



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:27 PM BST

PDB ID : 3J78  
EMDB ID: : EMD-5977  
Title : Structures of yeast 80S ribosome-tRNA complexes in the rotated and non-rotated conformations (Class I - non-rotated ribosome with 2 tRNAs)  
Authors : Svidritskiy, E.; Brilot, A.F.; Koh, C.S.; Grigorieff, N.; Korostelev, A.A.  
Deposited on : 2014-05-29  
Resolution : 6.30 Å(reported)  
Based on PDB ID : 3U5E, 3U5D, 3U5C, 3U5B, 3J3B, 3I9B

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

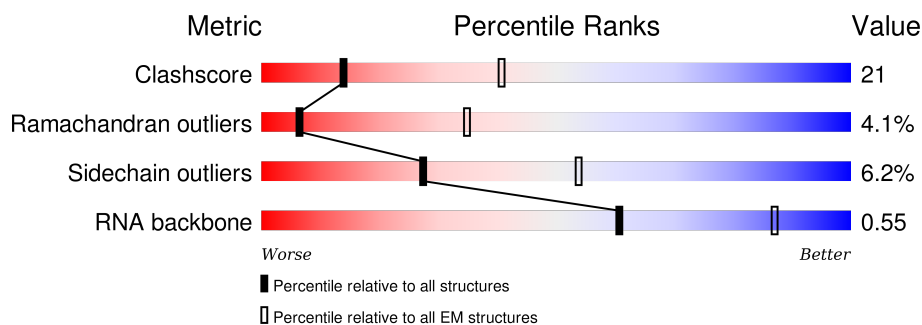
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 6.30 Å.

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









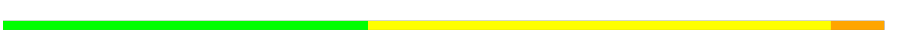





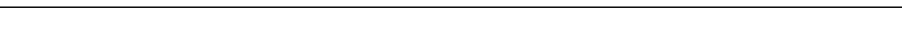

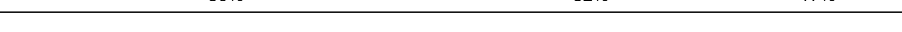

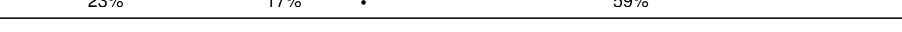








Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	L1	217	47% 39% 9% 6%
2	L2	254	43% 51% 5% .
3	L3	387	51% 46% .
4	L4	362	51% 44% .
5	L5	297	52% 44% .
6	L6	176	50% 35% . 11%
7	L7	244	42% 45% . . 9%
8	L8	256	42% 43% 6% 9%

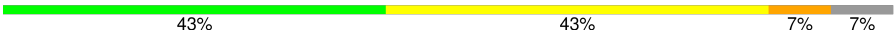









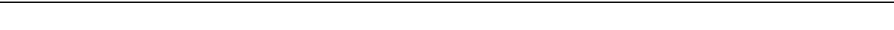

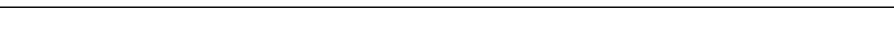
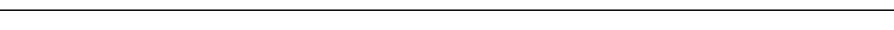











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Mol	Chain	Length	Quality of chain
9	L9	191	
10	60	221	
11	61	174	
12	62	165	
13	63	199	
14	64	138	
15	65	204	
16	66	199	
17	67	184	
18	68	186	
19	69	189	
20	70	172	
21	71	160	
22	72	121	
23	73	137	
24	74	155	
25	75	142	
26	76	127	
27	77	136	
28	78	149	
29	79	59	
30	80	105	
31	81	113	
32	82	130	
33	83	107	



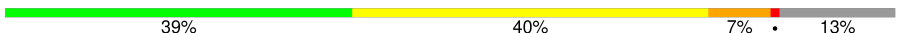








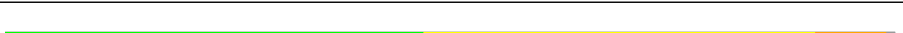













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Mol	Chain	Length	Quality of chain
34	84	121	
35	85	120	
36	86	100	
37	87	88	
38	88	78	
39	89	51	
40	90	128	
41	91	25	
42	92	106	
43	93	92	
44	P0	312	
45	RC	319	
46	S0	252	
47	S1	255	
48	S2	254	
49	S3	240	
50	S4	261	
51	S5	225	
52	S6	236	
53	S7	190	
54	S8	200	
55	S9	197	
56	10	105	
57	11	156	
58	12	143	

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Mol	Chain	Length	Quality of chain
59	13	151	
60	14	137	
61	15	142	
62	16	143	
63	17	136	
64	18	146	
65	19	144	
66	20	121	
67	21	87	
68	22	130	
69	23	145	
70	24	135	
71	25	108	
72	26	119	
73	27	82	
74	28	67	
75	29	56	
76	30	63	
77	31	152	
78	1S	1798	
79	2S	3395	
80	8S	158	
81	5S	121	
82	ET	77	
82	PT	77	

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Mol	Chain	Length	Quality of chain
83	MR	14	 <div> <div>36%</div> <div>21%</div> <div>7%</div> <div>36%</div> </div>

## 2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 209136 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 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L1	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 2 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L2	252	Total	C	N	O	S	0	0
			1918	1193	389	335	1		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L3	386	Total	C	N	O	S	0	0
			3082	1956	584	534	8		

- Molecule 4 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L4	361	Total	C	N	O	S	0	0
			2750	1730	522	495	3		

- Molecule 5 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L5	296	Total	C	N	O	S	0	0
			2376	1501	414	459	2		

- Molecule 6 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L6	156	Total	C	N	O	S	0	0
			1240	800	222	217	1		

- Molecule 7 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L7	222	Total	C	N	O	S	0	0
			1785	1151	324	309	1		

- Molecule 8 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L8	233	Total	C	N	O	S	0	0
			1818	1159	326	330	3		

- Molecule 9 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L9	191	Total	C	N	O	S	0	0
			1519	963	274	278	4		

- Molecule 10 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	60	211	Total	C	N	O	S	0	0
			1718	1089	325	298	6		

- Molecule 11 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	61	169	Total	C	N	O	S	0	0
			1354	847	253	250	4		

- Molecule 12 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	62	143	Total	C	N	O	0	0
			703	417	143	143		

- Molecule 13 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	63	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 14 is a protein called 60S ribosomal protein L14.



Mol	Chain	Residues	Atoms					AltConf	Trace
14	64	136	Total	C	N	O	S	0	0
			1054	675	199	178	2		

- Molecule 15 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	65	203	Total	C	N	O	S	0	0
			1721	1077	361	282	1		

- Molecule 16 is a protein called 60S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	66	197	Total	C	N	O	S	0	0
			1556	1003	289	263	1		

- Molecule 17 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	67	183	Total	C	N	O		0	0
			1443	896	287	260			

- Molecule 18 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	68	185	Total	C	N	O	S	0	0
			1442	908	290	242	2		

- Molecule 19 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	69	188	Total	C	N	O		0	0
			1522	935	326	261			

- Molecule 20 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	70	172	Total	C	N	O	S	0	0
			1446	930	267	245	4		

- Molecule 21 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	71	159	Total	C	N	O	S	0	0
			1277	805	246	222	4		

- Molecule 22 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	72	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 23 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	73	136	Total	C	N	O	S	0	0
			1004	628	189	180	7		

- Molecule 24 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	74	64	Total	C	N	O	S	0	0
			528	340	103	84	1		

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	75	121	Total	C	N	O	S	0	0
			969	623	170	174	2		

- Molecule 26 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	76	126	Total	C	N	O		0	0
			994	625	192	177			

- Molecule 27 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	77	135	Total	C	N	O		0	0
			1093	710	202	181			

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	78	148	Total	C	N	O	S	0	0
			1174	749	231	191	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	79	58	Total	C	N	O		0	0
			463	289	100	74			

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	80	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 31 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	81	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	82	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	83	106	Total	C	N	O	S	0	0
			851	540	165	145	1		

- Molecule 34 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	84	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 35 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	85	119	Total	C	N	O	S	0	0
			970	615	186	168	1		

- Molecule 36 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	86	99	Total	C	N	O	S	0	0
			772	481	156	133	2		

- Molecule 37 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	87	87	Total	C	N	O	S	0	0
			682	414	148	115	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	88	77	Total	C	N	O		0	0
			613	391	115	107			

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	89	50	Total	C	N	O	S	0	0
			437	272	97	66	2		

- Molecule 40 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	90	52	Total	C	N	O	S	0	0
			418	259	86	68	5		

- Molecule 41 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	91	25	Total	C	N	O	S	0	0
			234	142	63	28	1		

- Molecule 42 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	92	105	Total	C	N	O	S	0	0
			848	534	170	139	5		

- Molecule 43 is a protein called 60S ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	93	91	Total	C	N	O	S	0	0
			695	429	138	122	6		

- Molecule 44 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	P0	125	Total	C	N	O	S	0	0
			987	633	174	177	3		

- Molecule 45 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	RC	318	Total	C	N	O	S	0	0
			2445	1546	419	472	8		

- Molecule 46 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S0	206	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 47 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S1	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 48 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S2	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S3	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 50 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S4	260	Total	C	N	O	S	0	0
			2069	1316	389	361	3		

- Molecule 51 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S5	206	Total	C	N	O	S	0	0
			1610	1007	300	300	3		

- Molecule 52 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S6	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 53 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	S7	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 54 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	S8	188	Total	C	N	O	S	0	0
			1490	925	298	265	2		

- Molecule 55 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S9	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 56 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	10	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 57 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	11	155	Total	C	N	O	S	0	0
			1245	798	235	209	3		

- Molecule 58 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	12	124	Total	C	N	O	S	0	0
			935	587	165	181	2		

- Molecule 59 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	13	150	Total	C	N	O	S	0	0
			1193	759	224	208	2		

- Molecule 60 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	14	127	Total	C	N	O	S	0	0
			942	578	186	175	3		

- Molecule 61 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	15	124	Total	C	N	O	S	0	0
			991	631	187	166	7		

- Molecule 62 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	16	141	Total	C	N	O	0	0
			1106	708	203	195		

- Molecule 63 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	17	120	Total	C	N	O	S	0	0
			965	603	183	177	2		

- Molecule 64 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	18	145	Total	C	N	O	S	0	0
			1193	743	237	211	2		

- Molecule 65 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	19	143	Total	C	N	O	S	0	0
			1113	694	208	209	2		

- Molecule 66 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	20	107	Total	C	N	O	S	0	0
			856	539	156	160	1		

- Molecule 67 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	21	87	Total	C	N	O	S	0	0
			685	420	125	138	2		

- Molecule 68 is a protein called 40S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	22	129	Total	C	N	O	S	0	0
			1022	650	188	181	3		

- Molecule 69 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	23	144	Total	C	N	O	S	0	0
			1122	708	220	192	2		

- Molecule 70 is a protein called 40S ribosomal protein S24.



Mol	Chain	Residues	Atoms				AltConf	Trace
70	24	134	Total	C	N	O	0	0
			1074	676	208	190		

- Molecule 71 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	25	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 72 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	26	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 73 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	27	81	Total	C	N	O	S	0	0
			611	382	110	114	5		

- Molecule 74 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	28	63	Total	C	N	O	S	0	0
			498	306	99	92	1		

- Molecule 75 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	29	53	Total	C	N	O	S	0	0
			444	275	92	73	4		

- Molecule 76 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	30	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 77 is a protein called 40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	31	71	Total	C	N	O	S	0	0
			498	309	93	92	4		

- Molecule 78 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	1S	1781	Total	C	N	O	P	0	0
			37949	16965	6715	12488	1781		

- Molecule 79 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	2S	3302	Total	C	N	O	P	0	0
			70616	31540	12710	23064	3302		

- Molecule 80 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	8S	158	Total	C	N	O	P	0	0
			3354	1500	586	1110	158		

- Molecule 81 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	5S	121	Total	C	N	O	P	0	0
			2580	1152	461	846	121		

- Molecule 82 is a RNA chain called P/E-site initiator transfer RNA<sup>fMet</sup>.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	ET	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		
82	PT	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

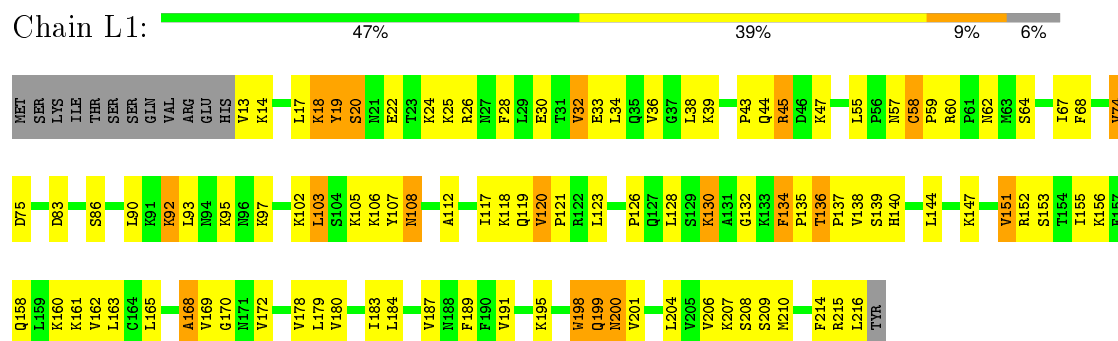
- Molecule 83 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	MR	9	Total	C	N	O	P	0	0
			195	88	39	59	9		

