



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Dec 11, 2019 – 01:47 AM EST

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

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

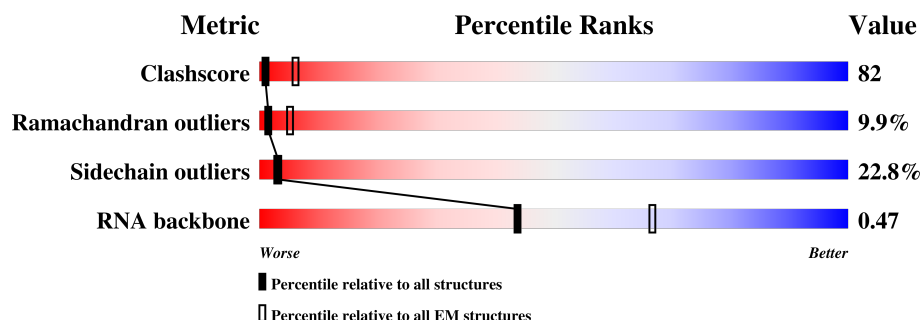
1 Overall quality at a glance

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.




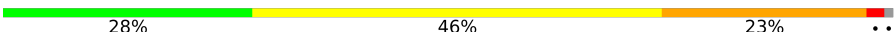
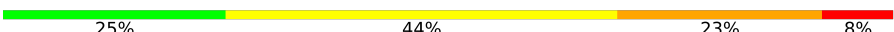

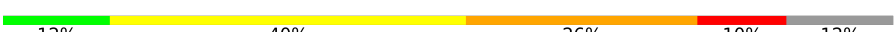
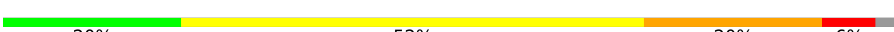
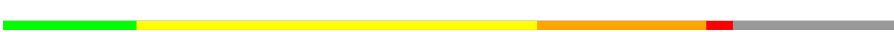





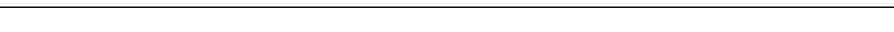

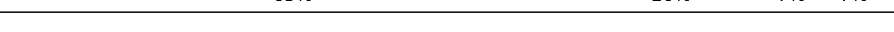

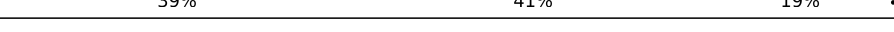
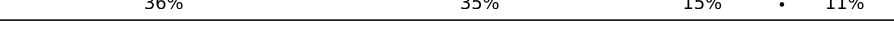

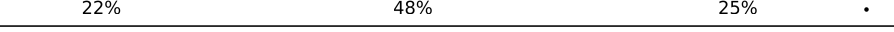




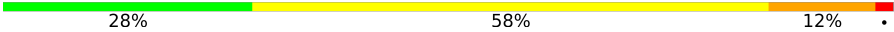
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 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%



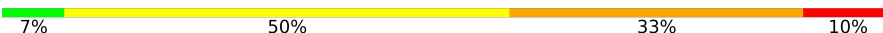



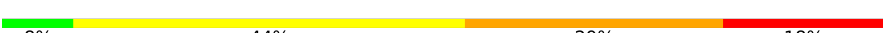








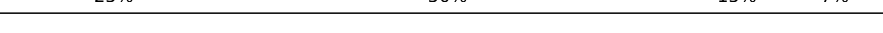

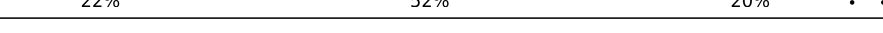







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Mol	Chain	Length	Quality of chain
9	Ad	56	
10	AN	151	
11	AL	158	
12	AR	135	
13	AP	145	
14	AT	145	
15	AB	264	
16	AA	295	
17	AV	83	
18	AY	133	
19	AZ	125	
20	Aa	115	
21	Ab	84	
22	Ac	69	
23	AD	243	
24	Ae	59	
25	Af	80	
26	AJ	194	
27	AE	263	
28	AC	293	
29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






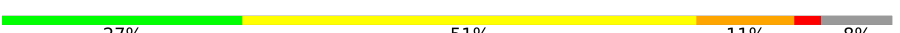
















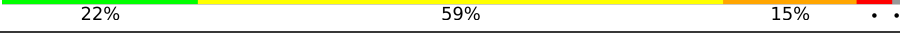


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Mol	Chain	Length	Quality of chain
34	AQ	146	
35	Ah	408	
36	B2	1869	
37	BC	75	
38	Cz	217	
39	Cq	317	
40	CK	165	
41	CO	203	
42	CL	211	
43	CV	140	
44	CM	215	
45	Ca	148	
46	CN	204	
47	CI	214	
48	CD	297	
49	CQ	188	
50	CR	196	
51	CA	257	
52	CS	176	
53	CT	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%44%24%6%15%</div></div>
86	A7	121	<div><div></div><div>59%31%7%</div></div>
87	A8	157	<div><div></div><div>5%57%27%11%</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		

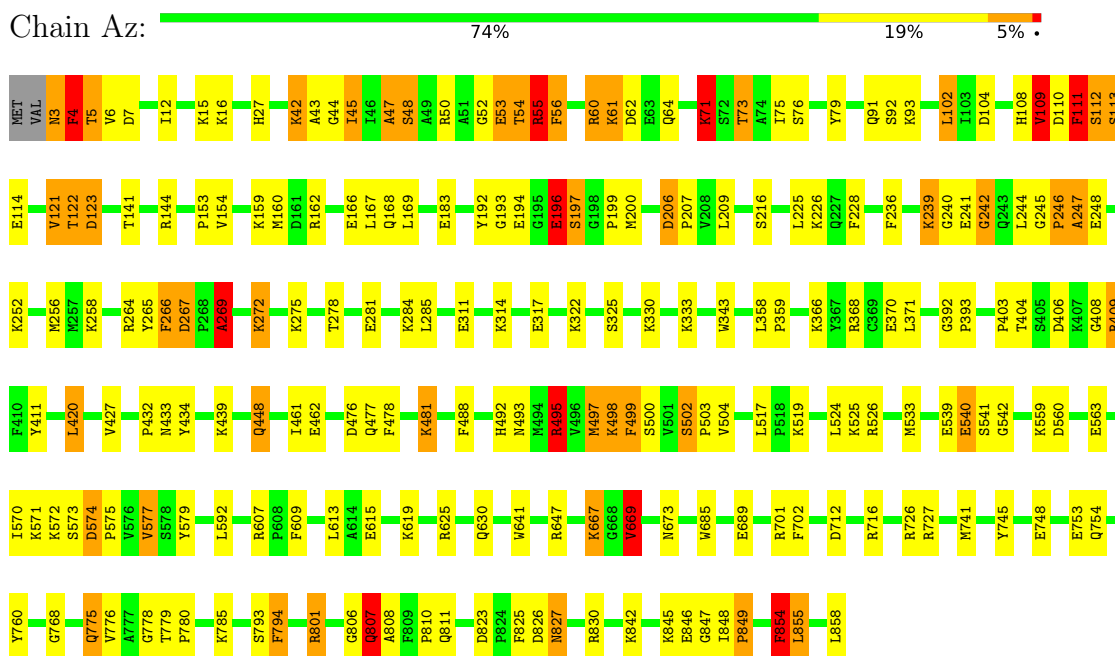
- Molecule 87 is a RNA chain called 5.8S ribosomal RNA.

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

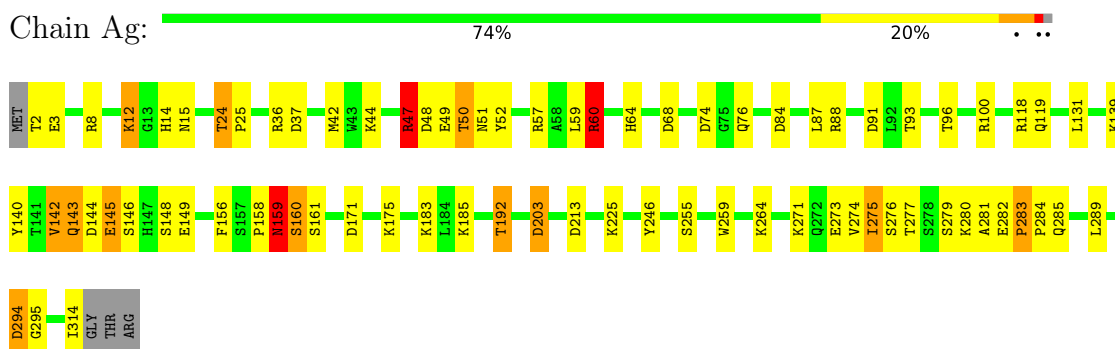
3 Residue-property plots

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

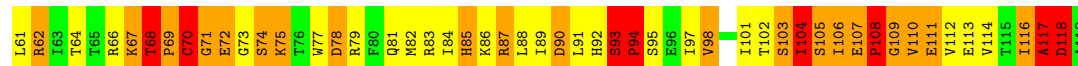


- Molecule 2: Guanine nucleotide-binding protein subunit beta-2-like 1



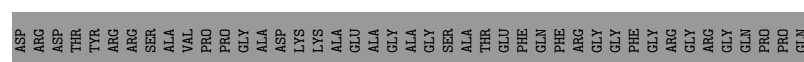
- Molecule 3: 40S ribosomal protein S20





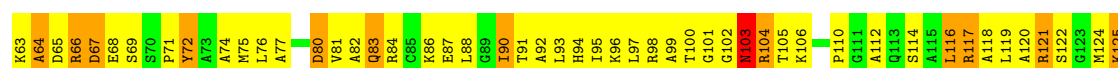
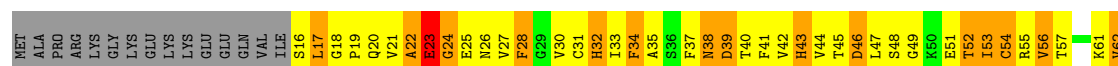
• Molecule 4: 40S ribosomal protein S10

Chain AK: 6% 27% 15% 12% 41%



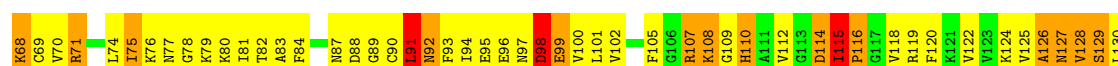
• Molecule 5: 40S ribosomal protein S14

Chain AO: 16% 48% 24% 10%



• Molecule 6: 40S ribosomal protein S23

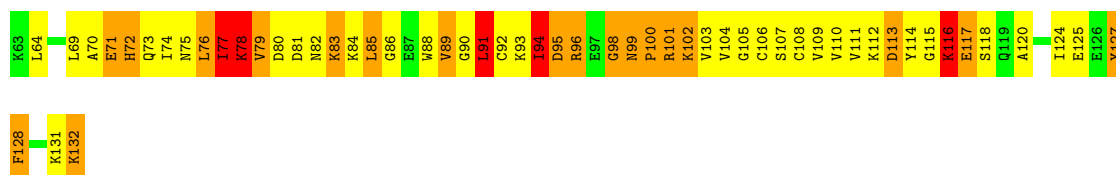
Chain AX: 26% 49% 19% 6%



• Molecule 7: 40S ribosomal protein S12

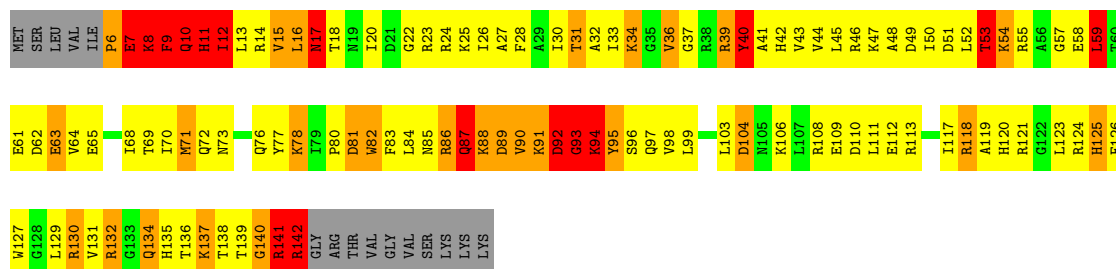
Chain AM: 20% 45% 23% 6% 6%





• Molecule 8: 40S ribosomal protein S18

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



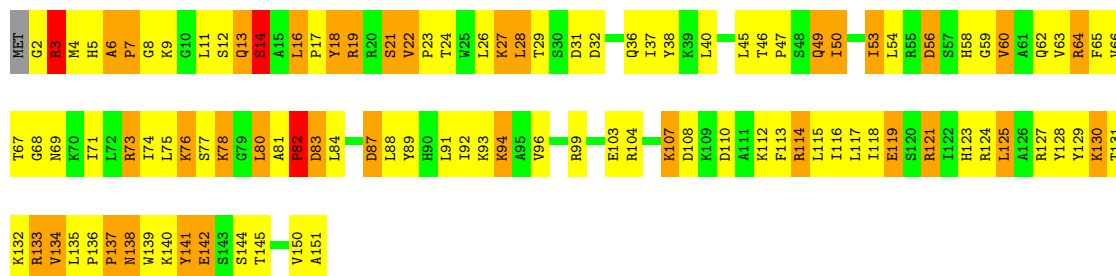
• Molecule 9: 40S ribosomal protein S29

Chain Ad: 66% 27% 5%



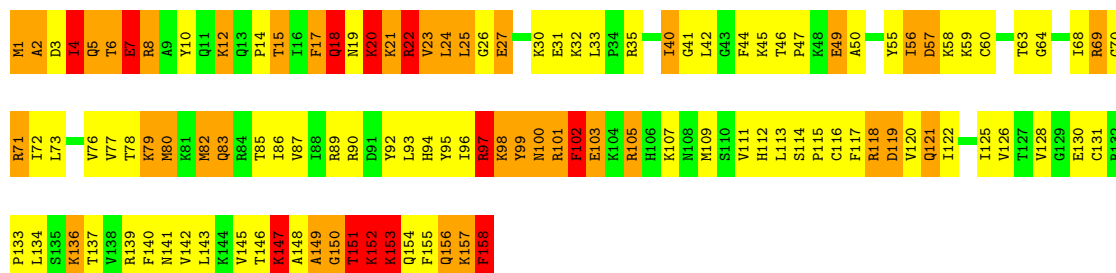
• Molecule 10: 40S ribosomal protein S13

