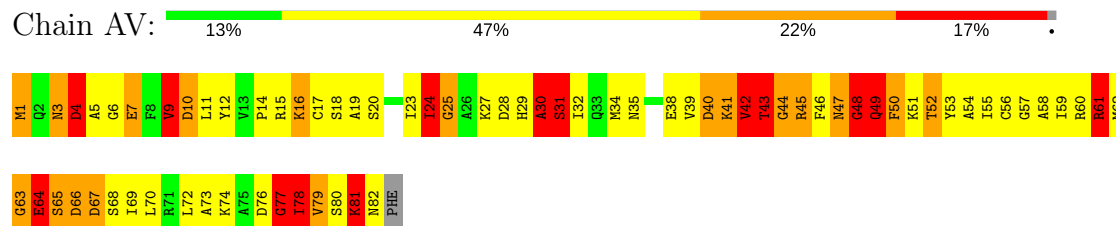




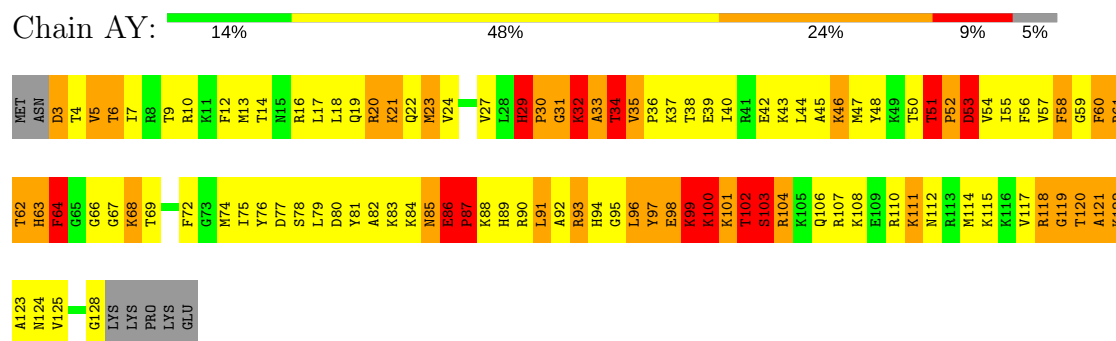
• Molecule 16: 40S ribosomal protein SA



• Molecule 17: 40S ribosomal protein S21

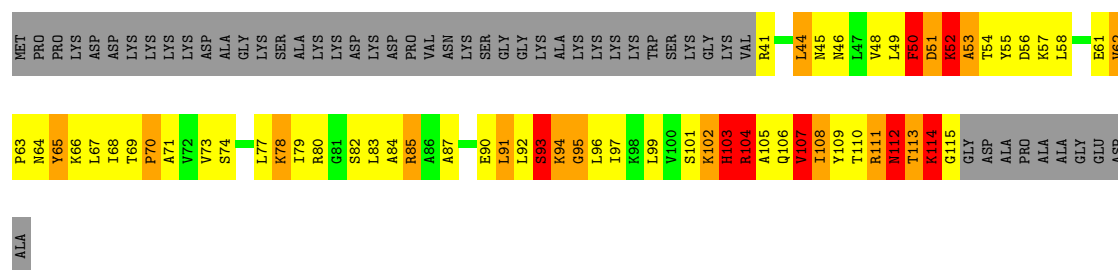


• Molecule 18: 40S ribosomal protein S24

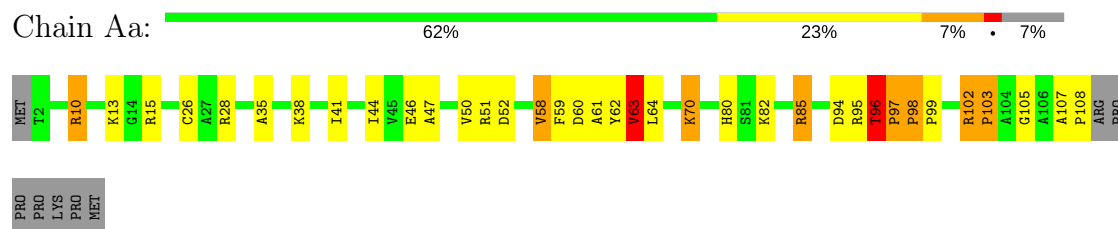


• Molecule 19: 40S ribosomal protein S25

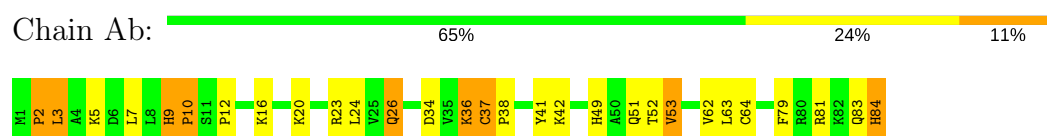




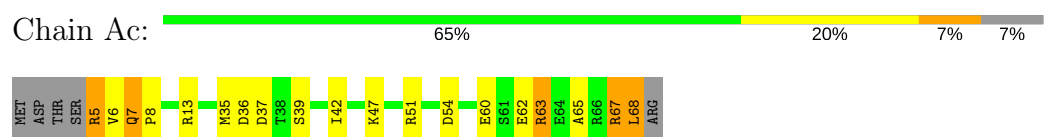
- Molecule 20: 40S ribosomal protein S26



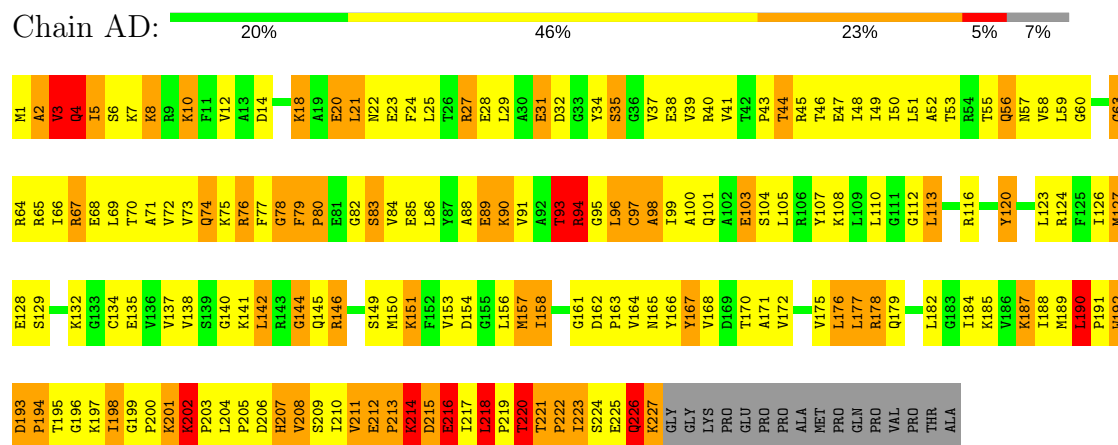
- Molecule 21: 40S ribosomal protein S27



- Molecule 22: 40S ribosomal protein S28

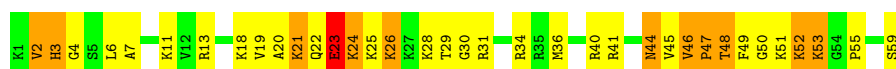


- Molecule 23: 40S ribosomal protein S3



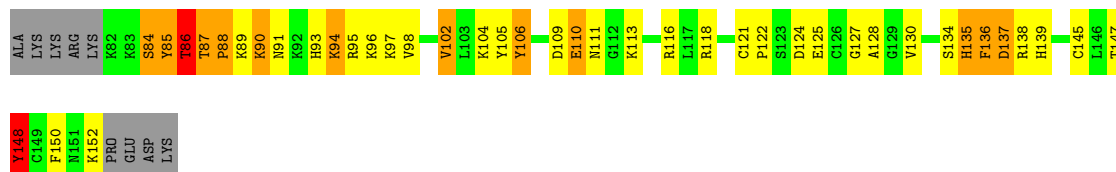
- Molecule 24: 40S ribosomal protein S30





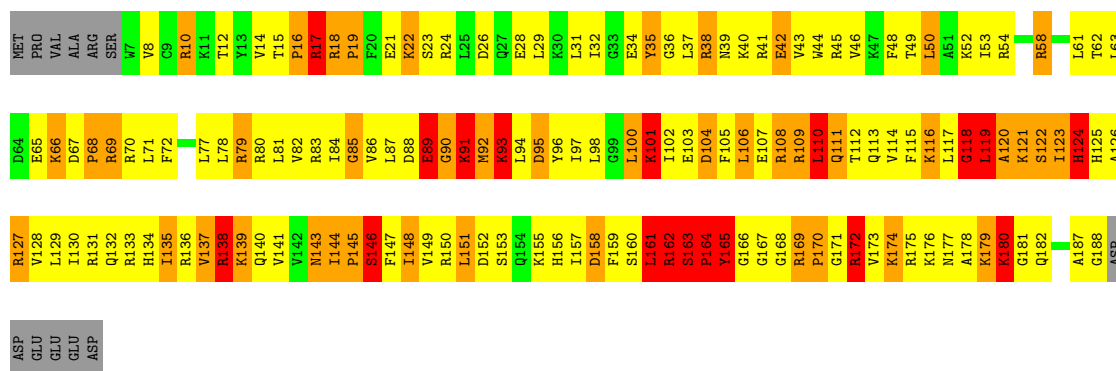
• Molecule 25: 40S ribosomal protein S27a

Chain Af: 36% 35% 15% 11%



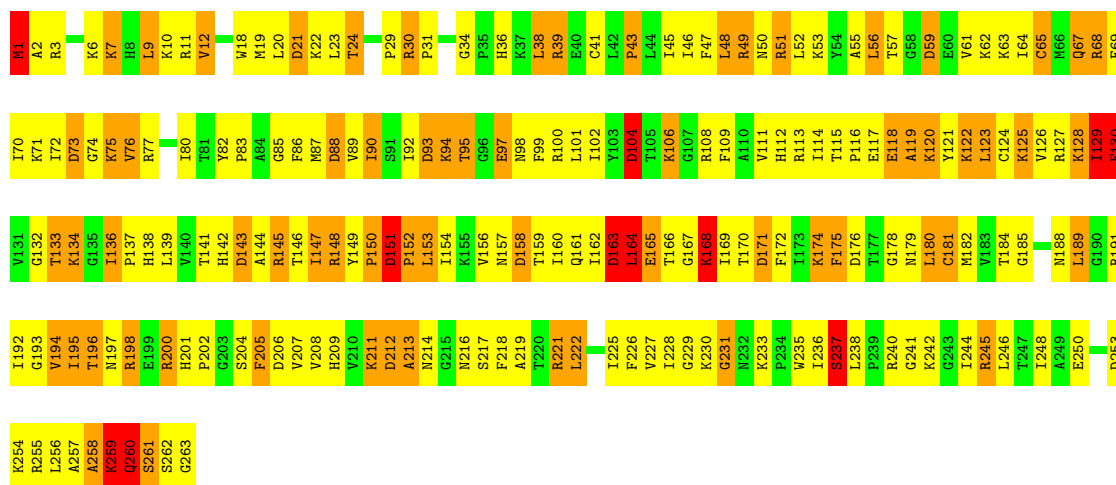
• Molecule 26: 40S ribosomal protein S9

Chain AJ: 14% 48% 22% 9% 6%



• Molecule 27: 40S ribosomal protein S4, X isoform

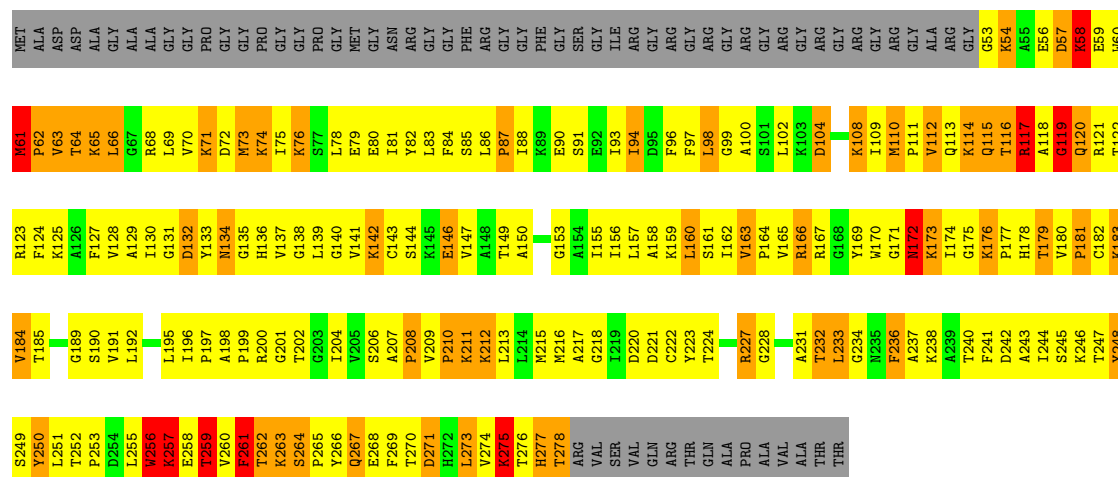
Chain AE: 22% 48% 25%



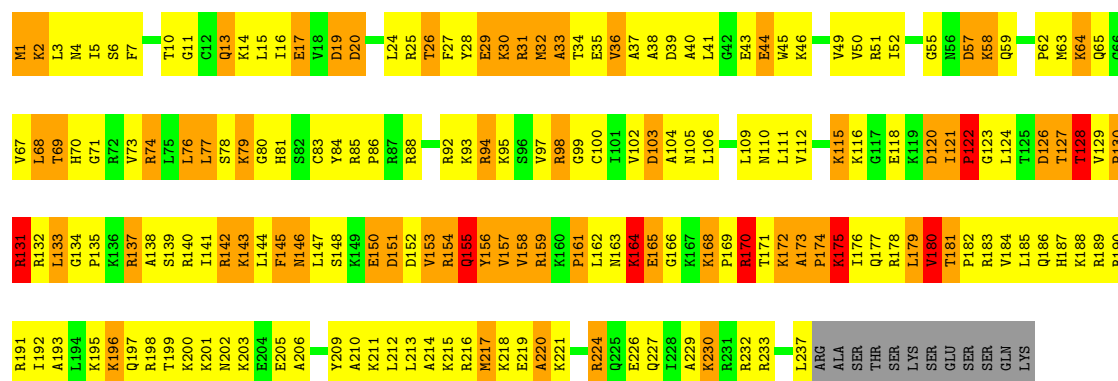
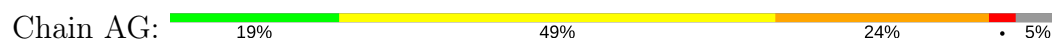
• Molecule 28: 40S ribosomal protein S2

Chain AC: 12% 44% 18% 23%

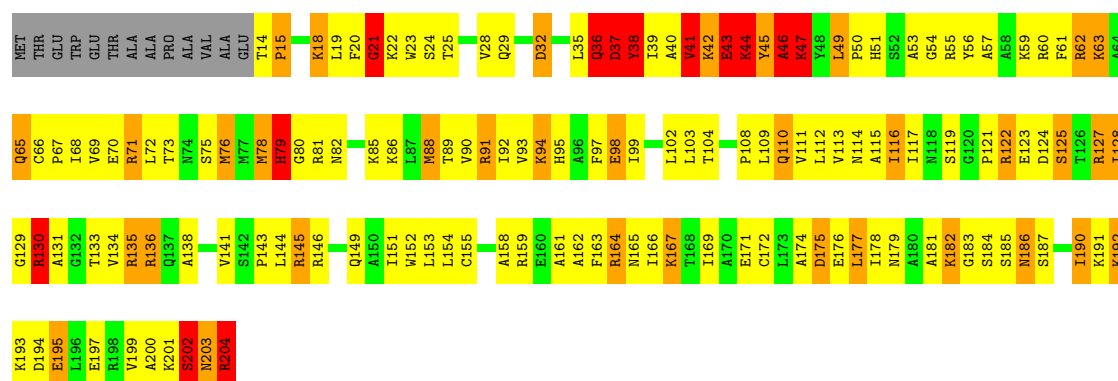




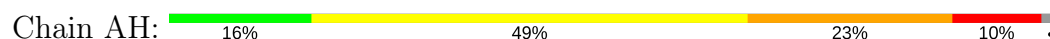
- Molecule 29: 40S ribosomal protein S6

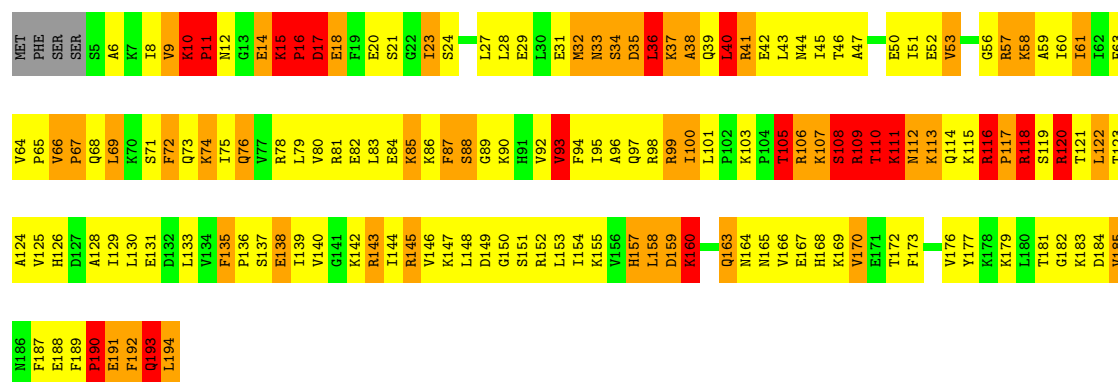


- Molecule 30: 40S ribosomal protein S5



- Molecule 31: 40S ribosomal protein S7





Chain Ah:



GLY	GLY	ILE	SER	D183	GLY	THR	MET
ARG	ARG	ARG	TYR	G184	LYS	ASN	PRO
GLY	GLY	PRO	TYR	L186	ILE	ASP	HIS
GLY	GLY	ASN	SER	S187	ASP	ALA	LEU
ARG	GLY	GLY	ASP	R188	ARG	ALA	GLN
GLY	GLY		LEU		ARG	GLY	GLY
ALA	GLY	ALA	ASP		PRO	LYS	GLY
ARG	ARG	GLN	ASN	PHE	ARG	GLN	PHE
GLY	GLY	GLY	SER	ASP	PRO	LYS	CYS
GLY	GLY	TRP	VAL	ASP	ARG	VAL	VAL
ARG	ARG	LYS	THR	ARG	PRO	GLY	THR
GLY	ARG	LYS	GLY	HIS	GLY	SER	ASN
PRO	PRO	GLY	GLY	SER	GLY	GLN	THR
ASN	ASN	PHE	THR	GLY	ARG	ARG	ARG
VAL	VAL	VAL	PRO	SER	ARG	ASP	PHE
GLY	GLY	HIS	GLY	ASP	PHE	ARG	ASP
SER	SER	GLY	GLY	ARG	E199	LYS	GLN
ARG	ARG	LYS	GLY	SER	K140	ASN	LEU
THR	THR	SER	GLY	SER	P141	PRO	PHE
ASP	ASP	HIS	HIS	PHE	L142	LEU	ASP
LYS	LYS	SER	PRO	SER	E143	PRO	ASP
SER	SER	GLY	VAL	HIS	E144	PRO	GLY
SER	SER	GLY	PRO	TYR	K145	SER	SER
ALA	ALA	ALA	ALA	GLY	E146	VAL	ASP
ALA	ALA	HIS	ASP	GLY	G148	VAL	PHE
GLY	GLY	GLY	GLY	LYS	G149	VAL	GLY
PRO	PRO	GLY	GLY	LYS	E150	ASP	VAL
ASP	ASP	ASP	ASN	HIS	E150	ASP	VAL
VAL	VAL	SER	GLY	GLY	P151	LYS	LEU
ASP	ASP	GLY	GLY	ASP	S152	LYS	LYS
ASP	ASP	MET	ASN	LYS	V153	GLY	ALA
PRO	PRO	ASP	GLY	ARG	D154	GLY	ALA
GLY	GLY	HIS	VAL	GLY	R155	THR	GLY
ALA	ALA	HIS	GLY	GLY	P156	GLN	ASN
PHE	PHE	PHE	GLY	GLY	I157	PRO	LYS
PRO	PRO	ARG	VAL	GLY		PRO	LYS
ALA	ALA	LYS	K281	SER	R160	VAL	LYS
LEU	LEU	PRO	E282	HIS	P161	ALA	LYS
ALA	ALA	ASN	E283	ASN	I162	LEU	ALA
		ASN	G284	TRP		LYS	GLY
		ASP	P285	GLY	R165	LYS	GLY
		ILE	K286	THR	G167	GLY	GLY
		THR		VAL	L168	ILE	VAL
		SER		ASP	G169	ARG	GLY
		GLN	D291	GLY	R170	ARG	GLY
		LEU	K294	LEU	G171	VAL	PRO
		GLY	A295	LEU		GLN	ALA
		ILE	I296	THR	R172	GLY	ALA
		ASN	Q297	GLY	G173	ARG	ALA
		PHE	N298	SER	G174	ARG	LYS
		GLY	K299	PRO	R175	PRO	SER
		ASP	D300	LYS	G176	ASP	SER
		LEU		TYR	R177	GLN	ALA
		GLY	K303	ILE	G178	GLN	ALA
		ARG	VAL	GLN	M179	LEU	ALA
		PRO	GLY	LYS	G180	GLN	ALA
		GLY	PHE	GLY	R181	GLY	ALA

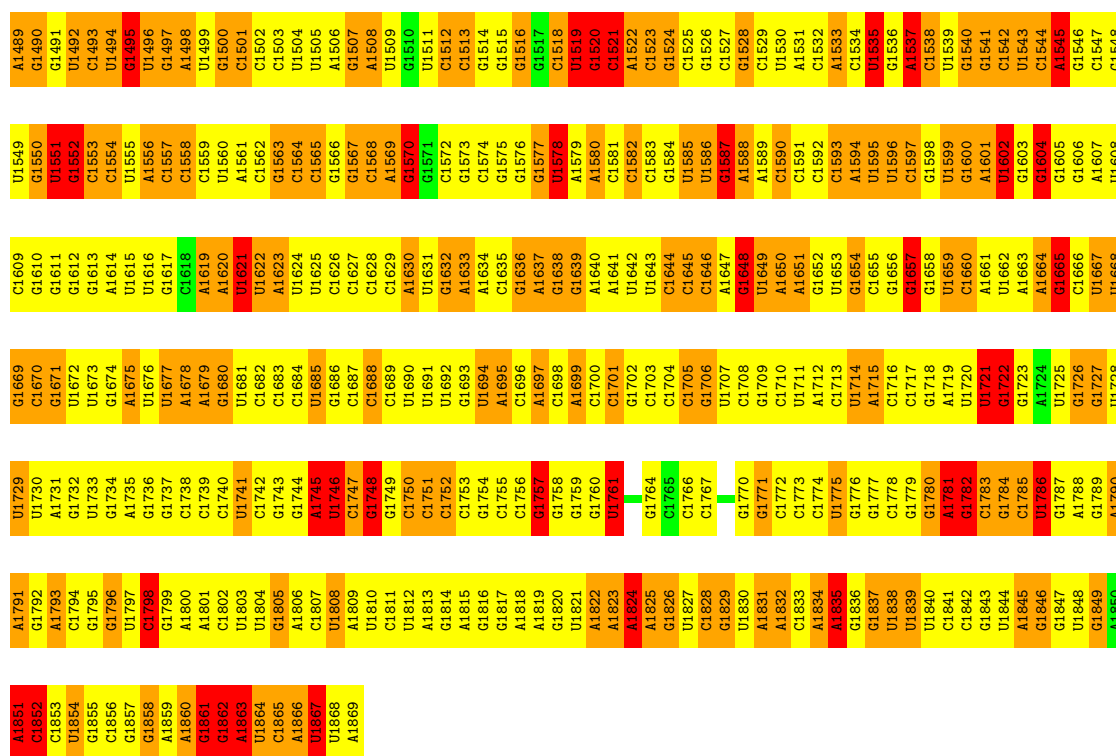
- Molecule 36: 18S ribosomal RNA

Chain B2:



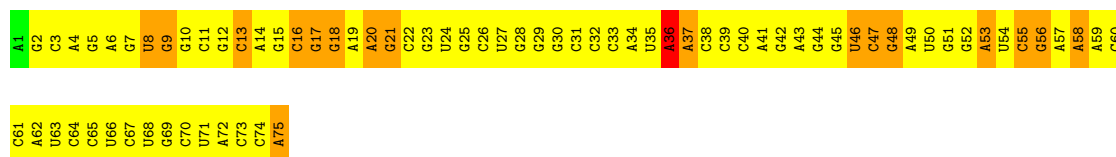
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G444	U384	C324	G184	G122	G62	A2
A445	G385	C325	G185	G123	U63	C3
G446	C386	C246	G186	U124	A64	C4
A447	G387	G327	G187	C125	G65	U5
A448	U388	U328	C188	G126	G66	G6
A449	A389	G329	U189	C127	G67	G7
G450	C390	G330	G190	C131	A68	U8
A451	C391	C331	A191	U132	G69	U9
G452	A392	G332	C192	G133	G70	G10
A453	G393	C333	C193	C134	G71	A11
U454	G394	C334	C194	G135	G72	U12
A455	G395	G335	C195	U136	G73	C13
G456	U396	A336	C196	C136	G74	C14
C457	G397	G337	U197	U137	G75	U15
A458	A398	G338	U198	C138	G76	G16
G459	C399	A339	C199	C139	A77	C17
A460	C400	C340	G200	C140	G78	C18
U461	A401	C341	C201	C141	A79	A19
G462	C402	A342	G202	C142	G80	G20
A463	G403	A343	G203	U143	U81	U21
A464	U404	U344	G204	U144	G82	A22
A465	G405	U345	G205	G145	A83	G23
G466	U406	C346	G206	G146	A84	C24
A467	G407	G347	G207	A147	A85	A25
A468	A408	A348	G208	U148	C86	U26
A469	C409	A349	A209	A149	U87	A27
G470	C410	C350	U210	A150	G88	U28
A471	G411	G351	G211	C151	C89	G29
C472	C412	U352	C212	U152	G90	C30
A473	G413	C353	G213	G153	A91	U31
G474	A414	U354	U214	U154	A92	U32
A475	A415	G355	G215	G155	G93	G33
G476	U416	C356	C216	G156	G94	U34
C477	C417	C357	A217	U157	G95	C35
A478	A418	C358	U218	A158	C96	U36
C479	G419	U359	U219	A159	U97	C37
G480	C420	A360	U220	U160	C98	A38
A481	C421	U361	A221	U161	A99	A39
G482	U422	C362	U222	C162	U100	A40
C483	C423	A363	C223	U163	C101	G41
A484	C424	A364	A224	A164	A102	A42
U485	G425	C365	G225	G165	A103	U43
A486	A426	U366	A226	A166	U104	A44
U488	U427	U367	G307	G167	U105	A45
A489	U428	U368	G228	C168	C106	A46
C490	C429	C369	G229	U169	A107	G47
C491	C430	G370	A230	U170	G108	C48
C492	G431	A371	A231	A171	U109	C49
A493	C432	U372	A232	U172	U110	A50
C494	A433	G373	C233	A173	A111	U51
U495	G434	G374	C234	C174	U112	G52
A496	A435	U375	A235	A175	G113	C53
C497	G436	C376	A236	U176	G114	A54
G498	C437	U377	C237	G177	U115	U55
A499	U438	U378	C238	C178	U116	A56
A500	A439	C379	C239	C179	C117	U57
C501	C440	G380	G240	G180	C118	C58
C502	C441	C381	G241	A181	U119	U59

G1429	A1369	U1308	U1248	A1188	C1127	C1067	C1007	U946	A886	A826	C750	A685	G625	G565	G504
C1430	A1370	C1249	C1249	A1189	C1128	G1068	A1008	G947	U887	A827	C751	U686	G626	U566	G505
G1431	U1371	A1190	A1250	A1191	G1129	U1089	A1009	C948	U888	G828	C752	G687	U627	C567	G506
U1432	C1310	C1131	A1251	C1191	G1130	U1070	A1010	C949	U889	C829	C753	U688	G628	C568	G507
C1433	C1312	C1252	C1252	U1192	G1071	G1071	A1011	C950	U890	A830	C754	U689	A829	A569	A508
C1434	A1313	U1253	U1253	U1193	C1132	U1072	A1012	C951	G891	G831	C755	G690	U630	C570	G509
G1435	C1374	C1254	C1254	A1194	U1133	U1073	U1013	G952	U892	G832	C756	G691	U631	U571	G510
C1436	A1375	U1314	U1314	A1195	U1133	C1074	G1014	C953	U893	C833	C757	G692	C632	U572	G511
C1437	U1377	G1256	G1256	A1196	C1135	C1075	U1015	U954	G894	C834	C758	A693	C633	U573	G512
A1438	C1317	G1257	G1257	A1197	U1136	C1076	U1016	A955	G895	C835		G694	A634	A574	G513
U1439	A1378	U1198	U1198	G1137	U1137	U1077	U1017	A956	U896	G836		G695	A635	A575	
C1440	C1319	A1258	A1258	A1199	C1138	C1078	U1018	A957	U897	A837	U767	G696	G636	A576	C617
U1441	A1380	U1260	A1260	A1200	C1139	C1079	U1019	G958	U898	G838	U770	G697	U637	U577	C618
U1442	G1321	C1261	C1261	U1201	G1140	A1080	A1020	G959	U899	C839	A771	G698	C638	C578	G518
C1443	A1383	U1202	U1202	U1202	G1141	A1081	U1021	U960	C900	C840	C772	G700	C639	C579	A519
U1444	C1322	G1262	G1262	U1203	G1142	U1082	U1022	U961	G901	G841	C773	G701	A640	U580	A520
U1445	U1263	U1263	U1263	A1083	A1143	A1083	A1023	A962	G902	C842			A641	U581	A521
A1446	G1324	C1264	C1264	A1204	A1144	A1084	A1024	A963	A903	C843	U780	U706	U642	U582	A522
U1447	A1395	A1265	A1265	C1205	A1145	C1085	U1025	A964	A904	U844			A643	A583	A523
G1448	G1387	G1266	C1266	G1206	A1145	C1086	C1026	G965	C905	C845		U707	G644	A584	U524
A1449	A1388	C1267	C1267	G1207	C1147	A1087	U1027	U966	U906	G846		C708	G645	A585	U525
U1450	G1328	A1208	A1208	U1208	C1148	U1088	A1028	U967	C907	A847	C785	G709	G646	G586	A526
G1451	U1329	G1269	G1269	A1148	G1149	U1089	G1029	U968	A908	U848	C786		G647	A587	C527
U1452	C1330	U1270	U1270	G1210	A1149	G1090	A1030	U969	G909	A849	C787	C	U647	G587	A528
A1453	C1331	C1271	C1271	G1211	A1150	C1091	A1031	G970	G910	C850	C788	C	A648	G588	
C1454	U1332	G1272	G1272	G1212	G1151	C1092	C1032	G971	C911	C851	C789	C	U649	G589	A529
A1454	A1333	C1273	C1273	C1213	U1152	G1093	G1033	C972	C912	G852	C790	G	A650	A590	U530
U1455	U1334	G1274	G1274	A1214	C1153	A1094	A1034	C973	A913	C853	C791	G	U651	U591	A531
A1456	C1335	C1275	C1275	C1215	U1154	C1095	A1035	C974	U914	C854	C792	A	U652	C532	C532
U1457	U1336	A1276	A1276	C1216	U1155	C1096	A1036	G975	G915	A855	C793	G	A653	C593	A533
G1458	C1337	C1277	C1277	G1217	U1156	G1097	G1037	G976	A916	G856	C794	C	A654	A594	G534
U1459	G1338	A1278	A1278	C1218	G1157	C1098	U1038	C977	U917	U857	C795	C718	G655	U595	G535
C1460	U1339	C1279	C1279	G1219	G1158	C1099	C1039	C978	U918	A858	C796		G656	U596	A536
G1461	A1401	G1280	G1280	A1220	G1159	G1099	U1040	G979	A919	G859	C797	G721	U657	G597	C537
U1462	U1342	G1281	G1281	G1221	U1160	U1101	G1041	A980	A920	G860	U799	G722	U658	G598	U538
C1463	A1343	A1282	A1282	G1222	U1161	G1102	A1042	A981	G921	A861	U799	C723	C660	A599	C539
A1464	U1404	C1283	C1283	G1223	C1162	G1103	G1043	G982	A922	A862	U800	A724	U661	G600	U540
A1465	A1344	G1224	G1224	A1224	C1163	C1104	G1044	A983	G923	U863	A802	C726	G662	G601	U541
G1466	G1345	U1225	U1225	U1225	G1164	G1104	U1045	C984	G924	A864			C663	G602	U542
C1467	U1346	G1226	G1226	G1226	G1165	G1105	C1046	G985	G925	A865	C803	C729	C664	C603	C543
U1468	U1347	A1287	A1287	G1227	G1166	G1106	C1047	G986	A926	U866	U805	C730	U665	A604	C544
A1469	G1348	U1288	U1288	A1228	G1167	G1107	C1048	A987	C927	G867		G731	U666	A605	A545
C1470	A1410	U1289	U1289	G1229	G1168	G1108	U1049	A988	G928	G868		U732	U667	G606	G546
U1471	G1411	G1290	G1290	C1230	G1169	C1109	A1050	C989	G929	A869	A808	C733	U668	U607	G547
C1472	A1291	U1291	U1291	C1231	A1170	U1110	A1051	C990	G930	A870	A809	C734	A668	C608	C548
G1473	G1352	C1292	C1292	U1232	G1171	U1111	G1052	A991	C931	U871	A810	C735	A669	U609	C549
U1474	A1414	G1293	G1293	C1233	U1172	U1112	C1053	G992	G932	A872	A811		A670	G610	C550
G1475	C1415	C1294	C1294	A1173	A1173	U1113	G1054	A993	G933	A873	A812	C736	A671	G611	U551
A1476	U1354	G1235	G1235	U1174	G1174	U1114	U1055	C994	G934	G874	A813	G737	A672	U612	G552
U1477	G1236	G1236	G1236	U1175	G1175	U1115	A1056	C995	G935	G875	U814	C738	G673	G613	U553
C1478	C1237	C1237	C1237	G1176	G1176	C1116	U1057	G996	G936	A876	U815	C739	C574	C614	A554
U1479	U1358	U1297	U1297	U1238	U1177	C1117	C1058		G937	C877	A816	C740	U675	C615	A555
C1480	U1359	G1298	G1298	U1239	U1178	C1118	U1059	A998	C937	C878	G817	C741	C676	A616	U556
A1481	A1420	A1299	A1299	U1239	U1179	C1119	G1059	G999	A938	G879	A818	U742	G677	G617	U557
C1482	U1421	U1300	U1300	A1241	G1179	U1120	A1060	C1000	U939	C879	G819	U743	G678	C618	G558
A1483	G1362	A1301	A1301	A1241	C1180	U1121	U1061	U940	G880	U820	U819	C744	A679	A619	G559
U1484	C1363	G1302	G1302	U1242	A1181	G1121	U1062	U941	G881	G821	G821	G745	G680	G620	A560
G1485	G1364	C1303	C1303	U1243	A1182	A1122	C1063	G942	G942	U882	U822	C746	U681	C621	A561
U1486	U1244	U1244	U1244	U1244		C1123	C1064	U1003	G943	U883	U823	U747	U682	C622	G562
A1487	C1305	G1245	G1245	U1245	C1185	C1124	C1065	U1004	A944	C884	C824	C748	U683	C623	G563
C1488	U1366	U1306	U1306	A1246	U1186	C1125	U1066	G1005	A945	C885	A825	U749	G684	C624	A564



