



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

Nov 16, 2017 – 07:21 PM EST

PDB ID : 5KPW  
EMDB ID: : EMD-8281  
Title : Structure of RelA bound to ribosome in presence of A/R tRNA (Structure III)  
Authors : Loveland, A.B.; Bah, E.; Madireddy, R.; Zhang, Y.; Brilot, A.F.; Grigorieff, N.; Korostelev, A.A.  
Deposited on : unknown  
Resolution : 3.90 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

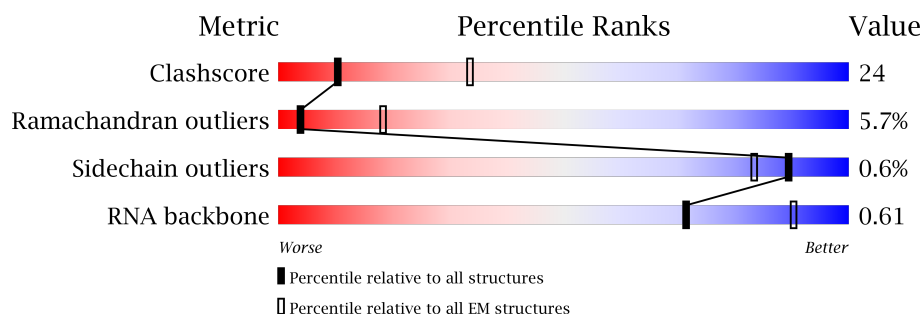
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.90 Å.

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





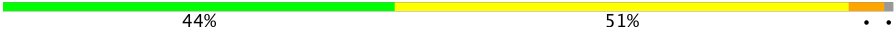








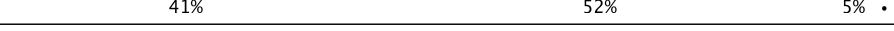







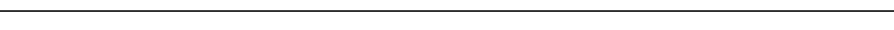

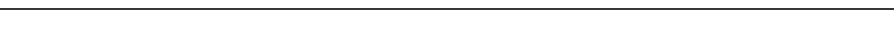
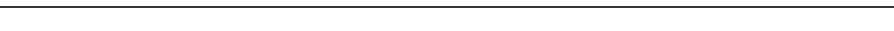


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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

Mol	Chain	Length	Quality of chain
1	A	273	58% 40% ..
2	B	209	46% 50% .
3	C	201	48% 49% .
4	D	179	41% 54% . .
5	E	177	50% 48% ..
6	F	149	40% 54% 5% .
7	G	165	17% 52% 10% 21%
8	H	142	29% 67% ..



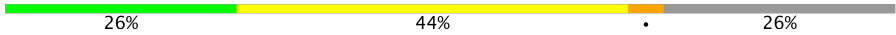
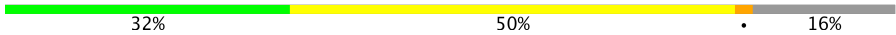

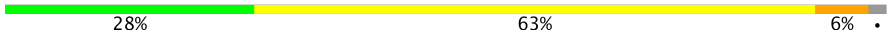
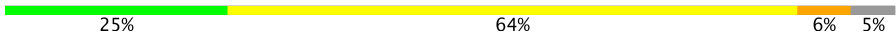
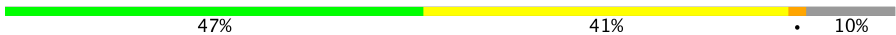
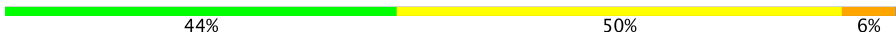
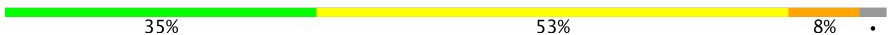
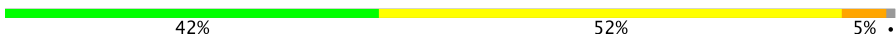

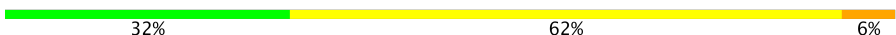
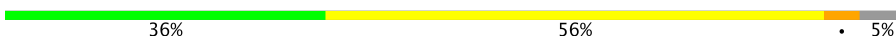








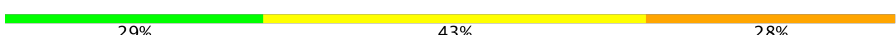

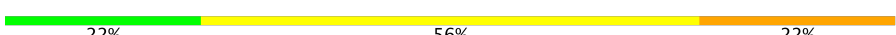
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Mol	Chain	Length	Quality of chain
9	I	142	
10	J	123	
11	K	144	
12	L	136	
13	M	127	
14	N	117	
15	O	115	
16	P	118	
17	Q	103	
18	R	110	
19	S	100	
20	T	104	
21	U	94	
22	V	85	
23	W	78	
24	X	63	
25	Y	59	
26	Z	70	
27	1	57	
28	2	55	
29	3	46	
30	4	65	
31	5	38	
32	6	241	
33	7	233	

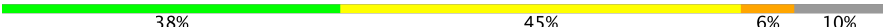
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Mol	Chain	Length	Quality of chain
34	8	206	
35	9	167	
36	10	135	
37	11	179	
38	12	130	
39	13	130	
40	14	103	
41	15	129	
42	16	124	
43	17	118	
44	18	101	
45	19	89	
46	20	82	
47	21	84	
48	22	75	
49	23	92	
50	24	87	
51	25	71	
52	26	1539	
53	27	2903	
54	28	120	
55	29	20	
56	30	76	
57	31	77	
58	32	77	

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Mol	Chain	Length	Quality of chain
59	33	750	 A horizontal bar chart showing the quality of chain 33. The bar is divided into four segments: green (38%), yellow (45%), orange (6%), and grey (10%). The percentages are labeled below the bar.

## 2 Entry composition [i](#)

There are 59 unique types of molecules in this entry. The entry contains 154603 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 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 21 is a protein called 50S ribosomal protein L25.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	2	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	6	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	8	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	9	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	10	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	11	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	12	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	13	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	14	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	15	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	16	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	17	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	18	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	19	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	20	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	21	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	22	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	23	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	24	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	25	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	26	1539	Total	C	N	O	P	0	0
			33016	14725	6052	10700	1539		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	27	2903	Total	C	N	O	P	0	0
			62322	27801	11468	20150	2903		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
27	747	C	U	conflict	GB 802133627
27	1847	G	A	conflict	GB 802133627

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	28	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
28	120	A	-	conflict	GB 1028475309

- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	29	20	Total	C	N	O	P	0	0
			432	195	86	132	19		

- Molecule 56 is a RNA chain called A-site tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	30	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 57 is a RNA chain called P-site tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	31	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

- Molecule 58 is a RNA chain called E-site tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	32	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 59 is a protein called GTP pyrophosphokinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	33	675	Total	C	N	O	S	0	0
			4911	3070	904	915	22		

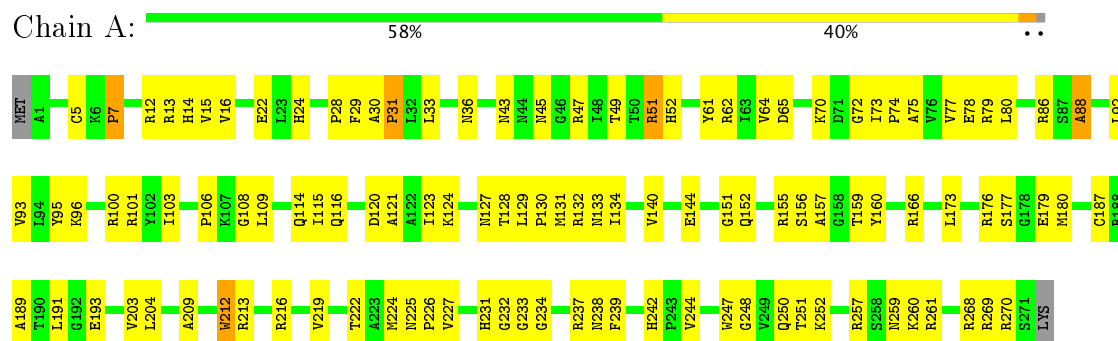
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
33	-5	MET	-	expression tag	UNP P0AG20
33	-4	HIS	-	expression tag	UNP P0AG20
33	-3	HIS	-	expression tag	UNP P0AG20
33	-2	HIS	-	expression tag	UNP P0AG20
33	-1	HIS	-	expression tag	UNP P0AG20
33	0	HIS	-	expression tag	UNP P0AG20
33	1	HIS	-	expression tag	UNP P0AG20