Chain AN: 28% 46% 23%

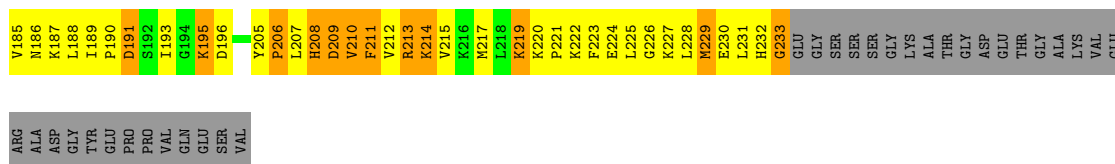


• Molecule 11: 40S ribosomal protein S11

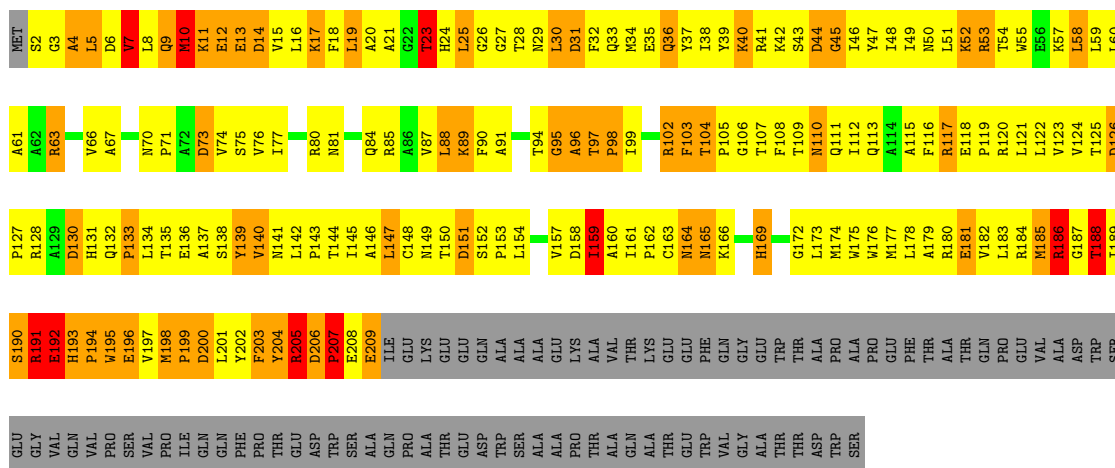
Chain AL: 25% 44% 23% 8%



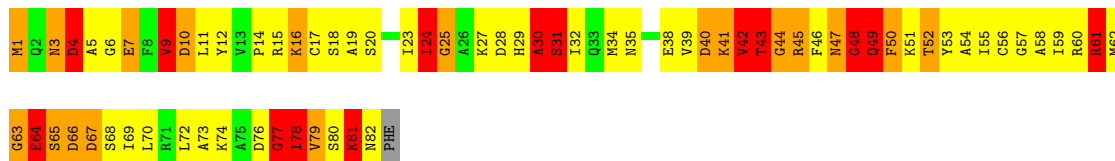
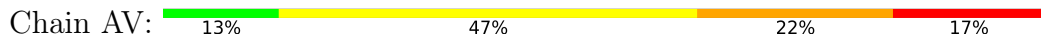
- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| A123 | A124 | H125 | H126 | V127 | K128 | L129 | T130 | H131 | G132 | L133 | L134 | L135 | L136 | L137 | F138 | F139 | V140 | G141 | F142 | T143 | K144 | K145 | R146 | M147 | M148 | Q149 | L150 | R151 | K152 | T153 | S154 | Y155 | A156 | Q157 | H158 | G159 | Q160 | V161 | R162 | R163 | R164 | R165 | K166 | K167 | M168 | M169 | M170 | T171 | R172 | T173 | R174 | E175 | V176 | Q177 | T178 | M179 | D180 | L181 | K182 | E183 | L184 | L185 | L186 | L187 | L188 | L189 | L190 | L191 | L192 | L193 | L194 | L195 | L196 | L197 | L198 | L199 | L200 |
| G61 | L62 | K63 | G64 | R65 | V66 | F67 | E68 | V69 | S70 | L71 | A72 | D73 | L74 | Q75 | N76 | D77 | E78 | V79 | A80 | F81 | R82 | K83 | F84 | R85 | L86 | L87 | T88 | E89 | D90 | V91 | Q92 | G93 | K94 | N95 | C96 | L97 | T98 | N99 | F100 | H101 | G102 | M103 | D104 | L105 | T106 | R107 | D108 | K109 | M110 | M113 | V114 | K115 | K116 | M117 | Q118 | T119 | M120 | | | | | | | | | | | | | | | | | | | | |
| ALA | VAL | GLY | LYS | ASN | LYS | ARG | LEU | THR | LYS | GLY | GLY | LYS | LYS | GLY | ALA | LYS | K19 | K20 | R21 | V22 | D23 | P24 | F25 | S26 | K27 | D28 | D29 | X30 | Y31 | D32 | V33 | K34 | A35 | P36 | A37 | M38 | F39 | N40 | I41 | R42 | M43 | I44 | G45 | K46 | T47 | L48 | V49 | T50 | R51 | T52 | Q53 | G54 | T55 | R56 | A58 | S59 | R60 | | | | | | | | | | | | | | | | | | | | |



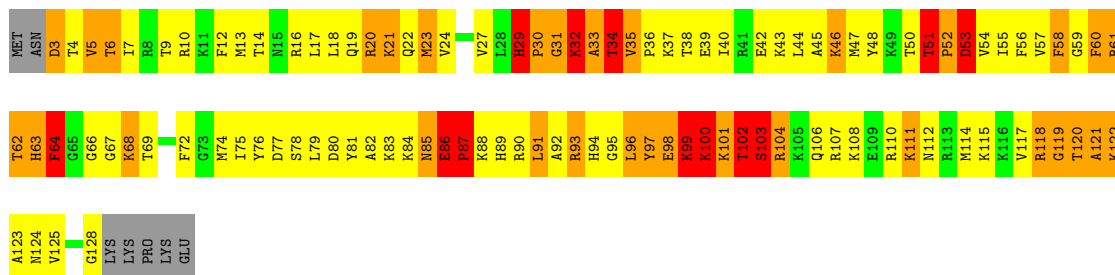
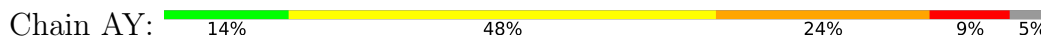
- Molecule 16: 40S ribosomal protein SA



- Molecule 17: 40S ribosomal protein S21

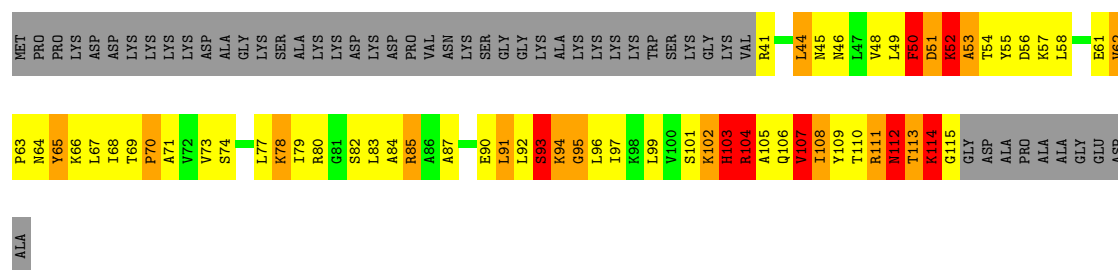


- Molecule 18: 40S ribosomal protein S24



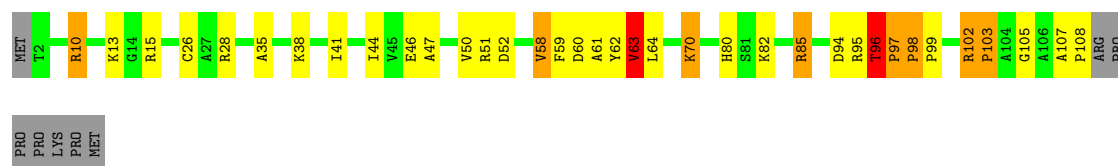
- Molecule 19: 40S ribosomal protein S25





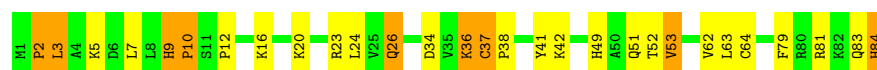
- Molecule 20: 40S ribosomal protein S26

Chain Aa: 



- Molecule 21: 40S ribosomal protein S27

Chain Ab:

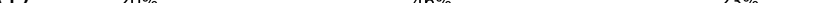


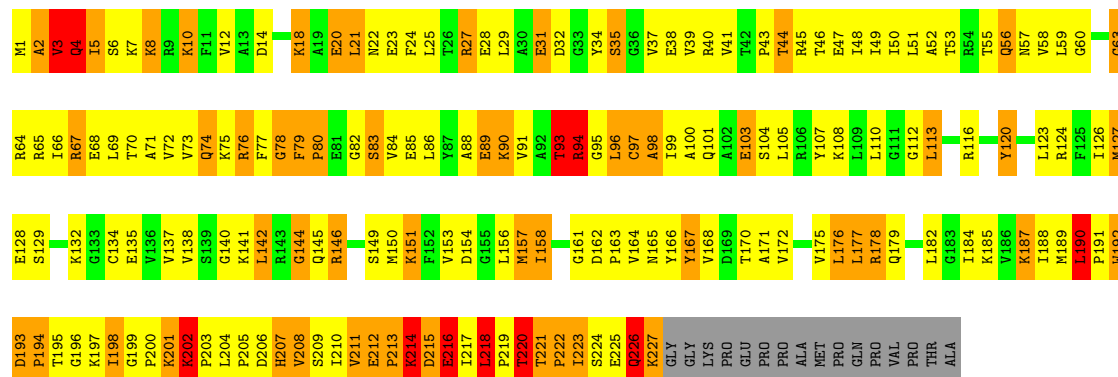
- Molecule 22: 40S ribosomal protein S28

Chain Ac: 



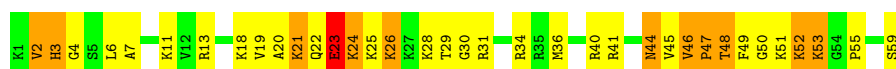
- Molecule 23: 40S ribosomal protein S3

Chain AD: 



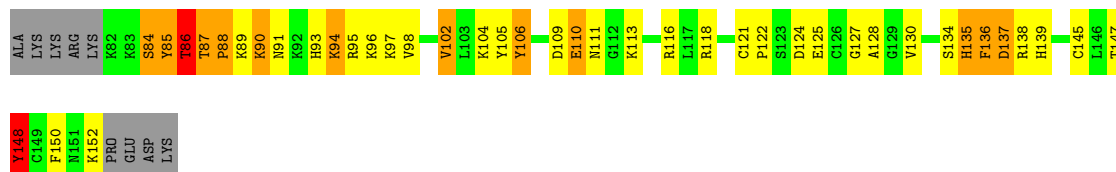
- Molecule 24: 40S ribosomal protein S30

Chain Ae:  39% 41% 19%



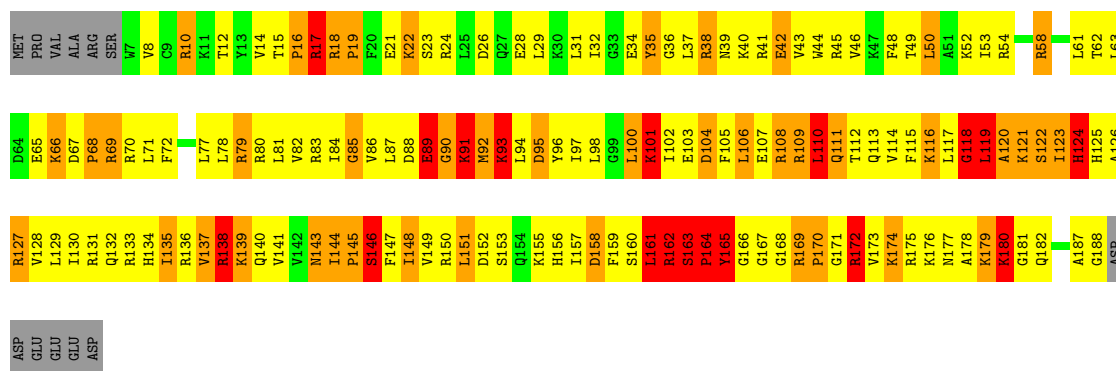
- Molecule 25: 40S ribosomal protein S27a

Chain Af: 36% 35% 15% 11%



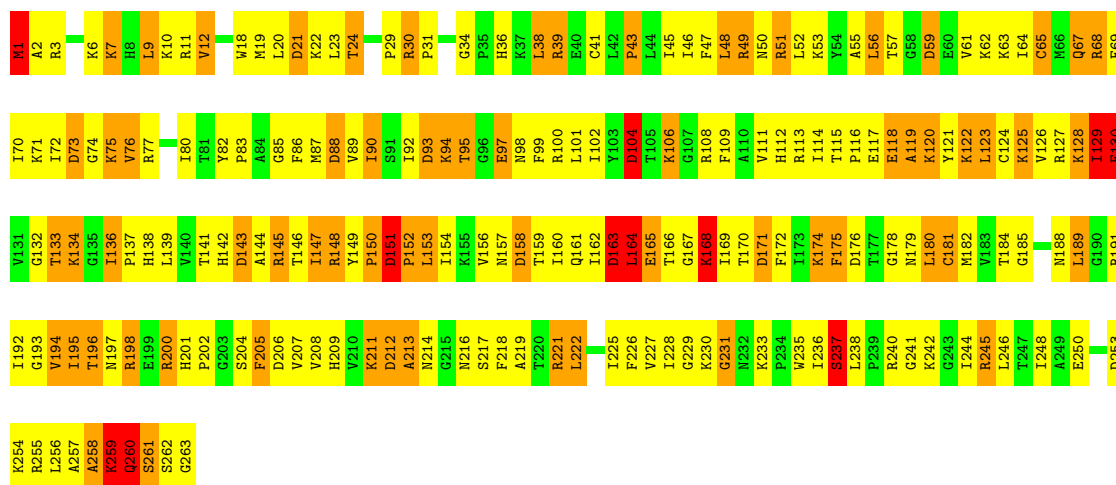
- Molecule 26: 40S ribosomal protein S9

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



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

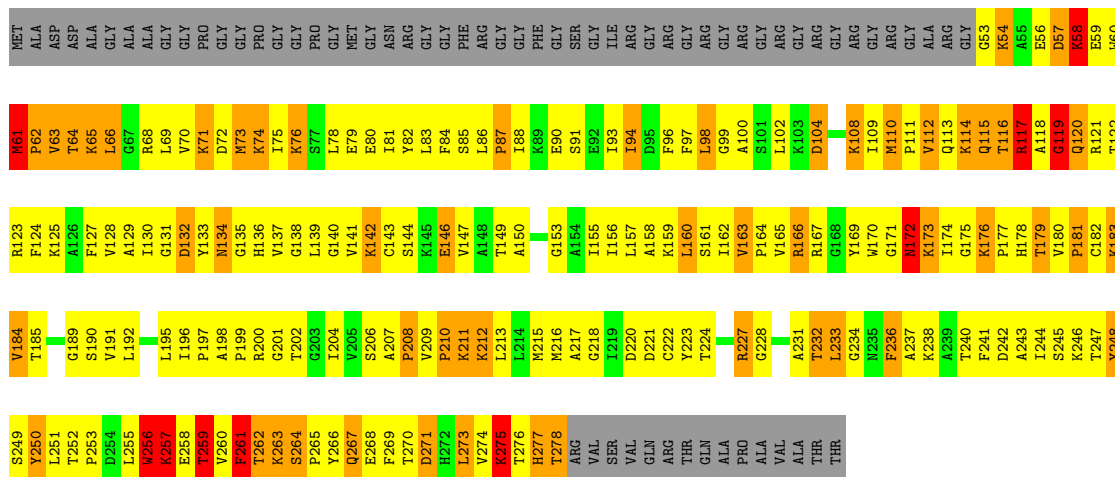
Chain AE: 22% 48% 25%



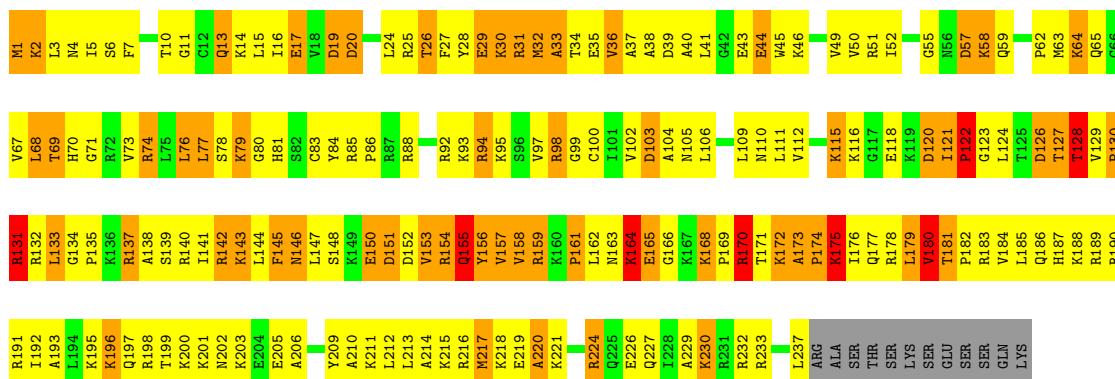
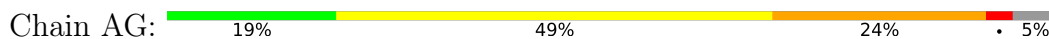
- Molecule 28: 40S ribosomal protein S2