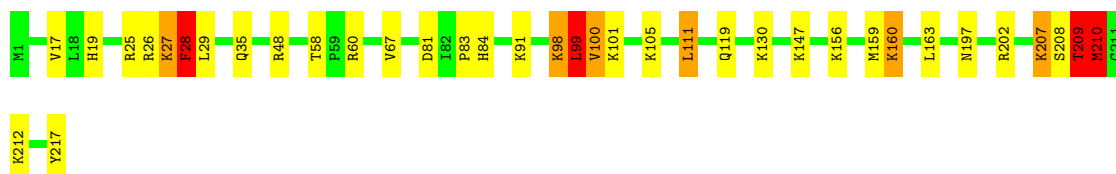
• Molecule 37: E-tRNA

Chain BC: 75% 23%



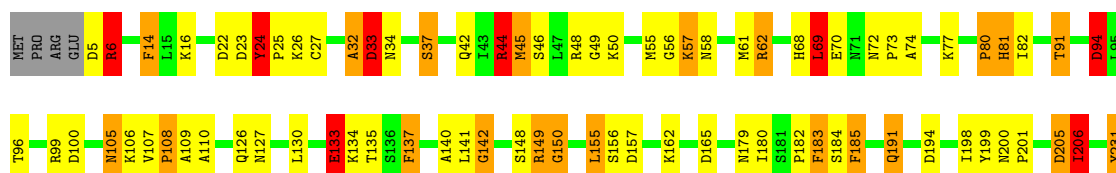
• Molecule 38: 60S ribosomal protein L10a

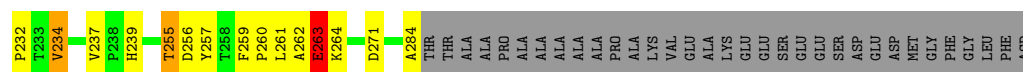
Chain Cz: 83% 12%



• Molecule 39: 60S acidic ribosomal protein P0

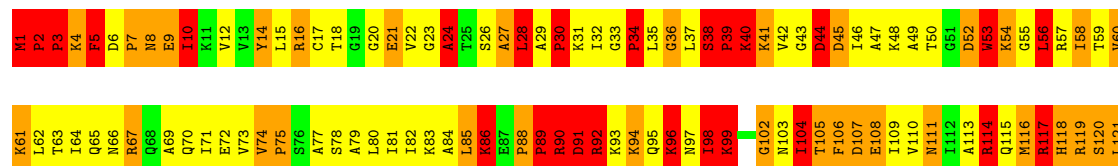
Chain Cq: 58% 20% 7% 12%





• Molecule 40: 60S ribosomal protein L12

Chain CK: 8% 44% 29% 18%



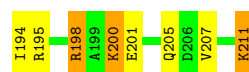
• Molecule 41: 60S ribosomal protein L13a

Chain CO: 29% 49% 21%



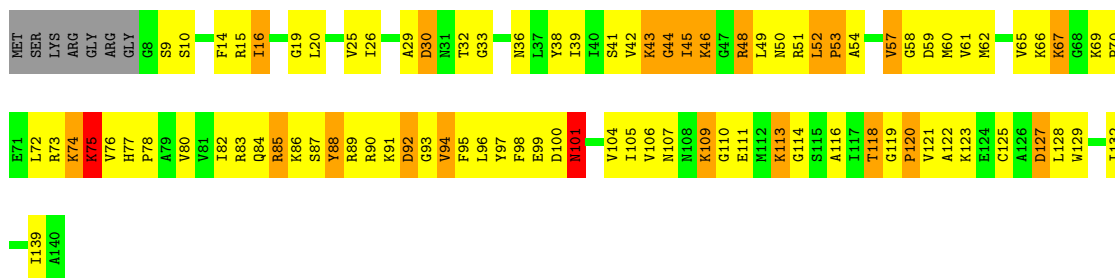
• Molecule 42: 60S ribosomal protein L13

Chain CL: 23% 45% 23% 9%

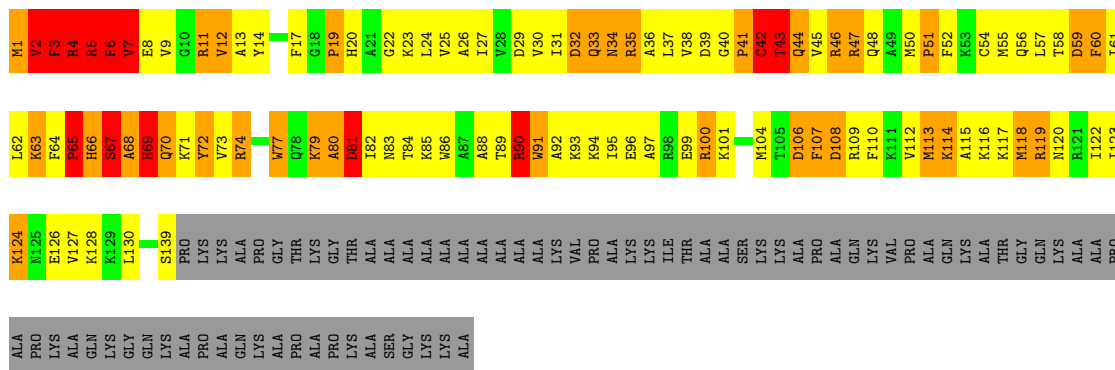


• Molecule 43: 60S ribosomal protein L23

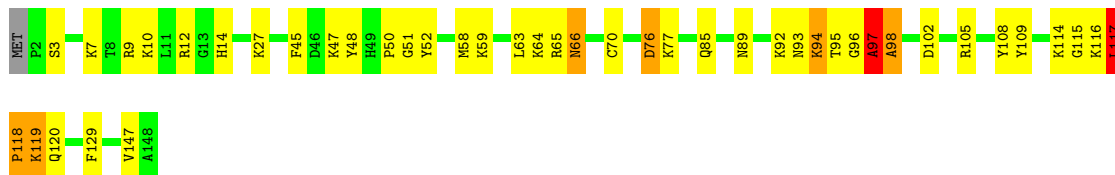
Chain CV: 31% 48% 15% 5%



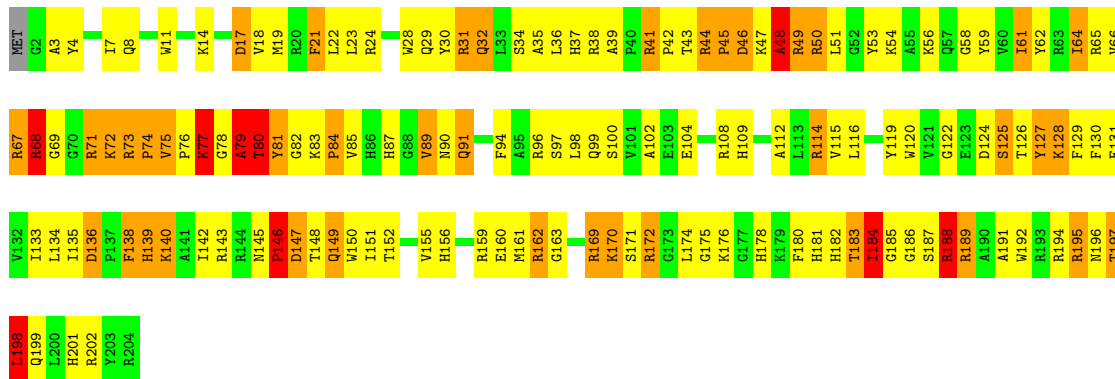
- Molecule 44: 60S ribosomal protein L14



- Molecule 45: 60S ribosomal protein L27a

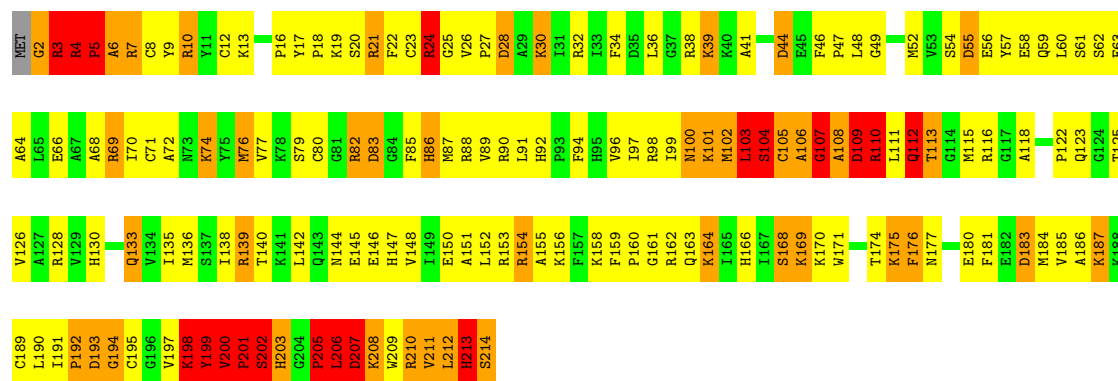


- Molecule 46: 60S ribosomal protein L15



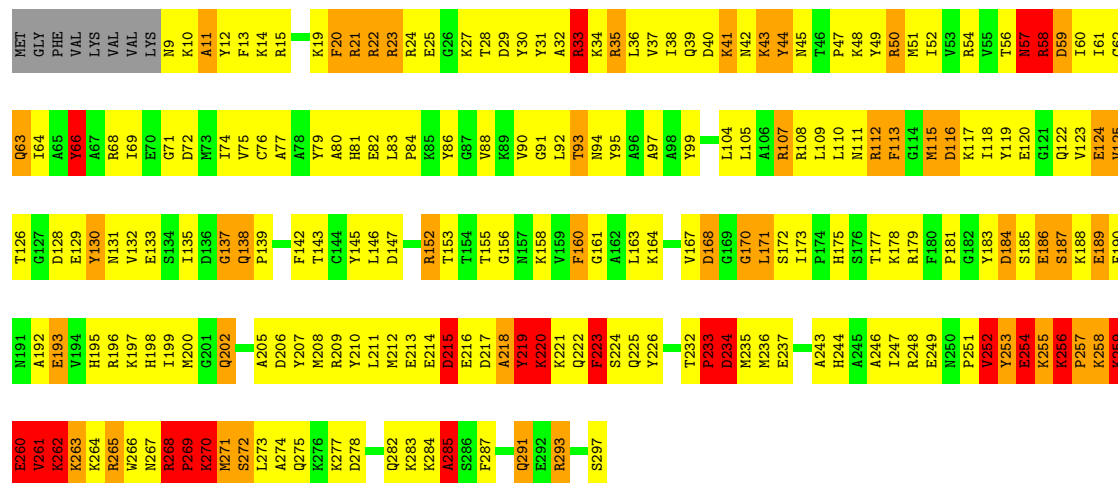
- Molecule 47: 60S ribosomal protein L10-like

Chain CI: 

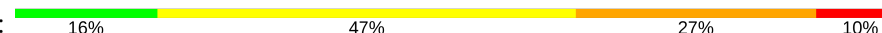


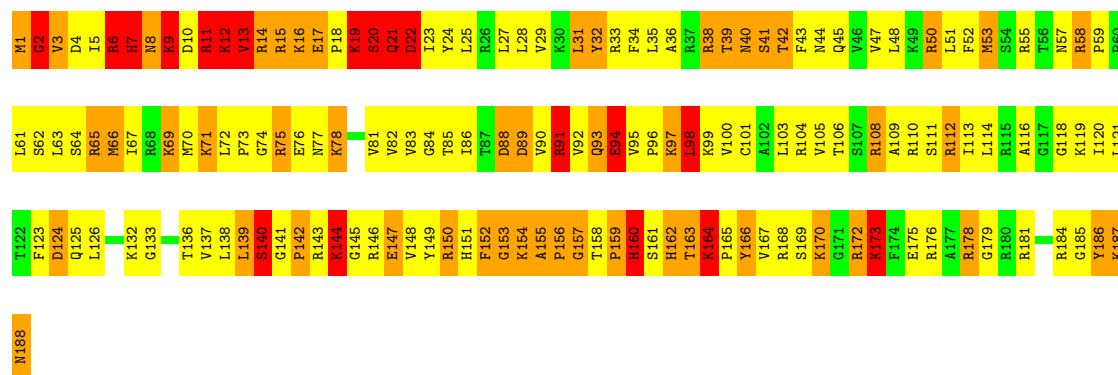
• Molecule 48: 60S ribosomal protein L5

Chain CD: 

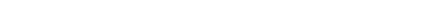


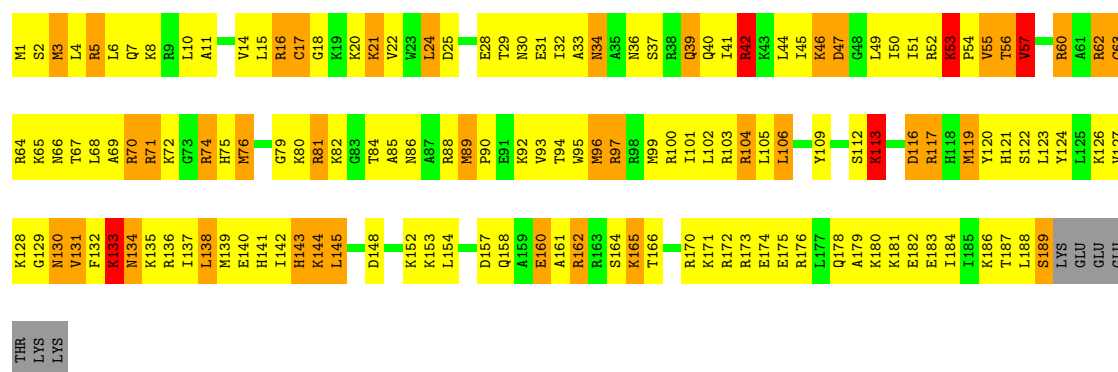
• Molecule 49: 60S ribosomal protein L18

Chain CQ: 



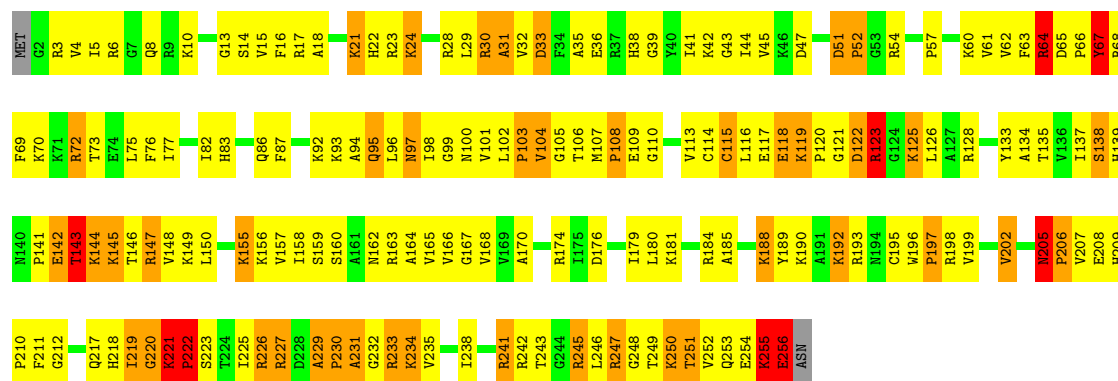
• Molecule 50: 60S ribosomal protein L19