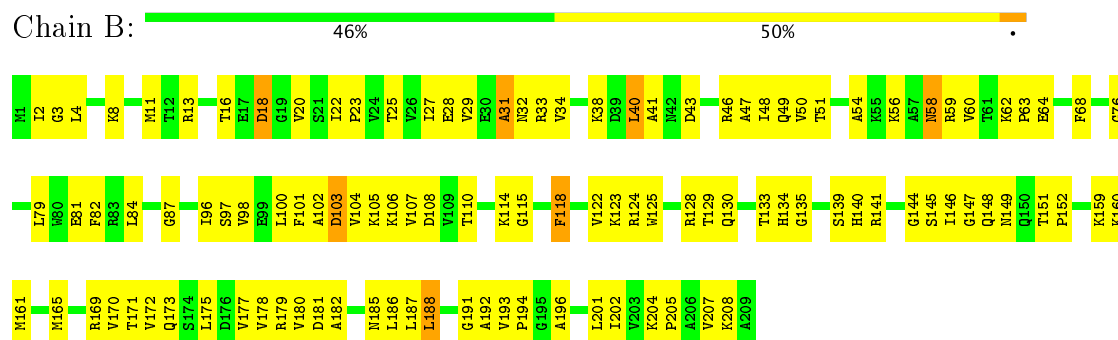
### 3 Residue-property plots

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.

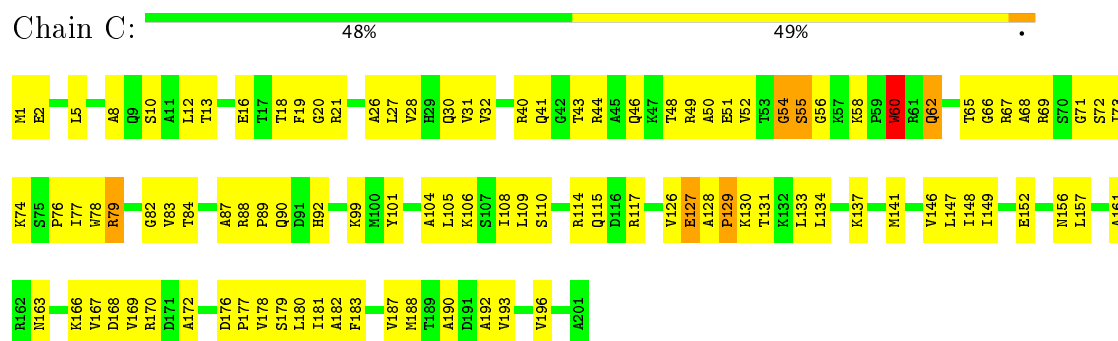
#### • Molecule 1: 50S ribosomal protein L2



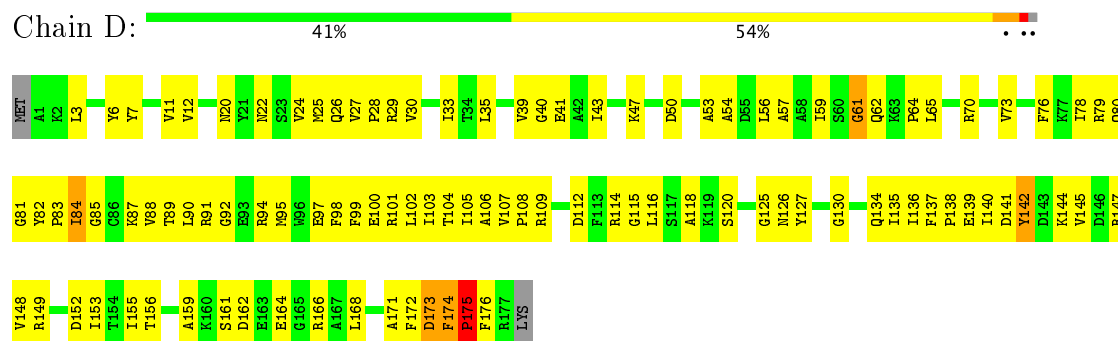
#### • Molecule 2: 50S ribosomal protein L3



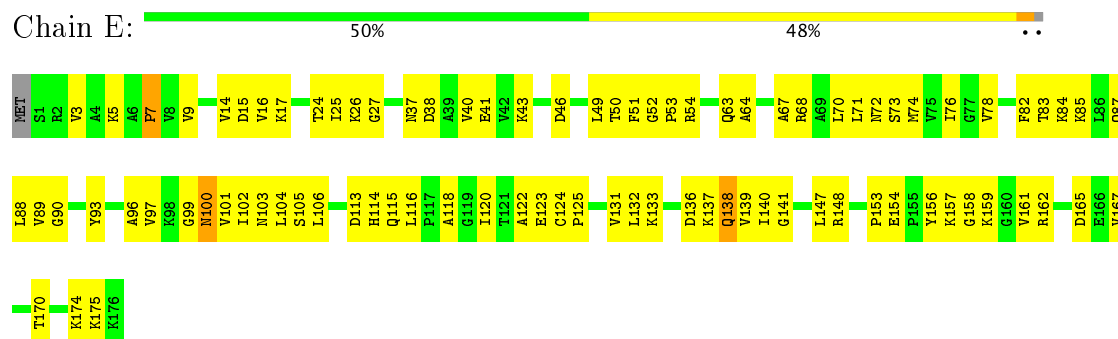
#### • Molecule 3: 50S ribosomal protein L4



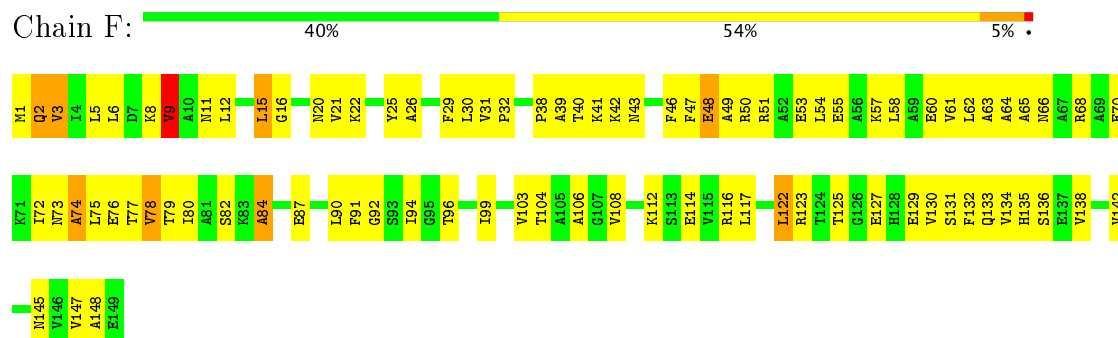
#### • Molecule 4: 50S ribosomal protein L5