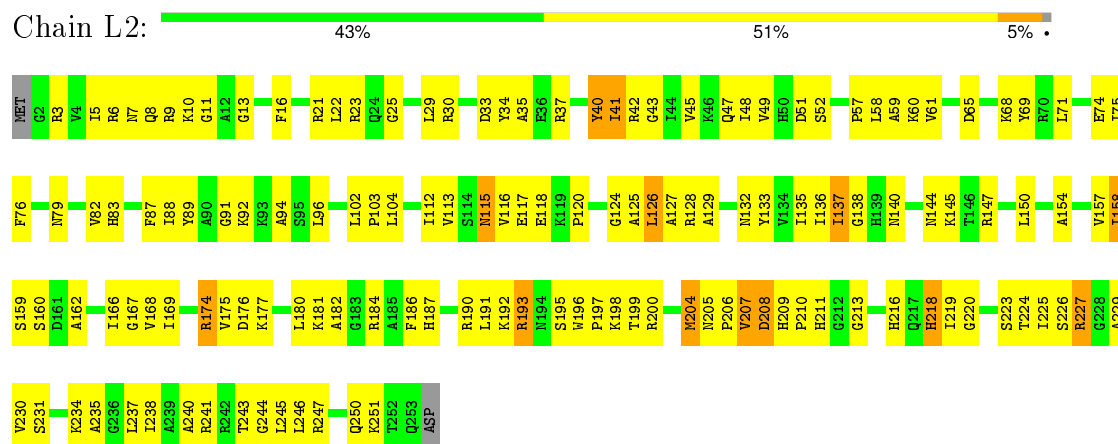
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

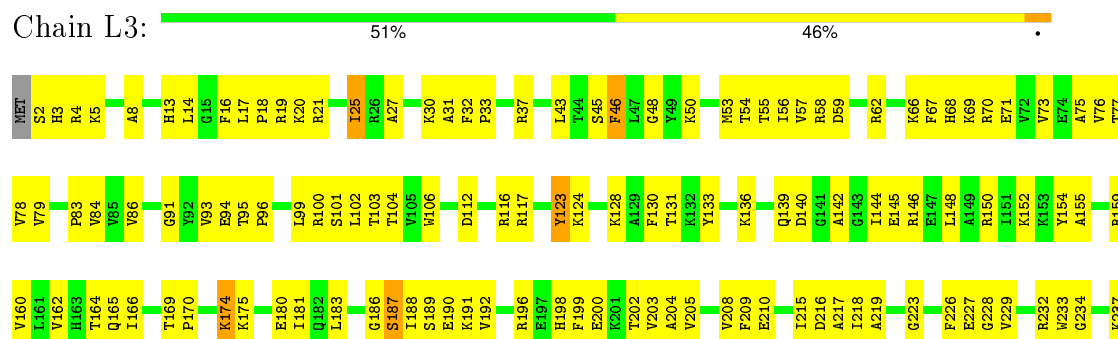
#### • Molecule 1: 60S ribosomal protein L1



#### • Molecule 2: 60S ribosomal protein L2

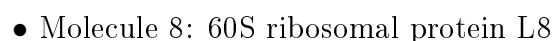


#### • Molecule 3: 60S ribosomal protein L3

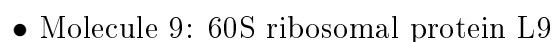




Response	Percentage
Yes	42%
No	45%
Don't know	9%



Response	Percentage
Yes	42%
No	43%
Don't know	6%
No answer	9%

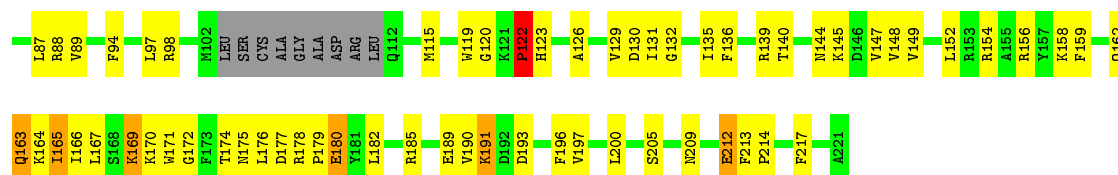


Response	Percentage
Yes	48%
No	48%
Don't know	5%



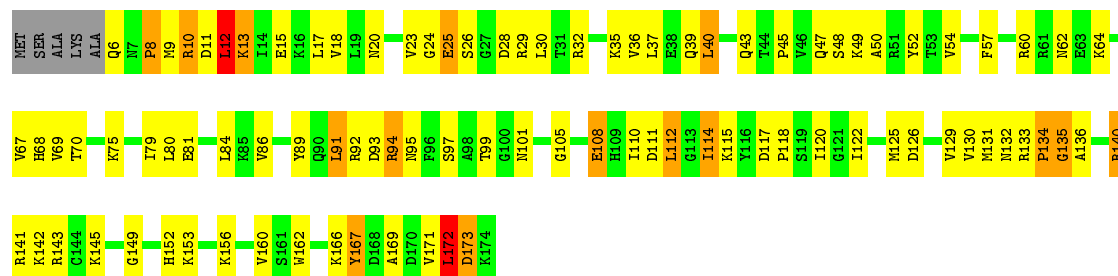
Response	Percentage
Yes	51%
No	40%
Don't know	5%
No answer	5%





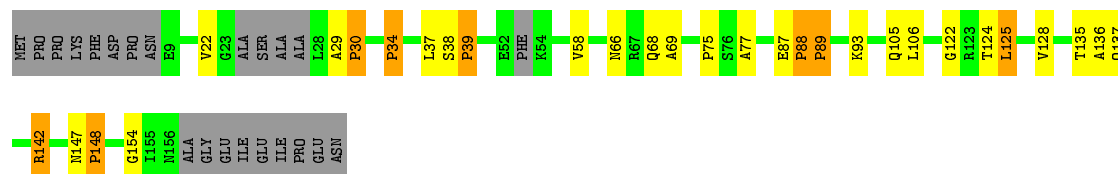
• Molecule 11: 60S ribosomal protein L11

Chain 61: 44% 44% 9% ..



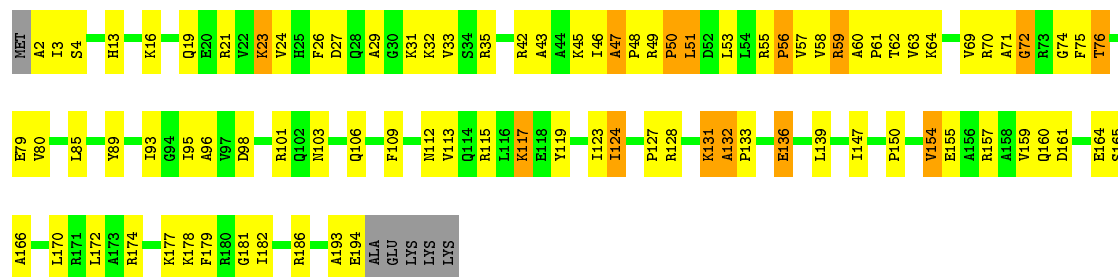
• Molecule 12: 60S ribosomal protein L12

Chain 62: 68% 13% 5% 13%



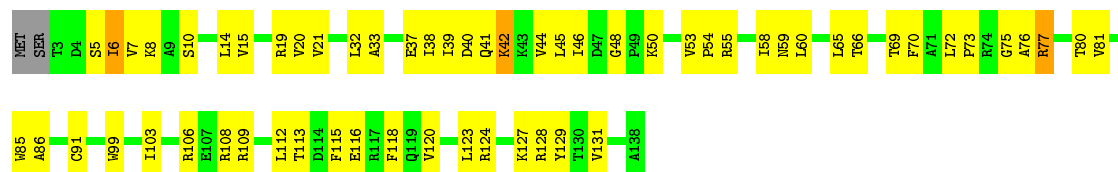
• Molecule 13: 60S ribosomal protein L13

Chain 63: 51% 39% 7% .



• Molecule 14: 60S ribosomal protein L14

Chain 64: 55% 41% ..



Chain 65:

Item	Category	Percentage
I133	Green	41%
I134	Green	41%
I138	Green	41%
I139	Green	41%
I140	Green	41%
I141	Green	41%
I142	Green	41%
I143	Green	41%
I144	Green	41%
I145	Green	41%
Y148	Green	41%
M149	Green	41%
M150	Green	41%
D153	Green	41%
P154	Green	41%
V155	Green	41%
H156	Green	41%
K157	Green	41%
H158	Green	41%
A159	Green	41%
E160	Green	41%
T165	Green	41%
A166	Green	41%
K169	Green	41%
K170	Green	41%
S171	Green	41%
G173	Green	41%
I174	Green	41%
M175	Green	41%
K176	Green	41%
K179	Green	41%
F180	Green	41%
K184	Green	41%
A185	Green	41%
G186	Green	41%
K187	Green	41%
K188	Green	41%
K189	Green	41%
T190	Green	41%
M191	Green	41%
Q194	Green	41%
N195	Green	41%
R201	Green	41%
Y202	Green	41%
R203	Green	41%
K204	Green	41%
V66	Yellow	52%
R67	Yellow	52%
R68	Yellow	52%
G69	Yellow	52%
N70	Yellow	52%
R71	Yellow	52%
F72	Yellow	52%
R73	Yellow	52%
F74	Yellow	52%
V75	Yellow	52%
T80	Yellow	52%
R81	Yellow	52%
G82	Yellow	52%
K83	Yellow	52%
P84	Yellow	52%
T85	Yellow	52%
R86	Yellow	52%
G87	Yellow	52%
G88	Yellow	52%
V89	Yellow	52%
L92	Yellow	52%
K93	Yellow	52%
F94	Yellow	52%
Q95	Yellow	52%
R96	Yellow	52%
S97	Yellow	52%
L98	Yellow	52%
R99	Yellow	52%
A102	Yellow	52%
E103	Yellow	52%
E104	Yellow	52%
F105	Yellow	52%
V106	Yellow	52%
R109	Yellow	52%
M112	Yellow	52%
I113	Yellow	52%
R114	Yellow	52%
V115	Yellow	52%
L116	Yellow	52%
M117	Yellow	52%
K118	Yellow	52%
S119	Yellow	52%
M120	Yellow	52%
V121	Yellow	52%
M122	Yellow	52%
Q123	Yellow	52%
D124	Yellow	52%
S125	Yellow	52%
T126	Yellow	52%
Y127	Yellow	52%
K128	Yellow	52%
Y129	Yellow	52%
F130	Yellow	52%
E131	Yellow	52%
F132	Yellow	52%
MET	Orange	6%
G2	Orange	6%
A3	Orange	6%
V4	Orange	6%
K5	Orange	6%
Y6	Orange	6%
L7	Orange	6%
B8	Orange	6%
E9	Orange	6%
L10	Orange	6%
O11	Orange	6%
R12	Orange	6%
K13	Orange	6%
K14	Orange	6%
Q15	Orange	6%
S16	Orange	6%
D17	Orange	6%
V18	Orange	6%
L19	Orange	6%
R20	Orange	6%
F21	Orange	6%
L22	Orange	6%
Q23	Orange	6%
R24	Orange	6%
V25	Orange	6%
R28	Orange	6%
Y30	Orange	6%
R31	Orange	6%
Q32	Orange	6%
K33	Orange	6%
R34	Orange	6%
V35	Orange	6%
R38	Orange	6%
A39	Orange	6%
P42	Orange	6%
T43	Orange	6%
R44	Orange	6%
P45	Orange	6%
P46	Orange	6%
K47	Orange	6%
A48	Orange	6%
R49	Orange	6%
R50	Orange	6%
L51	Orange	6%
G52	Orange	6%
R56	Orange	6%
G57	Orange	6%
S58	Orange	6%
F59	Orange	6%
R60	Orange	6%
L61	Orange	6%
V62	Orange	6%
R63	Orange	6%
V64	Orange	6%
R65	Orange	6%

[illegible]

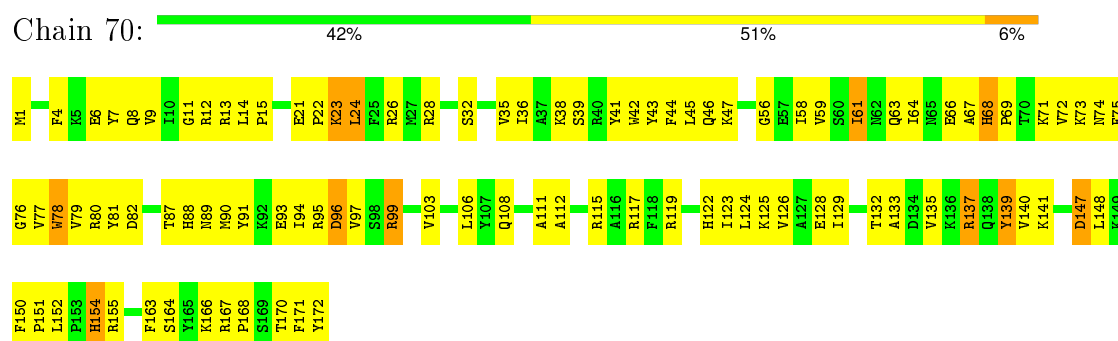
Chain 67:

Chain 68:

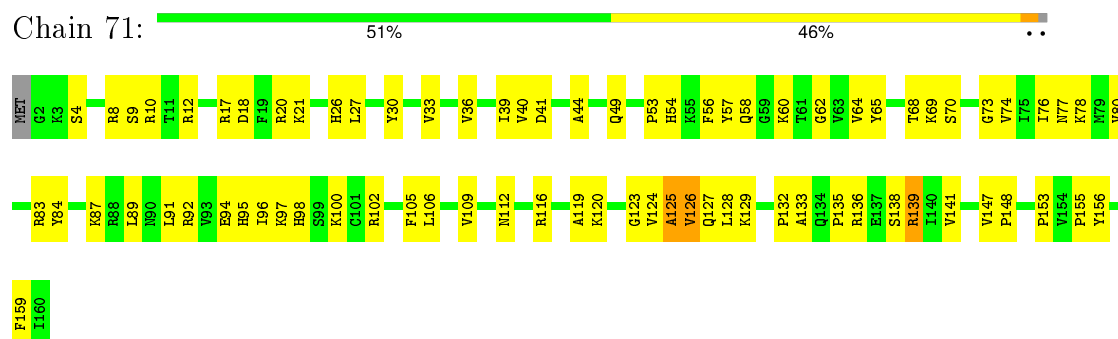
- Molecule 19: 60S ribosomal protein L19