Chain AC: 12% 44% 18% 23%

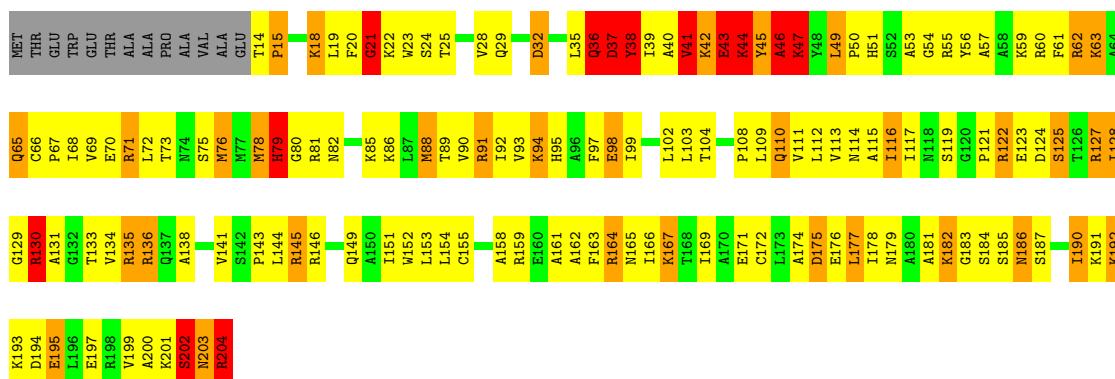




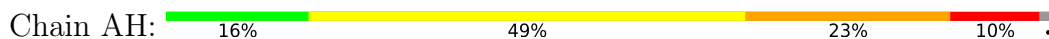
- Molecule 29: 40S ribosomal protein S6

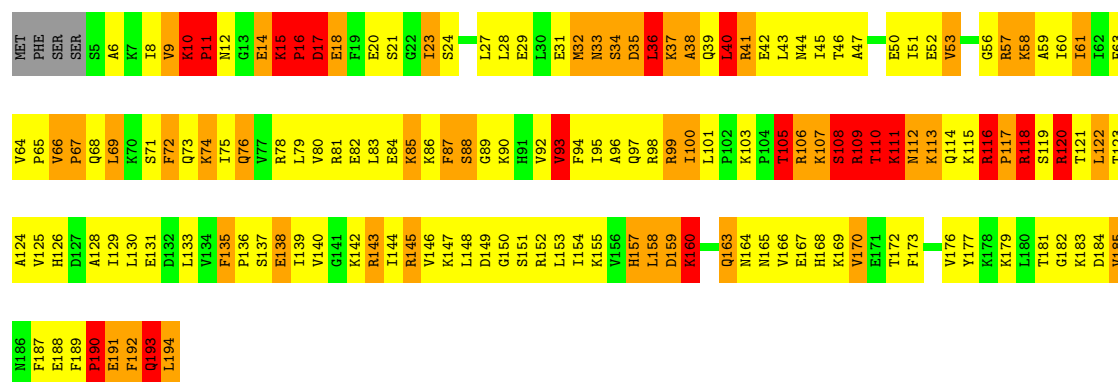


- Molecule 30: 40S ribosomal protein S5



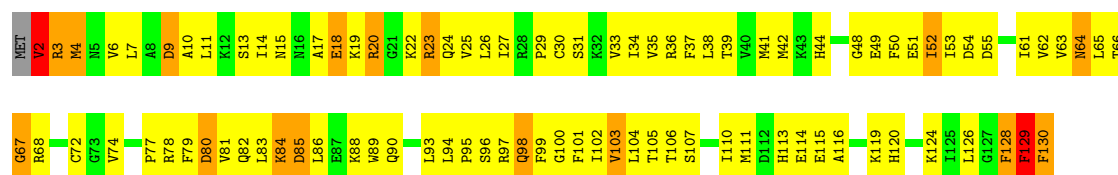
- Molecule 31: 40S ribosomal protein S7





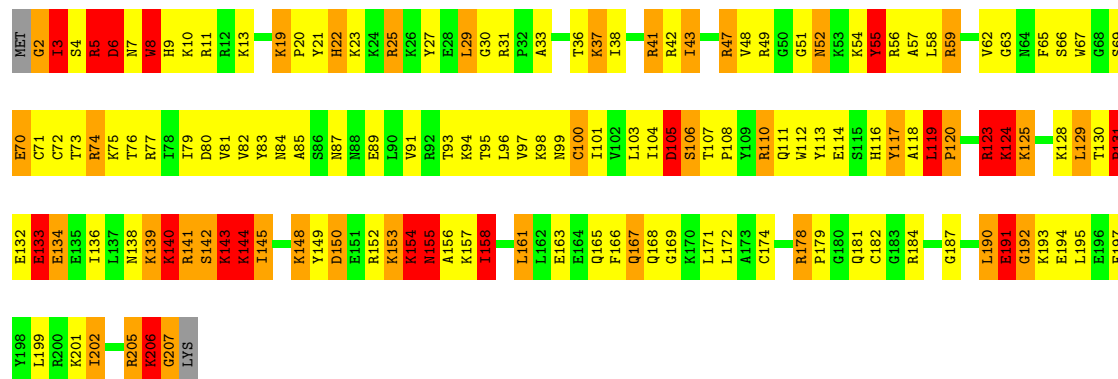
- Molecule 32: 40S ribosomal protein S15a

Chain AW: 28% 58% 12% ..



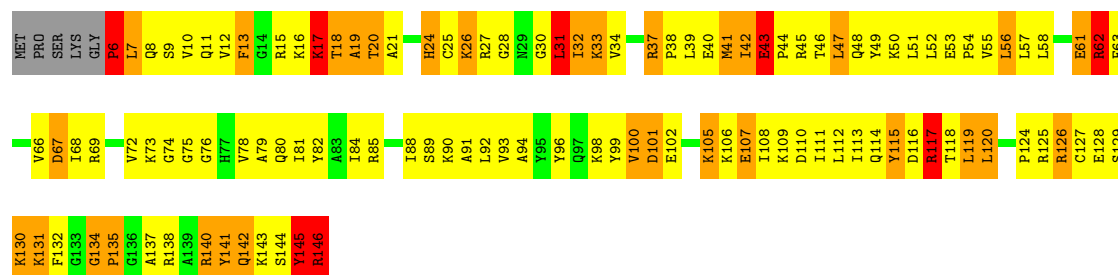
- Molecule 33: 40S ribosomal protein S8

Chain AI: 29% 44% 17% 9% .



- Molecule 34: 40S ribosomal protein S16

Chain AQ: 18% 52% 21% 5% .



- Molecule 35: Plasminogen activator inhibitor 1 RNA-binding protein

Chain Ah:  7% 8% . 82%

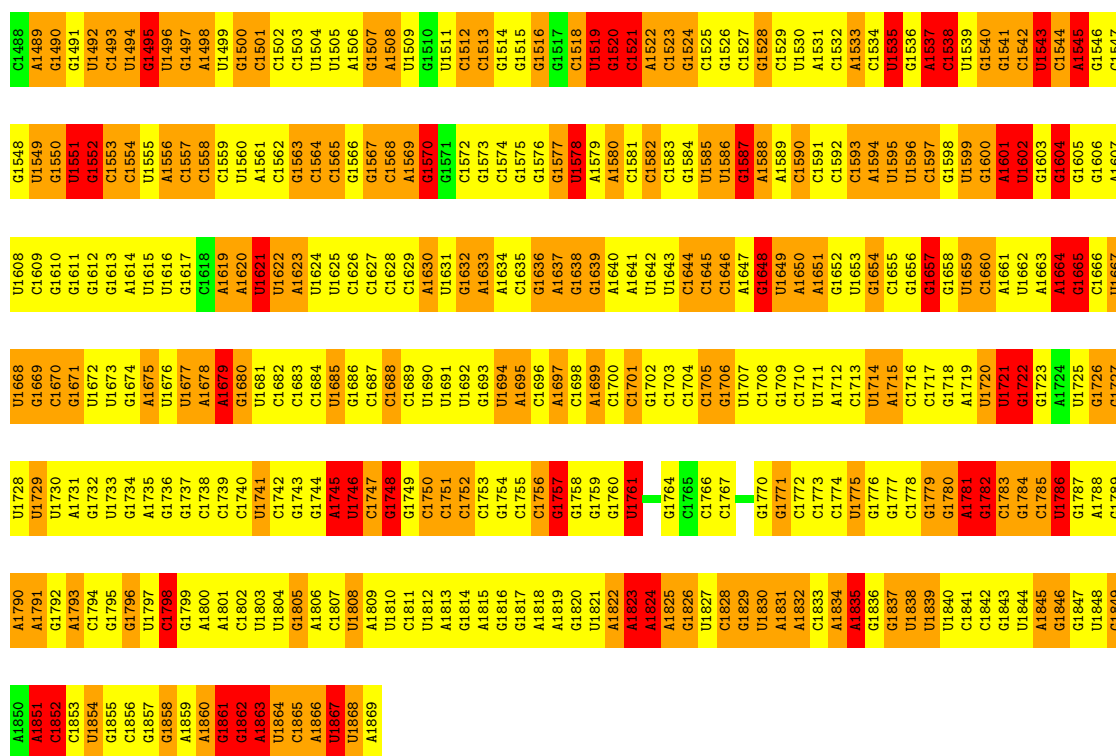
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GLY	ARG	ARG	TYR	G184	LYS	ASN	PRO
GLY	LYS	LYS	ASN	F185	ILE	ASP	GLY
GLY	PRO	PRO	TYR	L186	ASP	ALA	HIS
GLY	ASN	ASN	SER	S187	ILE	GLY	LEU
GLY	GLY	GLY	ASP	R188	ARG	ALA	GLN
GLY	ALA	ALA	LEU	GLY	ARG	GLY	GLY
GLY	ASP	ASP	ASP	LYS	PRO	LYS	PHE
GLY	GLN	GLN	GLN	ARG	GLY	GLN	GLY
GLY	GLY	GLY	SER	PHE	ARG	LEU	GLY
GLY	GLY	GLY	ASN	ASP	ARG	ARG	CYS
GLY	TRP	TRP	VAL	ASP	PRO	LYS	VAL
GLY	LYS	LYS	THR	ARG	PRO	GLY	VAL
ARG	LYS	LYS	GLY	HIS	ARG	SER	THR
PRO	PRO	GLY	GLY	SER	GLY	GLN	ASN
ASN	PHE	PHE	THR	GLY	ARG	LYS	ARG
VAL	VAL	VAL	PRO	SER	ARG	ASP	PHE
LEU	LEU	LEU	GLY	ASP	PHE	ARG	ASP
HIS	HIS	HIS	GLY	ARG	E189	LYS	GLN
LYS	LYS	LYS	GLY	SER	K190	ASN	LEU
SER	SER	SER	GLY	SER	P141	PRO	PHE
ASP	ASP	LYS	HIS	PHE	L142	LEU	ASP
SER	SER	SER	HIS	SER	E143	PRO	ASP
GLY	GLY	GLY	PRO	HIS	E144	PRO	GLY
SER	SER	GLY	VAL	THR	K145	SER	SER
ALA	ALA	ALA	ALA	SER	G146	VAL	ASP
ALA	ALA	ALA	THR	GLY	E147	GLY	PRO
GLY	GLY	GLY	GLY	LEU	G148	VAL	PHE
PRO	PRO	GLY	GLY	LYS	G149	VAL	GLY
ASP	ASP	ASP	ASN	HIS	E150	ASP	VAL
VAL	VAL	LYS	LYS	GLY	P161	LYS	LEU
ASP	ASP	VAL	GLY	ASP	G152	LYS	LYS
PRO	PRO	MET	ASN	LYS	V153	GLY	ALA
GLY	GLY	ASP	GLY	ARG	D154	GLY	ALA
ALA	HIS	VAL	VAL	GLY	R155	THR	GLY
PHE	PHE	GLY	GLY	GLY	P156	GLN	ASN
PRO	PRO	GLY	GLY	SER	I157	PRO	LYS
ALA	ALA	VAL	VAL	GLY	G160	PRO	LYS
LEU	PRO	ARG	LYS	SER	R160	VAL	LYS
ALA	ALA	PRO	HIS	ASN	P161	ALA	GLY
ALA	ASN	ASN	E283	TRP	I162	LEU	ALA
ASP	ASP	ASP	G284	GLY	R166	LYS	GLY
THR	THR	THR	K286	THR	G166	GLY	GLY
THR	THR	THR	D291	GLY	G167	GLY	GLY
GLN	GLN	GLN	D291	ASP	L168	ILE	VAL
LEU	LEU	LEU	K294	LEU	R170	ARG	GLY
GLY	GLY	GLY	K296	THR	G171	VAL	PRO
ILE	ILE	ILE	T296	THR	R172	GLY	PRO
ASN	ASN	ASN	Q297	GLY	G173	ARG	ALA
PHE	PHE	PHE	N298	SER	G174	ARG	LYS
GLY	GLY	GLY	K299	PRO	R175	PRO	SER
ASP	ASP	ASP	D300	LYS	G176	ASP	ALA
LEU	LEU	LEU	K303	TYR	R177	GLN	ALA
GLY	GLY	GLY	VAL	ILE	G178	GLN	ALA
ARG	ARG	ARG	VAL	GLN	M179	LEU	ALA
PRO	PRO	PRO	GLY	LYS	G180	GLN	ALA
GLY	GLY	GLY	PHE	GLY	R181	GLY	GLY
ASN	ASN	ASN	ASN	ILE	G182	GLY	GLN

- Molecule 36: 18S ribosomal RNA

Chain B2: 7% 50% 33% 10%

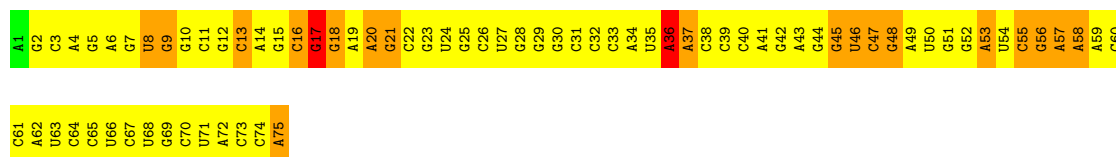
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G446	C386	C246	C186	U124	A64	C4
A447	G387	G327	G187	C125	G65	U5
U448	U388	U252	C188	G126	G66	G6
A449	G389	G329	U188	C127	G67	G7
C450	C390	G282	G190		A68	U8
G451	C391	G331	A191	C131	C69	U9
A452	A392	G286	C192	U132	G70	G10
G453	U393	G334	C193	C133	G71	A11
U454	G394	C271	C194	G134	C72	U12
A455	G395	G272	C195	U135	G73	C13
C456	U396	G273	C196	C136	G74	U14
G457	C397	G274	U197	U137	G75	C15
U458	A398	C275	C198	G137	G76	U16
C459	G399	G276	U198	C139	A77	C17
A460	C400	C340	G200	C140	C78	C18
U461	A401	C341	C201	A141	A79	A19
C462	G402	G280	G202	C142	G80	G20
A463	G403	G281	C203	U143	U81	U21
U464	C404	G282	G204	C144	G82	A22
A465	G405	G283	G205	U145	A83	G23
C466	U406	C284	G206	G146	A84	C24
G467	G407	U285	G207	C147	A85	A25
		G286	C208	U148	C86	U26
		G287	G209	C149	U87	A27
A468	C408	C348	A209	U150	G88	U28
U469	G409	G288	G210	A150	C89	G29
C470	G410	C289	G211	C151	G90	C30
G471	C411	U290	C212	U152	A91	U31
U472	G412	G291	G213	G153	A92	C32
A473	C413		U214	C154	U93	G33
G474	A414	U294	G215	G155	G94	U34
C475	U415	C295	C216	C156	G95	C35
U476	A416	G355	G217	U157	C96	U36
A477	C417	C357	A217	A158	U97	C37
G478	U418	C358	U218	C159	C98	A38
C479	G419	U359	U219	U160	A99	U39
U480	C420	A360	G220	C162	U100	A40
A481	G421	U361	A221	U161	C41	G41
C482	U422	C362	U222	C163	U101	A42
G483	U423	A363	C223	A164	A102	C43
A484	C424	C364	A224	G165	A103	U44
	G425	C365	G225	C166	U105	A45
	A426	C366	A226	G167	C106	A46
	U427	U367	G227	C168	A107	G47
A488	U428	C368	C228	U169	C108	C48
U489	C429	C369	A229	A170	U109	G49
C490	G430	G370	C230	A171	U110	A50
A491	C431	C371	A231	C172	A111	U51
C492	G432	A372	C232	C173	U112	G52
A493	A433	U373	C233	C174	G113	C53
C494	G434	G374	C234	A175	C114	A54
U495	A435	U375	A235	U176	U115	U55
A496	G436	C376	G236	G177	C116	G56
C497	U437	U377	C237	C178	C117	U57
G498	A438	G378	A238	C179	C118	C58
U499	C439	C379	C239	G180	U119	A59
A500	G440	G380	G240	C181	U120	G60
C501	U441	C381	C241	C182		
G502	C442	C382	G242			