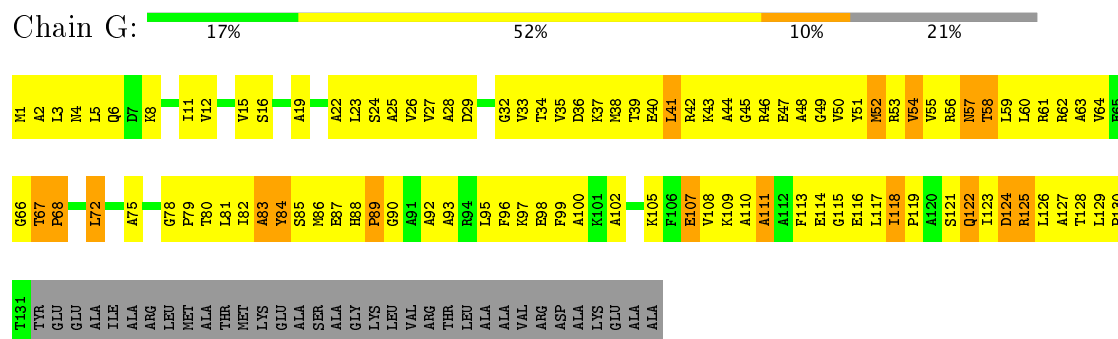
• Molecule 5: 50S ribosomal protein L6



• Molecule 6: 50S ribosomal protein L9



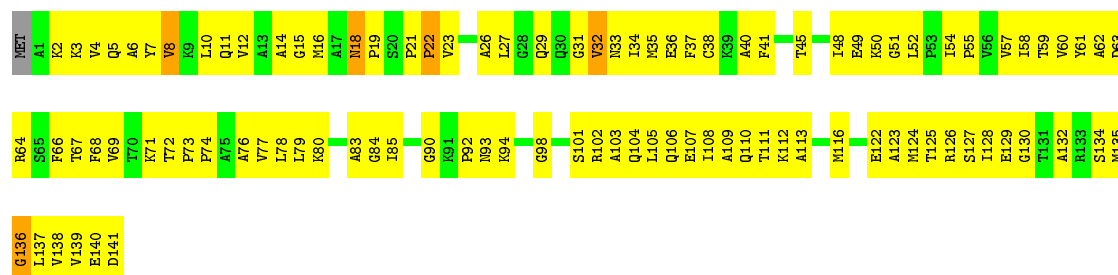
• Molecule 7: 50S ribosomal protein L10



• Molecule 8: 50S ribosomal protein L11

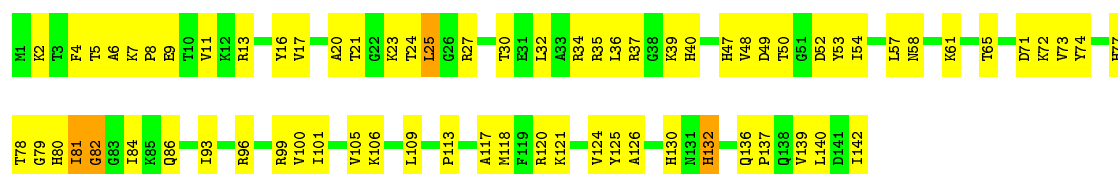


Chain H: 



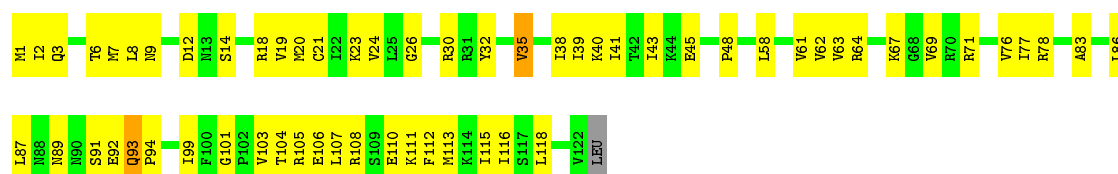
- Molecule 9: 50S ribosomal protein L13

Chain I: 



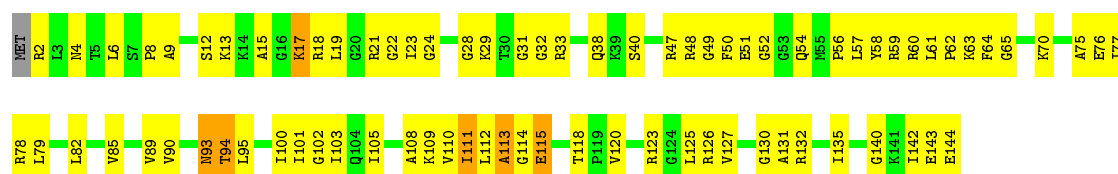
- Molecule 10: 50S ribosomal protein L14

Chain J: 



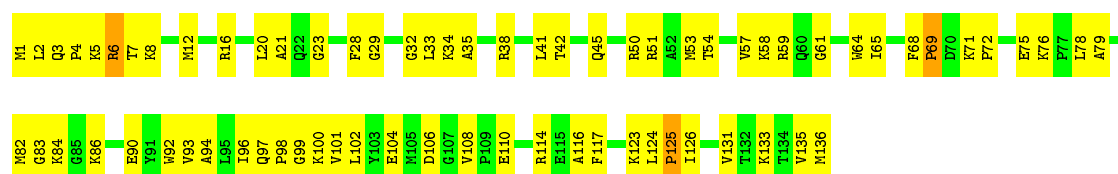
- Molecule 11: 50S ribosomal protein L15

Chain K: 

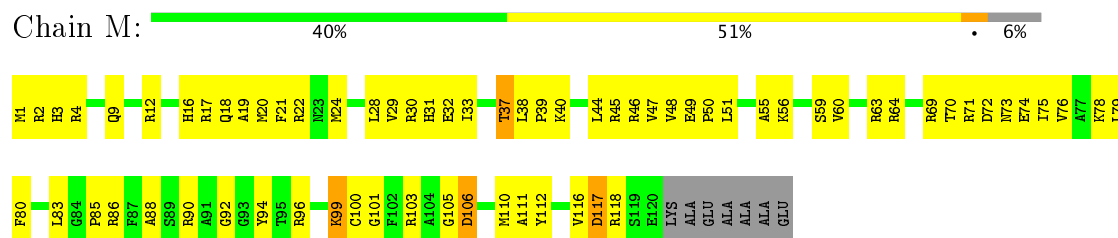


- Molecule 12: 50S ribosomal protein L16

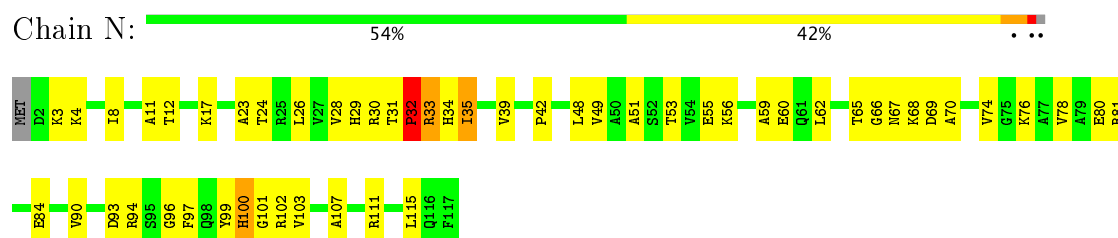
Chain L: 



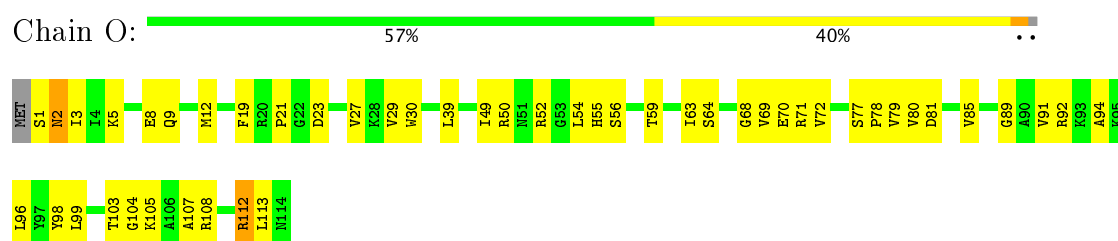
- Molecule 13: 50S ribosomal protein L17



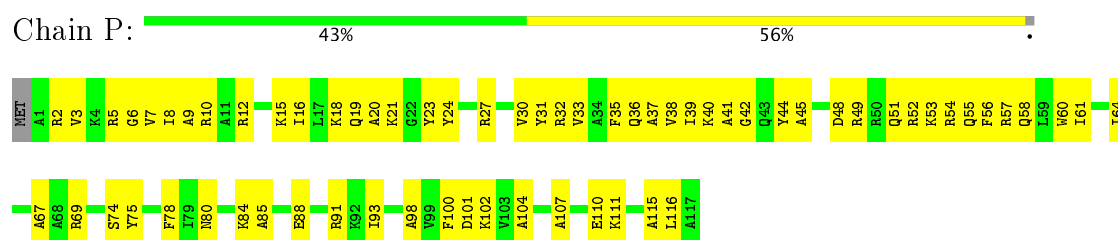
- Molecule 14: 50S ribosomal protein L18



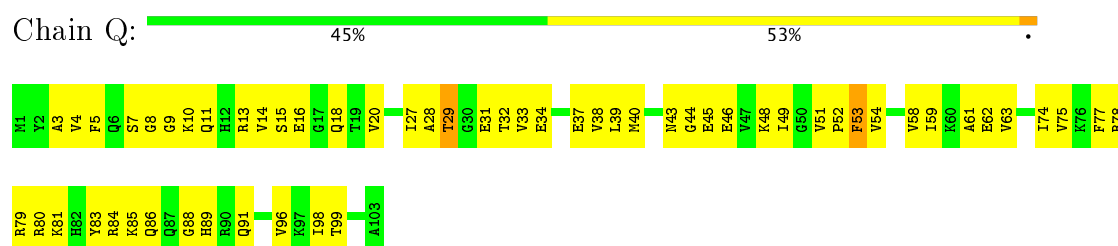
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20