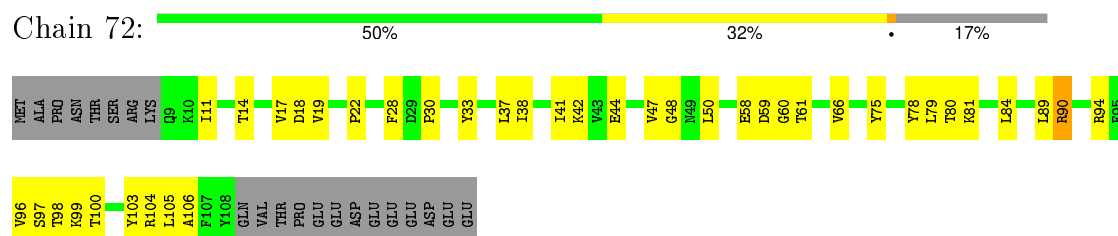
- Molecule 20: 60S ribosomal protein L20



- Molecule 21: 60S ribosomal protein L21

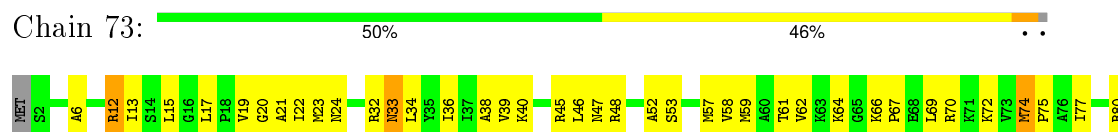


- Molecule 22: 60S ribosomal protein L22

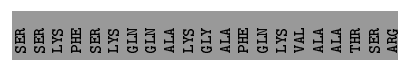
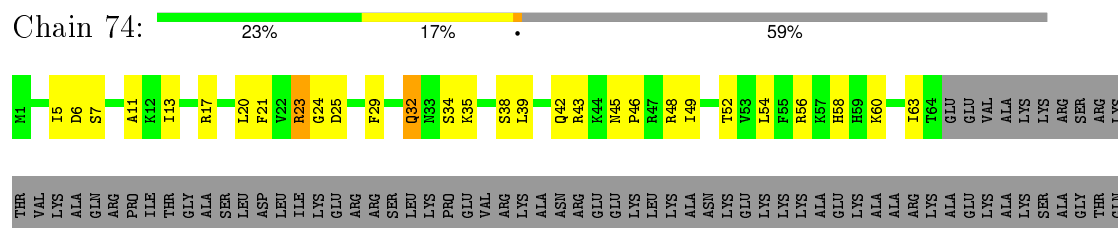


- Molecule 23: 60S ribosomal protein L23

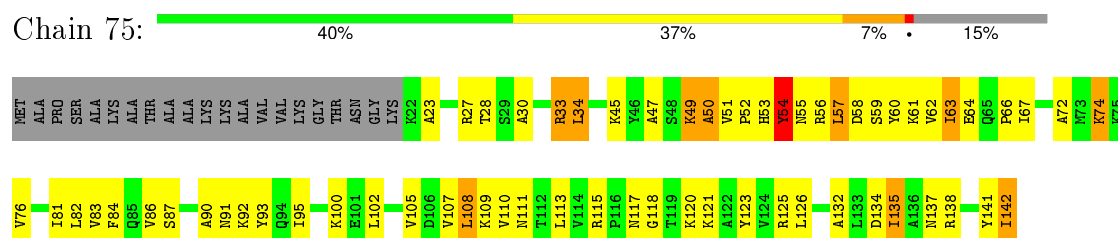




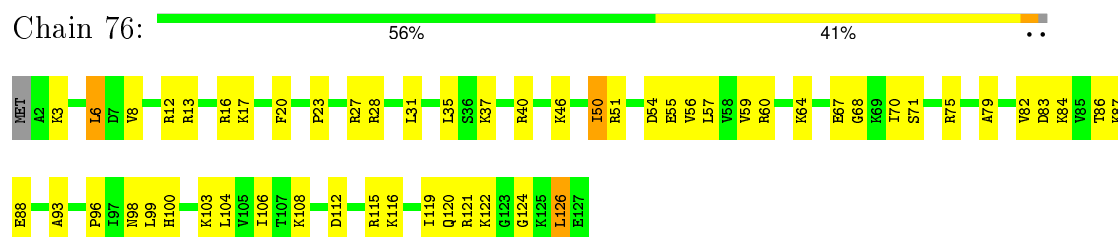
- Molecule 24: 60S ribosomal protein L24



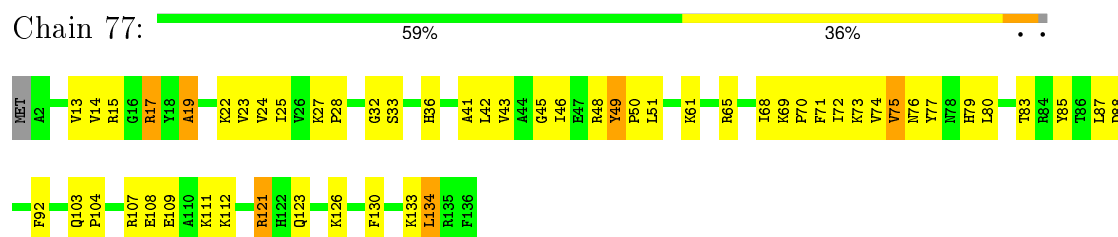
- Molecule 25: 60S ribosomal protein L25



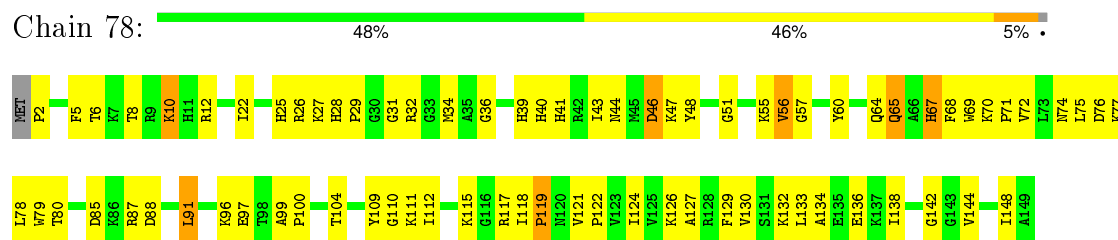
- Molecule 26: 60S ribosomal protein L26



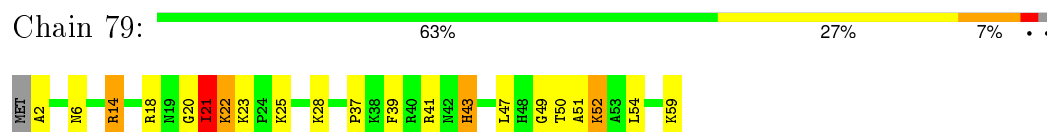
- Molecule 27: 60S ribosomal protein L27



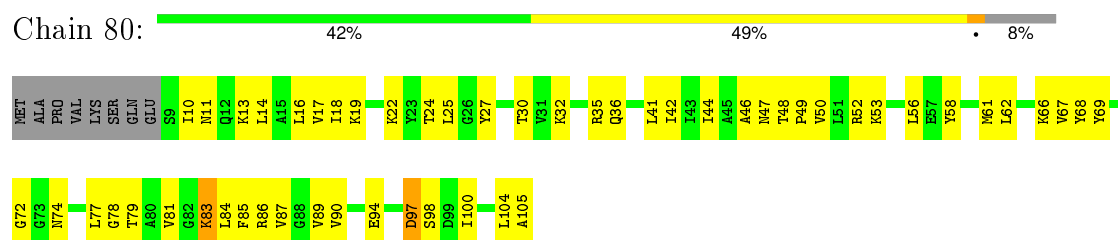
- Molecule 28: 60S ribosomal protein L28



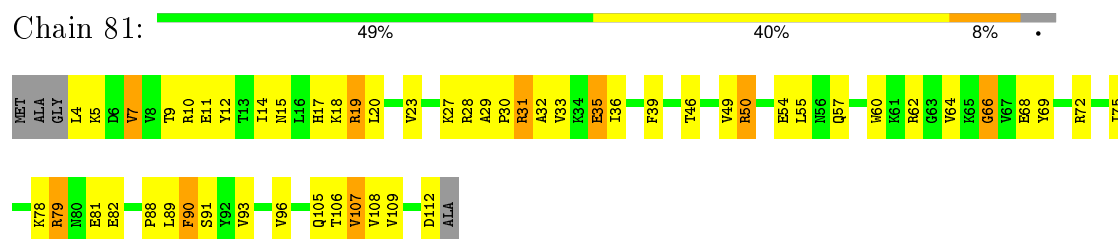
- Molecule 29: 60S ribosomal protein L29



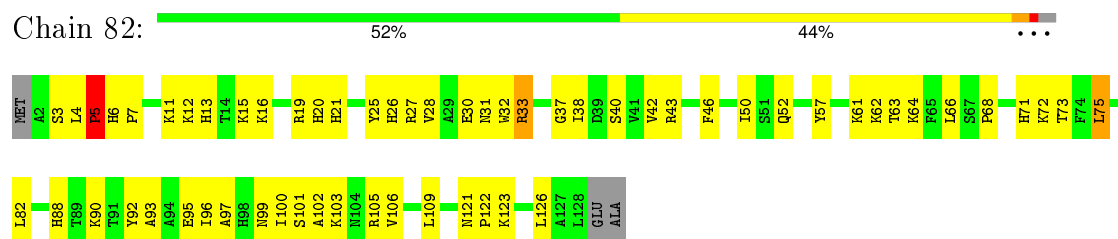
- Molecule 30: 60S ribosomal protein L30



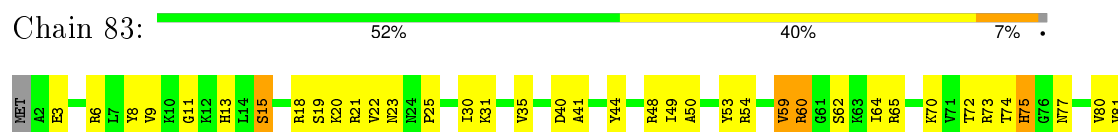
- Molecule 31: 60S ribosomal protein L31



- Molecule 32: 60S ribosomal protein L32



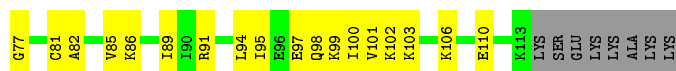
- Molecule 33: 60S ribosomal protein L33





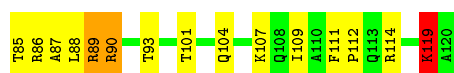
- Molecule 34: 60S ribosomal protein L34

Chain 84: 43% 43% 7% 7%



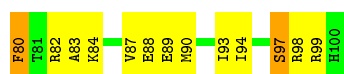
- Molecule 35: 60S ribosomal protein L35

Chain 85: 56% 39% ..



- Molecule 36: 60S ribosomal protein L36

Chain 86: 46% 45% 8% .



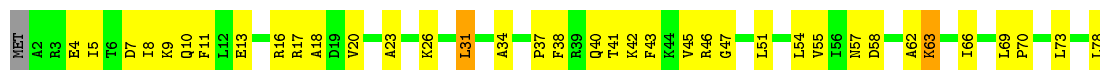
- Molecule 37: 60S ribosomal protein L37

Chain 87: 58% 38% ..



- Molecule 38: 60S ribosomal protein L38

Chain 88: 51% 45% ..