G1428	U1368	C1247	G1187	G1126	U1066	C1006	U945	U885	A825	U749	C624	A564	G504
G1429	A1369	U1248	A1188	C1127	C1067	C1007	U946	A886	A826	C750	G625	G565	G505
G1430	A1370	C1249	A1189	C1128	U1068	A1008	G947	U887	A827	G751	G626	U566	G506
C1431	U1371	A1250	A1190	G1129	U1069	A1009	C948	U888	G828	G752	U627	C567	G507
C1432	U1372	C1251	C1191	G1130	A1070	G1010	G949	U889	C829	C753	A628	C568	A508
C1433	G1373	C1252	C1192	G1131	G1071	A1011	C950	U890	A830	G754	A629	A569	G509
C1434	C1374	A1253	U1193	C1132	U1072	A1012	C951	G891	G831	C755	U630	C570	G510
C1435	G1375	C1254	A1194	A1133	U1073	U1013	G952	U892	G832	C756	U631	U571	G511
C1436	A1376	G1255	A1195	G1134	C1074	U1014	C953	U893	G833	C757	G632	U572	A512
A1437	U1377	G1256	A1196	C1135	C1075	U1015	U954	G894	C834	C758	C633	U573	G513
A1438	C1378	G1257	G1197	U1136	G1076	U1016	A955	G895	C835		A634	A574	U514
A1439	A1378	A1258	G1198	U1137	A1077	U1017	G956	U896	A836	U767	G635	A575	G515
C1440	C1380	A1259	A1199	G1138	C1078	U1018	A957	U897	A837		C536	A576	A516
U1441	G1381	A1260	A1200	C1139	C1079	C1019	G958	U898	G838	U770	U637	U577	C517
U1442	A1382	C1261	U1201	G1140	A1080	A1020	G959	U899	C839	A771	C638	C578	G518
C1443	C1383	C1262	U1202	G1141	U1081	U1021	U960	C900	C840	G772	C639	C579	A519
U1444	C1384	U1263	G1203	G1142	U1082	U1022	A961	G901	G841	C773	G700	U580	A520
U1445	G1385	C1264	A1204	A1143	A1083	A1023	G962	G902	C842		A641	U581	A521
A1446	A1386	C1265	C1205	A1144	A1084	A1024	A963	A903	C843	U780	U642	U582	A522
G1447	U1387	G1266	G1206	A1145	C1085	U1025	A964	A904	U844		A643	A583	A523
G1448	C1388	C1267	G1207	C1146	G1086	C1026	U965	C905	G845	G784	A644	A584	U524
G1449	U1389	C1268	A1208	C1147	A1087	A1027	U966	U906	G846	C785	C645	C585	A525
G1450	C1390	G1269	A1209	A1148	U1088	A1028	C967	G907	A847	G786	G646	C586	A526
G1451	C1391	G1270	G1210	A1149	U1089	G1029	U968	A908	U848	G787	U647	A587	C527
A1452	U1392	C1271	G1211	A1150	C1090	A1030	U969	G909	A849	G788	G648	G588	A528
C1453	G1393	C1272	G1212	G1151	C1091	A1031	G970	G910	C850	G789	U649	G589	A529
A1454	U1394	C1273	U1152	C1153	G1092	C1032	G971	C911	C851	G790	A650	A590	U530
A1455	C1395	G1274	A1214	U1153	A1093	G1033	A972	C912	G852	C791	U651	U591	A531
G1456	A1396	G1275	C1215	U1154	C1094	A1034	C973	A913	C853	C792	U652	C592	C532
U1457	U1397	A1276	U1155	U1155	C1095	A1035	C974	U914	A854	G793	A653	C593	A533
G1458	G1398	C1277	U1217	U1156	G1096	A1036	G975	G915	G855	A794	A654	A594	G534
G1459	C1399	A1278	C1218	G1157	C1097	G1037	G976	A916	C856	G795	A655	U595	G535
C1460	U1400	C1279	C1219	G1158	C1098	U1038	G977	U917	U857	G796		U596	A536
G1461	A1401	G1280	A1220	U1159	G1099	C1039	C978	U918	A858	C797	U657	G597	C537
U1462	A1402	G1281	G1221	U1160	A1100	G1040	A980	A919	G859	G798	G658	G598	U538
C1463	U1342	A1282	G1222	U1161	U1101	G1041	A920	A920	G860	C723	G659	A599	C539
C1464	A1404	C1283	A1223	C1162	G1102	A1042	A981	G921	A861	U800	C660	G600	U540
A1465	A1405	A1284	G1224	C1163	C1103	G1043	G982	A922	A862	U801	U661	G601	U541
G1466	G1406	G1285	U1225	G1164	G1104	U1044	A983	G923	U863	C726	G662	G602	U542
C1467	U1407	G1286	G1226	G1165	G1105	U1045	C984	G924	A864	C803	C663	C603	C543
C1468	U1408	A1287	G1227	G1166	C1106	U1046	G985	A925	A865	C730	G664	A604	A544
A1469	G1348	U1288	G1228	G1167	G1107	C1047	G986	G926	U866	G731	U665	A605	A545
C1470	C1409	U1289	G1229	G1168	G1108	G1048	A987	C927	G867	U732	U666	G606	G546
G1471	U1350	G1290	C1230	G1169	C1109	A1049	C988	G928	G868	U733	U667	U607	G547
C1472	G1351	A1291	C1231	A1170	G1110	U1050	C989	G929	A869	C608		C608	C548
G1473	C1352	G1292	U1232	G1171	U1111	G1051	A990	C930	C870	U609	A669	U609	C549
A1474	A1414	C1293	U1233	U1172	U1112	A1052	G991	C931	U871	C735	A670	G610	C550
C1475	G1415	G1294	C1234	A1173	A1113	C1053	A992	G932	A872	C736	A671	G611	U551
G1476	C1416	A1295	G1235	U1174	U1114	G1054	G993	G933	G873	G737	A672	U612	G552
U1477	C1417	U1296	G1236	G1175	U1115	A1055	C994	G934	G874	C738	G673	G613	U553
C1478	U1358	U1297	C1237	G1176	C1116	U1056		G935	A875	C739	C674	C614	A554
G1479	U1359	U1298	U1238	U1177	C1117	C1057		G936	C876	C740	U675	C615	A555
A1480	G1420	A1299	U1239	U1178	U1118	A1058	A998	C937	C877	C741	C676	A616	U556
G1481	G1361	U1300	A1240	G1179	A1119	G1059	G999	A938	G878	U742	G677	G617	U557
C1482	A1421	U1301	A1241	C1180	U1120	U1060	U939	U939	C879	U743	U678	C618	G558
C1483	G1422	G1302	U1242	A1181	G1121	A1061	A1000	U940	G880	G744	A679	A619	G559
A1484	G1424	C1303	U1243	A1182	A1122	A1062	U1002	C941	G881	C745	G680	G620	A560
U1485	G1425	U1304	U1244		C1123	C1063	U1003	G942	U882	C746	G681	C621	A561
A1486	U1486	G1365	G1245	C1185	C1185	C1064	U1004	U943	U883	U747	U682	C622	U562
A1487	C1427	U1306	A1246	U1186	C1125	G1065	G1005	A944	C884	C748	G683	G623	G563



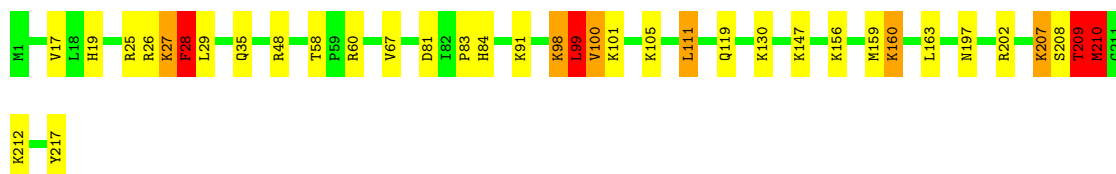
• Molecule 37: E-tRNA

Chain BC: 72% 24%



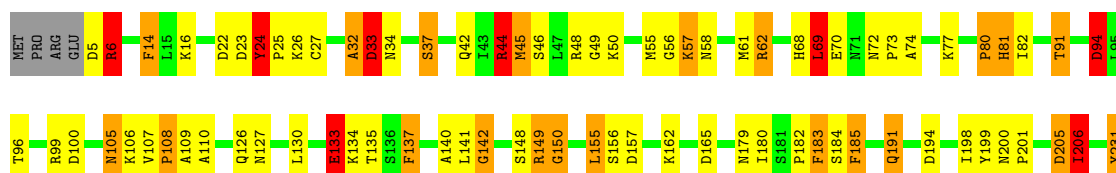
• Molecule 38: 60S ribosomal protein L10a

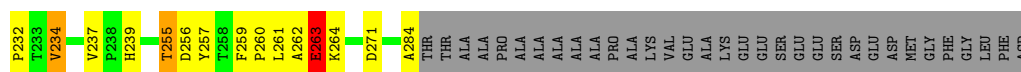
Chain Cz: 83% 12%



• Molecule 39: 60S acidic ribosomal protein P0

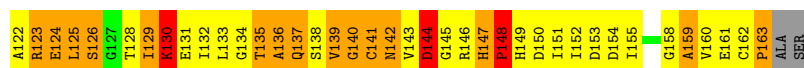
Chain Cq: 58% 20% 7% 12%





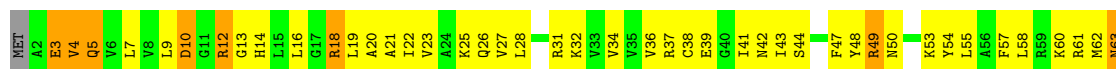
• Molecule 40: 60S ribosomal protein L12

Chain CK: 8% 44% 29% 18%



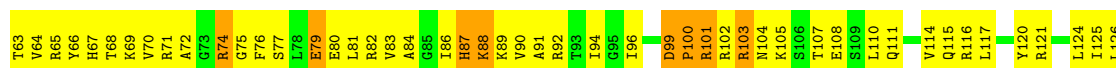
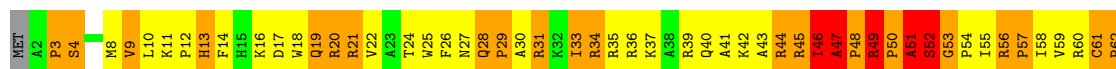
• Molecule 41: 60S ribosomal protein L13a

Chain CO: 29% 49% 21%



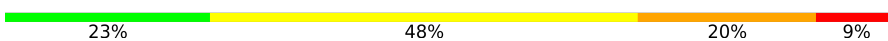
• Molecule 42: 60S ribosomal protein L13

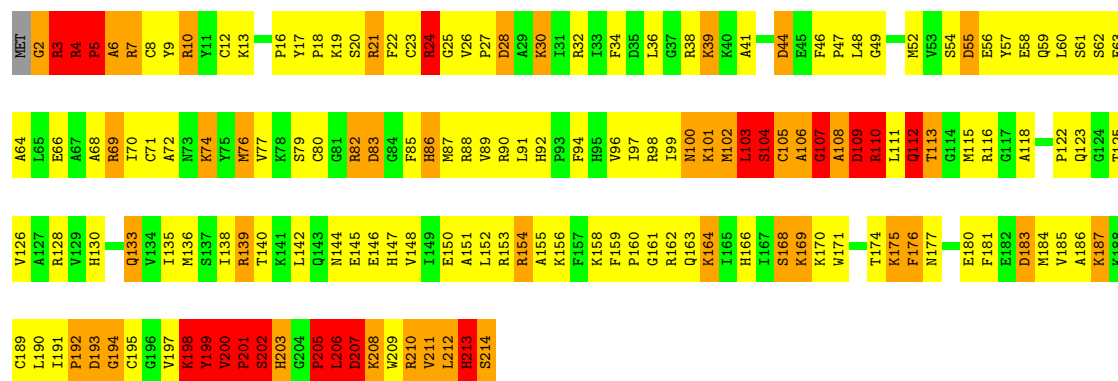
Chain CL: 23% 45% 23% 9%



• Molecule 43: 60S ribosomal protein L23

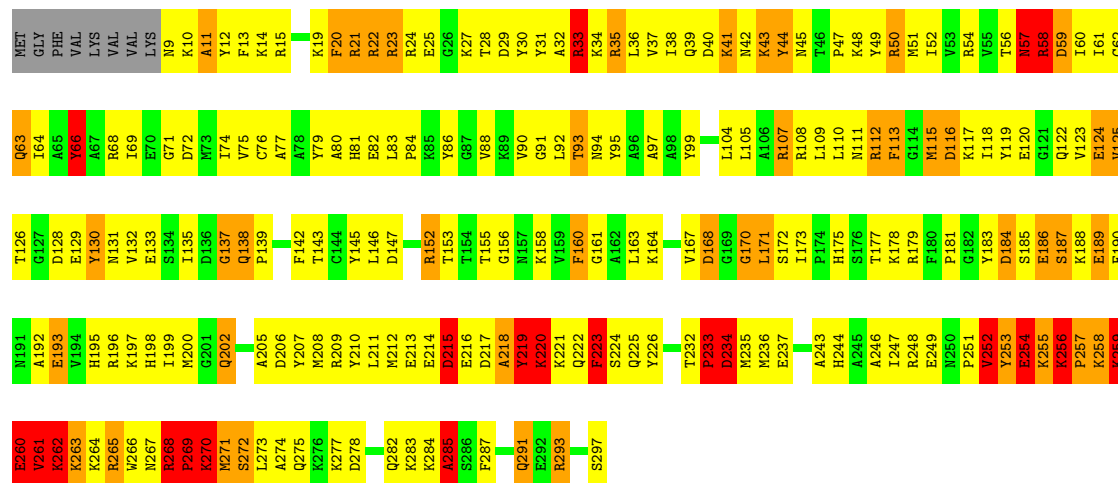
Chain CV: 31% 48% 15% 5%

Chain CI: 

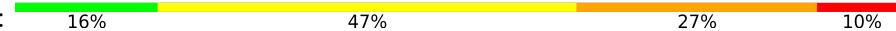


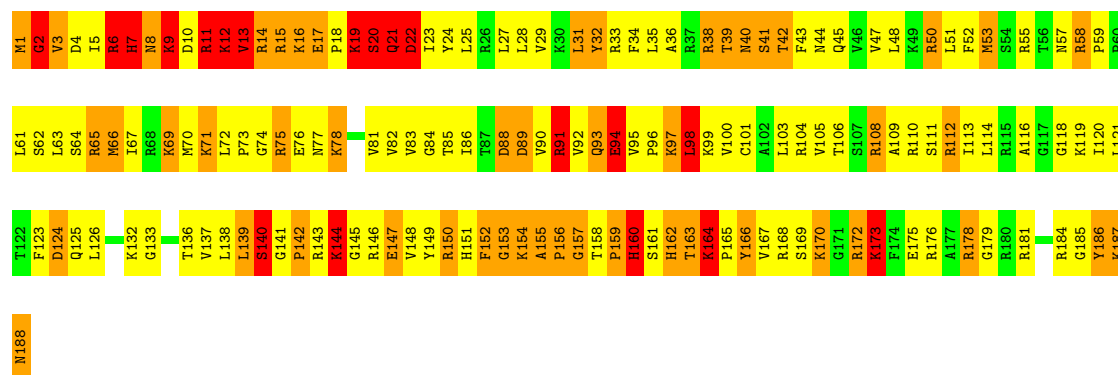
• Molecule 48: 60S ribosomal protein L5

Chain CD: 

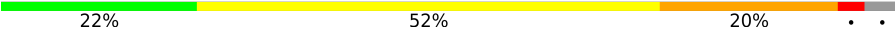


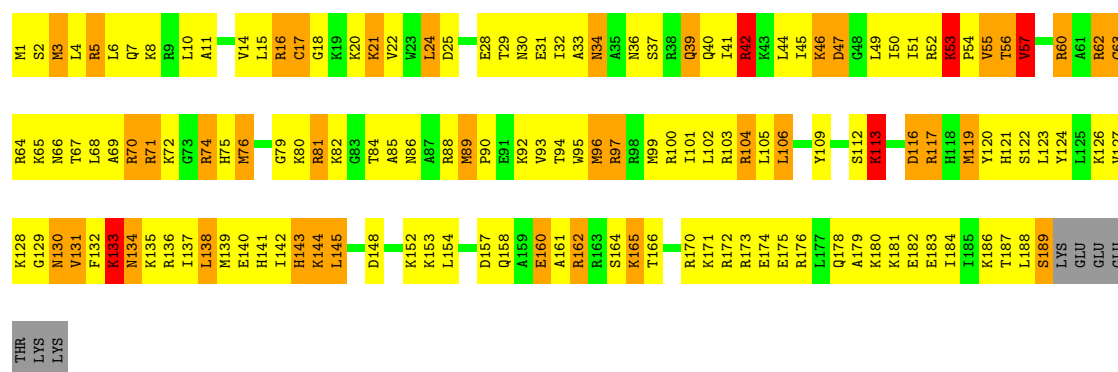
• Molecule 49: 60S ribosomal protein L18

Chain CQ: 