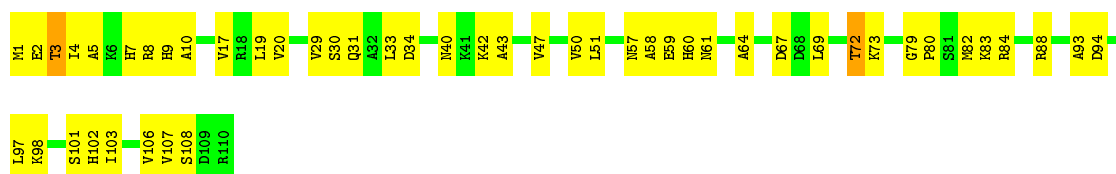


- Molecule 17: 50S ribosomal protein L21



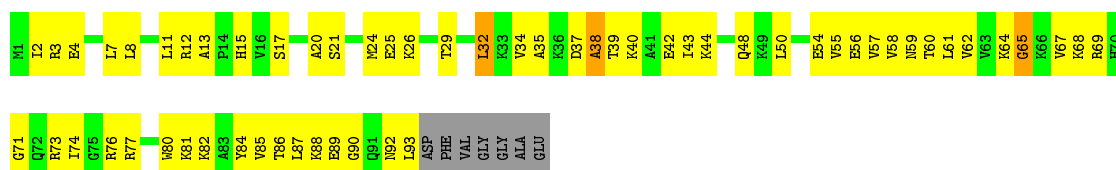
- Molecule 18: 50S ribosomal protein L22





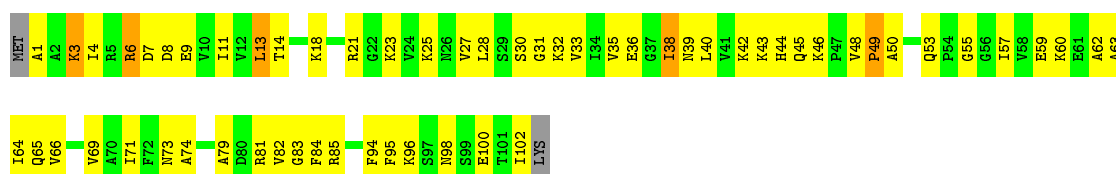
- Molecule 19: 50S ribosomal protein L23

Chain S:



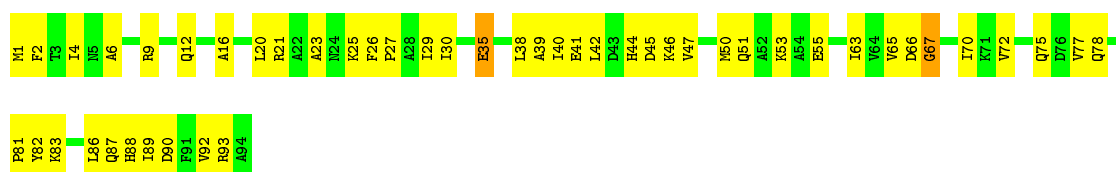
- Molecule 20: 50S ribosomal protein L24

Chain T:



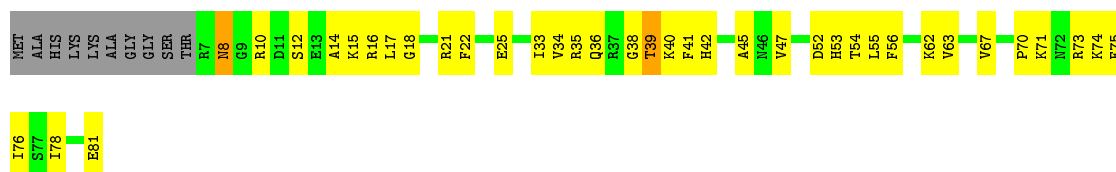
- Molecule 21: 50S ribosomal protein L25

Chain U:



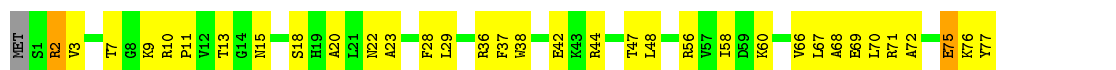
- Molecule 22: 50S ribosomal protein L27

Chain V:

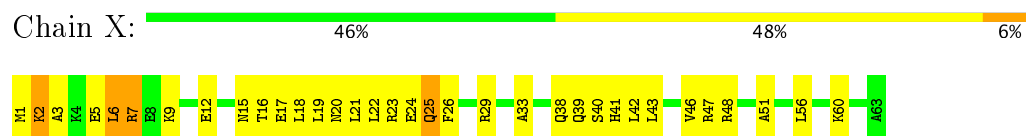


- Molecule 23: 50S ribosomal protein L28

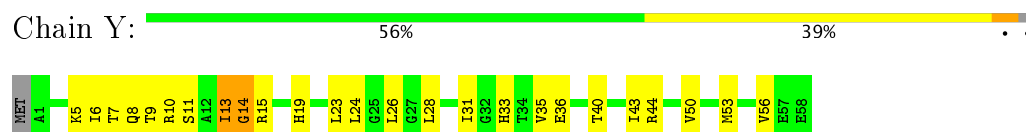
Chain W:



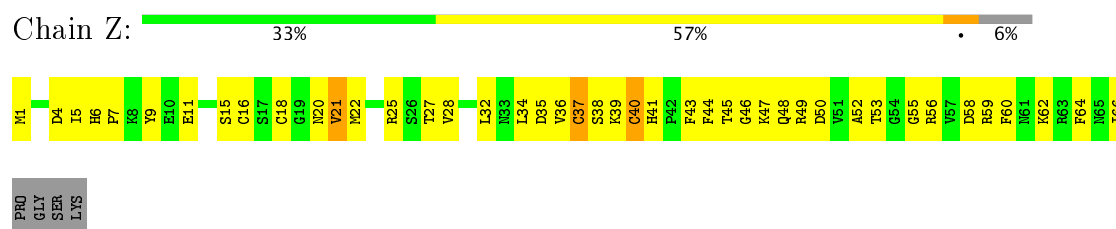
- Molecule 24: 50S ribosomal protein L29



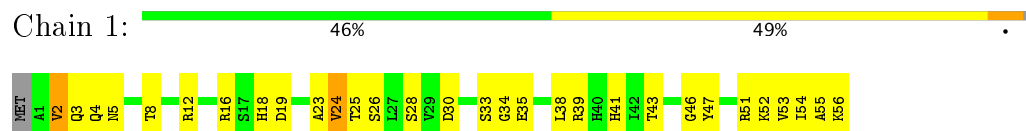
- Molecule 25: 50S ribosomal protein L30



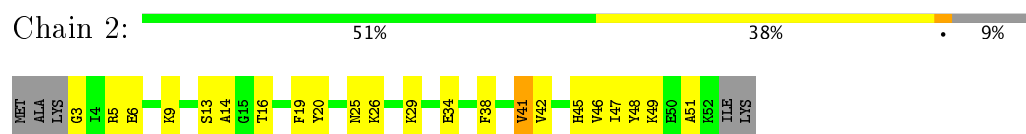
- Molecule 26: 50S ribosomal protein L31



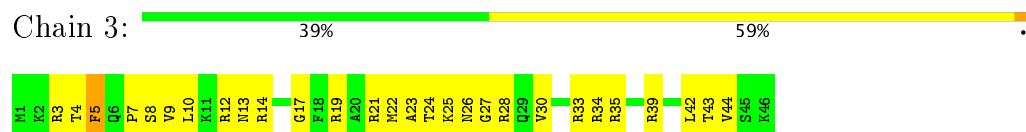
- Molecule 27: 50S ribosomal protein L32



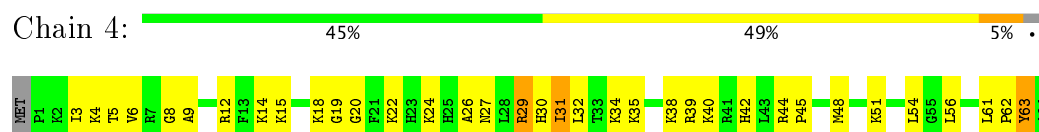
- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