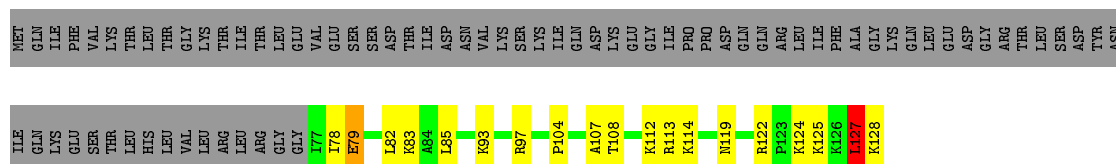
- Molecule 39: 60S ribosomal protein L39

Chain 89: 



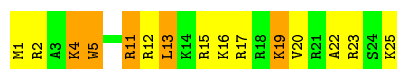
- Molecule 40: 60S ribosomal protein L40

Chain 90: 



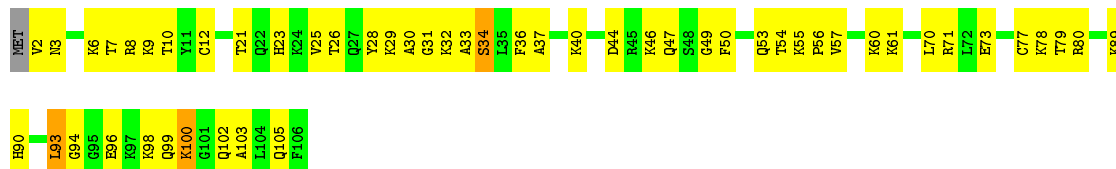
- Molecule 41: 60S ribosomal protein L41

Chain 91: 



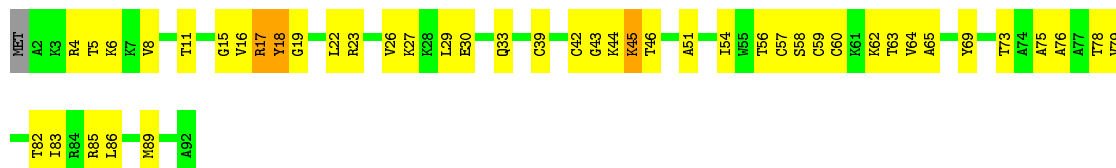
- Molecule 42: 60S ribosomal protein L42

Chain 92: 



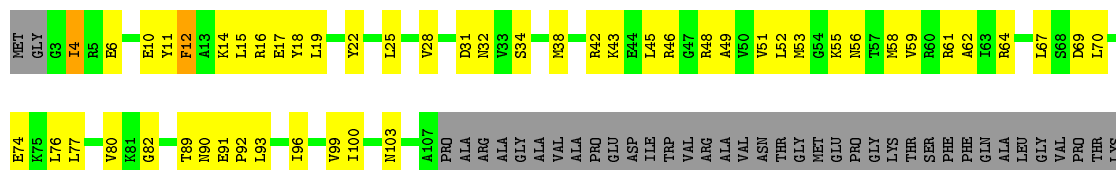
- Molecule 43: 60S ribosomal protein L43

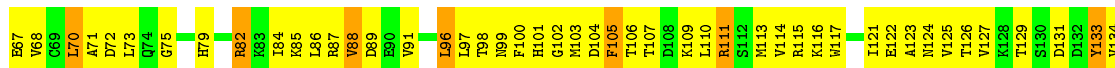
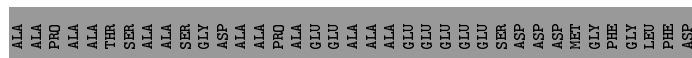
Chain 93: 

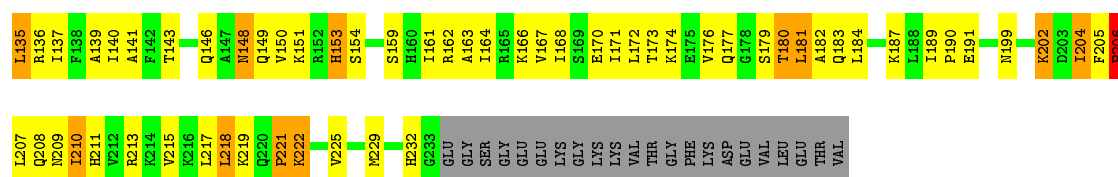


- Molecule 44: 60S acidic ribosomal protein P0

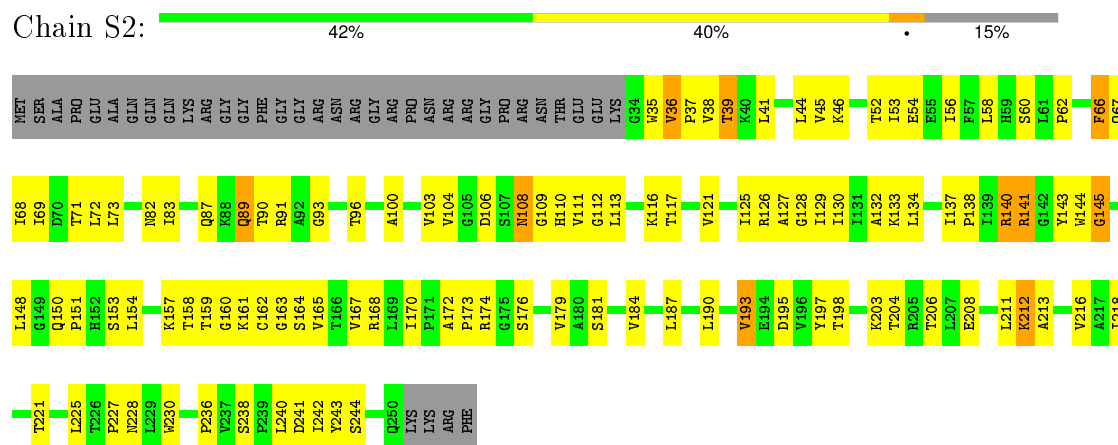
Chain P0: 







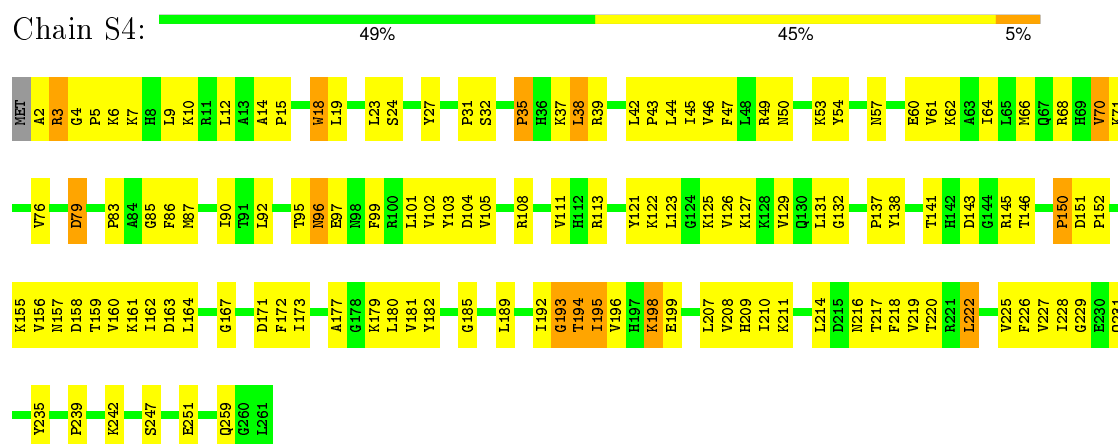
• Molecule 48: 40S ribosomal protein S2



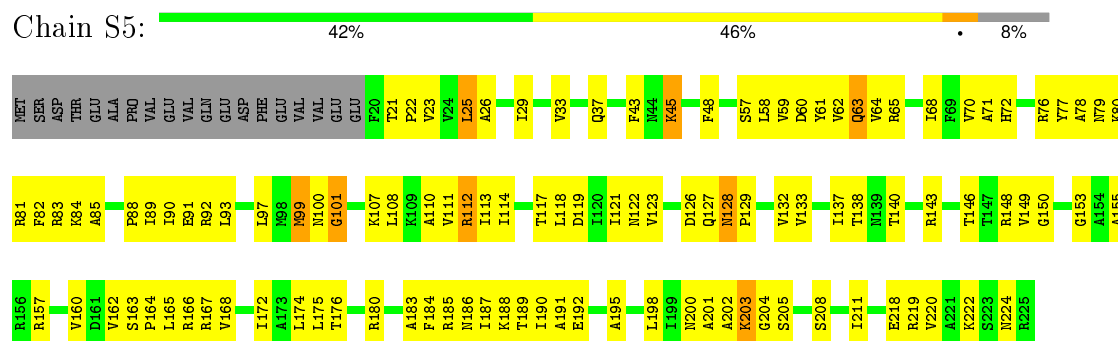
• Molecule 49: 40S ribosomal protein S3



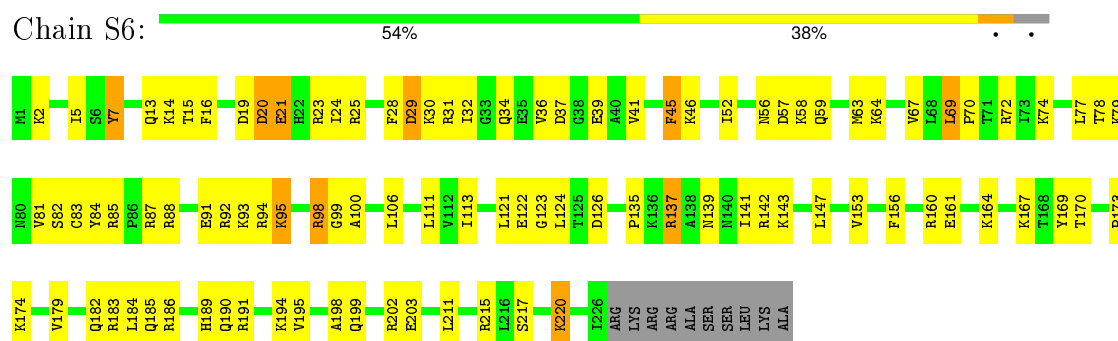
• Molecule 50: 40S ribosomal protein S4



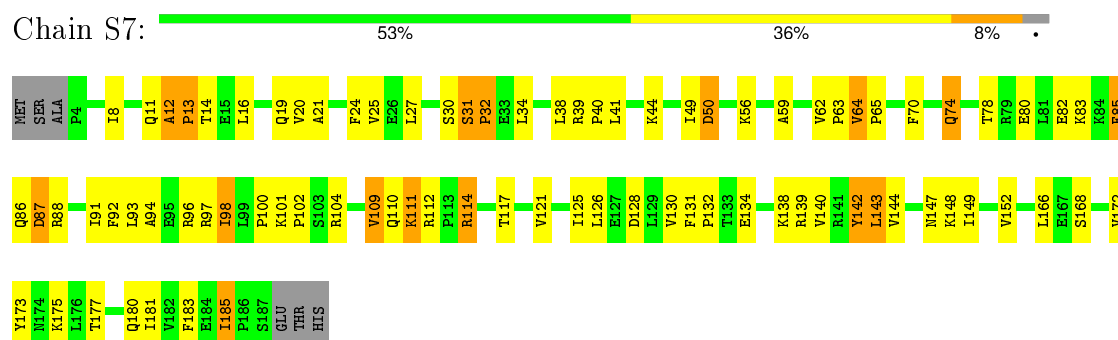
• Molecule 51: 40S ribosomal protein S5



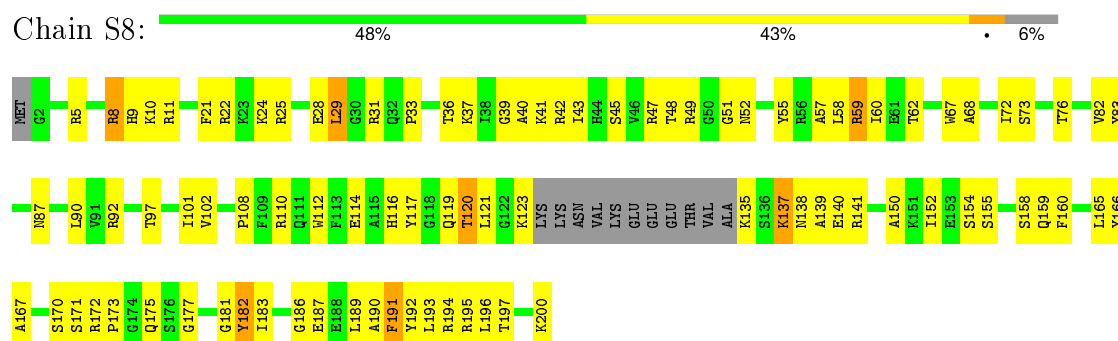
- Molecule 52: 40S ribosomal protein S6



- Molecule 53: 40S ribosomal protein S7



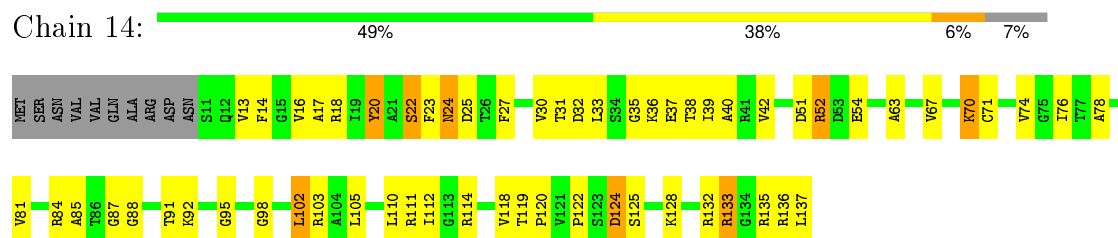
- Molecule 54: 40S ribosomal protein S8



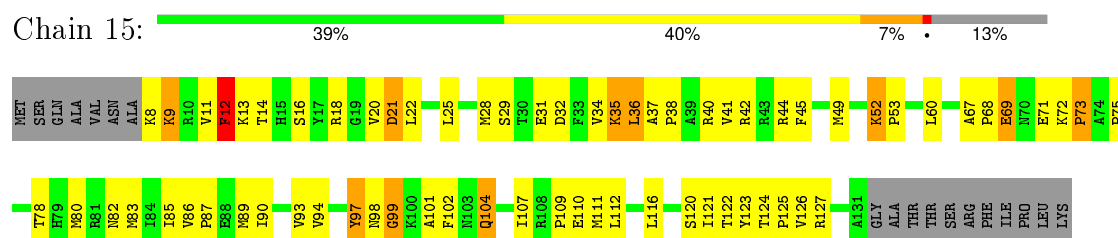
- Molecule 55: 40S ribosomal protein S9

- Molecule 60: 40S ribosomal protein S14

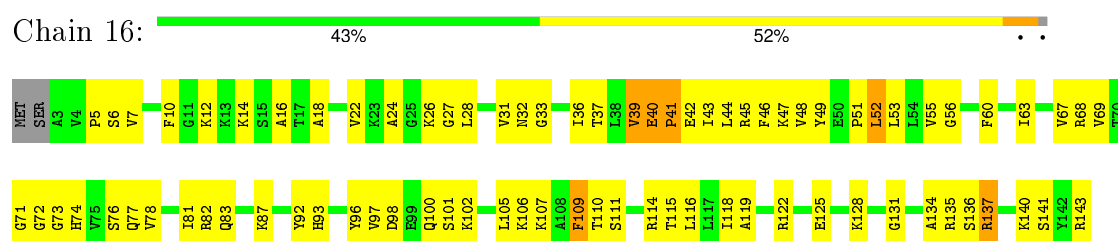




- Molecule 61: 40S ribosomal protein S15



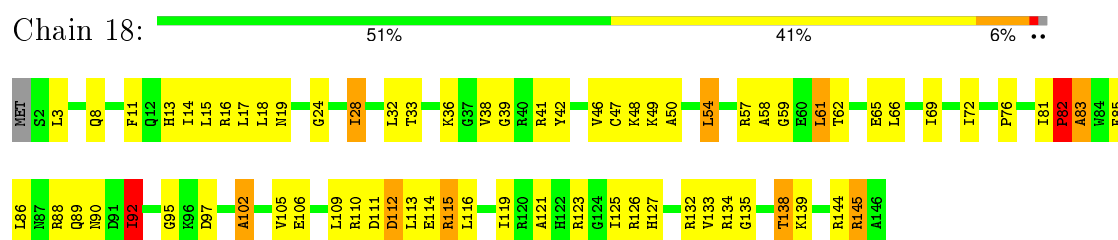
- Molecule 62: 40S ribosomal protein S16