Chain CR: 

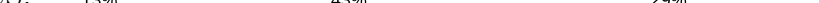


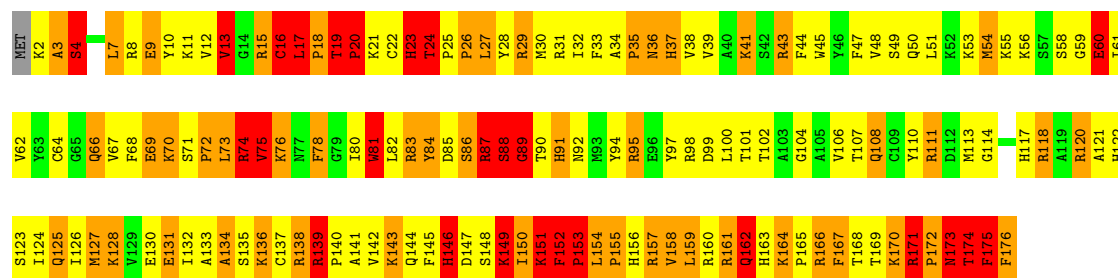
- Molecule 51: 60S ribosomal protein L8

Chain CA: 

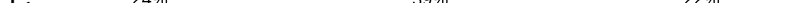


- Molecule 52: 60S ribosomal protein L18a

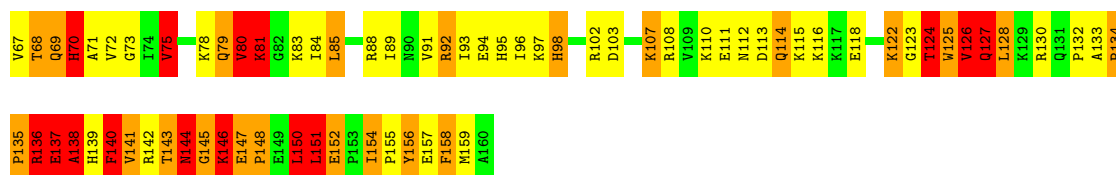
Chain CS: 



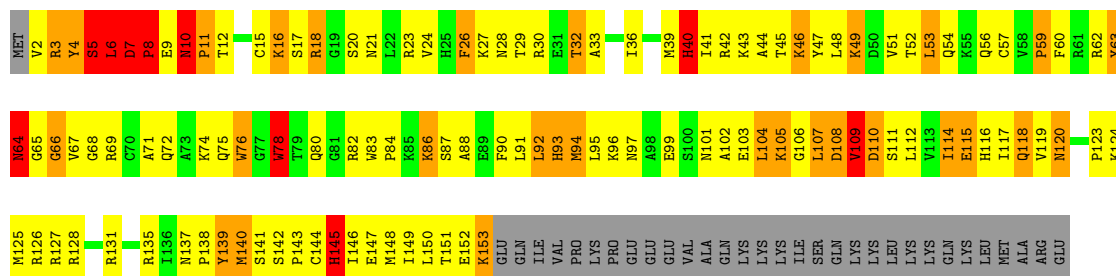
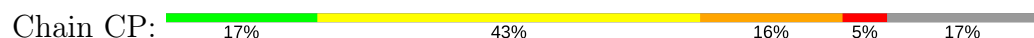
- Molecule 53: 60S ribosomal protein L21

Chain CT: 

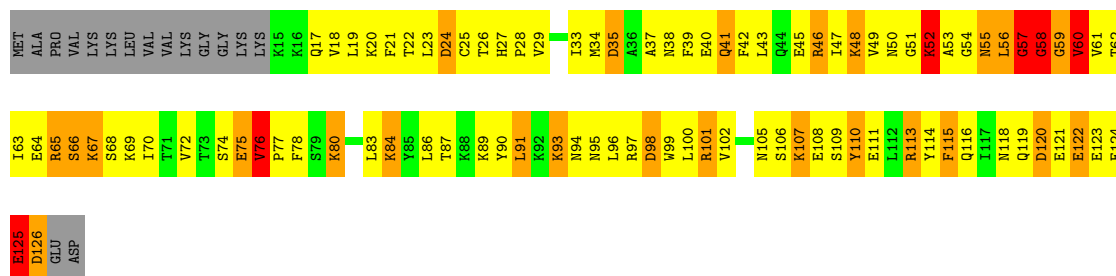
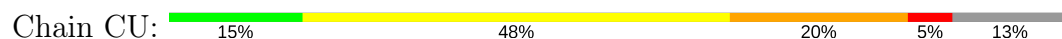




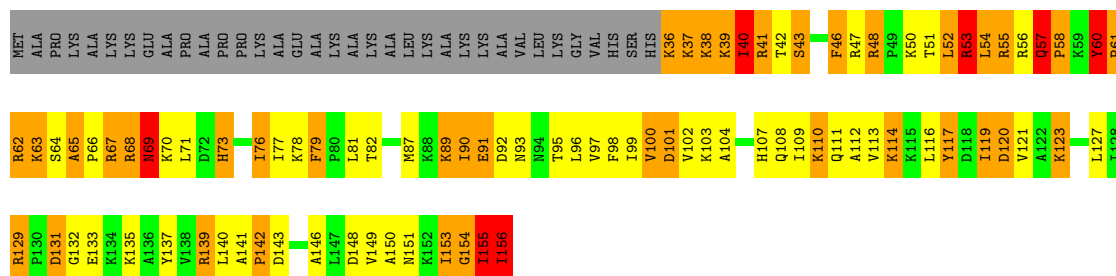
- Molecule 54: 60S ribosomal protein L17



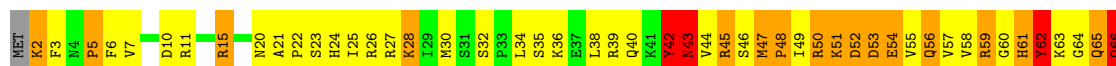
- Molecule 55: 60S ribosomal protein L22

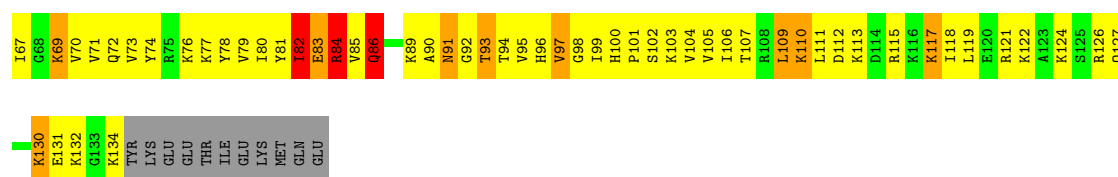


- Molecule 56: 60S ribosomal protein L23a

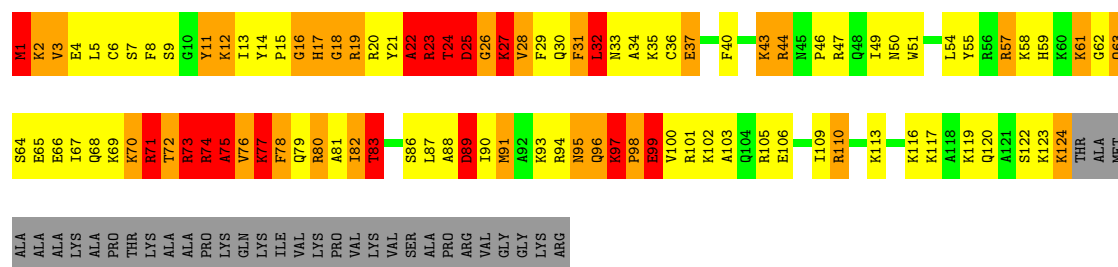


- Molecule 57: 60S ribosomal protein L26

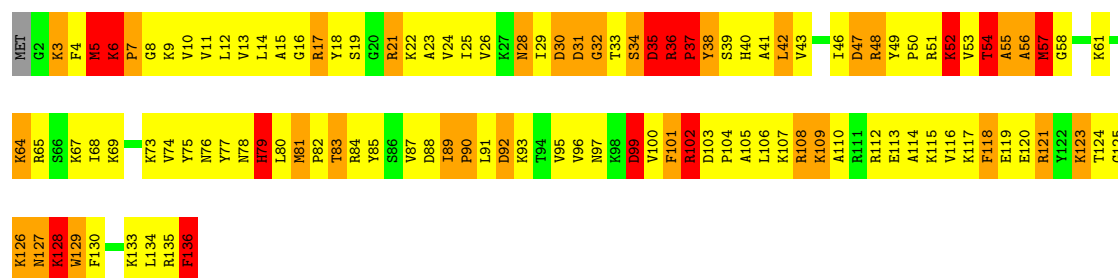
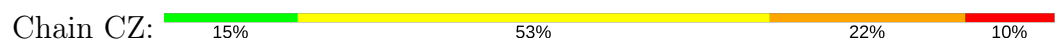




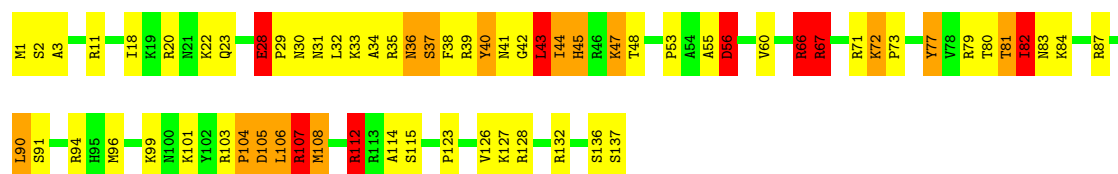
• Molecule 58: 60S ribosomal protein L24



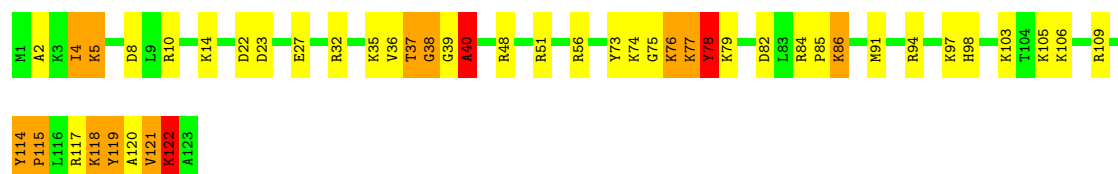
• Molecule 59: 60S ribosomal protein L27



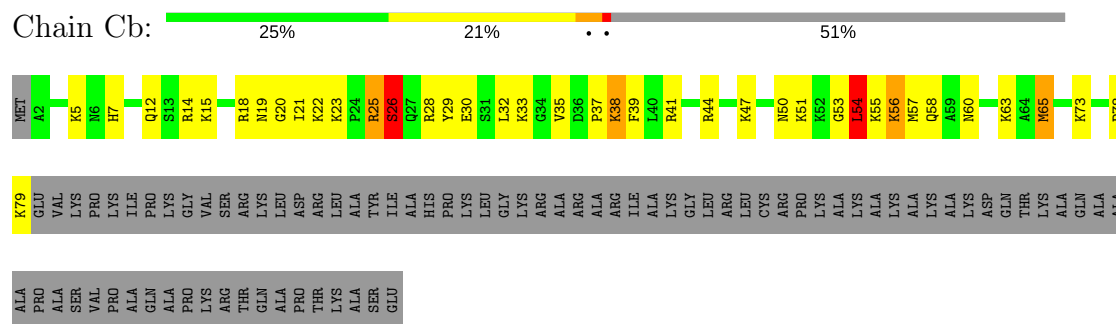
• Molecule 60: 60S ribosomal protein L28



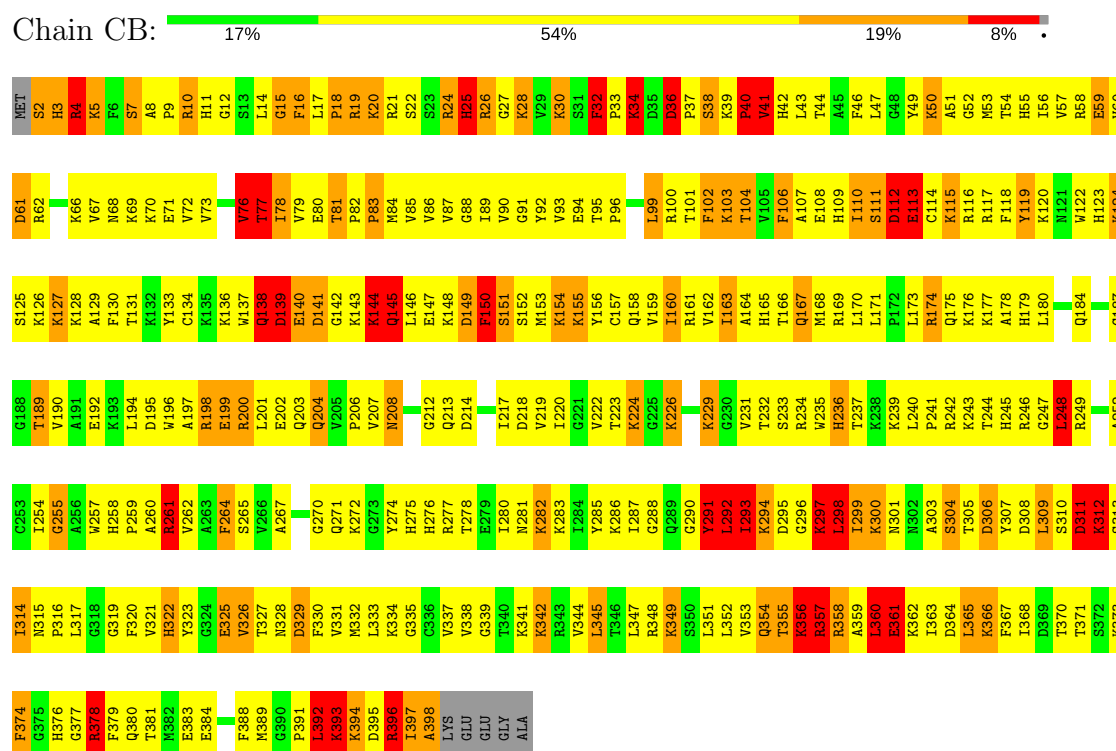
• Molecule 61: 60S ribosomal protein L35

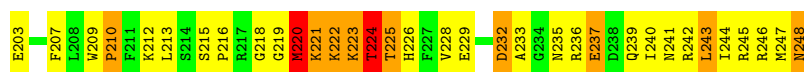


• Molecule 62: 60S ribosomal protein L29



• Molecule 63: 60S ribosomal protein L3





- Molecule 65: 60S ribosomal protein L30

Chain Cc:  70% 13% • 13%



- Molecule 66: 60S ribosomal protein L31

Chain Cd: 



- Molecule 67: 60S ribosomal protein L32

Chain Ce: 



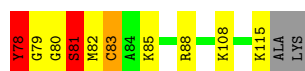
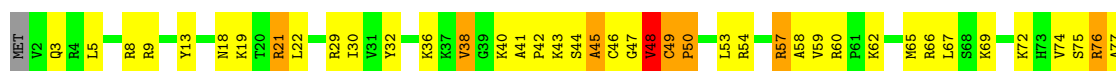
- Molecule 68: 60S ribosomal protein L35a

Chain Cf: 

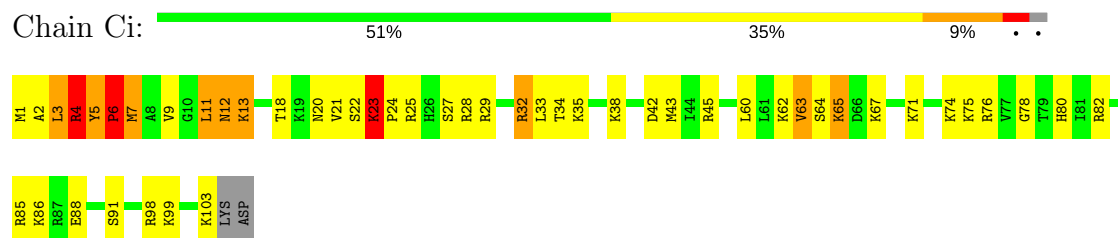


- Molecule 69: 60S ribosomal protein L34

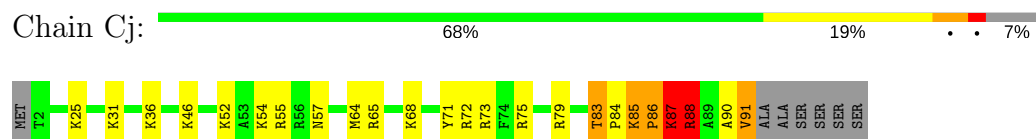
Chain Cg:  54% 34% 7% . .