- Molecule 30: 50S ribosomal protein L35



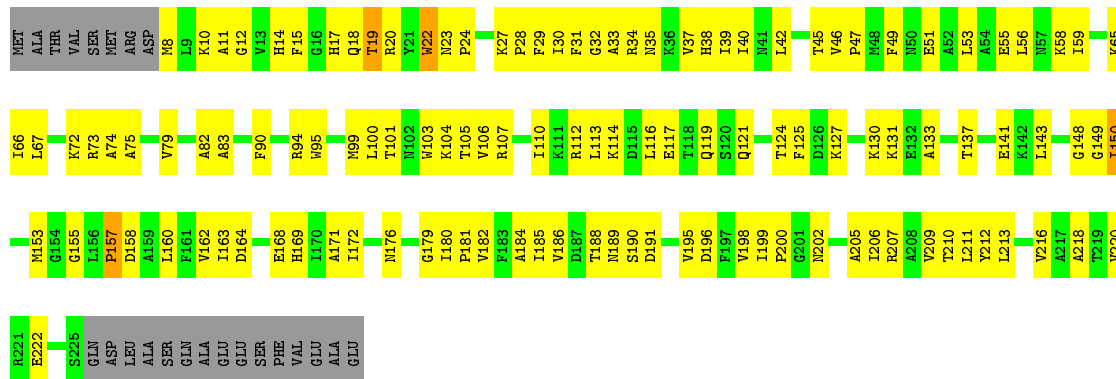
- Molecule 31: 50S ribosomal protein L36

Chain 5: 



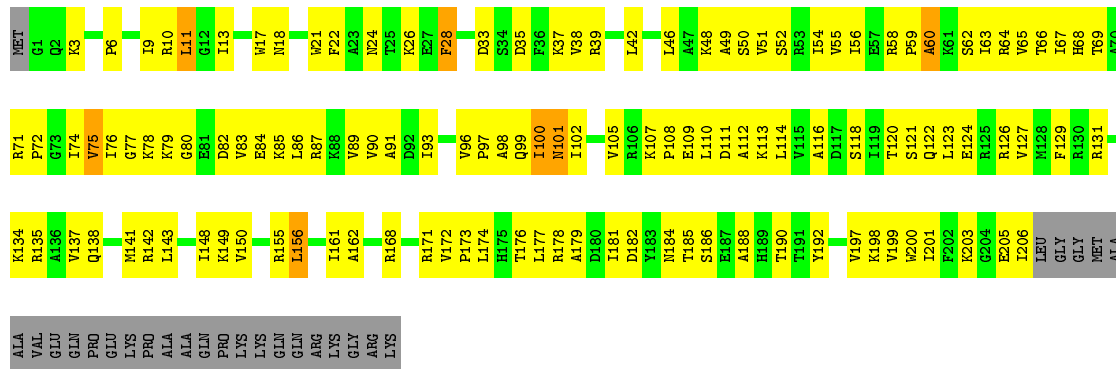
- Molecule 32: 30S ribosomal protein S2

Chain 6: 



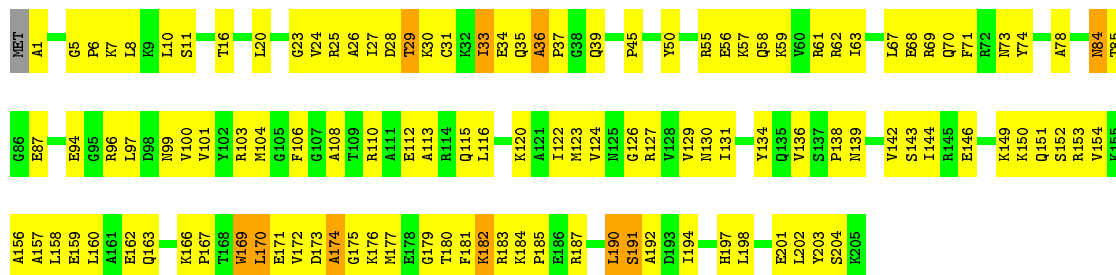
- Molecule 33: 30S ribosomal protein S3

Chain 7: 

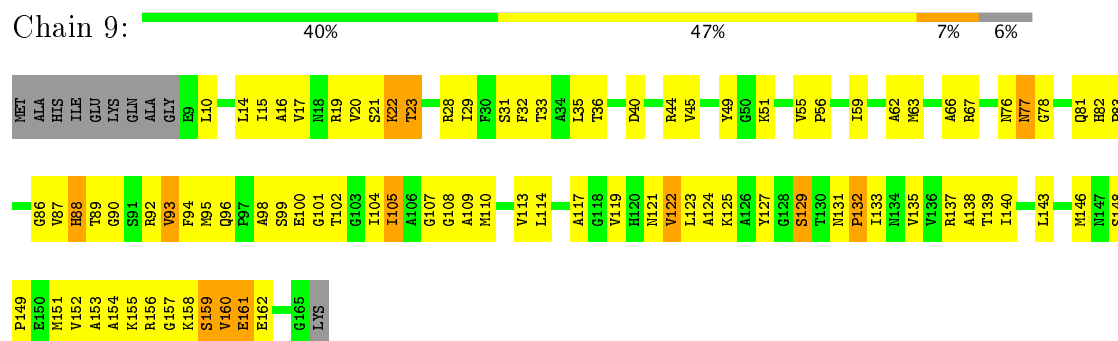


- Molecule 34: 30S ribosomal protein S4

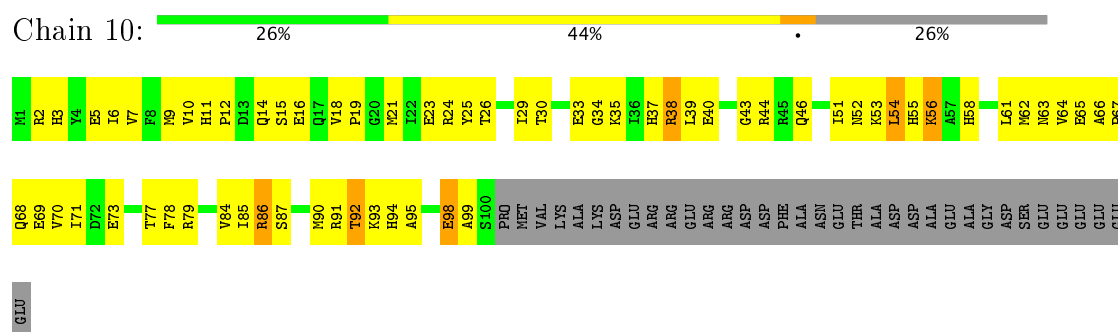
Chain 8: 