- Molecule 63: 40S ribosomal protein S17

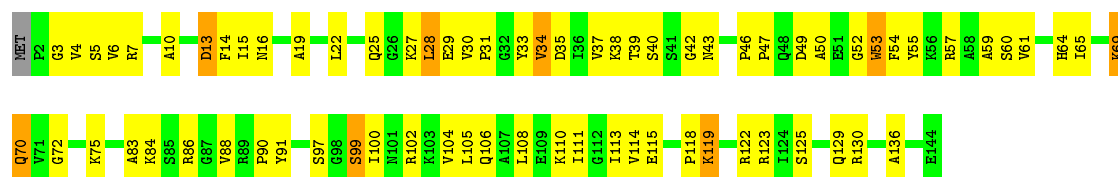


- Molecule 64: 40S ribosomal protein S18



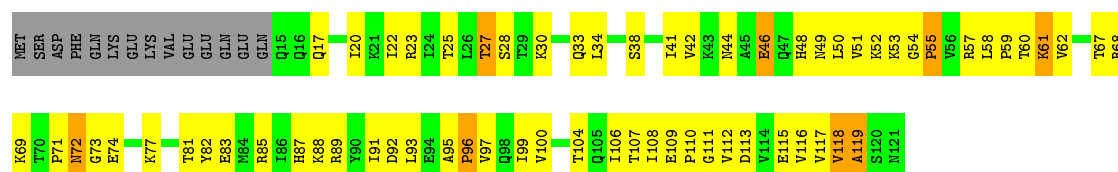
- Molecule 65: 40S ribosomal protein S19





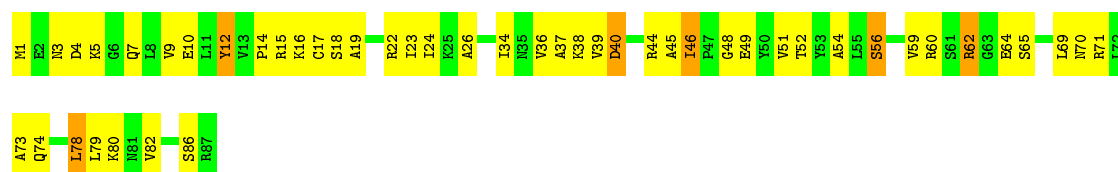
- Molecule 66: 40S ribosomal protein S20

Chain 20: 34% 48% 7% 12%



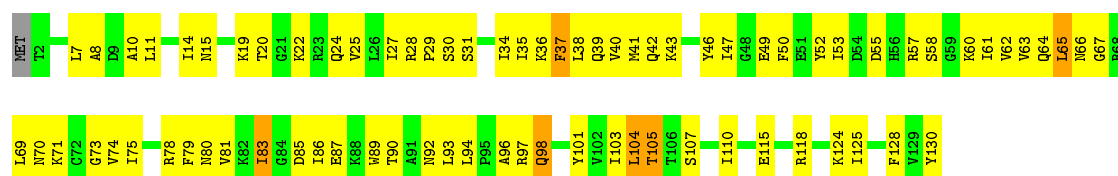
- Molecule 67: 40S ribosomal protein S21

Chain 21: 45% 48% 7%



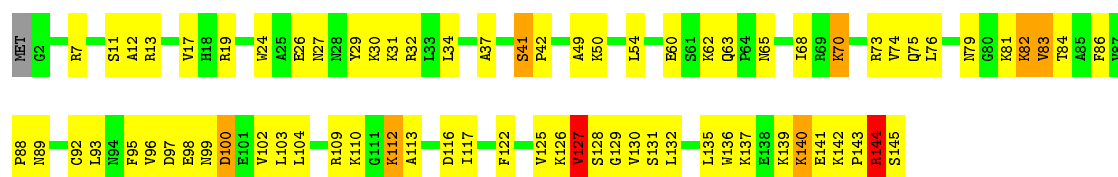
- Molecule 68: 40S ribosomal protein S22

Chain 22: 40% 55% 5%



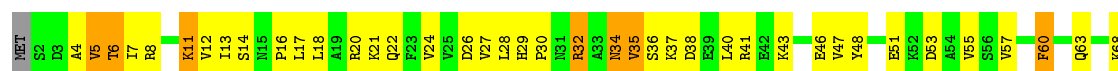
- Molecule 69: 40S ribosomal protein S23

Chain 23: 48% 45% 5%



- Molecule 70: 40S ribosomal protein S24

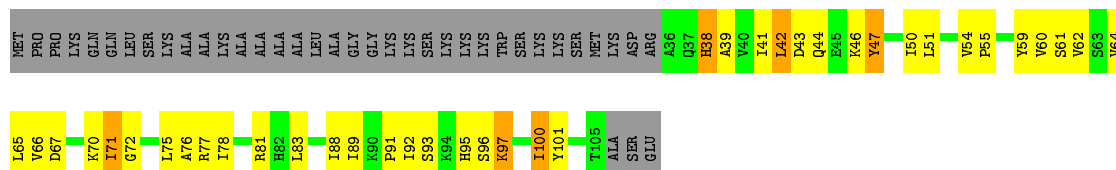
Chain 24: 47% 44% 8%





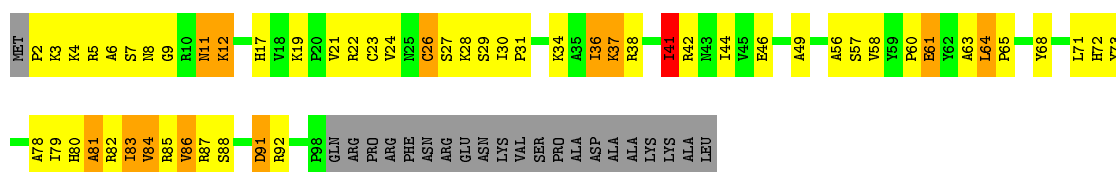
- Molecule 71: 40S ribosomal protein S25

Chain 25: 29% 31% 6% 35%



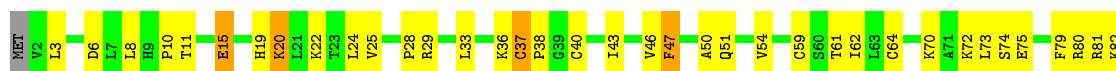
- Molecule 72: 40S ribosomal protein S26

Chain 26: 34% 36% 10% 18%



- Molecule 73: 40S ribosomal protein S27

Chain 27: 54% 40% 5%



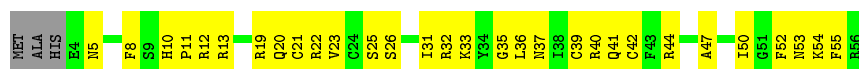
- Molecule 74: 40S ribosomal protein S28

Chain 28: 43% 43% 7% 6%



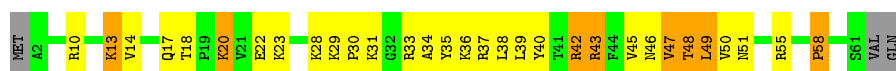
- Molecule 75: 40S ribosomal protein S29

Chain 29: 41% 54% 5%



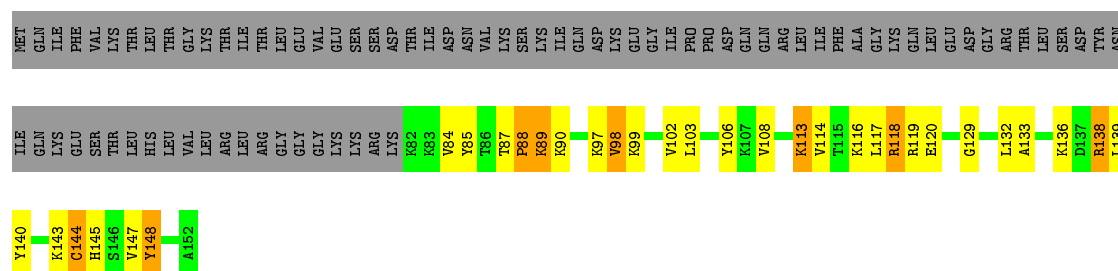
- Molecule 76: 40S ribosomal protein S30

Chain 30: 46% 37% 13% 5%



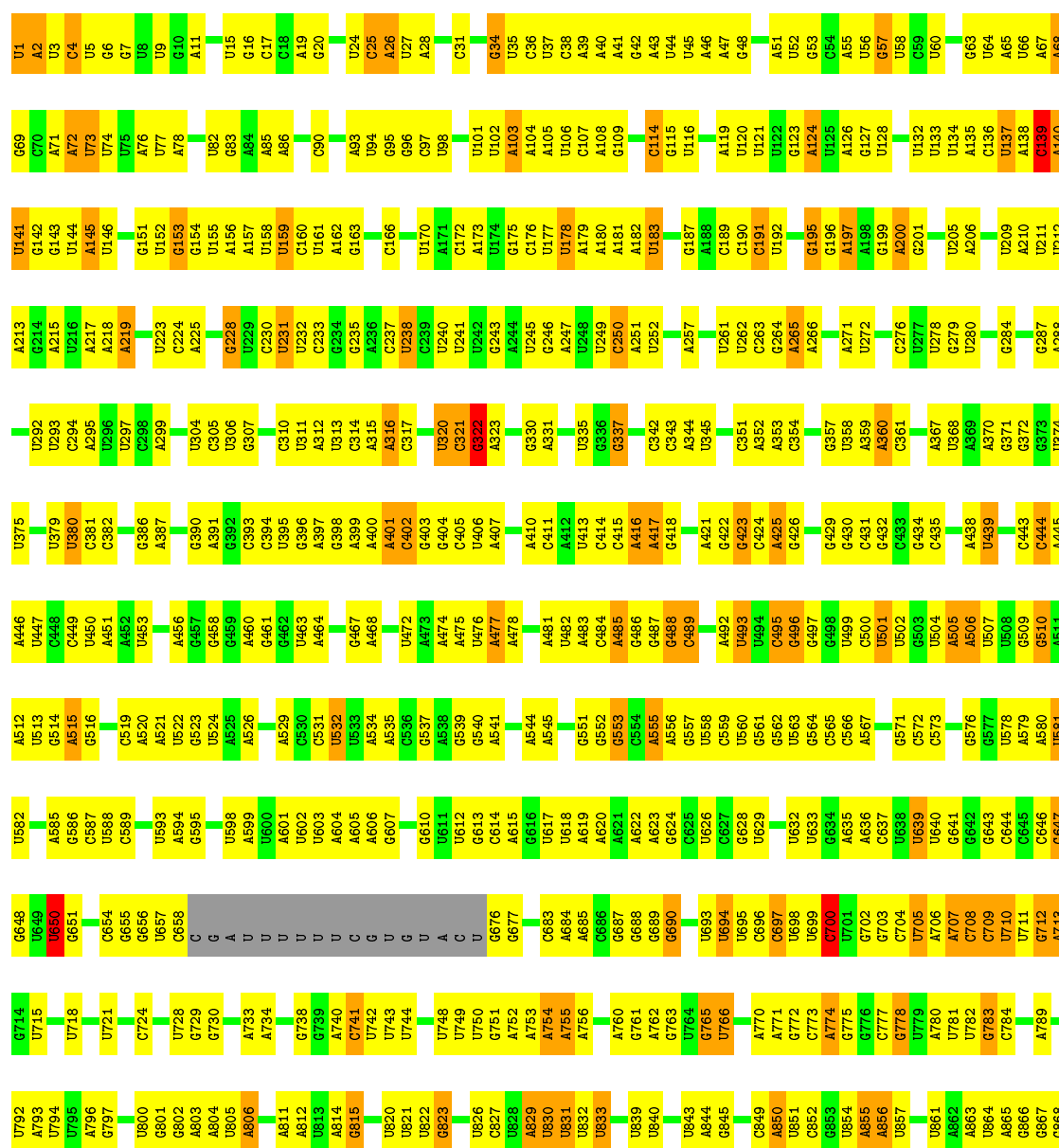
- Molecule 77: 40S ribosomal protein S31

Chain 31: 



● Molecule 78: 18S ribosomal RNA

Chain 1S: 