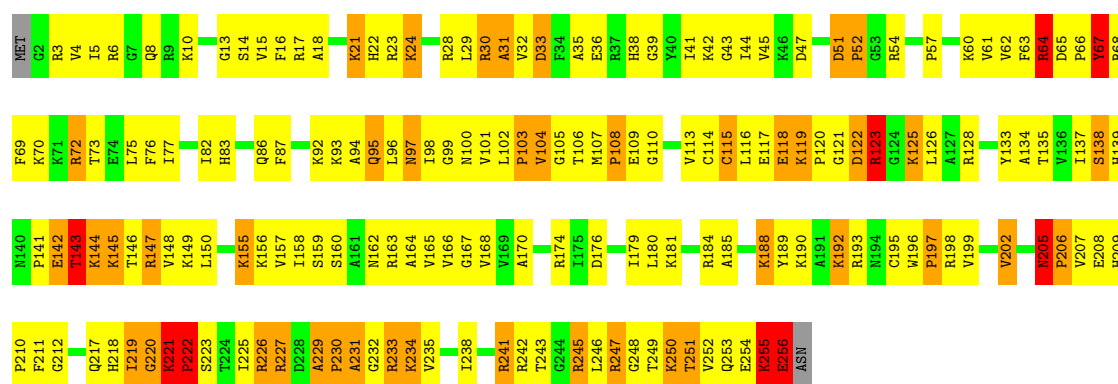
• Molecule 50: 60S ribosomal protein L19

Chain CR:  22% 52% 20%

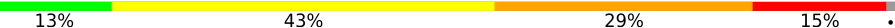


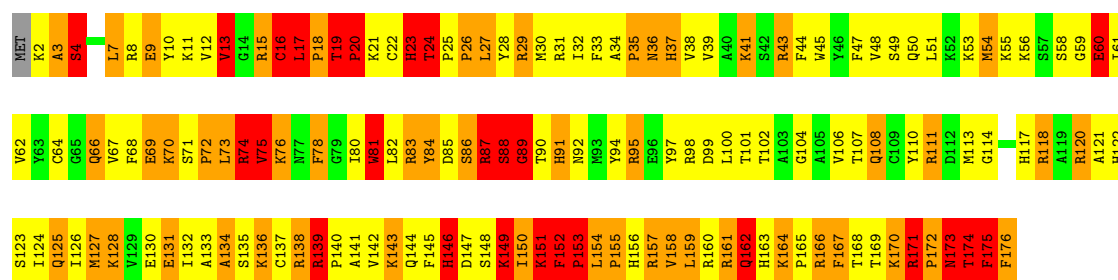
- Molecule 51: 60S ribosomal protein L8

Chain CA:  30% 49% 17%




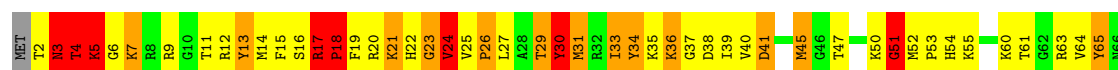
- Molecule 52: 60S ribosomal protein L18a

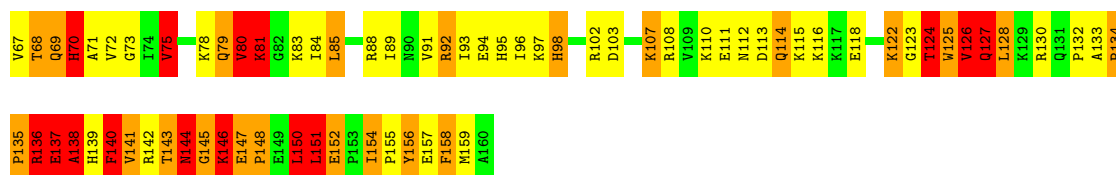
Chain CS:  13% 43% 29%



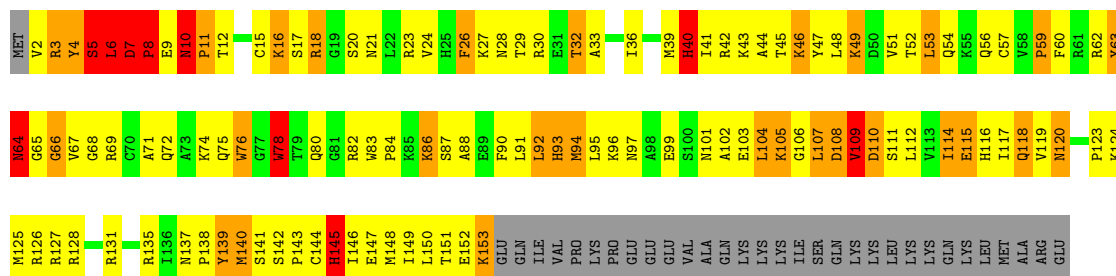
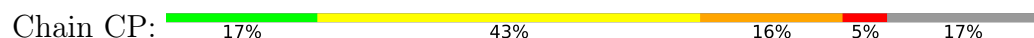
- Molecule 53: 60S ribosomal protein L21

Chain CT:  24% 39% 22%

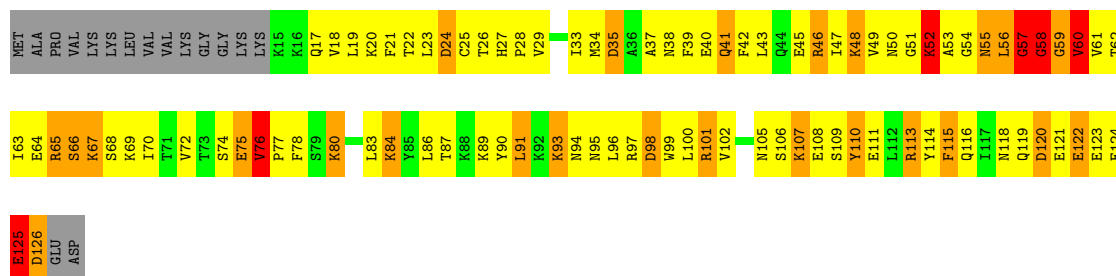
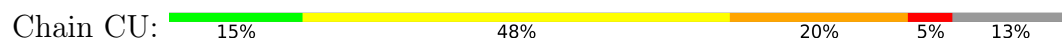




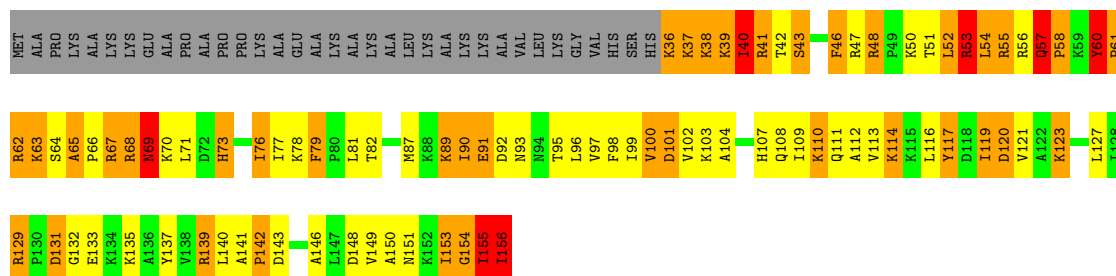
- Molecule 54: 60S ribosomal protein L17



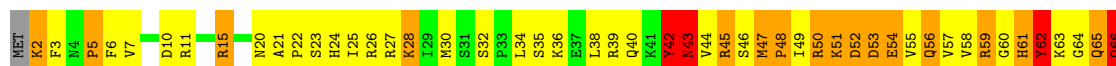
- Molecule 55: 60S ribosomal protein L22

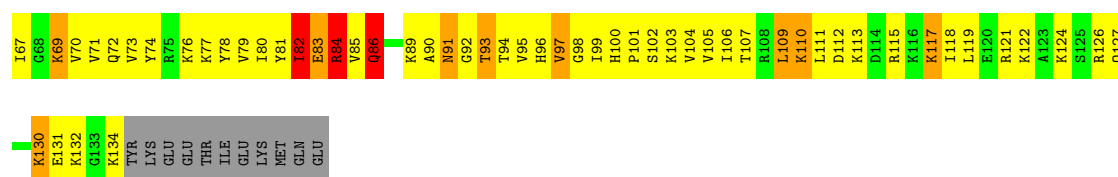


- Molecule 56: 60S ribosomal protein L23a

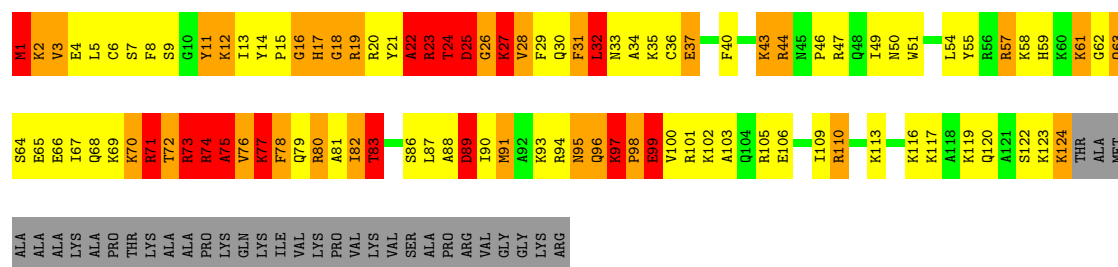


- Molecule 57: 60S ribosomal protein L26

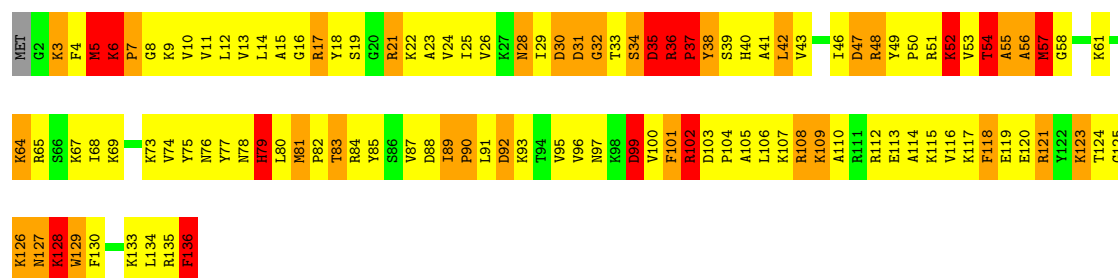
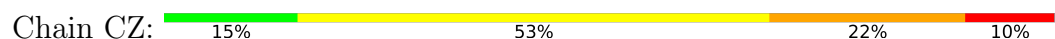




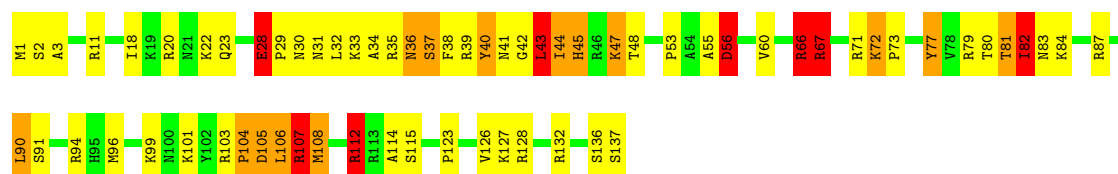
• Molecule 58: 60S ribosomal protein L24



• Molecule 59: 60S ribosomal protein L27



• Molecule 60: 60S ribosomal protein L28

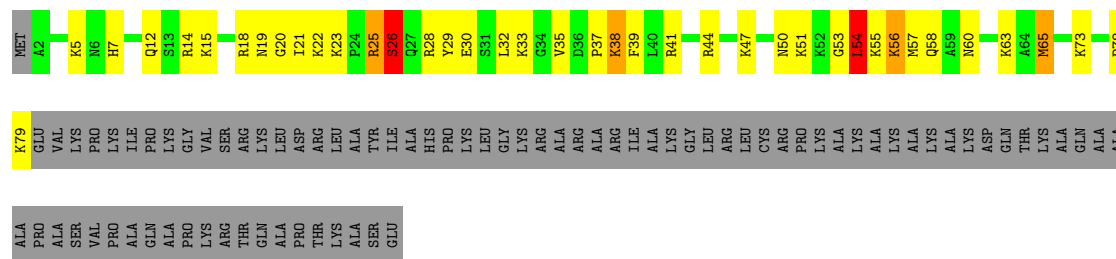


• Molecule 61: 60S ribosomal protein L35

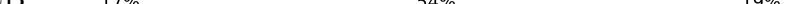


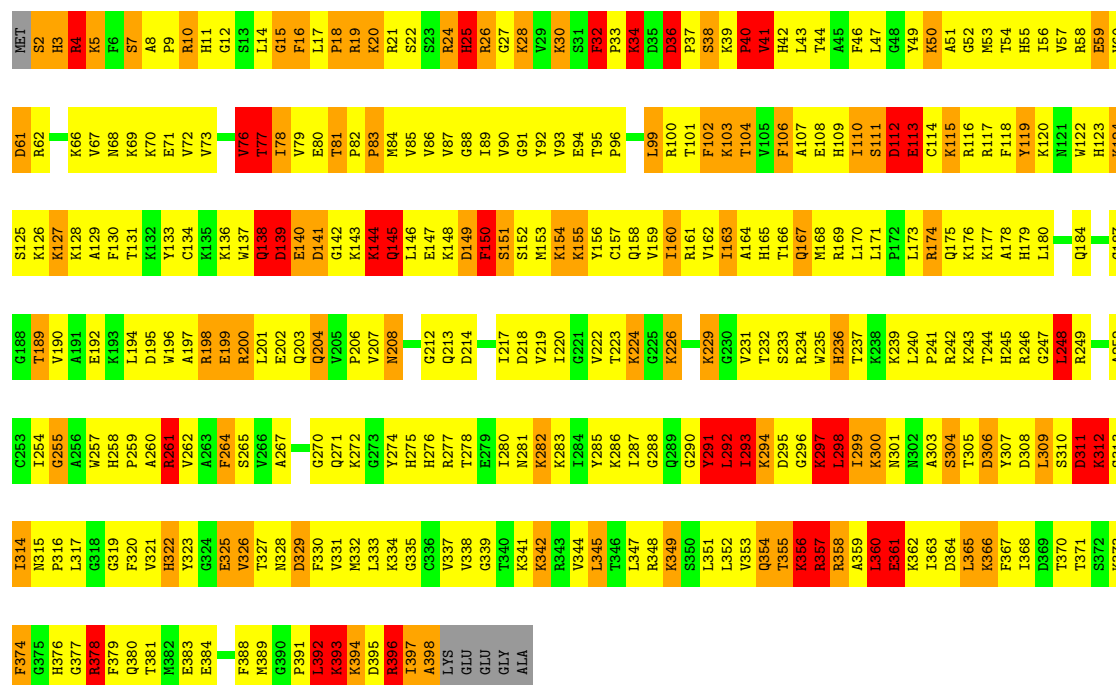
- Molecule 62: 60S ribosomal protein L29

Chain Cb:  25% 21% . . 51%



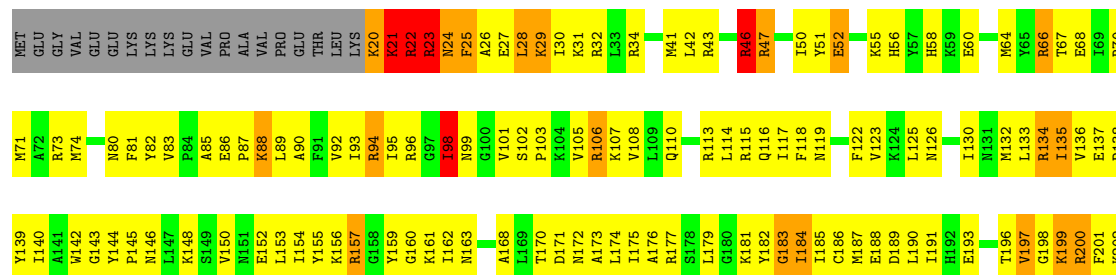
- Molecule 63: 60S ribosomal protein L3

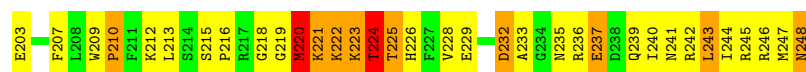
Chain CB: 



- Molecule 64: 60S ribosomal protein L7

Chain CF: 





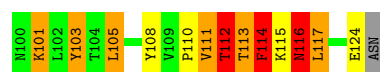
- Molecule 65: 60S ribosomal protein L30

Chain Cc: 70% 13% 13%



- Molecule 66: 60S ribosomal protein L31

Chain Cd: 53% 26% 8% 10%



- Molecule 67: 60S ribosomal protein L32

Chain Ce: 61% 25% 11%



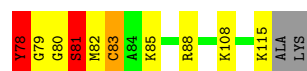
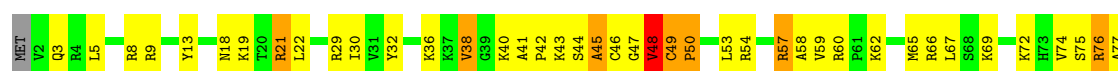
- Molecule 68: 60S ribosomal protein L35a