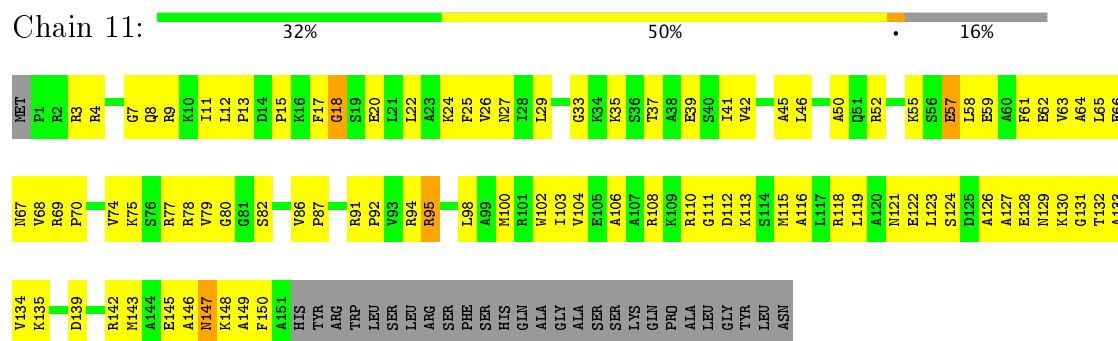
- Molecule 35: 30S ribosomal protein S5



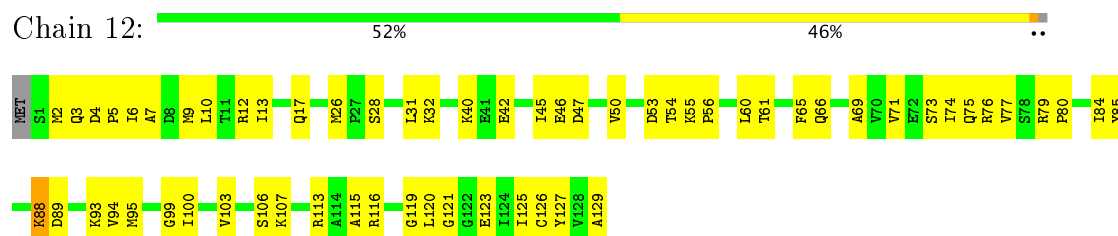
- Molecule 36: 30S ribosomal protein S6



- Molecule 37: 30S ribosomal protein S7

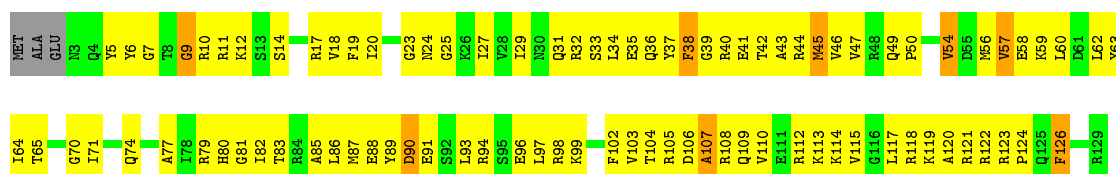


- Molecule 38: 30S ribosomal protein S8

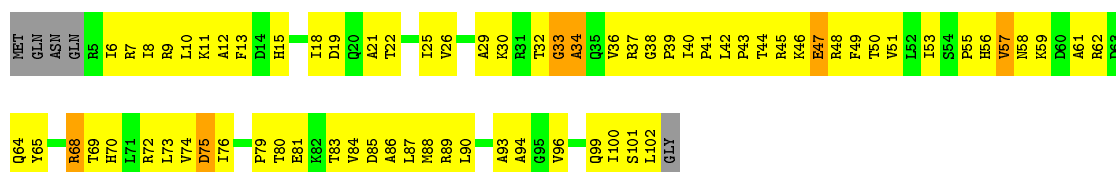


- Molecule 39: 30S ribosomal protein S9

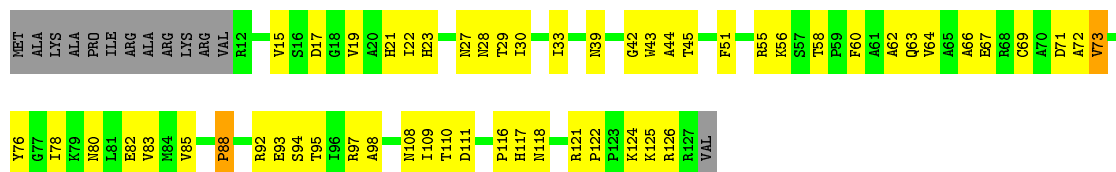




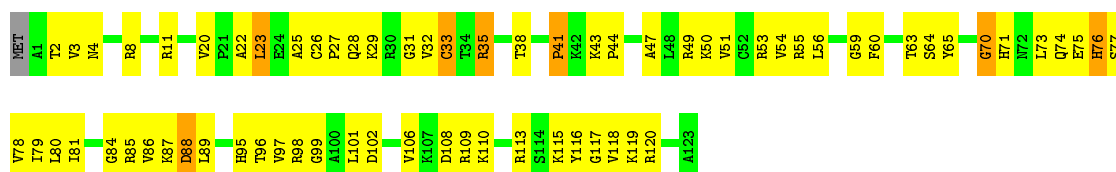
- Molecule 40: 30S ribosomal protein S10



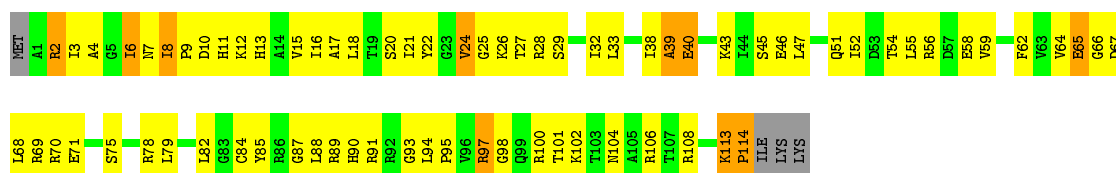
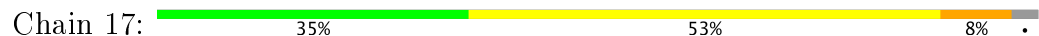
- Molecule 41: 30S ribosomal protein S11



- Molecule 42: 30S ribosomal protein S12

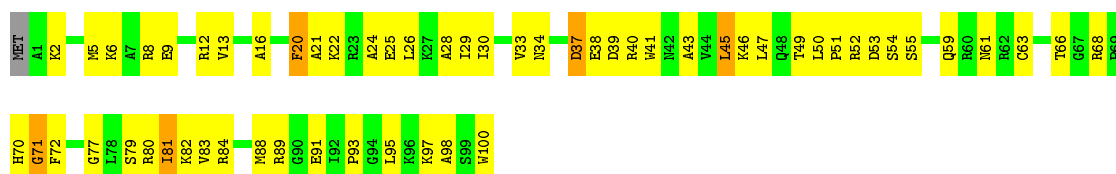


- Molecule 43: 30S ribosomal protein S13



- Molecule 44: 30S ribosomal protein S14





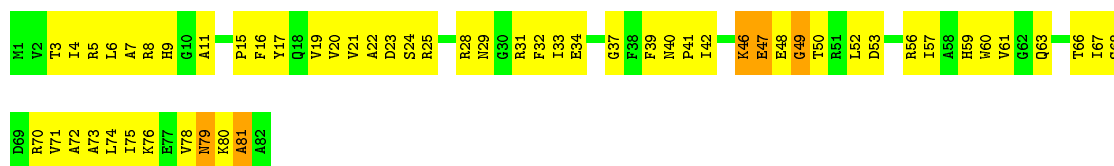
- Molecule 45: 30S ribosomal protein S15

Chain 19: 63% 34% ..



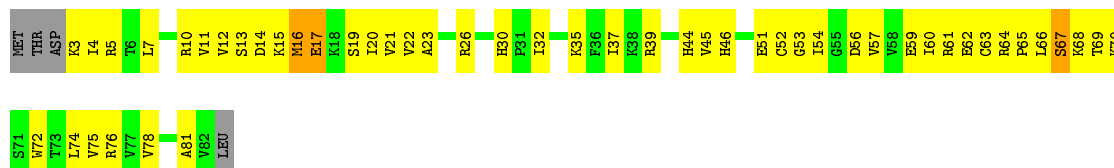
- Molecule 46: 30S ribosomal protein S16

Chain 20: 32% 62% 6%



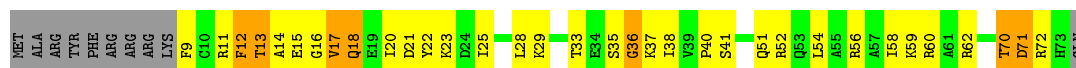
- Molecule 47: 30S ribosomal protein S17

Chain 21: 36% 56% 5%



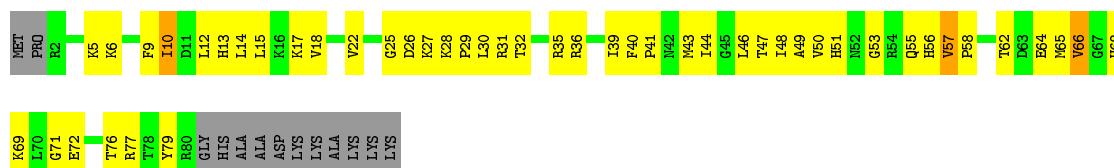
- Molecule 48: 30S ribosomal protein S18

Chain 22: 41% 36% 9% 13%



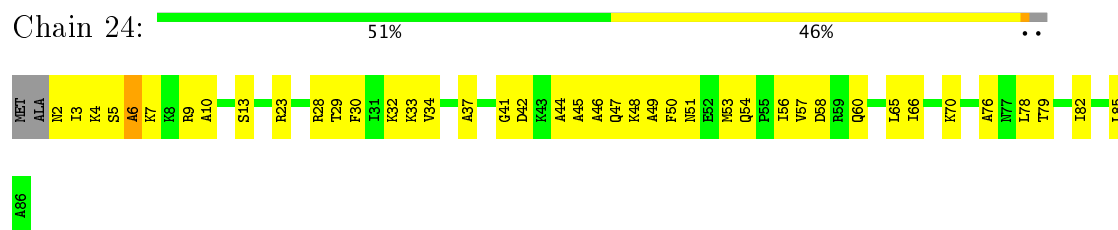
- Molecule 49: 30S ribosomal protein S19