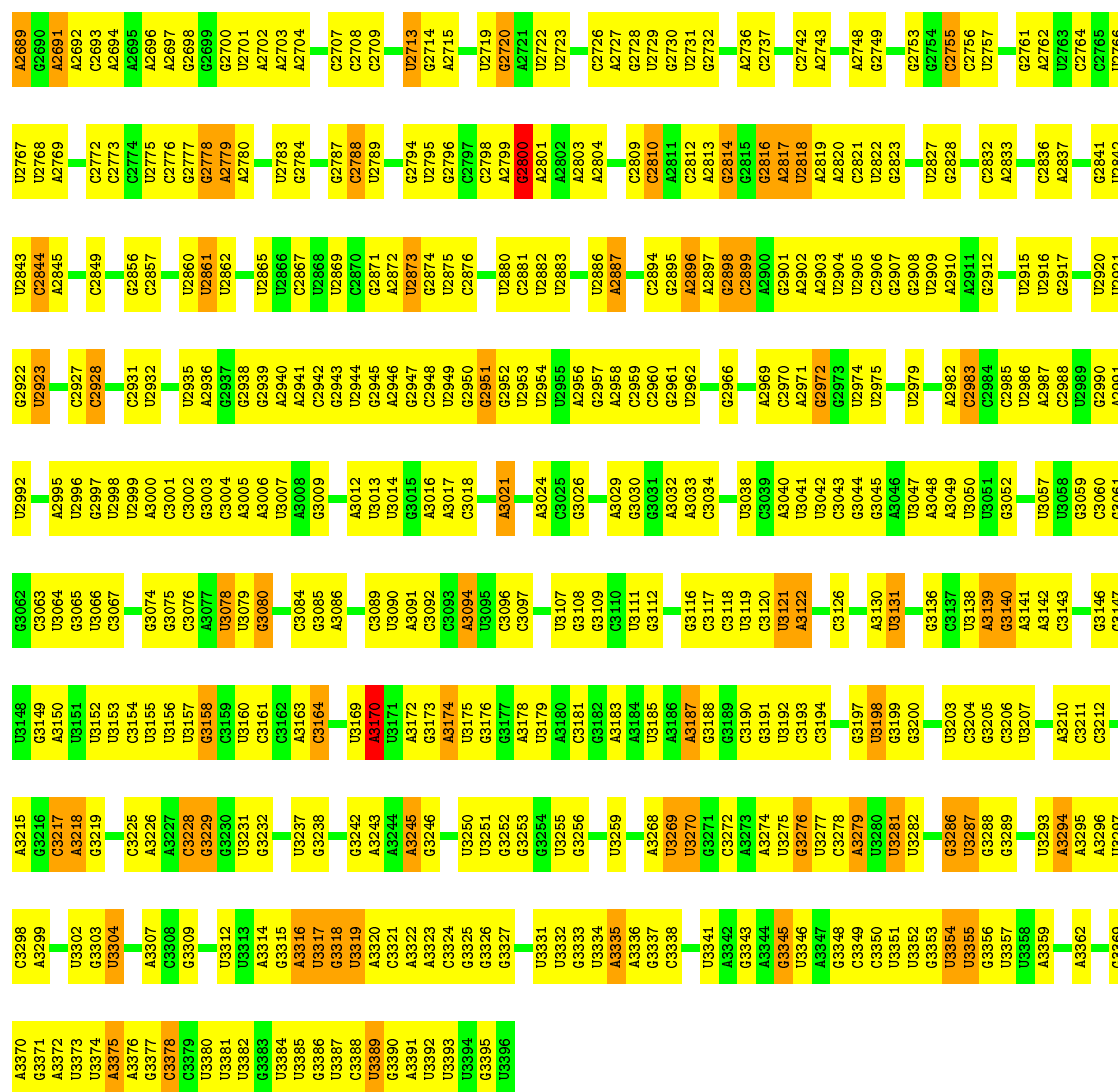


- Molecule 79: 25S ribosomal RNA

G76	G77	G78	G79	G80	G81	G82	G83	G84	G85	G86	G87	G88	G89	G90	G91	G92	G93	G94	G95	G96	G97	G98	G99	G100	G101	G102	G103	G104	G105	G106	G107	G108	G109	G110	G111	G112	G113	G114	G115	G116	G117	G118	G119	G120	G121	G122	G123	G124	G125	G126	G127	G128	G129	G130	G131	G132	G133	G134	G135	G136	G137	G138	G139	G140	G141	G142	G143	G144	G145	G146	G147	G148	G149	G150	G151	G152	G153	G154	G155	G156	G157	G158	G159	G160	G161	G162	G163	G164	G165	G166	G167	G168	G169	G170	G171	G172	G173	G174	G175	G176	G177	G178	G179	G180	G181	G182	G183	G184	G185	G186	G187	G188	G189	G190	G191	G192	G193	G194	G195	G196	G197	G198	G199	G200	G201	G202	G203	G204	G205	G206	G207	G208	G209	G210	G211	G212	G213	G214	G215	G216	G217	G218	G219	G220	G221	G222	G223	G224	G225	G226	G227	G228	G229	G230	G231	G232	G233	G234	G235	G236	G237	G238	G239	G240	G241	G242	G243	G244	G245	G246	G247	G248	G249	G250	G251	G252	G253	G254	G255	G256	G257	G258	G259	G260	G261	G262	G263	G264	G265	G266	G267	G268	G269	G270	G271	G272	G273	G274	G275	G276	G277	G278	G279	G280	G281	G282	G283	G284	G285	G286	G287	G288	G289	G290	G291	G292	G293	G294	G295	G296	G297	G298	G299	G300	G301	G302	G303	G304	G305	G306	G307	G308	G309	G310	G311	G312	G313	G314	G315	G316	G317	G318	G319	G320	G321	G322	G323	G324	G325	G326	G327	G328	G329	G330	G331	G332	G333	G334	G335	G336	G337	G338	G339	G340	G341	G342	G343	G344	G345	G346	G347	G348	G349	G350	G351	G352	G353	G354	G355	G356	G357	G358	G359	G360	G361	G362	G363	G364	G365	G366	G367	G368	G369	G370	G371	G372	G373	G374	G375	G376	G377	G378	G379	G380	G381	G382	G383	G384	G385	G386	G387	G388	G389	G390	G391	G392	G393	G394	G395	G396	G397	G398	G399	G400	G401	G402	G403	G404	G405	G406	G407	G408	G409	G410	G411	G412	G413	G414	G415	G416	G417	G418	G419	G420	G421	G422	G423	G424	G425	G426	G427	G428	G429	G430	G431	G432	G433	G434	G435	G436	G437	G438	G439	G440	G441	G442	G443	G444	G445	G446	G447	G448	G449	G450	G451	G452	G453	G454	G455	G456	G457	G458	G459	G460	G461	G462	G463	G464	G465	G466	G467	G468	G469	G470	G471	G472	G473	G474	G475	G476	G477	G478	G479	G480	G481	G482	G483	G484	G485	G486	G487	G488	G489	G490	G491	G492	G493	G494	G495	G496	G497	G498	G499	G500	G501	G502	G503	G504	G505	G506	G507	G508	G509	G510	G511	G512	G513	G514	G515	G516	G517	G518	G519	G520	G521	G522	G523	G524	G525	G526	G527	G528	G529	G530	G531	G532	G533	G534	G535	G536	G537	G538	G539	G540	G541	G542	G543	G544	G545	G546	G547	G548	G549	G550	G551	G552	G553	G554	G555	G556	G557	G558	G559	G560	G561	G562	G563	G564	G565	G566	G567	G568	G569	G570	G571	G572	G573	G574	G575	G576	G577	G578	G579	G580	G581	G582	G583	G584	G585	G586	G587	G588	G589
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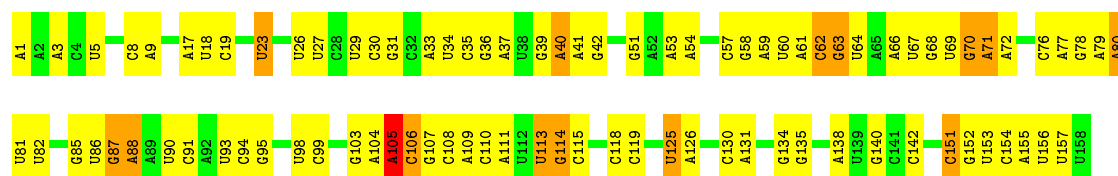
G1371	A1301	G1222	A1150	U1067	A992	G924	G856	A784	U627	U536	C	U381	G297	A219	U153
G1372	A1302	A1223	A1151	U1081	G993	A925	G857	G785	A628	U540	U	U382	U298	G220	U154
G1377	U1305	C1224	G1152	U1081	A996	A926	A858	A786	A629	U541	U	G393	G299	A221	G155
U1378	G1306	G1225	A1153	A1084	A997	C927	G859	G787	A630	G542	U	A386	G301	U223	G156
G1382	A1308	G1226	A1154	A1085	A998	A928	G861	A788	U631	G543	U	A389	U305	C224	A157
G1383	U1309	C1228	G1155	C1086	G999	U930	U862	U790	C633	C544	G	A394	U306	C225	G158
U1384	G1310	G1229	G1156	A1093	G1000	C931	C863	U791	C634	U545	U	G397	A307	C226	A159
C1385	G1311	A1231	A1157	U1094	G1001	U932	G864	G792	G635	U546	U	G394	A308	G229	G160
A1386	C1312	C1232	A1158	U1095	A933	A933	U865	G793	C636	G547	A	A395	A308	U230	G161
G1387	G1313	G1233	A1159	U1096	G934	U935	A866	U794	C637	G548	G	A396	U314	U168	U169
U1388	C1314	G1234	U1162	U1097	U936	U936	G867	G795	C638	U549	G	A397	C311	G241	G170
G1389	U1315	U1235	U1163	A1098	A936	A936	U871	U796	C639	A550	G	A398	C312	G171	G172
G1392	C1316	G1236	A1165	U1007	G937	G937	U872	U797	U640	U551	U	A399	C313	C233	A164
A1393	U1322	G1237	G1166	U1008	C938	C938	U873	G798	C641	A552	U	A400	C315	G234	A165
A1394	G1323	C1238	A1170	A1009	U939	U939	U874	A801	C642	U553	A	A401	U314	A235	C166
U1398	U1324	A1240	A1171	A1103	G940	G941	U875	C802	U643	A554	A	A402	C315	U167	U168
U1399	U1325	U1241	G1174	G1104	U942	U942	A876	C803	G644	G560	C	C403	A319	U240	U169
A1400	C1326	G1242	C1175	A1105	U943	U943	C877	G804	A645	C561	U	G404	U322	C242	G170
G1403	C1327	A1244	G1176	U1107	C944	C944	C878	G805	A646	C562	C	U405	A323	G243	G171
G1404	U1328	G1245	A1177	U1108	U1014	U1014	U879	A806	A647	U563	G	A406	U328	U250	U178
U1405	A1330	G1246	G1178	U1109	C1017	C1017	G880	A807	C648	U571	C	A407	U329	G251	C179
A1406	U1331	U1247	A1179	U1110	A951	A951	C886	A808	G652	A572	U	U487	A338	U252	C180
A1407	A1332	U1248	A1180	U1111	A952	A952	C887	U811	A653	U573	U	U488	C339	U257	U181
A1408	G1333	G1250	A1181	A1112	U955	U955	A888	G812	C654	C577	U	A418	C340	G258	G183
G1409	C1334	A1251	C1183	U1114	U956	U956	U889	G815	C655	U578	U	G421	C341	C259	U184
U1414	U1335	G1256	A1184	G1115	U1028	U1028	G891	A816	A656	A579	U	A422	C344	C260	C185
U1415	U1336	C1257	C1185	U1116	G1029	G1029	U892	A817	A657	U580	U	U426	A344	G267	U186
C1416	C1337	U1258	G1186	G1117	C959	C959	A895	C818	U662	A585	U	C427	C346	A268	A187
A1418	U1338	G1261	A1190	U1118	U960	U960	A896	U819	C663	G590	U	A428	C347	A269	U188
A1419	G1340	A1260	U1191	A1120	C961	C961	U897	A820	U664	G591	U	U429	C350	G269	G189
U1427	C1342	G1262	G1192	U1121	G963	G963	U898	G822	U671	A592	U	U434	C351	C271	U190
A1428	U1348	A1263	G1193	U1122	U1042	U1042	U899	C823	A672	C593	U	C435	A352	G272	U191
A1433	G1349	G1264	U1194	U1123	G968	G968	U900	C824	U673	U594	U	U436	A353	A273	C192
G1434	U1351	U1265	A1195	C1045	C969	C969	U903	U829	C674	A598	U	G437	C353	G274	G196
G1435	A1352	G1266	G1196	A1046	A970	A970	A904	A830	C675	C599	U	A438	U359	U275	A197
C1437	U1353	A1274	C1199	A1047	A971	A971	U905	G831	A677	G600	U	A440	A361	U276	A198
U1438	G1354	C1275	A1200	G1127	A972	A972	G907	U762	U681	A603	U	U441	A362	U277	A199
U1439	U1355	U1276	C1201	U1128	G974	G974	G908	U763	U682	G604	U	G442	U364	U278	C200
G1440	A1356	A1277	A1202	A1130	C975	C975	G909	U764	U683	A608	U	G443	C364	G282	A201
G1441	C1357	C1279	A1203	G1131	U1052	U1052	G910	U765	U684	G609	U	U444	C364	G283	G203
U1444	U1358	G1281	A1204	A1132	A1053	A1053	C911	U766	G685	G610	U	G445	C367	A284	A204
G1445	G1361	U1282	G1209	G1134	U1054	U1054	G912	U767	G686	A611	U	U446	A367	A285	G206
U1446	A1362	G1283	U1210	A1135	A1055	A1055	A913	G768	U687	U612	U	U447	A369	U286	U207
A1447	U1363	A1284	U1211	A1136	C982	C982	A914	G769	G688	U613	U	U448	U370	G287	C208
U1448	G1364	U1285	U1212	C1137	A983	A983	A915	A771	A690	G616	C	U449	C	A288	A209
U1449	U1365	A1286	G1213	U1138	G984	G984	G916	U772	U698	G617	C	U450	U371	G289	U210
A1450	A1366	U1287	U1214	U1139	U985	U985	A917	G773	A699	A618	U	U451	A372	G290	A211
C1451	G1367	A1290	U1215	G1140	U986	U986	C918	U776	A699	C619	U	U452	A373	C291	G212
U1452	U1368	U1291	A1062	C1141	U987	U987	U919	U777	C700	U620	U	U453	A374	U292	G213
A1453	A1369	G1292	G1142	U1142	U988	U988	A920	U778	G701	A622	U	U454	A375	C293	G214
	U1370	U1293	G1145	U1146	A1065	A1065	U921	U779	A780	A623	U	U455	C379	U294	G215
					G1066	G1066	C923	U781	A705				U380	A296	G218