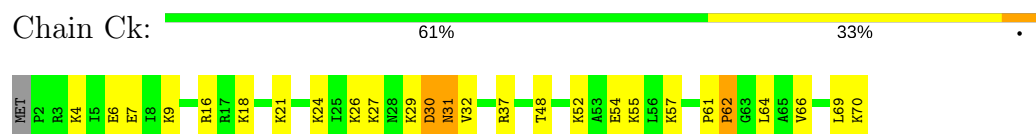
- Molecule 70: 60S ribosomal protein L36



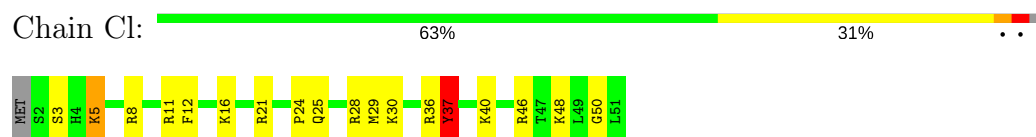
- Molecule 71: 60S ribosomal protein L37



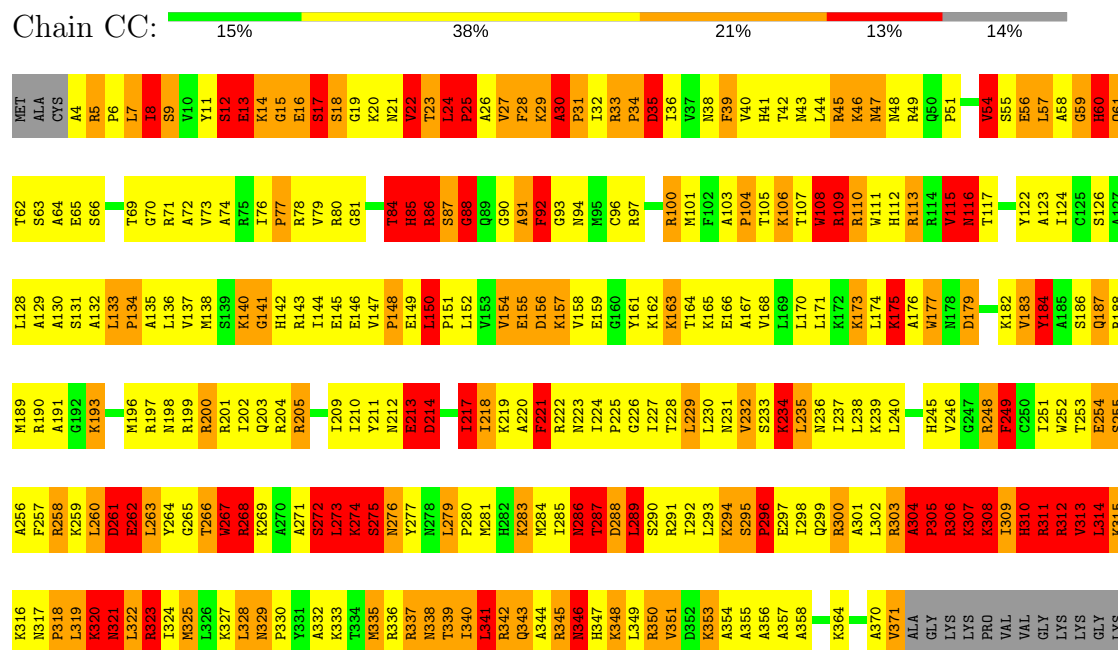
- Molecule 72: 60S ribosomal protein L38



- Molecule 73: 60S ribosomal protein L39



- Molecule 74: 60S ribosomal protein L4



LYS
ALA
ALA
VAL
GLY
VAL
LYS
LYS
GLN
LYS
LYS
PRO
LEU
VAL
GLY
LYS
LYS
ALA
ALA
ALA
THR
LYS
LYS
PRO
ALA
PRO
GLU
LYS
LYS
PRO
ALA
GLU
LYS
LYS
PRO
THR
THR
GLU
GLU
LYS
LYS
PRO
ALA
ALA

- Molecule 75: 60S ribosomal protein L40

Chain Cm:  60% 31% 8% •

I77
I78
E79
R83
Q84
L85
K88
C91
D92
K93
R97
K98
H104
P105
R106
R111
K112
K113
K114
K125
K126
V127
K128

- Molecule 76: 60S ribosomal protein L41

Chain Cn:  56% 44%

M1
W5
R6
K7
K8
R9
M10
R15
R18
K19
R20
Q22
R23
S24
K25

- Molecule 77: 60S ribosomal protein L37a

Chain Cp:  68% 27% • •

ME1
ALA
K3
R4
T5
K6
R17
Y18
K24
K25
V26
K27
K28
L29
E30
C42
K46
K47
K48
R49
R50
A51
V52
S53
I54
V55
H56
K62
S75
R84
R85
L86
K87
K90
D91
Q92

- Molecule 78: 60S ribosomal protein L36a

Chain Co:  53% 36% 8% • •

ME1
Y2
R3
K6
T7
R8
K13
K14
C15
T24
K27
K28
D31
S32
L33
T34
R40
Y41
D42
R43
K44
Q45
I55
K58
K59
A60
K61
T62
T63
K64
K65
T66
V67
E71
C72
V73
E74
P75
N76
C77
R78
R81
M82
L83
R87
S88
R89
H90
F91

E92
L93
D96
K97
K98
R99
K100
I104
Q105
F106

- Molecule 79: 60S ribosomal protein L11

Chain CJ:  30% 51% 12% • 6%

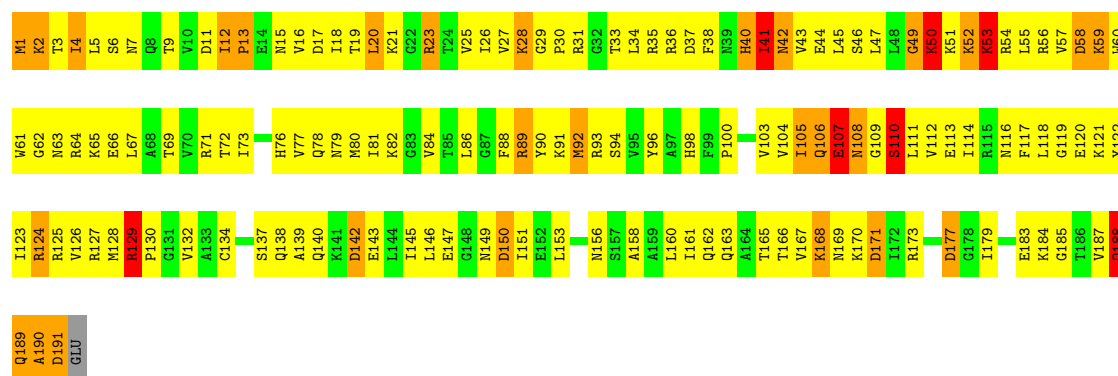
ME1
ALA
GLN
ASP
GLN
GLY
GLU
LYS
E9
P10
P11
M12
M13
R13
E14
L15
R16
I17
R18
K19
L20
C21
L22
V26
S29
G30
D31
Q32
L33
T34
R35
A36
A37
K38
Q42
L43
P48
V49
F50
A53
R54
Y55
T56
V57
R58
S59
F60
G61
I62
R63
R64
N65
I68
A69
V70

H71
C72
T73
V74
R75
A79
I82
L83
E84
K85
G86
L87
R88
W89
R90
E91
Y92
E93
L94
R95
K96
N97
R98
F99
S100
D101
M102
G103
V104
N104
F105
G106
F107
G108
D109
I109
Q110
E111
H112
I113
D114
L115
F115
G116
I117
K118
Y119
D120
T121
S122
I123
G124
I125
Y126
G127
L128
D129
F130
Y131
V132
V133

L134
G135
R136
P137
G138
F139
S140
I141
A142
K143
K144
K145
R146
R147
T148
I151
K154
H155
R156
I157
S158
K159
E160
E161
A162
M163
R164
V165
F166
Q167
Q168
K169
Y170
D171
I171
G172
I173
I174
L175
P176
GLY
LYS

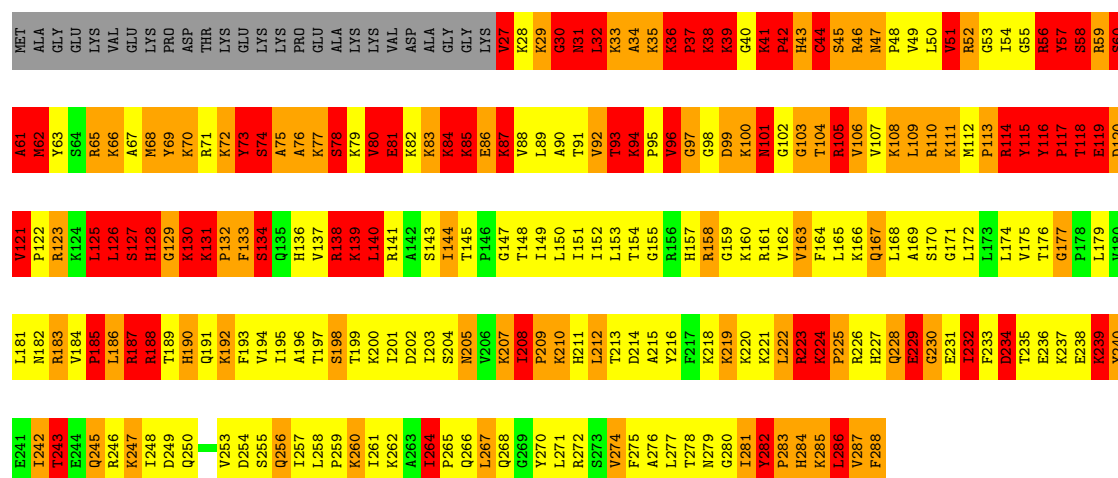
- Molecule 80: 60S ribosomal protein L9

Chain CH:  22% 59% 15% • •



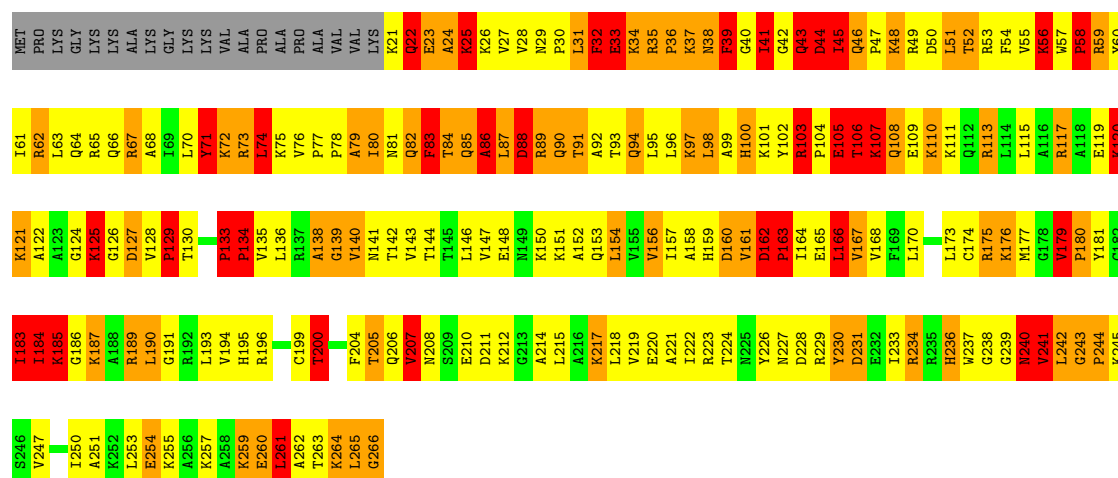
• Molecule 81: 60S ribosomal protein L6

Chain CE: 6% 38% 25% 22% 9%



• Molecule 82: 60S ribosomal protein L7a

Chain CG: 14% 41% 24% 14% 8%



• Molecule 83: 60S acidic ribosomal protein P1

Chain Cs: 

MET ALA SER MET VAL SER GLU L7 D18 D19 D26 P41 P44 V63 GLY ALA GLY GLY PRO PRO ALA ALA ALA ALA PRO ALA GLY PRO PRO PRO SER THR ALA ALA ALA PRO ALA ALA GLU GLU LYS LYS LYS VAL VAL ALA LYS LYS LYS GLU SER GLU SER ASP

ASP ASP MET GLY PHE LEU PHE ASP


• Molecule 83: 60S acidic ribosomal protein P1

Chain Ct: 

MET ALA SER MET VAL SER GLU L7 D18 D19 D26 P41 P44 V63 GLY ALA GLY GLY PRO PRO ALA ALA ALA ALA PRO ALA GLY PRO PRO PRO SER THR ALA ALA ALA PRO ALA ALA GLU GLU LYS LYS LYS VAL VAL ALA LYS LYS LYS GLU SER GLU SER ASP

ASP ASP MET GLY PHE LEU PHE ASP

• Molecule 84: 60S acidic ribosomal protein P2

Chain Cu: 

H1 S16 S17 P18 D22 D28 D35 D36 D37 S44 E45 L46 K49 D53 A56 GLN GLY ILE GLY LYS LEU ALA SER VAL PRO GLY GLY GLY VAL VAL ALA ALA ALA PRO GLY SER GLY SER ALA PRO ALA ALA GLY SER ALA ALA PRO ALA ALA GLU

LYS LYS ASP GLU LYS LYS LYS GLU GLU SER GLU GLU GLU SER ASP ASP MET GLY PHE LEU PHE ASP


• Molecule 84: 60S acidic ribosomal protein P2

Chain Cv: 

H1 R2 S16 S17 P18 D22 D28 D35 D36 D37 D53 A56 GLN GLY ILE GLY LYS LEU ALA SER VAL PRO GLY GLY GLY VAL VAL ALA ALA ALA PRO GLY SER GLY SER ALA PRO ALA ALA GLY SER ALA ALA PRO ALA ALA GLU LYS LYS ASP ASP LYS

LYS GLU SER GLU GLU GLU SER ASP ASP MET GLY PHE GLY LEU PHE ASP

• Molecule 85: 28S ribosomal RNA

Chain A5: 

G1 G2 C3 G4 A5 C6 C7 U8 C9 A10 G11 A12 G13 U13 C14 A15 G16 U17 C18 G19 U20 G21 G22 C23 G24 A25 C26 C27 C28 G29 G30 G31 U31 G32 A33 A34 U35 U36 U37 A38 A39 G40 G41 G42 U43 U44 U45 U46 G47 G48 U49 C50 A51 G52 C53 G54 G55 G56 A57 A58 G59 G60 A61 A62

G63 A64 A65 C66 U67 A68 A69 U70 C71 A72 C73 A74 G75 G76 A77 U78 C79 A80 C81 U82 C83 A84 G85 C86 U87 A88 C89 G90 C91 G92 C93 G94 A95 A96 U97 A98 A99 C100 A101 G102 A103 G104 A105 A106 C107 G108 A109 G110 C111 C112 A113 G114 C115 G116 G117 C118 G119 A120 A121 A122

C123 C124 C125 C126 G127 C128 C129 C130 C131 G132 C133 A134 G135 C136 G137 G138 G139 G140 C141 G142 C143 G144 G145 G146 A147 C148 A149 U150 G151 U152 C153 G154 G155 C156 U157 U158 A159 C160 G161 G162 A163 G164 A165 C166 C167 C168 G169 C170 U171 C172 C173 C174 C175 G176 G177 C178 G179 C180 A181 G182