Chain 23: 34% 49% 14%

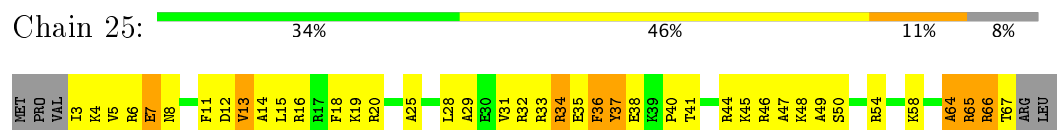


- Molecule 50: 30S ribosomal protein S20

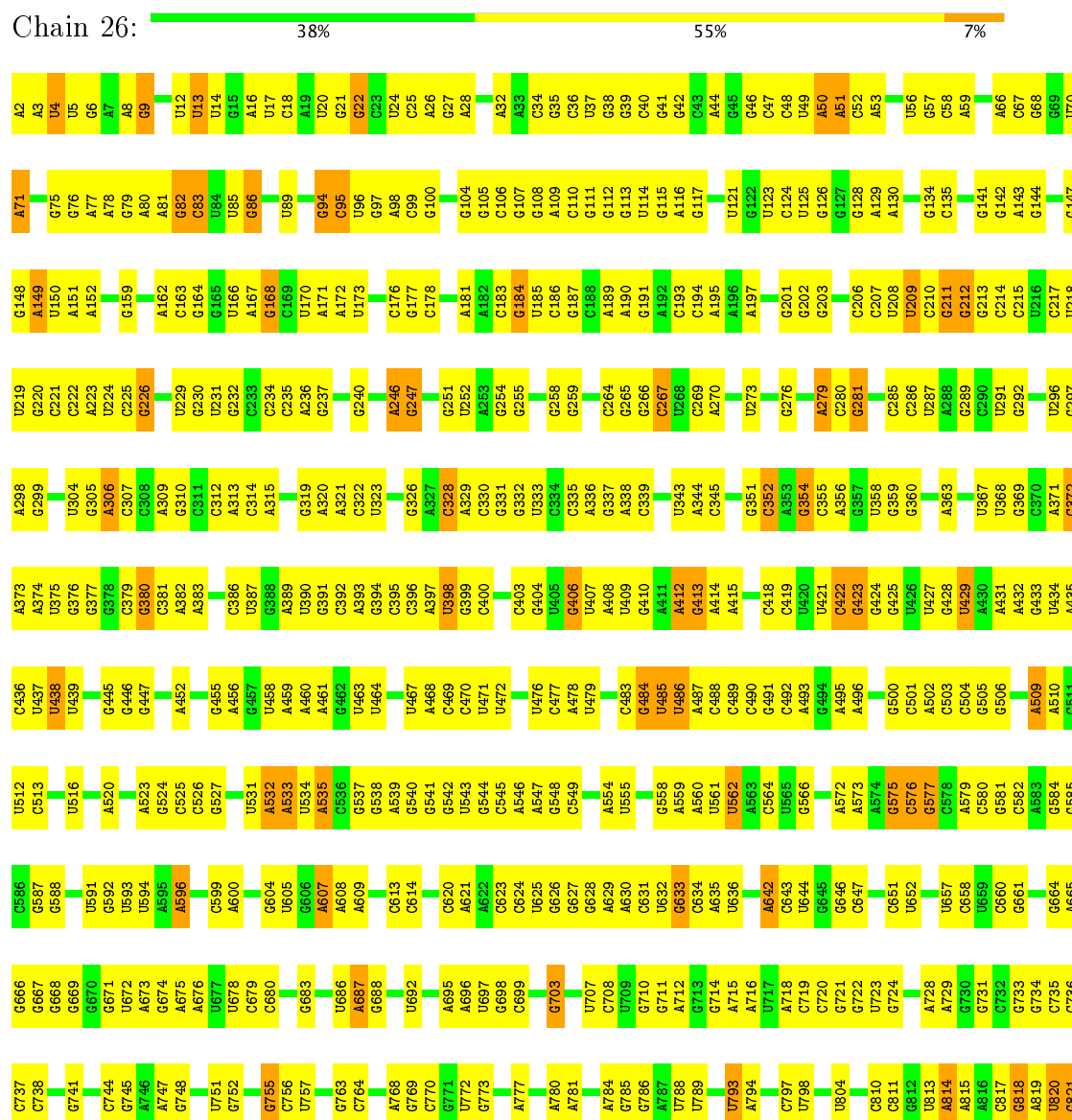


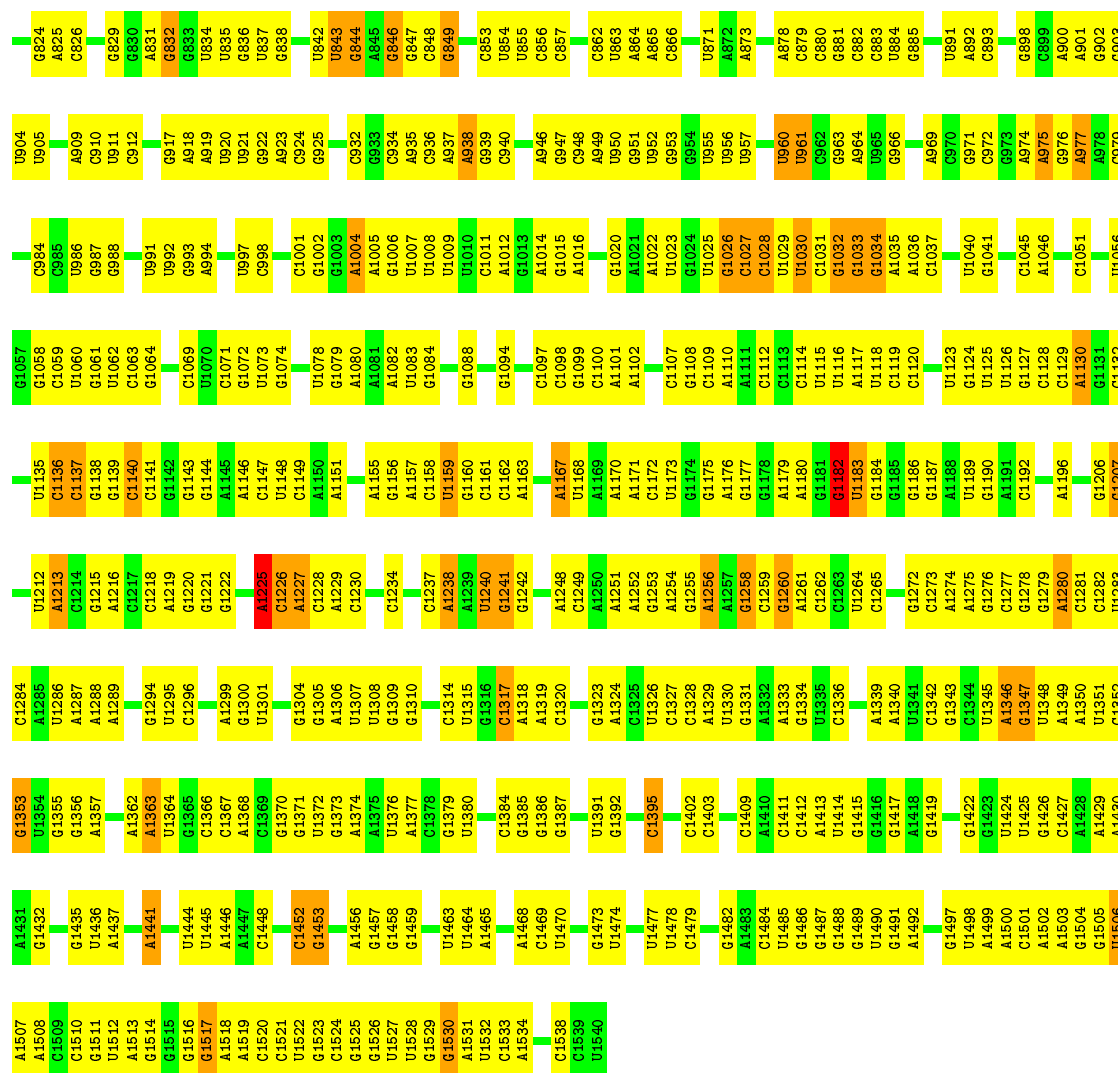


- Molecule 51: 30S ribosomal protein S21

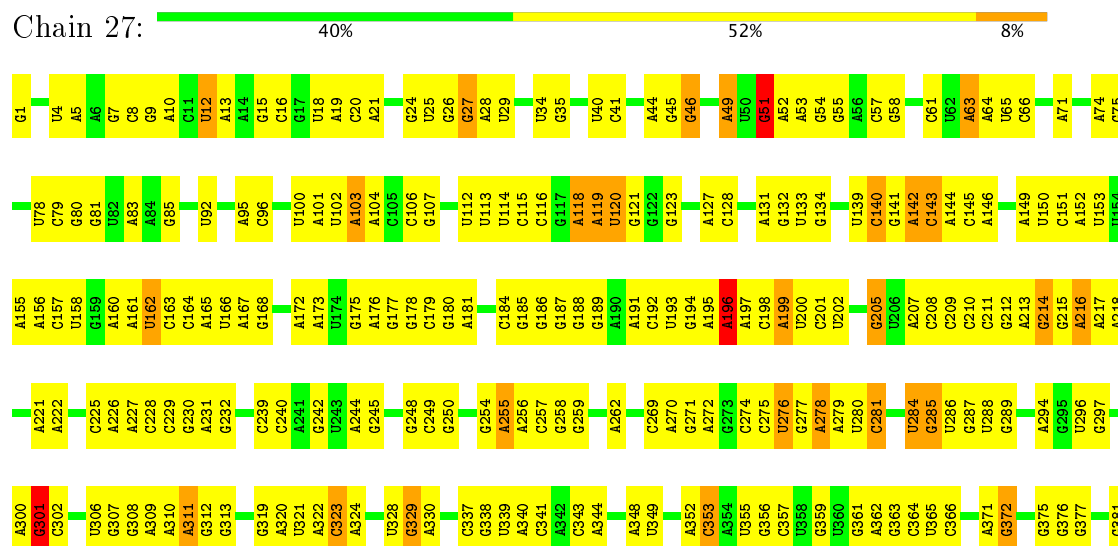


- Molecule 52: 16S ribosomal RNA



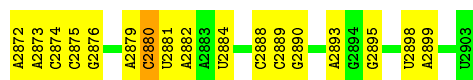


## • Molecule 53: 23S ribosomal RNA



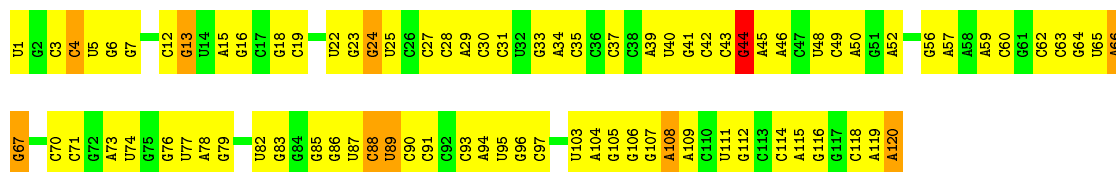
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G1482	U1394	A1301	G1229	C1146	A1077	G993	C922	U847	A764	C687	U615	U546	G386
G1483	A1395	A1304	G1229	A1147	U1078	C994	C922	C848	A764	C688	U615	U546	U387
U1484	U1396	C1305	A1230	G1149	C1079	C995	A925	A849	C765	A689	G620	A547	G388
U1485				C1150	U1081	C996	A926	U850	G768	C690	A621	G548	G389
U1486				U1316	U1082	C997	C926	C851	U769	C691	G622	G549	U390
U1487	U1400	U1317	U1234	A1151	U1083	C998	G930	U852	U769	C692	G622	C550	U391
U1488				U1318	A1084	C1005	U931	C853	G774	A693	C623	C550	U392
A1403	A1403	C1319	G1235	G1154	A1085	C1006	U932	G856	U773	G695	C624	G553	C394
A1404	C1320	C1320	G1236	C1155	A1086	C1007	A933	G857	G774	U694	G627	U554	U395
A1405	U1405	A1321	G1239	A1156	U1087	A1008	U934	G858	G776	G696	A627	G555	G396
U1406	U1406		U1240	G1157	A1088	A1009	C935	G859	G776	G697			U399
A1495	A1495	A1326		C1158	A1089			U860		U704	A633	U558	U400
A1496	U1411	U1327	C1243	U1159	A1090	U1012	G939	U861	A782	G705	C634	G559	A401
A1572	U1412	A1244	A1244	G1160	G1091	C1013	G940	G862	A783	G488	C635	G559	A402
C1498		U1329	G1245	C1161	C1092		A941	A863	G784	C490	G636	A563	U403
C1499	G1416	C1330	G1245	G1162	G1093	U1018	G942	G864	G785	C490	G637	C564	A404
G1500	C1417	G1331	G1248	G1163		U1019	A943	C865	G785	G708	G638	C565	U405
G1501	G1418	U1332	U1249	C1164	A1096	A1020	G944	C866	G795	U709	U639	U666	G406
A1502	A1419	G1333	G1250	A1165	U1097	A1021	A945	G867	G796	U710	C640	U667	G407
A1503	A1420	G1334	G1251	G1166	A1098	G1022	G946	U871	G797	G711	U641	U668	G408
A1504		C1335	G1252			U1023	A947	U872				U569	G410
A1505	A1427	A1336	G1253	G1171	A1103	G1024	C948	C873	G801	U714	A644	G570	G411