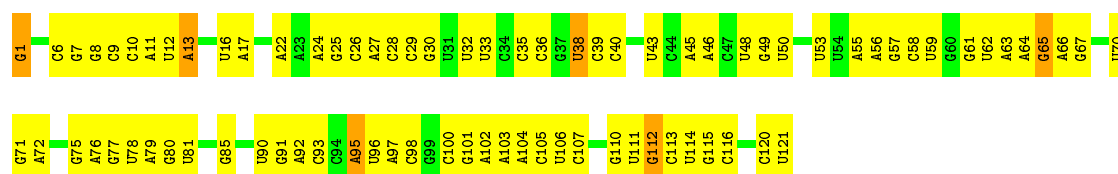
• Molecule 80: 5.8S ribosomal RNA

Chain 8S: 44% 47% 9%



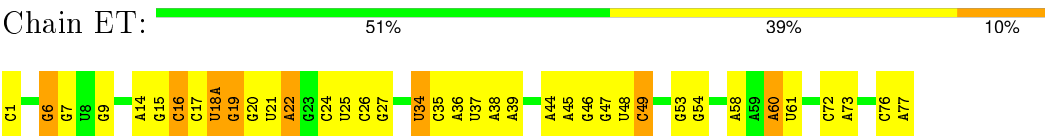
• Molecule 81: 5S ribosomal RNA

Chain 5S: 33% 62% 5%

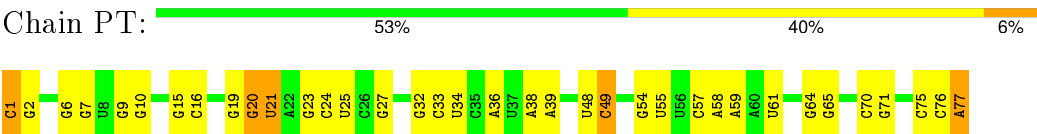




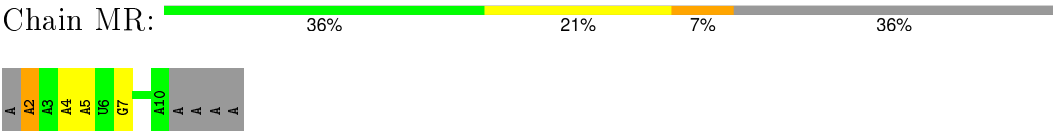
● Molecule 82: P/E-site initiator transfer RNAfMet



● Molecule 82: P/E-site initiator transfer RNAfMet



● Molecule 83: messenger RNA



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	23163	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	CTFFIND3, FREALIGN per micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	1159	Depositor
Maximum defocus (nm)	4844	Depositor
Magnification	133333	Depositor
Image detector	FEI FALCON I (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	L1	0.61	0/1634	0.67	0/2195
10	60	0.49	0/1754	0.56	0/2350
11	61	0.51	0/1375	0.58	0/1842
12	62	0.52	0/700	0.72	7/968 (0.7%)
13	63	0.48	0/1568	0.60	0/2106
14	64	0.50	0/1069	0.56	0/1438
15	65	0.47	0/1758	0.54	0/2354
16	66	0.49	0/1586	0.57	0/2128
17	67	0.49	0/1466	0.56	0/1968
18	68	0.48	0/1466	0.57	0/1965
19	69	0.42	0/1539	0.56	0/2050
2	L2	0.43	0/1952	0.59	0/2622
20	70	0.52	0/1482	0.58	0/1990
21	71	0.50	0/1301	0.56	0/1743
22	72	0.57	0/812	0.57	0/1099
23	73	0.46	0/1019	0.57	0/1369
24	74	0.51	0/540	0.56	0/717
25	75	0.50	0/984	0.60	0/1325
26	76	0.46	0/1005	0.58	1/1341 (0.1%)
27	77	0.51	0/1119	0.53	0/1497
28	78	0.46	0/1205	0.59	0/1612
29	79	0.48	0/474	0.60	0/629
3	L3	0.48	0/3153	0.56	0/4239
30	80	0.52	0/751	0.55	0/1008
31	81	0.46	0/904	0.59	0/1213
32	82	0.46	0/1041	0.58	0/1394
33	83	0.51	0/869	0.56	0/1168
34	84	0.48	0/891	0.59	0/1191
35	85	0.45	0/979	0.57	0/1301
36	86	0.46	0/779	0.63	0/1034
37	87	0.48	0/697	0.54	0/923
38	88	0.52	0/619	0.55	0/826
39	89	0.46	0/444	0.54	0/588
4	L4	0.46	0/2802	0.58	0/3792

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
40	90	0.44	0/424	0.58	0/562
41	91	0.46	0/235	0.58	0/300
42	92	0.49	0/861	0.58	0/1136
43	93	0.44	0/702	0.55	0/934
44	P0	0.62	0/1002	0.65	0/1348
45	RC	0.54	0/2498	0.60	0/3398
46	S0	0.55	0/1653	0.60	0/2261
47	S1	0.50	0/1735	0.59	0/2335
48	S2	0.50	0/1665	0.59	0/2263
49	S3	0.52	0/1759	0.58	0/2368
5	L5	0.53	0/2426	0.58	0/3271
50	S4	0.50	0/2110	0.62	0/2839
51	S5	0.49	0/1630	0.59	0/2202
52	S6	0.51	0/1844	0.59	0/2464
53	S7	0.52	0/1506	0.62	0/2028
54	S8	0.49	0/1515	0.60	0/2021
55	S9	0.50	0/1519	0.62	0/2035
56	10	0.58	0/837	0.64	0/1131
57	11	0.53	0/1273	0.58	0/1712
58	12	0.56	0/943	0.68	0/1274
59	13	0.49	0/1216	0.59	0/1638
6	L6	0.52	0/1261	0.62	0/1694
60	14	0.48	0/953	0.58	0/1279
61	15	0.54	0/1012	0.65	0/1356
62	16	0.52	0/1126	0.63	0/1510
63	17	0.58	0/974	0.70	0/1304
64	18	0.50	0/1212	0.61	0/1628
65	19	0.52	0/1131	0.60	0/1517
66	20	0.54	0/866	0.57	0/1169
67	21	0.51	0/694	0.57	0/935
68	22	0.49	0/1039	0.60	0/1395
69	23	0.48	0/1140	0.59	0/1518
7	L7	0.50	0/1822	0.60	1/2451 (0.0%)
70	24	0.53	0/1088	0.58	0/1449
71	25	0.52	0/571	0.67	0/768
72	26	0.47	0/782	0.57	0/1047
73	27	0.51	0/621	0.57	0/838
74	28	0.50	0/500	0.59	0/670
75	29	0.55	0/454	0.59	0/602
76	30	0.51	0/483	0.63	0/643
77	31	0.56	0/505	0.72	2/682 (0.3%)
78	1S	0.76	3/42445 (0.0%)	0.74	18/66138 (0.0%)
79	2S	0.72	5/79038 (0.0%)	0.72	22/123226 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
8	L8	0.49	0/1850	0.60	0/2495
80	8S	0.72	1/3747 (0.0%)	0.71	0/5832
81	5S	0.73	1/2884 (0.0%)	0.70	0/4491
82	ET	0.83	1/1836 (0.1%)	0.73	0/2859
82	PT	0.76	1/1836 (0.1%)	0.73	0/2859
83	MR	0.93	1/219 (0.5%)	0.75	0/339
9	L9	0.50	0/1540	0.59	0/2073
All	All	0.65	13/224719 (0.0%)	0.68	51/330272 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
78	1S	0	23
79	2S	3	56
80	8S	0	6
All	All	3	85

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
80	8S	1	A	OP3-P	-7.03	1.52	1.61
78	1S	1	U	OP3-P	-6.96	1.52	1.61
81	5S	1	G	OP3-P	-6.89	1.52	1.61
79	2S	486	A	P-O5'	6.74	1.66	1.59
82	PT	1	C	OP3-P	-6.69	1.53	1.61

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
78	1S	829	A	C2'-C3'-O3'	9.04	129.39	109.50
79	2S	2065	U	C2'-C3'-O3'	8.72	128.69	109.50
79	2S	2512	C	C2'-C3'-O3'	8.22	127.58	109.50
79	2S	493	U	N1-C1'-C2'	7.81	124.15	114.00
77	31	144	CYS	N-CA-C	-6.92	92.32	111.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
79	2S	65	A	C3'

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Mol	Chain	Res	Type	Atom
79	2S	2065	U	C3'
79	2S	2512	C	C3'

5 of 85 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
78	1S	183	U	Sidechain
78	1S	199	G	Sidechain
78	1S	228	G	Sidechain
78	1S	287	G	Sidechain
78	1S	313	U	Sidechain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L1	1609	0	1701	103	0
2	L2	1918	0	1987	162	0
3	L3	3082	0	3165	181	0
4	L4	2750	0	2863	153	0
5	L5	2376	0	2325	130	0
6	L6	1240	0	1326	77	0
7	L7	1785	0	1862	126	0
8	L8	1818	0	1908	129	0
9	L9	1519	0	1587	90	0
10	60	1718	0	1754	88	0
11	61	1354	0	1383	81	0
12	62	703	0	324	7	0
13	63	1543	0	1608	85	0
14	64	1054	0	1149	55	0
15	65	1721	0	1779	132	0
16	66	1556	0	1659	93	0
17	67	1443	0	1485	85	0
18	68	1442	0	1543	113	0
19	69	1522	0	1617	82	0
20	70	1446	0	1487	97	0
21	71	1277	0	1323	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	72	796	0	812	36	0
23	73	1004	0	1048	77	0
24	74	528	0	558	30	0
25	75	969	0	1036	56	0
26	76	994	0	1081	47	0
27	77	1093	0	1155	44	0
28	78	1174	0	1215	74	0
29	79	463	0	491	18	0
30	80	743	0	797	43	0
31	81	890	0	938	52	0
32	82	1020	0	1090	54	0
33	83	851	0	880	59	0
34	84	881	0	949	62	0
35	85	970	0	1078	42	0
36	86	772	0	849	50	0
37	87	682	0	687	46	0
38	88	613	0	682	37	0
39	89	437	0	475	16	0
40	90	418	0	459	18	0
41	91	234	0	284	16	0
42	92	848	0	918	46	0
43	93	695	0	738	46	0
44	P0	987	0	999	46	0
45	RC	2445	0	2401	115	0
46	S0	1612	0	1623	107	0
47	S1	1709	0	1784	141	0
48	S2	1635	0	1723	101	0
49	S3	1734	0	1817	95	0
50	S4	2069	0	2154	121	0
51	S5	1610	0	1675	112	0
52	S6	1820	0	1918	81	0
53	S7	1481	0	1572	82	0
54	S8	1490	0	1525	80	0
55	S9	1494	0	1573	105	0
56	10	817	0	804	55	0
57	11	1245	0	1314	64	0
58	12	935	0	975	45	0
59	13	1193	0	1255	67	0
60	14	942	0	979	63	0
61	15	991	0	1035	62	0
62	16	1106	0	1166	82	0
63	17	965	0	1026	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	18	1193	0	1222	72	0
65	19	1113	0	1124	65	0
66	20	856	0	917	72	0
67	21	685	0	672	39	0
68	22	1022	0	1060	77	0
69	23	1122	0	1196	84	0
70	24	1074	0	1132	55	0
71	25	563	0	603	41	0
72	26	769	0	818	66	0
73	27	611	0	633	33	0
74	28	498	0	535	33	0
75	29	444	0	436	27	0
76	30	475	0	525	32	0
77	31	498	0	441	22	0
78	1S	37949	0	19093	951	0
79	2S	70616	0	35486	1791	0
80	8S	3354	0	1695	74	0
81	5S	2580	0	1304	75	0
82	ET	1644	0	836	30	0
82	PT	1644	0	836	25	0
83	MR	195	0	98	3	0
All	All	209136	0	154035	7478	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 21.