Chain Cf: 55% 25% 15%

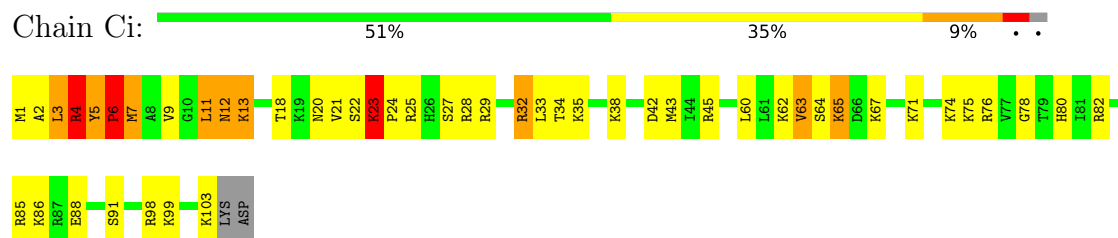


- Molecule 69: 60S ribosomal protein L34

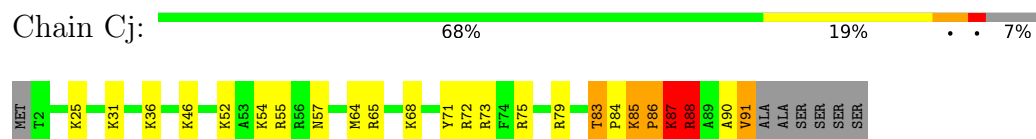
Chain Cg: 54% 34% 7%



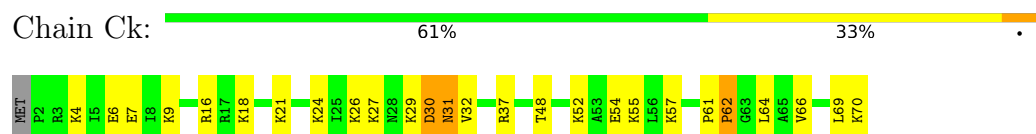
- Molecule 70: 60S ribosomal protein L36



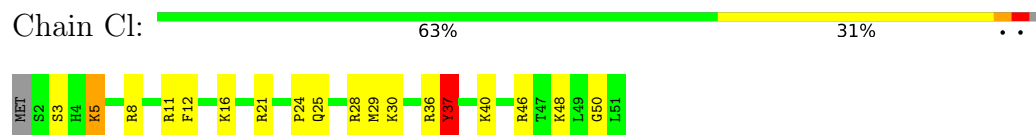
- Molecule 71: 60S ribosomal protein L37



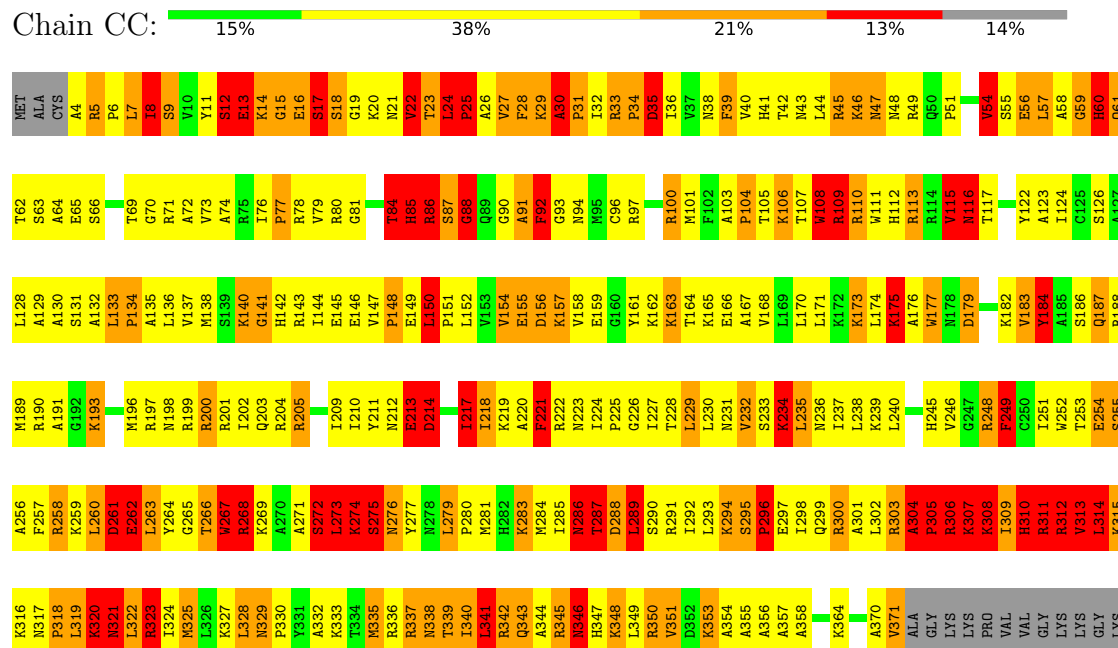
- Molecule 72: 60S ribosomal protein L38



- 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
Q21
R22
R23
S24
K25

- Molecule 77: 60S ribosomal protein L37a

Chain Cp:  68% 27% ••

ME1
ALA
K3
R4
T5
K6
R17
Y18
K24
M25
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

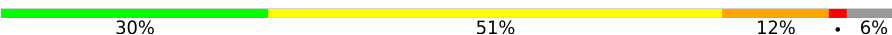
- Molecule 78: 60S ribosomal protein L36a

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%

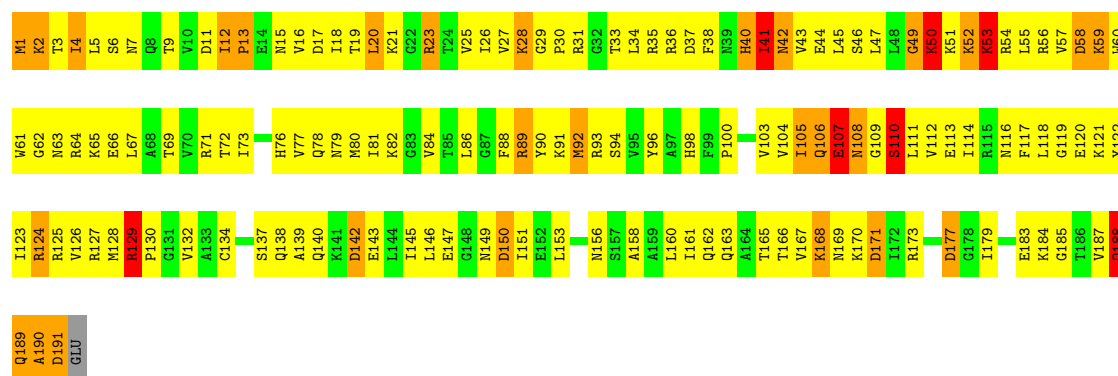
ME1
ALA
GLN
ASP
GLN
GLY
GLU
LYS
E9
P10
P11
M12
M13
E14
L15
R16
I17
R18
K19
L20
C21
L22
V26
S29
G30
D31
Q32
L33
T34
R35
A36
A37
K38
Q42
L43
P48
V49
F50
A53
R54
Y55
T56
P57
R58
S59
F60
G61
I62
R63
R64
N65
I68
A69
V70

H71
C72
T73
V74
R75
A79
I82
L83
E84
K85
G86
L87
R88
W89
E90
E91
Y92
E93
L94
R95
K96
N97
N98
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
F138
G139
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

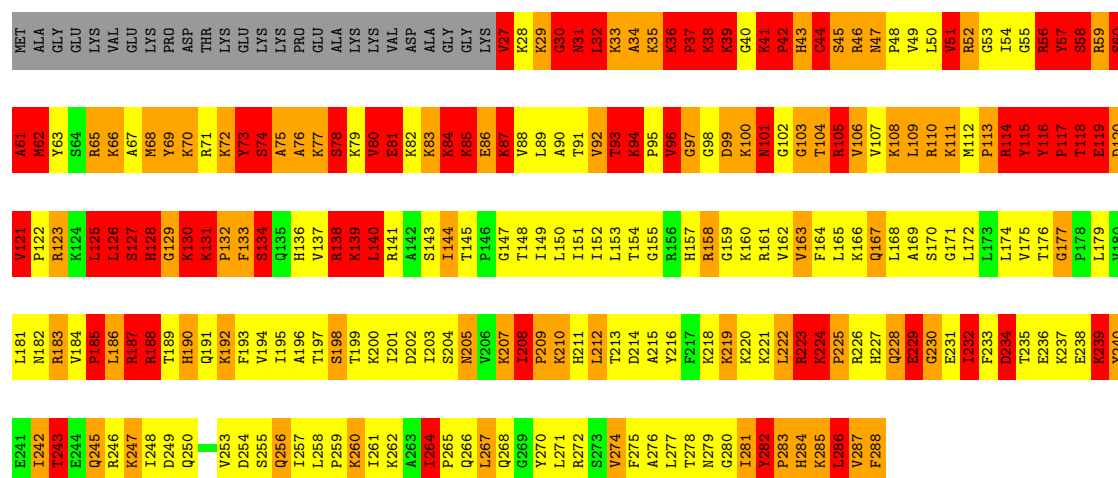
- Molecule 80: 60S ribosomal protein L9

Chain CH:  22% 59% 15% ••



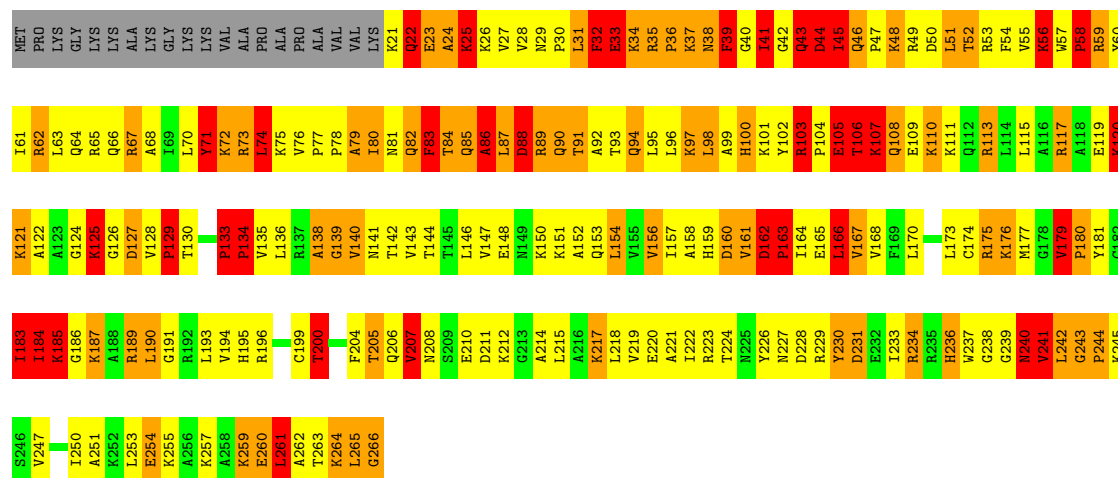
• Molecule 81: 60S ribosomal protein L6

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 GLU ALA LYS LYS LYS GLU SER GLU SER ASP

ASP ASP MET GLY PHE GLY 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 GLU ALA LYS LYS LYS GLU SER GLU SER ASP

ASP ASP MET GLY PHE GLY 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 ALA VAL ALA SER ALA ALA PRO GLY SER ALA ALA PRO GLY SER ALA ALA ALA ALA LYS LYS LYS ASP ASP

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 ALA VAL ALA SER ALA ALA PRO GLY SER ALA ALA PRO GLY SER ALA ALA ALA ALA LYS LYS LYS ASP ASP

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

• Molecule 85: 28S ribosomal RNA

Chain A5: 

G1 G2 C3 G4 A5 C6 C7 U8 C9 A10 G11 A12 G14 C14 A15 G16 A17 C18 G19 U20 G21 G22 G23 G24 A25 C26 C27 C28 G29 G30 G31 G32 G33 G34 A35 A36 A37 U38 A39 A40 G41 G42 A43 A44 A45 A46 A47 G48 U49 C50 A51 G52 C53 G54 G55 G56 G57 G58 A59 G60 A61 A62

G63 A64 A65 A66 C67 U68 A69 U70 C71 A72 A73 G74 G75 G76 A77 U78 C79 A80 C81 U82 C83 A84 G85 G86 A87 A88 C89 G90 G91 G92 G93 A94 A95 A96 U97 A98 A99 C100 A101 G102 A103 G104 A105 A106 G107 A108 G109 A110 C111 C112 A113 G114 G115 G116 G117 G118 G119 A120 A121 A122

C123 C124 C125 C126 G127 C128 C129 C130 C131 C132 C133 A134 G135 G136 G137 G138 G139 G140 C141 G142 C143 G144 G145 G146 A147 C148 A149 U150 G151 G152 G153 G154 G155 G156 U157 G158 A159 C160 G161 G162 A163 G164 A165 C166 C167 C168 G169 C170 U171 C172 C173 C174 C175 G176 G177 C178 G179 C180 C181 A182

A1303	C1243	G1183	C1099	G	C	G	C736	G676	A	C485	U425	G364	C303	A243	C183
C1304	G1244	A1184	U1100	A	G	G	C737	G677	G	C486	A426	U365	C304	G244	U184
C1305	C1245	G1185	C1101	C	G	C	C738	G678	G	C487	A427	A366	A305	C245	C185
C1306	C1246	U1186	U1102	G	G	C	C739	G679	G	C488	A428	C367	A306	G246	G186
A1307	U1247	G1187	C1103	G	C880	C	G740	G680	G	C489	A429	C368	A307	G247	U187
C1308	C1248	C1188	C1104	G	G881	C	C741	G681	G	C490	G430	C369	G308	G248	G188
C1309	C1249	C1189	C1105	G	G882	C	G742	G682	C	C491	G431	U370	C309	C249	G189
C1310	C1250	C1190	A1106	G	G883	C	G743	G683	C	U492	U432	A371	G310	C250	G190
C1311	C1251	C1191	A1107	U	G884	C	G744	G684	C	U493	A433	A372	G311	C251	G191
C1312	C1252	C1192	C1108	U	G885	C	G745	G685	C599	U494	A434	G373	G312	C252	G192
C1313	C1253	C1193	C1109	C	G886	C	G746	G686	C	U495	A435	G374	U313	G253	G193
C1314	A1254	G1194	C1032	C	C902	C	A747	U687	C608	U496	C436	G375	G314	G254	C194
C1315	A1255	G1195	C1033	U	C903	U	G748	U688	C	U497	G437	A376	G315	C255	C195
G1316	G1256	G1196	G1044	C	C904	C	G749	U689	C	C498	G438	A377	U316	G256	C196
U1317	A1257	G1197	G1045	C	C905	C	C750	G690	C	C499	G439	A378	A317	C257	A197
C1318	G1258	G1198	C1047	C	C906	C	U751	G691	C	G500	U440	G379	A318	G258	A198
U1319	G1259	G1199	C1048	C	C907	C	G752	G692	C	C501	U441	U380	A319	C259	G199
U1320	G1260	G1200	C1049	U	A908	U	C753	G693	C	C502	G442	U381	C320	C260	U200
C1321	G1261	U1201	C1050	G	C909	G	U754	G694	C	C503	G443	G382	U321	G261	C201
A1322	G1262	C1202	C1051	G	U911	G	C755	G695	C	C504	G444	A383	C322	G262	C202
C1323	A1263	C1203	C1052	G	G912	G	G756	G696	C	G505	U445	A384	C323	G263	U203
A1324	C1264	C1204	C1053	A	U913	A	G757	G697	C	C506	C446	A385	A324	C264	U204
C1325	G1265	G1205	C1059	G	U914	G	G758	G698	C	G507	C447	A386	U325	C265	C205
C1326	G1266	C1206	C1059	G	A915	G	G759	G699	C	G508	G448	G387	C326	C266	U206
C1327	G1267	C1207	C1059	G	C916	G	C760	G700	C	A509	G449	A388	U327	G267	G207
G1328	G1268	G1208	G1063	C	A917	C	C768	G701	C	U510	G450	A389	A328	G268	A208
G1329	G1269	U1209	G1064	C	G918	C	G768	G702	C	C511	C451	C390	A329	G269	U209
C1330	A1270	C1210	G1065	G	U919	G	G768	G703	C	C512	A452	U391	G330	U270	C210
C1331	G1271	G1211	C1066	C	C920	C	U768	G704	C	U513	G453	U392	C331	C271	G211
C1332	C1272	G1212	G1067	G	C921	C	C	G705	C	U514	U454	U393	C332	U272	A212
A1333	G1273	G1213	C1068	G	C922	G	C	G706	C	C515	C455	G394	U333	U273	G213
A1334	A1274	C1214	C1069	G	C923	G	C	G707	C	C516	C456	A395	A334	C274	G214
G1335	G1275	C1215	G1070	G	C924	G	U	G708	C	C517	G457	A396	A335	C275	C215
C1336	C1276	G1216	C1071	C	C925	C	C	G709	C	G518	C458	G397	A336	C276	C216
A1337	G1277	G1217	C1072	U	G926	U	C	G710	C	C519	C459	A398	U337	G277	C217
G1338	C1278	G1218	G1073	G	C927	G	U	A711	C	C520	C460	A399	C338	G278	A218
U1339	A1279	G1219	G1074	G	C928	G	C	G712	C	C521	G461	A400	C339	A279	G219
C1340	G1280	G1220	C1075	G	A929	G	C	G713	C	C522	G462	A402	C340	G280	C220
U1341	G1281	G1221	C1076	G	U930	G	U	G714	C	C523	A463	A403	G341	U281	C221
A1342	A1282	A1222	C1077	C	C931	C	U	G715	C	C524	A464	U404	G342	C282	C222
C1343	G1283	C1223	C1078	C	A932	C	C	G716	C	C525	A465	U405	A343	G283	G223
C1344	G1284	G1224	C1079	G	C933	G	U	U717	C	C526	A466	C406	A344	G284	U224
U1345	U1285	U1225	C1080	C	C934	C	C	G718	C	C527	U467	A407	C345	G285	G225
C1346	C1286	U1226	C1081	G	A935	G	C	G719	C	C528	U468	A408	G346	U286	G226
G1347	G1287	C1227	C1082	G	C936	G	C	G720	C	C529	C469	A409	A347	U287	A227
U1348	G1288	U1228	U1083	C	U937	C	C	G721	C	A660	A470	A410	C348	G288	C228
G1349	C1289	C1229	C1084	G	C938	G	C	G722	C	C661	A471	G411	A349	C289	G229
C1350	G1290	U1230	C1085	G	C939	G	C	A723	C	C662	C472	G412	C350	U290	G230
G1351	C1291	G1231	C1086	C	G940	C	U	G724	C	G663	C473	G413	C351	U291	U231
C1352	C1292	G1232	C1087	G	C941	G	C	G725	C	G664	C474	C414	G352	G292	G232
G1353	G1293	G1233	C1088	G	A942	G	U	G726	C	G665	G475	C415	U354	G293	U233
A1354	A1294	C1234	G1089	C	G943	C	C	G727	C	A667	G476	U416	A355	G294	G234
G1355	C1295	G1235	C1090	U	A944	C	C	U728	C	C668	C477	G417	G356	A295	A235
U1356	G1296	C1236	U1091	C	U945	G	C	G729	C	C669	G478	A418	U357	A296	G236
C1357	U1297	C1237	C1092	C	C946	G	C	G730	C	G670	G479	A419	C358	U297	G237
G1358	C1298	A1238	G1093	C	C947	C	C	G731	C	G671	C480	A420	A359	G298	C238
G1359	G1299	C1239	U1094	C	C948	G	C	A732	C	C672	G481	C421	A360	C299	C239
G1360	G1300	G1240	A1095	C	C949	U	C	A733	C	C673	G482	C422	C361	A300	G240
C1361	C1301	G1241	C1096	C	G950	G	C	G734	C	G674	G483	G423	A362	G301	G241
G1362	U1302	G1242	G1098	C	C951	C	C	G735	C	C675	U484	U424	A363	C302	U242