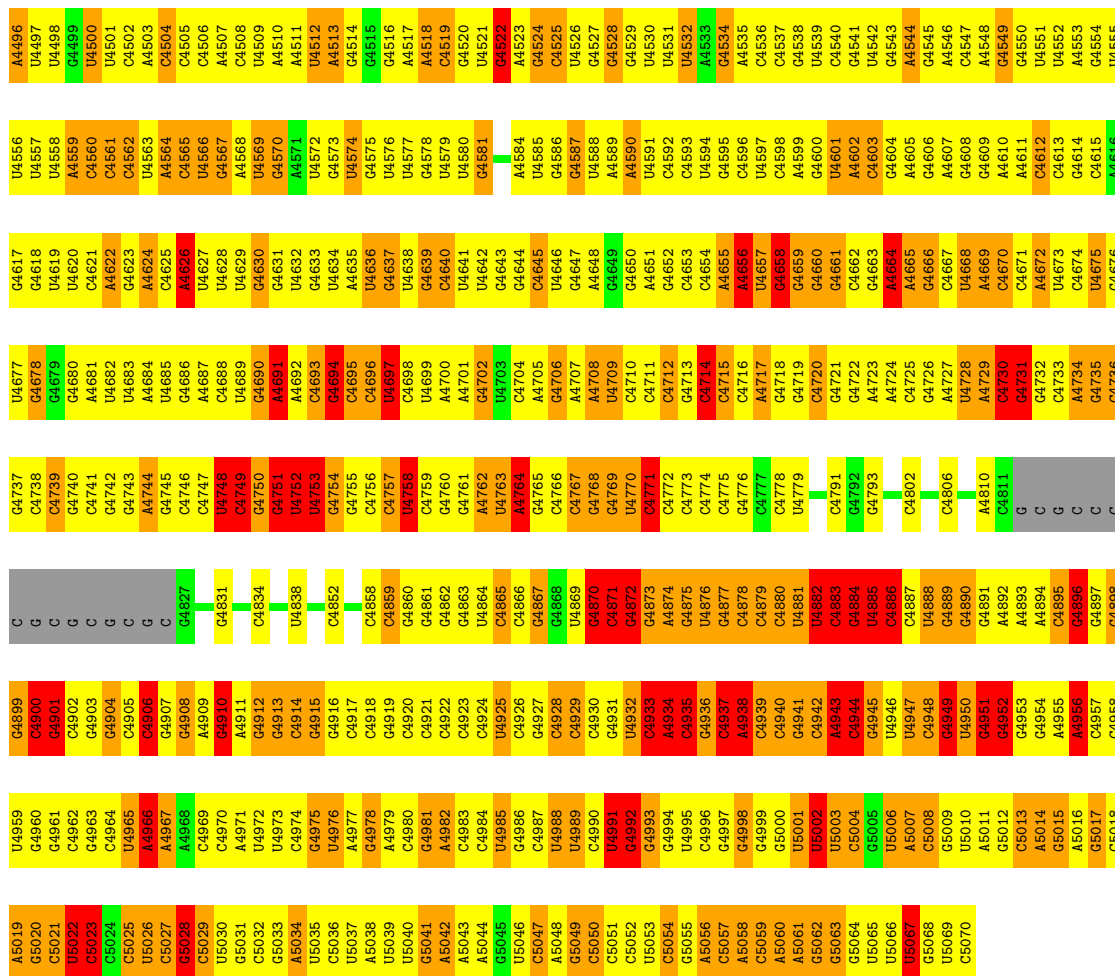
A1303	C1243	C1183	C1099	C952	C	G	C736	C676	A	C485	U425	G364	C303	A243	C183
C1304	G1244	A1184	U1100	C953	G	G	C737	C677	G	C486	A426	U365	C304	G244	U184
C1305	C1245	G1185	C1101	C954	G873	C	C738	C678	G	C487	A427	A366	A305	C245	C185
C1306	C1246	U1186	U1102	C955	G880	C	C739	C679	G	C488	A428	C367	A306	G246	G186
A1307	U1247	G1187	C1103	A956	C881	C	C740	C680	G	C489	A429	C368	A307	G247	U187
C1308	C1248	C1188	C1104	C957	G882	C	C741	C681	C	C490	G430	C369	G308	G248	G188
C1309	C1249	C1189	C1105	C958	G883	G	C742	C682	C	C491	G431	C370	C309	C249	G189
C1310	C1250	A1190	A1106	C959	G884	C	G743	C683	G893	U492	U432	A371	G310	C250	G190
C1311	C1251	C1191	C1107	A960	C886	C	G744	C684	C599	U494	A433	G372	G311	G251	G191
C1312	C1252	C1192	C1108	C961	C902	U	A745	C685	C	U495	A434	G373	G312	C252	G192
C1313	C1253	C1193	C1109	C962	C903	U	A746	C686	C	U496	A435	G374	U313	G253	G193
C1314	A1254	G1194	C1032	C963	C904	U	A747	C687	C608	U497	C436	G375	G314	G254	C194
C1315	A1255	A964	C1033	A965	C905	C	G748	C688	G	C498	G437	A376	G315	C255	C195
G1316	G1256	G985	G1044	C986	C906	C	G749	C689	G621	U499	G438	A377	U316	G256	C196
U1317	A1257	A966	G1045	A967	C907	C	U750	C690	G	U500	G439	A378	A317	G257	A197
C1318	G1258	G1198	C1047	C967	C908	C	G751	C691	G631	G501	U440	G379	A318	G258	A198
U1319	G1259	G1199	C1048	C968	C909	U	G752	C692	G632	C502	G441	U380	A319	G259	G199
U1320	G1260	G1200	C1049	C969	A909	U	C753	C693	G633	C503	G442	U381	C320	C260	U200
C1321	G1261	U1201	C1050	C970	C910	G	U754	C694	U634	C504	G443	G382	U321	G261	C201
A1322	G1262	C1202	C	U971	U911	G	C755	C695	G635	G504	G444	A383	C322	G262	C202
C1323	A1263	C1203	C	C972	G912	G	G756	C696	G636	G505	U445	A384	C323	G263	U203
A1324	C1264	C1204	C	C973	U913	A	G757	C697	G637	C506	C446	A385	A324	C264	U204
C1325	G1265	C974	C	C974	U914	G	G758	C698	G638	G507	C447	A386	U325	C265	C205
C1326	G1266	C975	C	C975	A915	G	G759	C699	U639	G508	G448	G387	C326	C266	U206
C1327	G1267	C1206	G	C976	C916	G	G760	C700	G640	A509	G449	A388	U327	G267	G207
C1328	G1268	G1208	G	C977	A917	C	G768	C701	G641	U510	G450	A389	A328	G268	A208
G1329	G1269	U1209	A	C978	G918	C	G778	U702	G642	C511	C451	C390	A329	G269	U209
C1330	A1270	C1210	C	C979	C919	G	G778	C703	C643	U512	A452	U391	G330	U270	C210
C1331	G1271	G1211	G	C980	C920	C	U	C704	G644	U513	G453	U392	C331	C271	G211
C1332	C1272	G1212	C	C981	C921	C	C	C705	G645	U514	U454	U393	C332	U272	A212
A1333	G1273	C1213	G	U982	C922	G	C	C706	G646	C515	C455	C394	U333	U273	G213
A1334	A1274	G1214	G	C983	C923	G	C	C707	G647	C516	C456	A395	A334	C274	G214
G1335	G1275	C1215	C	C984	C924	G	U	C708	G648	C517	G457	A396	A335	C275	G215
C1336	C1276	C1216	C	C985	C925	U	C	C709	A649	G518	C458	G397	A336	C276	C216
A1337	G1277	G1217	C	C986	G926	C	C	C710	C650	C519	C459	A398	U337	G277	C217
G1338	C1278	G1218	C	C987	C927	G	U	A711	C651	C520	C460	A399	C338	G278	A218
U1339	A1279	G1219	C	C988	C928	G	C	C712	C652	C521	G461	A402	C340	A279	G219
C1340	G1280	G1220	C	U989	A929	G	C	C713	U653	C522	G462	A403	G341	G280	C220
U1341	G1281	G1221	C	C990	G930	G	U	G714	C654	C523	A463	U404	G342	U281	C221
A1342	C1282	A1222	C	C991	C931	C	U	C715	C655	C524	A464	U405	A343	C282	C222
C1343	G1283	C1223	C	C992	A932	G	C	C716	C656	C	A465	C406	A344	G283	G223
C1344	G1284	G1224	C	C993	C933	G	U	U717	C657	U630	A466	A407	C345	G284	U224
A1345	U1285	U1225	C	C994	C934	C	C	C718	C658	C	U467	A408	C346	G285	G225
C1346	C1286	U1226	C	C995	A935	G	C	C719	G659	C	U468	A409	G347	U286	G226
G1347	C1287	C1227	C	C996	C936	G	C	C720	A660	C	C469	A410	A347	U287	A227
U1348	G1288	U1228	C	C997	U937	C	C	G721	C661	C	A470	G411	A348	G288	C228
G1349	C1289	C1229	C	C998	C938	G	C	C722	C662	C	A471	G412	A349	C289	G229
C1350	G1290	U1230	C	C999	C939	G	G	A723	G663	C	C472	G413	C350	U290	G230
G1351	C1291	G1231	C	A1000	C940	C	U	C724	G664	C	C473	G414	C351	U291	U231
C1352	C1292	G1232	C	A1012	C941	G	C	G725	C665	C	C474	C415	C	G292	G232
G1353	G1293	G1233	C	A	C942	G	U	C726	G666	U	G475	G416	U354	G293	U233
A1354	A1294	C1234	A	U	A943	C	C	C727	A667	C	G476	U417	A355	G294	G234
G1355	C1295	G1235	U	C	A944	C	C	U728	C668	C	C477	G418	G356	A295	A235
U1356	G1296	C1236	C	U	U945	G	G	G729	C669	U	C478	A419	U357	A296	G236
C1357	C1297	U1237	C	C	C946	C	C	C730	G670	C	G479	A420	C358	U297	G237
G1358	C1298	A1238	C	C	C947	G	C	G731	G671	C	C480	A421	A359	G298	C238
G1359	G1299	C1239	C	C	C948	G	C	A732	C672	C	G481	C422	A360	C299	C239
G1360	G1300	G1240	C	C	C949	U	C	A733	C673	C	G482	G423	C361	A300	G240
C1361	C1301	G1241	G	C	G950	G	C	G734	C674	G	G483	G424	A362	G301	G241
G1362	U1302	G1242	C	C	G951	C	C	G735	C675	C	U484	U424	A363	C302	U242

A2285	U2220	C	U2090	A2030	A1970	G1910	A1850	U1790	U1730	U1664	G1603	G1543	C1483	U1423	C1363
G2286	C2221	G	C2091	C2031	C1971	C1911	G1851	U1791	C1731	C1665	G1604	G1544	G1484	G1424	U1364
G2287	C2222	G	G2092	U2032	G1972	C1912	U1852	U1792	G1732	C1666	G1605	G1545	C1485	G1425	C1365
G2288	C2223	C	A2093	A2033	G1973	C1913	G1853	A1793	G1733	C1667	U1606	G1546	C1486	G1426	G1366
G2289	C2224	G	G2094	G2034	U1974	C1914	G1854	A1794	G1734	A1668	C1607	G1547	C1487	A1427	C1367
G2290	C2225	G	A2095	C2035	G1975	C1915	G1855	A1795	U1735	A1669	G1608	G1548	G1488	U1428	A1368
G2291	G2226	C	G2096	C2036	G1976	G1916	C1856	U1796	A1736	G1670	U1609	G1549	G1489	C1429	C1369
G2292	C2227	G	U2097	C2037	C1977	A1917	C1857	G1797	A1737	U1671	C1610	G1550	G1490	A1430	G1370
G2293	C2228	G	G2098	U2038	G1978	U1918	A1858	G1798	A1738	U1672	C1611	C1551	A1491	C1431	A1371
G2294	C2229	C	G2099	A2039	A1979	G1919	C1859	U1799	G1739	U1673	G1612	G1552	G1492	G1432	A1372
G2295	C2230	G	A2100	G2040	U1980	C1920	U1860	U1800	C1740	C1674	G1613	G1493	A1373	A1373	
G2296	C2231	C	C2101	A2041	G1981	G1921	U1861	A1801	G1741	C1675	G1614	U1494	G1374	G1374	
G2297	C2232	G	G1982	A2042	G1982	G1922	U1862	A1802	A1742	C1676	C1615	G1555	G1495	G1435	C1375
U2298	C2233	G	A1983	A2043	A1983	A1923	U1863	G1803	A1743	U1677	U1616	C1556	G1496	C1436	C1376
G2299	C2234	G	A1984	U2044	A1984	A1924	G1864	A1804	U1744	C1678	G1617	C1557	A1497	U1437	G1377
A2300	G2245	G	A2105	G2045	G1985	G1925	G1865	A1805	A1745	A1679	G1618	C1558	U1498	U1438	C1378
G2301	C2246	G	G2106	G2046	U1986	G1926	U1866	A1806	A1746	G1680	G1619	C1559	C1499	C1439	C1379
C2302	A2247	G	C2107	A2047	G1987	U1927	A1867	C1807	U1747	G1681	U1620	A1560	A1500	U1440	G1380
C2303	U2048	U	G1988	G2048	G1988	C1928	A1868	C1808	U1748	A1682	A1621	G1561	C1501	C1441	U1381
U2304	G2049	G	G1989	G2049	G1989	A1929	G1869	C1809	A1749	U1683	U1622	G1562	A1502	C1442	G1382
U2305	C2050	U	A1990	G2050	A1990	C1930	C1870	G1810	G1750	A1684	A1623	A1563	A1503	A1443	G1383
G2306	C2051	G	G2111	C2051	A1991	A1931	A1871	G1811	A1751	C1685	G1624	A1564	G1504	G1444	C1384
A2307	G2247	G	G2112	G2052	U1992	A1932	G1872	C1812	G1752	C1686	G1625	A1565	C1505	U1445	G1385
A2308	C2248	G	G1993	C2053	G1993	G1933	A1873	U1813	G1753	U1687	G1626	C1566	G1506	C1446	C1386
G2309	C2249	G	G2114	U2054	C1994	A1934	A1874	C1814	U1754	G1688	G1627	U1567	C1507	G1447	A1387
C2310	C2250	U	G2115	G2055	G1995	C1935	C1875	G1815	C1755	G1689	C1628	C1568	A1508	G1448	A1388
C2311	G2251	C	C2116	G2056	C1996	C1936	U1876	C1816	U1756	C1690	G1629	U1569	C1509	C1449	U1389
C2312	G2252	C	G2117	A2057	U1997	C1937	G1877	U1817	U1757	G1691	A1630	G1570	C1510	C1450	C1390
A2313	A2253	U	C2118	G2058	A1998	C1938	G1878	C1818	G1758	C1692	A1631	G1571	U1511	G1451	A1391
G2314	C2247	U	C2119	C2059	A1999	A1939	C1879	G1819	G1759	U1693	A1632	U1572	G1512	A1452	A1392
G2315	C2255	C	G2120	G2060	G2000	G1940	G1880	C1820	G1760	C1694	G1633	G1573	U1513	G1453	G1393
C2316	C2256	C	C2121	U2061	G2001	A1941	C1881	G1821	G1761	U1695	A1634	G1574	U1514	G1454	C1394
C2317	C2257	C	G2122	C2062	A2002	A1942	U1882	U1822	C1762	C1696	C1635	G1575	A1515	G1455	U1395
G2318	C2258	C	C2123	G2063	G2003	A1943	G1883	G1823	C1763	G1697	U1636	G1576	C1516	G1456	C1396
C2319	G2259	C	G2124	G2064	U2004	A1944	C1884	G1824	G1764	C1698	A1637	G1577	G1517	G1457	A1397
G2320	C2260	G	C2125	G2065	G2005	G1945	G1885	A1825	A1765	A1699	U1638	U1578	A1518	C1458	A1398
G2321	G2261	C	G2126	C2066	U2006	G1946	G1886	G1826	G1766	G1700	U1639	U1579	C1519	A1459	A1399
G2322	G2262	C	C2127	C2067	G2007	U1947	G1887	C1827	A1767	A1701	C1640	C1580	G1520	C1460	G1400
C2323	A2263	C	G2128	C2068	U2008	G1948	A1888	C1828	C1768	C1702	G1641	G1581	C1521	C1461	C1401
C2324	C2264	C	C2129	A2069	A2009	U1949	U1889	G1829	G1769	C1703	A1642	U1582	G1522	A1462	C1402
G2325	G2265	C	G2130	U2070	A2010	G1950	G1890	G1830	A1770	C1704	A1643	A1583	A1523	C1463	G1403
C2326	C2266	C	C2131	A2071	C2011	G1951	A1891	C1831	U1771	G1705	C1644	G1584	A1524	G1464	G1404
G2327	U2267	C	G2132	C2072	A2012	G1952	A1892	C1832	C1772	G1708	C1645	G1585	A1525	G1465	C1405
C2328	A2268	C	C2133	C2073	A2013	U1953	C1893	G1833	U1773	C1709	A1646	G1586	G1526	G1466	C1406
U2329	C2269	C	C2134	C2074	C2014	U1954	C1894	U1834	C1774	C1709	U1647	G1587	A1527	C1467	C1407
G2330	G2270	C	G2135	G2075	U2015	G1955	G1895	G1835	A1775	C1714	C1648	U1588	G1528	G1468	G1408
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A2332	C2272	A	G2144	C2077	A2017	U1957	A1897	A1837	C1777	C1714	A1650	C1590	G1530	U1470	U1410
G2333	G2273	C	U2145	G2078	C2018	A1958	C1898	A1838	C1778	G1718	G1651	U1591	U1531	U1471	C1411
C2334	C2274	G	U2146	G2079	C2019	U1959	G1899	G1839	U1779	A1719	U1652	G1592	G1532	C1472	G1412
C2335	G2275	C	C2147	U2080	U2020	A1960	C1900	G1840	A1780	C1720	A1653	A1593	A1533	U1473	C1413
G2336	A2276	C	G2148	C2081	G2021	G1961	C1901	C1841	U1781	G1721	C1654	C1594	A1534	C1474	C1414
C2337	C2277	U	C2149	G2082	C2022	A1962	G1902	G1842	U1782	G1722	C1655	U1595	C1535	G1475	G1415
C2338	G2278	C	G2152	C2083	C2023	C1963	G1903	A1843	C1783	A1723	U1656	U1596	U1536	C1476	G1416
A2339	A2279	U	G2153	G2084	G2024	A1964	G1904	G1844	U1784	G1724	C1657	G1597	A1537	C1477	C1417
C2340	G2280	U	G2154	G2085	A2025	G1965	U1905	U1845	C1785	U1725	G1657	C1598	U1538	G1478	C1418
A2341	U2281	C	G2155	G2086	A2026	C1966	U1906	G1846	A1786	U1726	U1660	A1599	G1539	G1479	G1419
G2342	A2282	C	C	C2087	U2027	A1967	A1907	C1847	A1787	U1727	C1661	A1600	C1540	C1480	A1420
G2343	G2283	G	G	A2088	C2028	G1968	A1908	C1848	A1788	U1728	C1662	A1601	C1541	C1481	G1421
U2344	G2284	G	C2218	G2089	A2029	G1969	G1909	U1849	C1789	A1729	C1663	U1602	U1542	G1482	G1422