The worst 5 of 7478 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)
1:L1:30:GLU:HB2	1:L1:34:LEU:HD11	1.32	1.10
78:1S:712:G:H2'	78:1S:713:A:H5''	1.34	1.09
79:2S:1604:G:H4'	79:2S:1835:A:H4'	1.35	1.08
1:L1:93:LEU:HD21	1:L1:118:LYS:HD2	1.35	1.08
79:2S:1971:C:H2'	79:2S:1972:A:H4'	1.27	1.07

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	L1	202/217 (93%)	140 (69%)	50 (25%)	12 (6%)	2	26
2	L2	250/254 (98%)	205 (82%)	34 (14%)	11 (4%)	3	33
3	L3	384/387 (99%)	328 (85%)	47 (12%)	9 (2%)	8	48
4	L4	359/362 (99%)	290 (81%)	53 (15%)	16 (4%)	3	33
5	L5	294/297 (99%)	251 (85%)	32 (11%)	11 (4%)	4	37
6	L6	152/176 (86%)	131 (86%)	19 (12%)	2 (1%)	15	59
7	L7	220/244 (90%)	182 (83%)	32 (14%)	6 (3%)	6	44
8	L8	231/256 (90%)	191 (83%)	30 (13%)	10 (4%)	3	34
9	L9	189/191 (99%)	163 (86%)	22 (12%)	4 (2%)	9	50
10	60	207/221 (94%)	183 (88%)	21 (10%)	3 (1%)	14	58
11	61	167/174 (96%)	131 (78%)	23 (14%)	13 (8%)	1	20
12	62	137/165 (83%)	79 (58%)	37 (27%)	21 (15%)	0	5
13	63	191/199 (96%)	158 (83%)	20 (10%)	13 (7%)	1	23
14	64	134/138 (97%)	110 (82%)	21 (16%)	3 (2%)	8	49
15	65	201/204 (98%)	160 (80%)	33 (16%)	8 (4%)	4	35
16	66	195/199 (98%)	173 (89%)	17 (9%)	5 (3%)	7	45
17	67	181/184 (98%)	153 (84%)	23 (13%)	5 (3%)	6	44
18	68	183/186 (98%)	155 (85%)	21 (12%)	7 (4%)	4	37
19	69	186/189 (98%)	169 (91%)	16 (9%)	1 (0%)	34	76
20	70	170/172 (99%)	142 (84%)	21 (12%)	7 (4%)	3	34
21	71	157/160 (98%)	137 (87%)	15 (10%)	5 (3%)	5	40
22	72	98/121 (81%)	81 (83%)	14 (14%)	3 (3%)	5	41
23	73	134/137 (98%)	118 (88%)	14 (10%)	2 (2%)	13	57
24	74	62/155 (40%)	50 (81%)	10 (16%)	2 (3%)	5	40
25	75	119/142 (84%)	99 (83%)	14 (12%)	6 (5%)	3	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	76	124/127 (98%)	116 (94%)	8 (6%)	0	100	100
27	77	133/136 (98%)	102 (77%)	25 (19%)	6 (4%)	3	33
28	78	146/149 (98%)	119 (82%)	22 (15%)	5 (3%)	5	40
29	79	56/59 (95%)	50 (89%)	4 (7%)	2 (4%)	4	38
30	80	95/105 (90%)	82 (86%)	11 (12%)	2 (2%)	9	50
31	81	107/113 (95%)	93 (87%)	11 (10%)	3 (3%)	6	44
32	82	125/130 (96%)	111 (89%)	13 (10%)	1 (1%)	24	69
33	83	104/107 (97%)	82 (79%)	14 (14%)	8 (8%)	1	20
34	84	110/121 (91%)	87 (79%)	18 (16%)	5 (4%)	3	33
35	85	117/120 (98%)	108 (92%)	7 (6%)	2 (2%)	11	55
36	86	97/100 (97%)	83 (86%)	8 (8%)	6 (6%)	2	25
37	87	85/88 (97%)	70 (82%)	14 (16%)	1 (1%)	16	61
38	88	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	15	59
39	89	48/51 (94%)	40 (83%)	7 (15%)	1 (2%)	9	50
40	90	50/128 (39%)	41 (82%)	7 (14%)	2 (4%)	4	35
41	91	23/25 (92%)	23 (100%)	0	0	100	100
42	92	103/106 (97%)	83 (81%)	18 (18%)	2 (2%)	10	52
43	93	89/92 (97%)	77 (86%)	11 (12%)	1 (1%)	17	63
44	P0	121/312 (39%)	107 (88%)	13 (11%)	1 (1%)	24	69
45	RC	316/319 (99%)	262 (83%)	44 (14%)	10 (3%)	5	40
46	S0	204/252 (81%)	161 (79%)	37 (18%)	6 (3%)	6	43
47	S1	212/255 (83%)	162 (76%)	39 (18%)	11 (5%)	2	29
48	S2	215/254 (85%)	177 (82%)	30 (14%)	8 (4%)	4	37
49	S3	221/240 (92%)	188 (85%)	25 (11%)	8 (4%)	4	38
50	S4	258/261 (99%)	202 (78%)	45 (17%)	11 (4%)	3	34
51	S5	204/225 (91%)	170 (83%)	25 (12%)	9 (4%)	3	33
52	S6	224/236 (95%)	196 (88%)	24 (11%)	4 (2%)	11	53
53	S7	182/190 (96%)	145 (80%)	27 (15%)	10 (6%)	2	28
54	S8	184/200 (92%)	141 (77%)	34 (18%)	9 (5%)	3	31
55	S9	183/197 (93%)	151 (82%)	20 (11%)	12 (7%)	1	24
56	10	94/105 (90%)	69 (73%)	17 (18%)	8 (8%)	1	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	11	153/156 (98%)	122 (80%)	23 (15%)	8 (5%)	2	29
58	12	122/143 (85%)	81 (66%)	26 (21%)	15 (12%)	0	8
59	13	148/151 (98%)	133 (90%)	11 (7%)	4 (3%)	6	44
60	14	125/137 (91%)	95 (76%)	25 (20%)	5 (4%)	4	35
61	15	122/142 (86%)	97 (80%)	18 (15%)	7 (6%)	2	27
62	16	139/143 (97%)	118 (85%)	17 (12%)	4 (3%)	6	43
63	17	116/136 (85%)	90 (78%)	18 (16%)	8 (7%)	1	22
64	18	143/146 (98%)	114 (80%)	20 (14%)	9 (6%)	2	25
65	19	141/144 (98%)	118 (84%)	16 (11%)	7 (5%)	3	31
66	20	105/121 (87%)	83 (79%)	16 (15%)	6 (6%)	2	27
67	21	85/87 (98%)	68 (80%)	11 (13%)	6 (7%)	1	22
68	22	127/130 (98%)	112 (88%)	11 (9%)	4 (3%)	5	41
69	23	142/145 (98%)	107 (75%)	30 (21%)	5 (4%)	4	39
70	24	132/135 (98%)	106 (80%)	18 (14%)	8 (6%)	2	25
71	25	68/108 (63%)	51 (75%)	14 (21%)	3 (4%)	3	33
72	26	95/119 (80%)	64 (67%)	20 (21%)	11 (12%)	0	9
73	27	79/82 (96%)	61 (77%)	18 (23%)	0	100	100
74	28	61/67 (91%)	46 (75%)	13 (21%)	2 (3%)	5	40
75	29	51/56 (91%)	43 (84%)	7 (14%)	1 (2%)	9	51
76	30	58/63 (92%)	44 (76%)	8 (14%)	6 (10%)	1	12
77	31	69/152 (45%)	44 (64%)	14 (20%)	11 (16%)	0	5
All	All	11389/12574 (91%)	9340 (82%)	1579 (14%)	470 (4%)	6	34

5 of 470 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L1	20	SER
1	L1	151	VAL
2	L2	41	ILE
2	L2	115	ASN
2	L2	192	LYS

### 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	L1	185/198 (93%)	172 (93%)	13 (7%)	19	56
2	L2	194/196 (99%)	185 (95%)	9 (5%)	33	68
3	L3	322/323 (100%)	310 (96%)	12 (4%)	41	73
4	L4	288/289 (100%)	276 (96%)	12 (4%)	36	70
5	L5	244/245 (100%)	236 (97%)	8 (3%)	45	76
6	L6	134/153 (88%)	128 (96%)	6 (4%)	34	69
7	L7	186/205 (91%)	178 (96%)	8 (4%)	35	70
8	L8	191/208 (92%)	178 (93%)	13 (7%)	20	57
9	L9	171/171 (100%)	158 (92%)	13 (8%)	16	53
10	60	180/187 (96%)	167 (93%)	13 (7%)	18	55
11	61	147/150 (98%)	134 (91%)	13 (9%)	12	45
13	63	154/159 (97%)	146 (95%)	8 (5%)	29	65
14	64	107/109 (98%)	103 (96%)	4 (4%)	41	73
15	65	175/176 (99%)	163 (93%)	12 (7%)	19	56
16	66	160/162 (99%)	150 (94%)	10 (6%)	22	59
17	67	145/146 (99%)	135 (93%)	10 (7%)	19	56
18	68	150/151 (99%)	142 (95%)	8 (5%)	28	64
19	69	153/154 (99%)	142 (93%)	11 (7%)	18	55
20	70	156/156 (100%)	145 (93%)	11 (7%)	18	55
21	71	136/137 (99%)	132 (97%)	4 (3%)	50	78
22	72	87/107 (81%)	84 (97%)	3 (3%)	44	75
23	73	104/105 (99%)	99 (95%)	5 (5%)	31	67
24	74	56/129 (43%)	55 (98%)	1 (2%)	66	87
25	75	105/118 (89%)	93 (89%)	12 (11%)	7	32
26	76	109/110 (99%)	103 (94%)	6 (6%)	27	63
27	77	115/116 (99%)	111 (96%)	4 (4%)	43	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	78	118/119 (99%)	111 (94%)	7 (6%)	24	61
29	79	46/47 (98%)	40 (87%)	6 (13%)	5	28
30	80	81/88 (92%)	76 (94%)	5 (6%)	23	60
31	81	96/97 (99%)	88 (92%)	8 (8%)	14	49
32	82	109/111 (98%)	103 (94%)	6 (6%)	27	63
33	83	90/91 (99%)	88 (98%)	2 (2%)	60	83
34	84	95/103 (92%)	89 (94%)	6 (6%)	22	59
35	85	104/105 (99%)	98 (94%)	6 (6%)	25	61
36	86	81/82 (99%)	74 (91%)	7 (9%)	13	47
37	87	70/71 (99%)	68 (97%)	2 (3%)	50	78
38	88	68/69 (99%)	63 (93%)	5 (7%)	17	54
39	89	45/46 (98%)	39 (87%)	6 (13%)	5	28
40	90	47/116 (40%)	46 (98%)	1 (2%)	61	84
41	91	23/23 (100%)	18 (78%)	5 (22%)	1	9
42	92	90/91 (99%)	87 (97%)	3 (3%)	45	76
43	93	71/72 (99%)	69 (97%)	2 (3%)	51	78
44	P0	105/254 (41%)	98 (93%)	7 (7%)	20	57
45	RC	261/262 (100%)	242 (93%)	19 (7%)	17	54
46	S0	173/210 (82%)	158 (91%)	15 (9%)	13	45
47	S1	191/224 (85%)	171 (90%)	20 (10%)	8	36
48	S2	176/205 (86%)	167 (95%)	9 (5%)	29	66
49	S3	182/195 (93%)	167 (92%)	15 (8%)	14	49
50	S4	221/222 (100%)	209 (95%)	12 (5%)	27	64
51	S5	173/191 (91%)	166 (96%)	7 (4%)	38	71
52	S6	193/201 (96%)	183 (95%)	10 (5%)	29	65
53	S7	165/170 (97%)	154 (93%)	11 (7%)	20	57
54	S8	150/161 (93%)	143 (95%)	7 (5%)	32	68
55	S9	158/166 (95%)	151 (96%)	7 (4%)	35	69
56	10	89/98 (91%)	79 (89%)	10 (11%)	7	33
57	11	136/137 (99%)	128 (94%)	8 (6%)	24	61
58	12	100/119 (84%)	90 (90%)	10 (10%)	9	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	13	127/128 (99%)	118 (93%)	9 (7%)	18	55
60	14	96/105 (91%)	89 (93%)	7 (7%)	17	54
61	15	104/118 (88%)	95 (91%)	9 (9%)	13	45
62	16	117/119 (98%)	111 (95%)	6 (5%)	29	66
63	17	109/124 (88%)	95 (87%)	14 (13%)	5	29
64	18	128/129 (99%)	116 (91%)	12 (9%)	11	42
65	19	115/116 (99%)	109 (95%)	6 (5%)	29	65
66	20	100/114 (88%)	94 (94%)	6 (6%)	24	60
67	21	74/74 (100%)	69 (93%)	5 (7%)	20	57
68	22	110/111 (99%)	103 (94%)	7 (6%)	22	58
69	23	119/120 (99%)	112 (94%)	7 (6%)	24	61
70	24	112/113 (99%)	105 (94%)	7 (6%)	22	59
71	25	61/89 (68%)	55 (90%)	6 (10%)	10	39
72	26	83/101 (82%)	76 (92%)	7 (8%)	14	48
73	27	70/71 (99%)	65 (93%)	5 (7%)	18	55
74	28	56/60 (93%)	53 (95%)	3 (5%)	27	64
75	29	47/49 (96%)	47 (100%)	0	100	100
76	30	51/54 (94%)	47 (92%)	4 (8%)	16	51
77	31	43/135 (32%)	38 (88%)	5 (12%)	7	32
All	All	9583/10436 (92%)	8985 (94%)	598 (6%)	27	60

5 of 598 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	85	71	LYS
46	S0	41	ARG
68	22	104	LEU
36	86	59	ASP
42	92	105	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 223 such sidechains are listed below:

Mol	Chain	Res	Type
32	82	31	ASN

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Mol	Chain	Res	Type
42	92	99	GLN
67	21	74	GLN
32	82	52	GLN
35	85	68	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
78	1S	1780/1798 (98%)	329 (18%)	16 (0%)
79	2S	3298/3395 (97%)	474 (14%)	23 (0%)
80	8S	157/158 (99%)	22 (14%)	1 (0%)
81	5S	120/121 (99%)	8 (6%)	0
82	ET	76/77 (98%)	11 (14%)	1 (1%)
82	PT	76/77 (98%)	7 (9%)	0
83	MR	8/14 (57%)	1 (12%)	0
All	All	5515/5640 (97%)	852 (15%)	41 (0%)

5 of 852 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
78	1S	2	A
78	1S	4	C
78	1S	25	C
78	1S	26	A
78	1S	34	G

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
79	2S	282	G
79	2S	1103	A
79	2S	3269	U
79	2S	517	G
79	2S	637	C

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

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

## 5.5 Carbohydrates [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](#)

There are no chain breaks in this entry.