A2285	U2220	C	U2090	A2030	A1970	G1910	A1850	U1790	U1730	U1664	G1603	G1543	G1483	U1423	C1363
G2286	C2221	G	C2091	C2031	C1971	C1911	G1851	U1791	C1731	C1665	G1604	G1544	G1484	G1424	U1364
G2287	C2222	G	G2092	U2032	G1972	C1913	G1852	U1792	G1732	C1666	G1605	G1545	C1485	G1425	C1365
G2288	C2225	C	A2093	A2033	G1973	C1914	G1853	A1793	G1733	C1667	U1606	C1546	C1486	G1426	G1366
G2289	C2226	G	G2094	G2034	U1974	C1915	G1854	A1794	G1734	A1668	C1607	A1547	G1487	A1427	C1367
G2290	G2206	G	A2095	C2035	G1975	C1916	G1855	A1795	U1735	A1669	G1608	G1548	G1488	U1428	A1368
G2291	G2207	C	G2096	C2036	G1976	G1917	C1856	U1796	A1736	G1670	U1609	G1549	G1489	C1429	C1369
G2292	C2228	G	U2097	C2037	C1977	A1917	C1857	G1797	A1737	U1671	C1610	G1550	G1490	A1430	G1370
G2293	C2229	G	G2098	U2038	G1978	U1918	A1858	G1798	A1738	U1672	C1611	C1551	A1491	C1431	A1371
G2294	C2230	C	G2099	A2039	A1979	G1919	G1859	U1799	G1739	U1673	G1612	G1552	G1492	G1432	A1372
G2295	C2232	G	A2100	A2040	U1980	C1920	U1860	U1800	C1740	C1674	G1613	C1493	A1373	A1373	A1373
G2296	A2041	C	C2101	G2041	G1981	G1921	U1861	A1801	G1741	C1675	G1614	U1494	G1434	G1374	G1374
G2297	C2235	G	G2102	A2042	G1982	G1922	U1862	A1802	A1742	C1676	C1615	G1555	G1495	G1435	C1375
U2298	C2236	G	G2103	A2043	A1983	A1923	U1863	G1803	A1743	U1677	U1616	C1556	G1496	C1436	C1376
G2299	C2239	G	U2044	G2044	A1984	G1924	G1864	A1804	U1744	C1678	G1617	C1557	A1497	U1437	G1377
A2300	G2045	G	A2105	G2045	G1985	G1925	G1865	A1805	A1745	A1679	G1618	C1558	U1498	U1438	C1378
G2301	G2046	G	U2046	A2046	U1986	G1926	U1866	A1806	A1746	G1680	G1619	C1559	C1499	C1439	C1379
G2302	A2047	U	G2107	U2047	G1987	U1927	A1867	C1807	U1747	G1681	U1620	A1560	A1500	U1440	G1380
G2303	U2048	U	G2108	U2048	G1988	C1928	A1868	C1808	U1748	A1682	A1621	G1561	C1501	C1441	U1381
U2304	G2049	G	G1989	G2049	G1989	A1929	G1869	C1809	A1749	U1683	U1622	G1562	G1502	C1442	G1382
U2305	G2050	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	G2052	G	G2112	G2052	U1992	A1932	G1872	C1812	G1752	C1686	G1625	A1565	C1505	U1445	G1385
G2308	C2053	G	G2113	C2053	G1993	G1933	A1873	U1813	G1753	G1687	G1626	C1566	G1506	C1446	C1386
G2309	C2248	G	G2114	U2054	C1994	A1934	A1874	C1814	U1754	G1688	G1627	U1567	C1507	G1447	A1387
G2310	G2055	U	G2115	G2055	G1995	C1935	C1875	G1815	C1755	G1689	C1628	C1568	A1508	G1448	A1388
G2311	G2251	C	C2116	G2056	C1996	C1936	U1876	C1816	U1756	C1690	G1629	U1569	C1509	C1449	U1389
G2312	G2252	C	G2117	A2057	C1997	G1937	U1817	G1817	U1757	G1691	A1630	G1570	G1510	C1450	C1390
A2313	A2253	U	C2118	G2058	A1998	C1938	G1878	C1818	G1758	C1692	A1631	G1571	U1511	G1451	A1391
G2314	C2247	U	G2119	C2059	A1999	A1939	C1879	G1819	G1759	U1693	A1632	U1572	G1512	A1452	A1392
G2315	G2254	U	G2120	G2060	G2000	G1940	G1880	C1820	G1760	C1694	G1633	G1573	U1513	G1453	G1393
G2316	C2255	C	C2121	U2061	G2001	A1941	C1881	G1821	G1761	U1695	A1634	G1574	U1514	G1454	G1394
C2317	C2257	C	C2122	C2062	A2002	A1942	U1882	U1822	C1762	C1696	C1635	A1575	A1515	G1455	U1395
G2318	C2258	C	G2123	G2063	C2003	A1943	G1883	G1823	C1763	C1697	U1636	G1576	C1516	G1456	C1396
G2319	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	A1519	A1459	A1399
G2322	G2262	C	C2127	C2067	G2007	U1947	G1887	G1827	A1767	A1701	C1640	C1580	G1520	C1460	G1400
C2323	C2263	C	G2128	C2068	U2008	G1948	A1888	C1828	C1768	C1702	G1641	U1581	C1521	C1461	C1401
G2324	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
G2326	C2266	C	C2131	A2071	C2011	G1951	A1891	G1831	U1771	G1705	C1644	C1584	A1524	G1464	G1404
G2327	U2267	C	G2132	C2072	A2012	G1952	A1892	G1832	C1772	C1706	C1645	C1585	A1525	G1465	G1405
G2328	A2268	C	C2133	C2073	A2013	U1953	C1893	G1833	U1773	G1708	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
G2331	C2271	C	C2144	C2076	C2016	A1956	A1896	G1836	A1776	C1715	U1649	G1589	G1529	C1469	C1409
A2332	C2272	A	G2145	C2077	A2017	U1957	A1897	A1837	C1777	C1716	A1650	C1590	G1530	U1470	U1410
G2333	G2273	C	C2146	G2078	C2018	A1958	C1898	A1838	C1778	G1718	G1651	U1591	U1531	U1471	C1411
G2334	C2274	G	U2146	G2079	C2019	U1959	G1899	U1839	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	G1961	G1961	C1901	C1841	U1781	G1721	C1654	C1594	A1534	C1474	C1414
C2337	C2277	U	C2149	G2082	C2021	A1962	G1902	G1842	U1782	C1722	C1655	G1595	C1535	G1475	G1415
G2338	C2278	C	G2152	C2083	C2022	C1963	G1903	A1843	C1783	A1723	U1656	U1596	U1536	C1476	G1416
G2339	A2279	U	G2153	G2084	G1964	A1964	G1904	U1844	U1784	G1724	C1657	C1597	A1537	C1477	C1417
C2340	G2280	U	C2154	G2085	A2025	G1965	U1905	U1845	C1785	U1725	C1658	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

[illegible]

U4436	C4375	A4315	A4255	G4195	G4135	U4075	C3978	G3918	C3858	U3798	G3678	C3618	U
U4437	A4376	G4316	A4256	G4196	G4136	G4076	C3979	C3919	G3859	A3799	U3679	G3619	C
U4438	A4377	A4317	A4257	G4197	C4137	A4077	G3980	U3920	A3860	A3799	U3680	C3620	C
U4439	A4378	C4318	C4258	G4198	C4138	C4078		U3921	A3861	U3801	U3681	C3621	U
G4440	A4379	C4319	C4259	G4199	G4139	A4079	C3997	G3922	A3862	A3682	A3682	C3622	C
A4441	A4380	G4320	U4260	G4200	C4140	C4080		A3923	C3863	A3803	G3743	C3623	G
U4442	A4381	U4321	C4261	G4201	G4141	G4081	G4000	C3924	C3864	G3804	G3744	A3624	G
C4443	G4382	G4322	C4262	U4202	C4142	G4082		U3925	A3865	U3805	U3745	G3625	U
C4444	G4383	A4323	C4263	A4203	G4143	U4083	G4004	C3926	C3866	G3806	C3686	C3626	C
U4445	C4384	A4324	G4264	C4204	C4144	A4084		U3927	A3867	A3807	A3747	C3627	C
U4446	A4385	A4325	U4265	G4205	C4145	A4085	G4007	A3928	C3868	C3808	U3688	G3628	C
C4447	C4386	G4326	G4266	C4206	G4146	G4086		U3929	C3869	G3809	G3689	A3629	C
C4448	C4387	G4327	G4267	C4207	G4147	G4087		U3930	C3870	C3810	U3690	C3630	C
A4449	A4388	G4328	A4268	U4208	C4148	C4088	G4014	C3931	A3871	G3811	G3751	U3631	C
C4450	C4389	G4329	G4269	G4209	C4149	G4089		U3932	A3872	C3812	C3752	C3632	C
U4451	A4390	G4330	C4270	G4210	G4150	G4090	G4017	G3933	C3873	A3813	U3693	C3633	C
U4452	G4391	A4331	A4271	C4211	G4151	G4091	G4018	G3934	G3874	U3814	U3694	G3634	C
C4453	C4392	G4332	A4272	G4212	G4152	G4092		U3935	C3875	G3815	U3695	A3635	C
G4454	A4393	A4333	A4273	A4213	C4153	G4093		A3936	A3876	A3816	A3756	C3636	C
C4455	A4394	U4334	A4274	A4214	C4154	G4094	G4034	C3937	A3877	A3817	G3757	U3637	C
C4456	U4395	G4335	G4275	C4215	C4155	G4095	G4035	G3938	C3878	U3818	U3758	G3638	C
U4457	A4396	A4336	G4276	G4216	G4156	C4096	G4036	G3939	G3879	G3819	A3759	U3639	G
A4458	A4397	G4337	G4277	C4217	A4157	G4097	C4037	U3940	G3880	G3820	A3760	U3640	C
U4459	C4398	G4338	C4278	U4218	C4158	A4098	C4038	G3941	G3881	A3821	C3761	U3641	C
U4460		A4339	A4279	A4219	C4159	G4099	G4039	A3942	C3882	U3822	U3762	A3642	G
C4461	G4401	U4340	A4280	A4220	C4160	C4100	C4040	A3943	U3883	G3823	A3763	A3643	C
C4462	U4402	C4341	A4281	C4221	G4161	C4101	C4041	G3944	C3884	A3824	U3764	U3644	C
U4463	U4403	A4342	A4282	G4222	C4162	C4102	G4042	A3945	C3885	A3825	A3765	A3645	A
A4464	U4404	U4343	G4283	C4223	C4163	G4103	G4043	G3946	C3886	G3826	A3766	A3646	C
U4465	A4405	A4344	A4284	A4224	C4164	G4104	U4044	A3947	C3887	G3827	C3767	A3647	C
C4466	U4406	G4345	U4285	G4225	C4165	A4105	G4045	C3948	G3888	A3828	U3768	C3648	C
U4467	U4407	U4346	C4286	G4226	C4166	G4106	A4046	A3949	C3889	G3829	C3769	A3649	C
G4468	G4408	G4347	G4287	U4227	G4167	G4107	A4047	U3950	A3890	U3770	C3650	G3590	G
U4469	C4409	A4348	C4288	G4228	G4168	G4108	A4048	G3951	C3891	U3831	U3771	A3651	C
G4470	U4410	C4349	U4289	U4229	G4169	G4109	U4049	A3952	U3892	A3832	A3712	C3592	C
U4471	G4411	C4350	U4290	C4230	A4170	C4110	A4050	G3953	C3893	U3773	U3713	C3593	G
G4472	C4412	U4351	G4291	C4231	C4171	U4111	C4051	A3954	A3894	A3774	G3714	G3654	A
A4473	C4413	U4352	U4292	U4232	A4172	C4112	C4052	G3955	C3895	A3775	U3715	C3655	G
A4474	A4414	U4353	U4293	A4233	G4173	U4113	A4053	G3956	C3896	A3656	C3716	A3656	G
G4475	U4415	C4354	C4294	G4234	U4174	C4114	C4054	U3957	C3897	A3657	A3717	G3597	G
C4476	G4416	A4355	U4295	G4235	G4175	G4115	U4055	G3958	C3898	U3838	A3778	C3658	C
A4477	C4417	G4356	U4296	G4236	C4176	C4116	A4056	U3959	G3899	G3839	A3779	A3599	C
G4478	U4418	G4357	G4297	C4237	C4177	U4117	C4057	A3960	C3900	U3840	G3780	C3660	C
U4479	U4419	U4358	A4298	G4238	A4178	U4118	U4058	G3961	A3901	C3841	C3781	C3661	C
A4480	U4420	U4359	U4299	A4239	G4179	C4119	C4059	A3962	A3902	C3842	G3782	A3662	C
U4481	C4421	U4360	U4300	G4240	G4180	U4120	U4060	A3963	A3903	C3843	A3783	A3663	G
U4482	U4422	U4361	U4301	C4241	U4181	G4121	G4061	U3964	G3904	U3844	A3784	G3664	G
C4483	U4423	A4362	U4302	U4242	G4182	C4122	A4062	A3965	A3905	A3845	G3785	C3665	C
A4484	A4424	C4363	C4303	C4243	G4183	C4123	U4063	A3966	A3906	C3846	U3786	C3666	C
C4485	G4425	A4364	A4304	A4244	G4184	C4124	C4064	G3967	C3907	C3847	A3787	U3667	C
C4486	C4426	C4365	G4305	G4245	C4185	G4125	G4065	U3968	A3908	U3848	C3788	C3668	C
A4487	G4427	A4366	U4306	G4246	A4186	C4126	U4066	C3969	C3909	A3849	C3789	G3669	G
A4488	A4428	G4367	A4307	C4247	G4187	A4127	U4067	G3970	C3910	C3850	U3790	C3670	U
G4489	C4429	C4368	C4308	A4248	U4188	A4128	U4068	G3971	C3911	U3851	C3791	A3611	C
C4490	A4430	A4369	C4309	G4249	U4189	G4129	U4069	A3972	U3912	A3852	G3792	G3672	C
G4491	U4431	G4370	C4310	C4250	U4190	C4130	U4070	G3973	G3913	U3853	U3793	C3673	C
U4492	C4432	G4371	A4251	A4251	G4191	C4131	U4071	C3974	U3914	C3854	C3794	G3674	C
G4493	G4433	U4372	C4252	C4252	A4192	C4132	C4072	C3975	U3915	C3855	A3795	G3675	C
U4494	A4434	C4373	A4253	C4253	G4193	C4133	A4073	C3976	C3916	A3856	U3796	G3676	C
G4495	U4435	U4374	G4254	G4254	U4194	C4134	C4074	C3977	A3917	G3857	A3797	G3677	C