WORLDWIDE PDB
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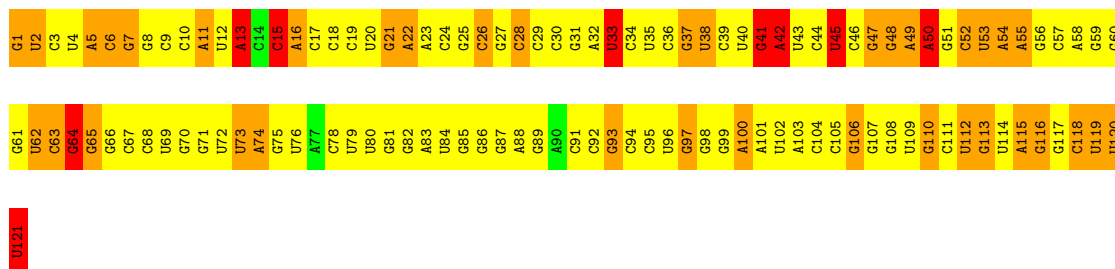
EMDataBank
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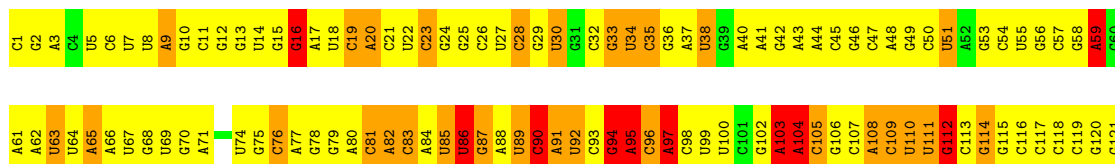
- Molecule 86: 5S ribosomal RNA

Chain A7:  60% 31% 7%



- Molecule 87: 5.8S ribosomal RNA

Chain A8: 5% 59% 27% 10%



G122	U123	U124	C125	C126	U127	C128	C129	C130	G131	G132	G133	G134	C135	U136	A137	C138	G139	C140	C141	U142	G143	U144	C145	U146	G147	A148	G149	C150	G151	U152	C153	G154	C155	U156	U157
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4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	343343	Depositor
Resolution determination method	FSC at 0.5 cut-off	Depositor
CTF correction method	each subvolume	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	90000	Depositor
Image detector	Eagle 4k CCD	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	Az	1.04	25/6804 (0.4%)	1.36	96/9189 (1.0%)
10	AN	0.82	4/1232 (0.3%)	1.00	14/1656 (0.8%)
11	AL	1.10	6/1319 (0.5%)	1.40	17/1761 (1.0%)
12	AR	1.23	10/1031 (1.0%)	1.64	30/1383 (2.2%)
13	AP	0.74	1/1081 (0.1%)	1.43	32/1440 (2.2%)
14	AT	0.96	3/1119 (0.3%)	1.27	13/1499 (0.9%)
15	AB	0.79	7/1774 (0.4%)	1.08	23/2372 (1.0%)
16	AA	0.76	2/1679 (0.1%)	1.05	17/2283 (0.7%)
17	AV	1.20	6/631 (1.0%)	1.69	24/844 (2.8%)
18	AY	0.92	3/1040 (0.3%)	1.42	21/1382 (1.5%)
19	AZ	1.04	6/604 (1.0%)	1.35	17/810 (2.1%)
2	Ag	0.91	1/2493 (0.0%)	1.29	27/3394 (0.8%)
20	Aa	0.96	5/863 (0.6%)	1.62	21/1159 (1.8%)
21	Ab	1.02	2/673 (0.3%)	1.36	13/902 (1.4%)
22	Ac	0.80	1/508 (0.2%)	1.17	8/680 (1.2%)
23	AD	1.03	6/1793 (0.3%)	1.30	22/2414 (0.9%)
24	Ae	1.50	5/474 (1.1%)	1.47	11/623 (1.8%)
25	Af	1.10	4/593 (0.7%)	1.49	16/786 (2.0%)
26	AJ	1.27	19/1522 (1.2%)	1.51	42/2031 (2.1%)
27	AE	0.76	4/2126 (0.2%)	0.98	23/2859 (0.8%)
28	AC	1.03	7/1788 (0.4%)	1.26	22/2414 (0.9%)
29	AG	1.05	17/1946 (0.9%)	1.28	29/2590 (1.1%)
3	AU	0.96	1/832 (0.1%)	1.59	30/1117 (2.7%)
30	AF	0.99	5/1531 (0.3%)	1.21	17/2059 (0.8%)
31	AH	1.09	8/1553 (0.5%)	2.20	29/2079 (1.4%)
32	AW	0.84	4/1051 (0.4%)	0.85	9/1406 (0.6%)
33	AI	1.11	7/1715 (0.4%)	1.51	33/2287 (1.4%)
34	AQ	0.70	3/1142 (0.3%)	1.11	15/1528 (1.0%)
35	Ah	1.51	9/572 (1.6%)	2.04	32/752 (4.3%)
36	B2	2.42	1909/42821 (4.5%)	2.23	2680/66606 (4.0%)
37	BC	2.31	82/1795 (4.6%)	2.06	106/2798 (3.8%)
38	Cz	1.50	16/1768 (0.9%)	1.87	43/2368 (1.8%)
39	Cq	1.02	14/2176 (0.6%)	1.48	58/2951 (2.0%)
4	AK	1.21	7/851 (0.8%)	1.78	32/1147 (2.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	CK	1.65	17/1257 (1.4%)	2.18	72/1697 (4.2%)
41	CO	0.83	5/1687 (0.3%)	0.87	12/2257 (0.5%)
42	CL	0.99	10/1732 (0.6%)	1.44	41/2315 (1.8%)
43	CV	0.71	3/1003 (0.3%)	0.84	6/1345 (0.4%)
44	CM	0.97	4/1161 (0.3%)	1.45	35/1552 (2.3%)
45	Ca	1.08	14/1191 (1.2%)	1.21	15/1591 (0.9%)
46	CN	0.71	3/1746 (0.2%)	0.96	16/2338 (0.7%)
47	CI	1.23	17/1751 (1.0%)	1.39	51/2340 (2.2%)
48	CD	0.90	11/2398 (0.5%)	1.30	50/3210 (1.6%)
49	CQ	1.40	14/1545 (0.9%)	1.74	36/2062 (1.7%)
5	AO	0.61	0/1029	1.05	12/1380 (0.9%)
50	CR	0.83	5/1596 (0.3%)	0.93	12/2109 (0.6%)
51	CA	0.77	9/1995 (0.5%)	1.07	18/2674 (0.7%)
52	CS	1.10	6/1493 (0.4%)	1.61	40/2003 (2.0%)
53	CT	1.33	17/1326 (1.3%)	1.51	35/1770 (2.0%)
54	CP	0.98	10/1259 (0.8%)	1.19	16/1689 (0.9%)
55	CU	0.89	4/935 (0.4%)	1.25	17/1253 (1.4%)
56	CX	1.19	7/1011 (0.7%)	1.51	29/1356 (2.1%)
57	CY	0.91	6/1124 (0.5%)	1.09	14/1494 (0.9%)
58	CW	1.29	14/1030 (1.4%)	1.76	36/1364 (2.6%)
59	CZ	1.01	6/1130 (0.5%)	1.29	21/1507 (1.4%)
6	AX	0.99	8/1124 (0.7%)	1.24	21/1500 (1.4%)
60	Cr	1.43	16/1120 (1.4%)	2.15	65/1497 (4.3%)
61	Ch	0.87	6/1031 (0.6%)	1.39	26/1361 (1.9%)
62	Cb	1.13	4/646 (0.6%)	1.23	12/853 (1.4%)
63	CB	1.06	13/3270 (0.4%)	1.43	35/4377 (0.8%)
64	CF	1.18	11/1945 (0.6%)	1.27	24/2589 (0.9%)
65	Cc	1.04	4/787 (0.5%)	1.12	8/1057 (0.8%)
66	Cd	1.18	6/946 (0.6%)	1.38	26/1272 (2.0%)
67	Ce	0.98	8/1114 (0.7%)	1.34	20/1485 (1.3%)
68	Cf	1.21	3/895 (0.3%)	1.76	29/1198 (2.4%)
69	Cg	1.23	8/916 (0.9%)	1.39	20/1220 (1.6%)
7	AM	0.99	3/970 (0.3%)	1.22	6/1300 (0.5%)
70	Ci	1.17	3/851 (0.4%)	1.25	13/1125 (1.2%)
71	Cj	0.71	1/748 (0.1%)	0.89	4/990 (0.4%)
72	Ck	1.06	3/575 (0.5%)	1.09	4/761 (0.5%)
73	Cl	1.26	8/454 (1.8%)	1.39	6/599 (1.0%)
74	CC	1.25	30/2979 (1.0%)	1.72	111/4001 (2.8%)
75	Cm	1.07	2/435 (0.5%)	1.04	6/575 (1.0%)
76	Cn	1.12	2/241 (0.8%)	0.46	1/305 (0.3%)
77	Cp	0.88	3/713 (0.4%)	0.93	4/946 (0.4%)
78	Co	1.11	6/877 (0.7%)	1.26	10/1156 (0.9%)
79	CJ	0.51	1/1372 (0.1%)	0.76	8/1836 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
8	AS	1.21	11/1157 (1.0%)	1.60	36/1548 (2.3%)
80	CH	0.67	4/1545 (0.3%)	0.85	9/2077 (0.4%)
81	CE	1.59	39/2153 (1.8%)	2.38	153/2878 (5.3%)
82	CG	1.26	10/2006 (0.5%)	1.39	43/2697 (1.6%)
83	Cs	0.73	1/433 (0.2%)	0.84	6/592 (1.0%)
83	Ct	0.72	1/433 (0.2%)	0.85	6/592 (1.0%)
84	Cu	0.74	1/421 (0.2%)	1.08	10/566 (1.8%)
84	Cv	0.71	1/421 (0.2%)	1.26	9/566 (1.6%)
85	A5	2.47	4305/94517 (4.6%)	2.18	5688/146662 (3.9%)
86	A7	2.55	144/2880 (5.0%)	2.04	177/4489 (3.9%)
87	A8	2.37	168/3723 (4.5%)	2.08	216/5800 (3.7%)
9	Ad	0.89	2/455 (0.4%)	0.79	3/603 (0.5%)
All	All	1.98	7227/254452 (2.8%)	1.92	11021/371948 (3.0%)

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
1	Az	2	41
10	AN	0	4
11	AL	0	7
12	AR	1	5
13	AP	0	10
14	AT	1	6
15	AB	0	4
16	AA	0	11
17	AV	0	11
18	AY	1	6
19	AZ	0	6
2	Ag	0	13
20	Aa	0	3
21	Ab	0	3
23	AD	0	5
24	Ae	0	5
25	Af	0	6
26	AJ	1	11
27	AE	1	2
28	AC	1	7
29	AG	0	1
3	AU	0	8

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Mol	Chain	#Chirality outliers	#Planarity outliers
30	AF	0	3
31	AH	0	10
32	AW	0	2
33	AI	0	8
34	AQ	0	4
35	Ah	0	4
36	B2	6	0
37	BC	1	0
38	Cz	2	6
39	Cq	0	14
4	AK	0	11
40	CK	1	8
41	CO	0	2
42	CL	0	19
43	CV	0	2
44	CM	0	8
45	Ca	1	9
46	CN	1	3
47	CI	0	13
48	CD	1	15
49	CQ	0	10
5	AO	0	1
50	CR	0	2
51	CA	0	1
52	CS	0	12
53	CT	0	13
54	CP	0	2
55	CU	0	4
56	CX	0	5
57	CY	0	6
58	CW	2	11
59	CZ	1	5
6	AX	0	4
60	Cr	0	14
61	Ch	1	8
62	Cb	0	3
63	CB	0	18
64	CF	1	4
65	Cc	0	3
66	Cd	0	10
67	Ce	1	5
68	Cf	0	14

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Mol	Chain	#Chirality outliers	#Planarity outliers
69	Cg	0	4
7	AM	0	1
70	Ci	0	6
71	Cj	0	1
72	Ck	0	2
74	CC	0	29
75	Cm	0	4
77	Cp	0	1
78	Co	0	4
8	AS	1	10
80	CH	0	8
81	CE	5	36
82	CG	1	10
84	Cu	1	0
85	A5	7	0
All	All	42	587

The worst 5 of 7227 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	A5	1359	G	C2'-C1'	-36.90	1.12	1.53
49	CQ	6	ARG	NE-CZ	30.14	1.72	1.33
40	CK	2	PRO	CA-CB	28.43	2.10	1.53
85	A5	1266	G	C2'-C1'	-27.46	1.23	1.53
74	CC	348	LYS	C-N	-26.18	0.73	1.34

The worst 5 of 11021 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	AH	109	ARG	NE-CZ-NH2	-53.46	93.57	120.30
31	AH	109	ARG	NE-CZ-NH1	42.77	141.69	120.30
63	CB	248	LEU	O-C-N	-38.89	60.47	122.70
36	B2	1780	G	P-O3'-C3'	38.27	165.63	119.70
49	CQ	6	ARG	NE-CZ-NH2	-36.36	102.12	120.30

5 of 42 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	Az	73	THR	CA
1	Az	854	PHE	CA
8	AS	92	ASP	CA
12	AR	3	ARG	CA

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Mol	Chain	Res	Type	Atom
14	AT	93	SER	CA

5 of 587 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Az	102	LEU	Mainchain
1	Az	108	HIS	Peptide
1	Az	4	PHE	Peptide
1	Az	42	LYS	Mainchain
1	Az	55	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Az	6673	0	6743	0	0
2	Ag	2436	0	2388	0	0
3	AU	822	0	886	216	0
4	AK	827	0	853	360	0
5	AO	1016	0	1039	296	0
6	AX	1106	0	1177	308	0
7	AM	960	0	988	264	0
8	AS	1139	0	1188	469	0
9	Ad	445	0	441	0	0
10	AN	1208	0	1294	265	0
11	AL	1296	0	1370	408	0
12	AR	1019	0	1070	375	0
13	AP	1062	0	1121	528	0
14	AT	1101	0	1135	398	0
15	AB	1747	0	1823	520	0
16	AA	1642	0	1644	649	0
17	AV	625	0	625	273	0
18	AY	1023	0	1088	512	0
19	AZ	598	0	652	212	0
20	Aa	847	0	899	0	0
21	Ab	659	0	680	0	0
22	Ac	506	0	536	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	AD	1765	0	1857	609	0
24	Ae	468	0	514	0	0
25	Af	581	0	598	0	0
26	AJ	1498	0	1599	546	0
27	AE	2084	0	2189	545	0
28	AC	1751	0	1831	594	0
29	AG	1923	0	2085	579	0
30	AF	1509	0	1560	476	0
31	AH	1530	0	1624	492	0
32	AW	1034	0	1079	275	0
33	AI	1686	0	1772	464	0
34	AQ	1124	0	1193	490	0
35	Ah	566	0	554	0	0
36	B2	38377	0	19188	780	0
37	BC	1604	0	816	7	0
38	Cz	1741	0	1853	0	0
39	Cq	2138	0	2191	0	0
40	CK	1238	0	1295	650	0
41	CO	1655	0	1795	546	0
42	CL	1701	0	1815	428	0
43	CV	989	0	1045	180	0
44	CM	1139	0	1209	431	0
45	Ca	1162	0	1210	0	0
46	CN	1701	0	1747	506	0
47	CI	1711	0	1746	471	0
48	CD	2353	0	2370	610	0
49	CQ	1521	0	1639	577	0
50	CR	1580	0	1746	396	0
51	CA	1957	0	2051	464	0
52	CS	1453	0	1485	648	0
53	CT	1298	0	1363	412	0
54	CP	1233	0	1260	304	0
55	CU	921	0	926	262	0
56	CX	994	0	1078	310	0
57	CY	1107	0	1193	349	0
58	CW	1015	0	1074	372	0
59	CZ	1107	0	1182	345	0
60	Cr	1104	0	1183	0	0
61	Ch	1023	0	1159	0	0
62	Cb	635	0	683	0	0
63	CB	3202	0	3335	1006	0
64	CF	1910	0	2046	322	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
65	Cc	776	0	812	0	0
66	Cd	931	0	979	0	0
67	Ce	1096	0	1188	0	0
68	Cf	876	0	910	0	0
69	Cg	906	0	999	0	0
70	Ci	840	0	925	0	0
71	Cj	733	0	773	0	0
72	Ck	569	0	637	0	0
73	Cl	444	0	483	0	0
74	CC	2925	0	3093	1079	0
75	Cm	429	0	469	0	0
76	Cn	240	0	289	0	0
77	Cp	703	0	755	0	0
78	Co	863	0	930	0	0
79	CJ	1349	0	1382	350	0
80	CH	1526	0	1603	415	0
81	CE	2113	0	2315	865	0
82	CG	1973	0	2123	864	0
83	Cs	426	0	436	0	0
83	Ct	426	0	436	0	0
84	Cu	419	0	433	0	0
84	Cv	419	0	433	0	0
85	A5	84946	0	41833	835	0
86	A7	2578	0	1306	55	0
87	A8	3334	0	1693	52	0
All	All	237685	0	177013	23825	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 82.