A5019	U4959	C4899	C4737	U4677	G4617	U4556	A4496
G5020	C4900	C4901	C4738	C4678	C4618	U4557	U4497
C5021	C4961	C4902	C4739	C4679	U4619	U4558	U4498
U5022	C4962	C4903	G4740	G4680	U4620	A4559	G4499
C5023	C4963	C4904	C4741	C4681	C4621	C4560	U4500
G5024	C4964	C4905	C4742	U4682	A4622	C4561	U4501
U4965	U4965	C4906	C4743	C4683	C4623	C4562	C4502
U4966	C4966	C4907	A4744	U4684	A4624	U4563	A4503
U4967	C4967	C4908	C4745	U4685	C4625	A4564	C4504
C4968	C4968	A4909	C4746	C4686	A4626	C4565	C4505
C5029	C4969	C4910	C4747	U4687	U4627	U4566	C4506
U5030	C4970	G4910	U4748	C4688	U4628	C4567	A4507
G5031	A4971	A4911	C4749	C4689	U4629	A4568	C4508
C5032	U4972	C4912	C4750	C4690	C4630	U4569	U4509
G5033	U4973	C4913	G4751	A4691	C4631	G4570	A4510
A5034	C4974	U4838	U4752	A4692	U4632	A4571	A4511
U5035	C4975	C4914	U4753	C4693	C4633	U4572	U4512
C5036	U4976	C4915	U4754	C4694	U4634	C4573	A4513
U5037	A4977	C4916	C4754	C4694	A4635	U4574	G4514
C5038	C4978	C4917	G4755	C4695	U4636	C4575	G4515
U5039	A4979	C4918	C4756	C4696	C4637	U4576	A4516
U5040	C4980	C4919	U4758	C4697	C4638	U4577	A4517
G5041	C4981	C4920	C4759	U4699	C4639	C4578	A4518
A5041	C4982	C4921	C4760	A4700	C4640	U4579	C4519
A5042	C4983	C4922	C4761	C4702	U4641	U4580	C4520
C5043	C4984	C4923	A4762	U4703	C4642	U4521	U4521
G5044	U4985	U4925	C4763	C4704	G4643		G4522
U5046	C4986	C4926	A4764	C4705	C4644	A4584	A4584
G5047	C4987	C4927	C4765	A4706	C4645	U4585	U4585
A5048	U4988	C4928	C4766	C4706	U4646	C4586	C4525
G5049	U4989	C4929	C4767	A4707	C4647	U4587	U4526
C5050	C4990	C4930	C4768	C4708	U4648	C4588	C4527
C5051	U4991	C4931	C4769	U4709	G4649	A4589	C4528
C5052	C4992	U4932	U4770	C4710	C4650	A4590	C4529
U5053	C4993	C4933	C4771	C4711	A4651	U4591	U4530
C5054	C4994	A4934	C4772	C4712	C4652	C4592	U4531
U4995	U4995	C4935	C4773	C4713	C4653	C4593	U4532
A5056	C4996	C4936	C4774	C4714	C4654	U4594	A4533
C5057	C4997	C4937	C4775	C4715	A4655	C4595	G4534
A5058	C4998	A4938	C4776	C4716	A4656	C4596	A4535
C5059	C4999	C4939	C4777	U4717	U4657	U4597	C4536
A5060	G5000	C4940	C4778	C4718	C4658	C4598	C4537
U5001	U5001	C4941	U4779	C4719	C4659	A4599	C4538
U5002	C5002	C4942		C4720	C4660	C4600	U4539
G5063	U5003	A4943	G4791	C4721	C4661	U4601	C4540
C5004	C5004	C4944	C4792	C4722	C4662	A4602	C4541
G5005	U5005	C4945	C4793	A4723	C4663	C4603	U4542
U5006	U5006	U4946		A4724	A4664	C4604	C4543
A5007	A5007	U4947	C4802	C4725	A4665	A4605	A4544
G5062	C5008	C4948		C4726	C4666	C4606	A4545
C5009	U5009	C4949	C4806	A4727	C4667	A4607	A4546
U5010	U5010	U4950	C4890	U4728	U4668	C4608	C4547
A5011	A5011	G4951	A4810	A4729	A4669	C4609	A4548
G5012	G5012	C4952	C4811	C4730	C4670	A4610	C4549
C5013	C4953	C4953	G	C4731	C4671	A4611	C4550
A5014	A5014	C4954	C	C4732	A4672	C4612	U4551
G5015	G5015	A4955	C	C4733	U4673	C4613	U4552
A5016	A5016	A4956	C4896	A4734	C4674	A4553	A4553
G5017	G5017	C4957	C4897	C4735	U4675	C4554	G4554
C5018	C5018	C4958	C	C4736	C4676	C4555	U4555

• Molecule 86: 5S ribosomal RNA

Chain A7: 59% 31% 7%

G61	U62	C63	G64	A65	C66	C67	C68	U69	G70	G71	U72	U73	A74	G75	U76	A77	C78	U79	U80	G81	C82	A83	U84	G85	C86	G87	A88	C89	A90	C91	C92	G93	C94	C95	U96	G97	C98	G99	A100	A101	U102	A103	C104	C105	G106	G107	C108	U109	G110	C111	U112	G113	U114	A115	G116	G117	C118	U119	U120
G1	U2	C3	U4	A5	C6	G7	G8	C9	C10	A11	U12	A13	C14	C15	A16	C17	C18	C19	U20	G21	A22	A23	C24	G25	C26	G27	C28	C29	C30	G31	A32	U33	C34	U35	C36	G37	U38	C39	U40	G41	A42	U43	C44	U45	C46	G47	G48	A49	U50	G51	C52	U53	A54	A55	G56	C57	A58	G59	G60

U121

• Molecule 87: 5.8S ribosomal RNA

Chain A8: 5% 57% 27% 11%

C1	G2	A3	C4	U5	C6	U7	U8	A9	C10	G11	C12	G13	U14	G15	A17	G18	U19	C20	A21	C22	C23	A24	U25	C26	U27	C28	U29	C30	U31	C32	G33	C34	C35	C36	A37	U38	C39	A40	U41	C42	A43	A44	C45	C46	A47	C48	U49	C50	U51	A52	C53	C54	U55	C56	C57	U58	C59	A60	G60
A61	A62	C63	U64	A65	C66	U67	C68	U69	G70	A71	U72	G73	C74	C75	A77	G78	C79	A80	C81	A82	C83	A84	U85	C86	A87	C88	U89	C90	A91	U92	C93	G94	A95	C96	A97	C98	U99	U100	C101	U102	A103	C104	C105	G106	C107	C108	U109	C110	U111	C112	C113	G114	C115	U116	C117	C118	C119	G120	C121

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, C1	Depositor
Number of particles used	343343	Depositor
Resolution determination method	FSC 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	FEI EAGLE (4k x 4k)	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

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	28
2	Ag	311/317 (98%)	271 (87%)	23 (7%)	17 (6%)	2	23
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	22
7	AM	122/132 (92%)	85 (70%)	16 (13%)	21 (17%)	0	3
8	AS	135/152 (89%)	106 (78%)	20 (15%)	9 (7%)	1	19
9	Ad	51/56 (91%)	46 (90%)	3 (6%)	2 (4%)	3	29
10	AN	148/151 (98%)	124 (84%)	18 (12%)	6 (4%)	3	28
11	AL	156/158 (99%)	132 (85%)	10 (6%)	14 (9%)	1	14
12	AR	124/135 (92%)	96 (77%)	13 (10%)	15 (12%)	0	6
13	AP	125/145 (86%)	92 (74%)	16 (13%)	17 (14%)	0	5
14	AT	139/145 (96%)	121 (87%)	8 (6%)	10 (7%)	1	18
15	AB	213/264 (81%)	174 (82%)	24 (11%)	15 (7%)	1	18
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	5
18	AY	124/133 (93%)	91 (73%)	15 (12%)	18 (14%)	0	4
19	AZ	73/125 (58%)	52 (71%)	12 (16%)	9 (12%)	0	6
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	5
22	Ac	62/69 (90%)	44 (71%)	13 (21%)	5 (8%)	1	15
23	AD	225/243 (93%)	180 (80%)	24 (11%)	21 (9%)	1	13
24	Ae	57/59 (97%)	39 (68%)	5 (9%)	13 (23%)	0	1
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	5
27	AE	261/263 (99%)	210 (80%)	29 (11%)	22 (8%)	1	14
28	AC	224/293 (76%)	203 (91%)	10 (4%)	11 (5%)	2	25
29	AG	235/249 (94%)	202 (86%)	18 (8%)	15 (6%)	1	20
30	AF	189/204 (93%)	162 (86%)	15 (8%)	12 (6%)	1	21
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	49
33	AI	204/208 (98%)	169 (83%)	13 (6%)	22 (11%)	0	9
34	AQ	139/146 (95%)	110 (79%)	19 (14%)	10 (7%)	1	18
35	Ah	69/408 (17%)	31 (45%)	15 (22%)	23 (33%)	0	0
38	Cz	213/217 (98%)	189 (89%)	16 (8%)	8 (4%)	3	30
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	39
42	CL	208/211 (99%)	165 (79%)	18 (9%)	25 (12%)	0	6
43	CV	131/140 (94%)	116 (88%)	11 (8%)	4 (3%)	4	35
44	CM	137/215 (64%)	112 (82%)	16 (12%)	9 (7%)	1	20
45	Ca	145/148 (98%)	120 (83%)	14 (10%)	11 (8%)	1	16
46	CN	201/204 (98%)	179 (89%)	9 (4%)	13 (6%)	1	20
47	CI	211/214 (99%)	165 (78%)	27 (13%)	19 (9%)	1	14
48	CD	287/297 (97%)	237 (83%)	24 (8%)	26 (9%)	1	13
49	CQ	186/188 (99%)	152 (82%)	18 (10%)	16 (9%)	1	14
50	CR	187/196 (95%)	165 (88%)	15 (8%)	7 (4%)	4	31
51	CA	253/257 (98%)	210 (83%)	23 (9%)	20 (8%)	1	16
52	CS	173/176 (98%)	137 (79%)	15 (9%)	21 (12%)	0	6
53	CT	157/160 (98%)	131 (83%)	11 (7%)	15 (10%)	1	12
54	CP	150/184 (82%)	134 (89%)	9 (6%)	7 (5%)	2	26
55	CU	110/128 (86%)	90 (82%)	13 (12%)	7 (6%)	1	20
56	CX	119/156 (76%)	98 (82%)	14 (12%)	7 (6%)	2	22
57	CY	131/145 (90%)	116 (88%)	11 (8%)	4 (3%)	4	35
58	CW	122/157 (78%)	94 (77%)	13 (11%)	15 (12%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	CZ	133/136 (98%)	109 (82%)	14 (10%)	10 (8%)	1	17
60	Cr	135/137 (98%)	86 (64%)	22 (16%)	27 (20%)	0	2
61	Ch	121/123 (98%)	93 (77%)	14 (12%)	14 (12%)	0	7
62	Cb	76/159 (48%)	58 (76%)	9 (12%)	9 (12%)	0	7
63	CB	395/403 (98%)	322 (82%)	34 (9%)	39 (10%)	1	11
64	CF	227/248 (92%)	209 (92%)	6 (3%)	12 (5%)	2	24
65	Cc	98/115 (85%)	90 (92%)	5 (5%)	3 (3%)	4	35
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	7
68	Cf	107/110 (97%)	82 (77%)	12 (11%)	13 (12%)	0	6
69	Cg	112/117 (96%)	91 (81%)	7 (6%)	14 (12%)	0	6
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	15
72	Ck	67/70 (96%)	59 (88%)	5 (8%)	3 (4%)	3	27
73	Cl	48/51 (94%)	37 (77%)	8 (17%)	3 (6%)	1	21
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	21
76	Cn	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
77	Cp	88/92 (96%)	75 (85%)	9 (10%)	4 (4%)	3	27
78	Co	103/106 (97%)	74 (72%)	14 (14%)	15 (15%)	0	4
79	CJ	166/178 (93%)	132 (80%)	20 (12%)	14 (8%)	1	14
80	CH	189/192 (98%)	163 (86%)	18 (10%)	8 (4%)	3	28
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	2
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	17
84	Cv	54/115 (47%)	51 (94%)	0	3 (6%)	2	23
All	All	13166/14959 (88%)	10588 (80%)	1270 (10%)	1308 (10%)	1	11

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	Ab	76/76 (100%)	63 (83%)	13 (17%)	2	15
22	Ac	57/62 (92%)	46 (81%)	11 (19%)	1	10
23	AD	190/202 (94%)	144 (76%)	46 (24%)	1	5
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	12
27	AE	225/225 (100%)	172 (76%)	53 (24%)	1	6
28	AC	190/225 (84%)	145 (76%)	45 (24%)	1	5
29	AG	207/218 (95%)	157 (76%)	50 (24%)	1	5
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	24
33	AI	178/180 (99%)	142 (80%)	36 (20%)	1	9
34	AQ	117/121 (97%)	89 (76%)	28 (24%)	1	5
35	Ah	55/328 (17%)	41 (74%)	14 (26%)	0	5
38	Cz	195/196 (100%)	174 (89%)	21 (11%)	7	30
39	Cq	232/258 (90%)	194 (84%)	38 (16%)	2	16
40	CK	136/137 (99%)	110 (81%)	26 (19%)	1	10
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	11
44	CM	118/161 (73%)	85 (72%)	33 (28%)	0	3
45	Ca	120/121 (99%)	100 (83%)	20 (17%)	2	16
46	CN	171/172 (99%)	132 (77%)	39 (23%)	1	6
47	CI	180/181 (99%)	150 (83%)	30 (17%)	2	16
48	CD	243/250 (97%)	210 (86%)	33 (14%)	4	22
49	CQ	165/165 (100%)	119 (72%)	46 (28%)	0	3
50	CR	168/175 (96%)	126 (75%)	42 (25%)	0	5
51	CA	197/199 (99%)	161 (82%)	36 (18%)	2	12
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	10
56	CX	109/133 (82%)	78 (72%)	31 (28%)	0	3
57	CY	123/135 (91%)	95 (77%)	28 (23%)	1	6
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%)	0	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	5
64	CF	198/215 (92%)	172 (87%)	26 (13%)	4	23
65	Cc	85/97 (88%)	73 (86%)	12 (14%)	4	22
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	41
80	CH	170/171 (99%)	146 (86%)	24 (14%)	4	22
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%)	55 77
84	Cv	46/83 (55%)	45 (98%)	1 (2%)	55 77
All	All	11438/12642 (90%)	8832 (77%)	2606 (23%)	3 6

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%)	128 (7%)
37	BC	74/75 (98%)	13 (17%)	3 (4%)
85	A5	3761/5070 (74%)	1048 (27%)	337 (8%)
86	A7	120/121 (99%)	24 (20%)	2 (1%)
87	A8	156/157 (99%)	38 (24%)	12 (7%)
All	All	5871/7292 (80%)	1626 (27%)	482 (8%)

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

5 of 482 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	A5	1214	C
85	A5	1442	C
85	A5	4874	A
85	A5	1239	C
85	A5	1294	A

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
74	CC	5
63	CB	4
26	AJ	3
82	CG	3
81	CE	3
8	AS	2

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Mol	Chain	Number of breaks
66	Cd	2
64	CF	2
29	AG	2
47	CI	2
58	CW	2
1	Az	2
35	Ah	1
70	Ci	1
28	AC	1
73	Cl	1
38	Cz	1
41	CO	1
61	Ch	1
56	CX	1
23	AD	1
53	CT	1
24	Ae	1
33	AI	1
3	AU	1
12	AR	1
69	Cg	1

The worst 5 of 47 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