The worst 5 of 23825 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)
82:CG:136:LEU:HD21	82:CG:204:PHE:CZ	1.19	1.70
48:CD:223:PHE:CD1	48:CD:226:TYR:CE2	1.77	1.70
40:CK:123:ARG:CD	40:CK:129:ILE:HD11	1.23	1.69
63:CB:40:PRO:HB2	63:CB:42:HIS:CD2	1.23	1.68
13:AP:53:GLN:HG2	13:AP:80:LEU:CD1	1.24	1.68

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	Az	854/858 (100%)	766 (90%)	51 (6%)	37 (4%)	3	30
2	Ag	311/317 (98%)	271 (87%)	23 (7%)	17 (6%)	2	25
3	AU	102/119 (86%)	77 (76%)	9 (9%)	16 (16%)	0	4
4	AK	96/165 (58%)	67 (70%)	11 (12%)	18 (19%)	0	3
5	AO	134/151 (89%)	101 (75%)	14 (10%)	19 (14%)	0	5
6	AX	140/143 (98%)	121 (86%)	11 (8%)	8 (6%)	2	24
7	AM	122/132 (92%)	85 (70%)	16 (13%)	21 (17%)	0	4
8	AS	135/152 (89%)	106 (78%)	20 (15%)	9 (7%)	1	21
9	Ad	51/56 (91%)	46 (90%)	3 (6%)	2 (4%)	3	32
10	AN	148/151 (98%)	124 (84%)	18 (12%)	6 (4%)	3	31
11	AL	156/158 (99%)	132 (85%)	10 (6%)	14 (9%)	1	15
12	AR	124/135 (92%)	96 (77%)	13 (10%)	15 (12%)	0	7
13	AP	125/145 (86%)	92 (74%)	16 (13%)	17 (14%)	0	6
14	AT	139/145 (96%)	121 (87%)	8 (6%)	10 (7%)	1	19
15	AB	213/264 (81%)	174 (82%)	24 (11%)	15 (7%)	1	20
16	AA	206/295 (70%)	156 (76%)	23 (11%)	27 (13%)	0	6
17	AV	80/83 (96%)	59 (74%)	10 (12%)	11 (14%)	0	6
18	AY	124/133 (93%)	91 (73%)	15 (12%)	18 (14%)	0	5
19	AZ	73/125 (58%)	52 (71%)	12 (16%)	9 (12%)	0	7
20	Aa	105/115 (91%)	74 (70%)	13 (12%)	18 (17%)	0	4
21	Ab	82/84 (98%)	57 (70%)	14 (17%)	11 (13%)	0	6
22	Ac	62/69 (90%)	44 (71%)	13 (21%)	5 (8%)	1	17
23	AD	225/243 (93%)	180 (80%)	24 (11%)	21 (9%)	1	14
24	Ae	57/59 (97%)	39 (68%)	5 (9%)	13 (23%)	0	2
25	Af	69/80 (86%)	38 (55%)	13 (19%)	18 (26%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	AJ	180/194 (93%)	138 (77%)	18 (10%)	24 (13%)	0	6
27	AE	261/263 (99%)	210 (80%)	29 (11%)	22 (8%)	1	16
28	AC	224/293 (76%)	203 (91%)	10 (4%)	11 (5%)	2	28
29	AG	235/249 (94%)	202 (86%)	18 (8%)	15 (6%)	1	22
30	AF	189/204 (93%)	162 (86%)	15 (8%)	12 (6%)	1	22
31	AH	188/194 (97%)	146 (78%)	11 (6%)	31 (16%)	0	4
32	AW	127/130 (98%)	111 (87%)	14 (11%)	2 (2%)	11	52
33	AI	204/208 (98%)	169 (83%)	13 (6%)	22 (11%)	0	10
34	AQ	139/146 (95%)	110 (79%)	19 (14%)	10 (7%)	1	19
35	Ah	69/408 (17%)	31 (45%)	15 (22%)	23 (33%)	0	0
38	Cz	213/217 (98%)	189 (89%)	16 (8%)	8 (4%)	4	33
39	Cq	278/317 (88%)	197 (71%)	31 (11%)	50 (18%)	0	3
40	CK	161/165 (98%)	77 (48%)	35 (22%)	49 (30%)	0	0
41	CO	200/203 (98%)	183 (92%)	12 (6%)	5 (2%)	6	42
42	CL	208/211 (99%)	165 (79%)	18 (9%)	25 (12%)	0	7
43	CV	131/140 (94%)	116 (88%)	11 (8%)	4 (3%)	5	38
44	CM	137/215 (64%)	112 (82%)	16 (12%)	9 (7%)	1	21
45	Ca	145/148 (98%)	120 (83%)	14 (10%)	11 (8%)	1	18
46	CN	201/204 (98%)	179 (89%)	9 (4%)	13 (6%)	1	22
47	CI	211/214 (99%)	165 (78%)	27 (13%)	19 (9%)	1	15
48	CD	287/297 (97%)	237 (83%)	24 (8%)	26 (9%)	1	15
49	CQ	186/188 (99%)	152 (82%)	18 (10%)	16 (9%)	1	15
50	CR	187/196 (95%)	165 (88%)	15 (8%)	7 (4%)	4	34
51	CA	253/257 (98%)	210 (83%)	23 (9%)	20 (8%)	1	17
52	CS	173/176 (98%)	137 (79%)	15 (9%)	21 (12%)	0	7
53	CT	157/160 (98%)	131 (83%)	11 (7%)	15 (10%)	1	13
54	CP	150/184 (82%)	134 (89%)	9 (6%)	7 (5%)	3	29
55	CU	110/128 (86%)	90 (82%)	13 (12%)	7 (6%)	1	22
56	CX	119/156 (76%)	98 (82%)	14 (12%)	7 (6%)	2	23
57	CY	131/145 (90%)	116 (88%)	11 (8%)	4 (3%)	5	38
58	CW	122/157 (78%)	94 (77%)	13 (11%)	15 (12%)	0	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	CZ	133/136 (98%)	109 (82%)	14 (10%)	10 (8%)	1	18
60	Cr	135/137 (98%)	86 (64%)	22 (16%)	27 (20%)	0	3
61	Ch	121/123 (98%)	93 (77%)	14 (12%)	14 (12%)	0	8
62	Cb	76/159 (48%)	58 (76%)	9 (12%)	9 (12%)	0	8
63	CB	395/403 (98%)	322 (82%)	34 (9%)	39 (10%)	1	12
64	CF	227/248 (92%)	209 (92%)	6 (3%)	12 (5%)	2	26
65	Cc	98/115 (85%)	90 (92%)	5 (5%)	3 (3%)	5	38
66	Cd	111/125 (89%)	75 (68%)	20 (18%)	16 (14%)	0	5
67	Ce	131/135 (97%)	102 (78%)	14 (11%)	15 (12%)	0	8
68	Cf	107/110 (97%)	82 (77%)	12 (11%)	13 (12%)	0	7
69	Cg	112/117 (96%)	91 (81%)	7 (6%)	14 (12%)	0	7
70	Ci	101/105 (96%)	78 (77%)	7 (7%)	16 (16%)	0	4
71	Cj	88/97 (91%)	74 (84%)	7 (8%)	7 (8%)	1	17
72	Ck	67/70 (96%)	59 (88%)	5 (8%)	3 (4%)	3	29
73	Cl	48/51 (94%)	37 (77%)	8 (17%)	3 (6%)	1	22
74	CC	366/427 (86%)	259 (71%)	41 (11%)	66 (18%)	0	3
75	Cm	50/52 (96%)	44 (88%)	3 (6%)	3 (6%)	2	23
76	Cn	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
77	Cp	88/92 (96%)	75 (85%)	9 (10%)	4 (4%)	3	29
78	Co	103/106 (97%)	74 (72%)	14 (14%)	15 (15%)	0	5
79	CJ	166/178 (93%)	132 (80%)	20 (12%)	14 (8%)	1	16
80	CH	189/192 (98%)	163 (86%)	18 (10%)	8 (4%)	3	31
81	CE	260/288 (90%)	164 (63%)	39 (15%)	57 (22%)	0	2
82	CG	244/266 (92%)	165 (68%)	31 (13%)	48 (20%)	0	3
83	Cs	55/114 (48%)	53 (96%)	2 (4%)	0	100	100
83	Ct	55/114 (48%)	55 (100%)	0	0	100	100
84	Cu	54/115 (47%)	49 (91%)	1 (2%)	4 (7%)	1	19
84	Cv	54/115 (47%)	51 (94%)	0	3 (6%)	2	25
All	All	13166/14959 (88%)	10588 (80%)	1270 (10%)	1308 (10%)	1	12

5 of 1308 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Az	4	PHE
1	Az	43	ALA
1	Az	44	GLY
1	Az	45	ILE
1	Az	47	ALA

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	Az	728/730 (100%)	586 (80%)	142 (20%)	1	11
2	Ag	272/275 (99%)	223 (82%)	49 (18%)	2	13
3	AU	94/107 (88%)	74 (79%)	20 (21%)	1	8
4	AK	89/136 (65%)	61 (68%)	28 (32%)	0	2
5	AO	106/119 (89%)	87 (82%)	19 (18%)	2	14
6	AX	114/115 (99%)	91 (80%)	23 (20%)	1	9
7	AM	104/108 (96%)	81 (78%)	23 (22%)	1	8
8	AS	119/132 (90%)	95 (80%)	24 (20%)	1	9
9	Ad	47/49 (96%)	35 (74%)	12 (26%)	0	5
10	AN	130/131 (99%)	103 (79%)	27 (21%)	1	8
11	AL	142/142 (100%)	105 (74%)	37 (26%)	0	4
12	AR	114/122 (93%)	90 (79%)	24 (21%)	1	8
13	AP	116/130 (89%)	84 (72%)	32 (28%)	0	4
14	AT	112/115 (97%)	85 (76%)	27 (24%)	1	6
15	AB	196/231 (85%)	154 (79%)	42 (21%)	1	8
16	AA	174/243 (72%)	140 (80%)	34 (20%)	1	11
17	AV	66/67 (98%)	47 (71%)	19 (29%)	0	3
18	AY	108/115 (94%)	85 (79%)	23 (21%)	1	8
19	AZ	66/103 (64%)	53 (80%)	13 (20%)	1	10
20	Aa	90/98 (92%)	75 (83%)	15 (17%)	2	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	Ab	76/76 (100%)	63 (83%)	13 (17%)	2	16
22	Ac	57/62 (92%)	46 (81%)	11 (19%)	1	11
23	AD	190/202 (94%)	144 (76%)	46 (24%)	1	6
24	Ae	48/48 (100%)	24 (50%)	24 (50%)	0	0
25	Af	64/72 (89%)	43 (67%)	21 (33%)	0	2
26	AJ	157/168 (94%)	128 (82%)	29 (18%)	2	13
27	AE	225/225 (100%)	172 (76%)	53 (24%)	1	6
28	AC	190/225 (84%)	145 (76%)	45 (24%)	1	6
29	AG	207/218 (95%)	157 (76%)	50 (24%)	1	6
30	AF	161/170 (95%)	117 (73%)	44 (27%)	0	4
31	AH	170/174 (98%)	125 (74%)	45 (26%)	0	4
32	AW	112/113 (99%)	98 (88%)	14 (12%)	5	27
33	AI	178/180 (99%)	142 (80%)	36 (20%)	1	9
34	AQ	117/121 (97%)	89 (76%)	28 (24%)	1	6
35	Ah	55/328 (17%)	41 (74%)	14 (26%)	0	5
38	Cz	195/196 (100%)	174 (89%)	21 (11%)	7	32
39	Cq	232/258 (90%)	194 (84%)	38 (16%)	2	17
40	CK	136/137 (99%)	110 (81%)	26 (19%)	2	11
41	CO	173/174 (99%)	137 (79%)	36 (21%)	1	8
42	CL	176/177 (99%)	135 (77%)	41 (23%)	1	6
43	CV	102/107 (95%)	83 (81%)	19 (19%)	2	12
44	CM	118/161 (73%)	85 (72%)	33 (28%)	0	4
45	Ca	120/121 (99%)	100 (83%)	20 (17%)	2	17
46	CN	171/172 (99%)	132 (77%)	39 (23%)	1	7
47	CI	180/181 (99%)	150 (83%)	30 (17%)	2	17
48	CD	243/250 (97%)	210 (86%)	33 (14%)	4	24
49	CQ	165/165 (100%)	119 (72%)	46 (28%)	0	4
50	CR	168/175 (96%)	126 (75%)	42 (25%)	1	5
51	CA	197/199 (99%)	161 (82%)	36 (18%)	2	13
52	CS	156/157 (99%)	97 (62%)	59 (38%)	0	1
53	CT	139/140 (99%)	102 (73%)	37 (27%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	CP	133/163 (82%)	94 (71%)	39 (29%)	0	3
55	CU	102/115 (89%)	82 (80%)	20 (20%)	1	11
56	CX	109/133 (82%)	78 (72%)	31 (28%)	0	3
57	CY	123/135 (91%)	95 (77%)	28 (23%)	1	7
58	CW	103/126 (82%)	75 (73%)	28 (27%)	0	4
59	CZ	117/118 (99%)	82 (70%)	35 (30%)	0	3
60	Cr	121/121 (100%)	91 (75%)	30 (25%)	1	5
61	Ch	110/110 (100%)	81 (74%)	29 (26%)	0	4
62	Cb	66/126 (52%)	41 (62%)	25 (38%)	0	1
63	CB	345/349 (99%)	261 (76%)	84 (24%)	1	6
64	CF	198/215 (92%)	172 (87%)	26 (13%)	5	25
65	Cc	85/97 (88%)	73 (86%)	12 (14%)	4	23
66	Cd	102/110 (93%)	78 (76%)	24 (24%)	1	6
67	Ce	119/121 (98%)	87 (73%)	32 (27%)	0	4
68	Cf	88/89 (99%)	57 (65%)	31 (35%)	0	1
69	Cg	98/100 (98%)	63 (64%)	35 (36%)	0	1
70	Ci	87/89 (98%)	51 (59%)	36 (41%)	0	0
71	Cj	75/80 (94%)	55 (73%)	20 (27%)	0	4
72	Ck	64/65 (98%)	45 (70%)	19 (30%)	0	3
73	Cl	47/48 (98%)	33 (70%)	14 (30%)	0	3
74	CC	305/348 (88%)	222 (73%)	83 (27%)	0	4
75	Cm	48/48 (100%)	31 (65%)	17 (35%)	0	1
76	Cn	24/24 (100%)	14 (58%)	10 (42%)	0	0
77	Cp	74/75 (99%)	53 (72%)	21 (28%)	0	3
78	Co	93/94 (99%)	60 (64%)	33 (36%)	0	1
79	CJ	142/149 (95%)	130 (92%)	12 (8%)	12	44
80	CH	170/171 (99%)	146 (86%)	24 (14%)	4	23
81	CE	232/252 (92%)	156 (67%)	76 (33%)	0	2
82	CG	209/223 (94%)	141 (68%)	68 (32%)	0	2
83	Cs	46/81 (57%)	46 (100%)	0	100	100
83	Ct	46/81 (57%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
84	Cu	46/83 (55%)	45 (98%)	1 (2%)	57 79
84	Cv	46/83 (55%)	45 (98%)	1 (2%)	57 79
All	All	11438/12642 (90%)	8832 (77%)	2606 (23%)	3 7

5 of 2606 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	CK	90	ARG
49	CQ	50	ARG
78	Co	66	ILE
41	CO	158	GLU
45	Ca	12	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 308 such sidechains are listed below:

Mol	Chain	Res	Type
41	CO	199	HIS
48	CD	122	GLN
80	CH	98	HIS
42	CL	115	GLN
46	CN	139	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
36	B2	1760/1869 (94%)	503 (28%)	0
37	BC	74/75 (98%)	13 (17%)	0
85	A5	3761/5070 (74%)	1048 (27%)	0
86	A7	120/121 (99%)	24 (20%)	0
87	A8	156/157 (99%)	38 (24%)	0
All	All	5871/7292 (80%)	1626 (27%)	0

5 of 1626 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
36	B2	2	A
36	B2	3	C
36	B2	4	C
36	B2	8	U

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Mol	Chain	Res	Type
36	B2	16	G

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no 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
38	Cz	1
26	AJ	1
74	CC	1
23	AD	1
53	CT	1
41	CO	1
35	Ah	1
24	Ae	1
70	Ci	1
47	CI	1
1	Az	1
64	CF	1
82	CG	1

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Cz	100:VAL	C	101:LYS	N	2.08
1	AD	5:ILE	C	6:SER	N	1.82
1	CI	205:PRO	C	206:LEU	N	1.82
1	CO	202:LEU	C	203:VAL	N	1.80
1	Ci	78:GLY	C	79:THR	N	1.80