U1506	C1428	G1337	A1254	C1172	G1104			C874		A715	U646	U571	A412
C1507	G1429	U1337	U1254	U1173	U1105	A1028	G949	G875	A804	A716	U646	U571	C413
A1509	G1430	U1340	G1256	U1174	G1106	A1029	G953	C876	G805	G717	G648	U573	C414
A1510	G1432		C1257	A1175		U1033	G954	A877	C806	A718	G649	A574	A504
A1511	A1433	U1344	U1258	U1176	G1110	G1334	U955	U878	C807	G719	G650	U576	A416
C1512	A1434	C1345	G1259	G1177	A1111	G1335	G956	G879	G808	U720	G651		U418
U1513	G1435	U1345	A1260	C1178	G1112	U1035	A959	G880	G809			U580	U419
G1514	A1436	C1351	C1261	G1179	U1113	G1036	A960	G881	U810	U724	A654	C581	C420
A1515	C1437	U1352	A1262	U1180	G1114	G1037	C961	G882	U811	G725	A655	A582	A421
U1516	U1438	A1353	A1263	U1181	G1115	G1038	G962	G883	C812	G726	G656	A583	A422
	A1439	A1354	A1264	U1182	G1118	A1039	G963	U887	C814	A727	U657	C584	A423
		G1355	A1265	U1183	C1118	A1040	U963	C888	C815	G728	U658	G585	G424
U1520	U1440	G1356	G1266	U1184	U1119		C964	C889	C816	G729	A659	A514	G425
G1521	U1442	G1361		G1185	G1120	C1045	U967	C890	C817	A730	G662	C587	
G1524	U1443	C1362	G1271	G1186	C1123	A1046	U967	C891	G818	C731	G662	U588	C435
	U1444		A1272	U1187	G1124	G1047	G969	A892	A819		U665	U589	C436
A1528	G1445	A1365		A1189	G1125	C1052	U970	A896	A820	U739	A666	U519	U441
G1529	C1446	C1366	C1278	G1190	A1126	U1053	G971	A897	A821	C740	A666	U520	G442
A1535	C1447	A1367	G1279	G1197	A1127	A1054	G972	C897		U742	G669	C594	
C1536	G1448	A1368	G1280	U1198	G1128	G1055	A973	C898	A825	A743	A670	U596	G445
		U1372	G1281	U1199	A1129	G1056	G974	A899	U826	U744	C571	G597	G446
	A1453	G1374	U1282	U1199	U1130	A1057	A975	A900	U827	G745	C572	U598	G447
U1539	C1454	A1374	G1283	G1200	G1131	U1058	G976	C901	U828	G746	C573	A599	U448
G1540	G1455	U1375	A1284		U1132	G1059		C902	A829	C747	G600	A528	U449
C1541		A1285		U1203	A1133	U1061	A979	A905	G830	G748	A675	C601	A449
U1542	U1458	A1378	A1286	A1204	A1134	U1060	A905	U906	G831		A676	A602	G450
G1543	G1459	U1379	A1287	A1205	C1135	G1062	G982		A832	A752	C677	A603	U451
A1544	U1460	G1288	G1288	G1206		G1063	A983		A833	A753	C678	G604	G452
A1545	C1461	G1381	C1289		G1138	C1064	A984	A910	G834	U754	C679	G605	C455
G1546		A1382		G1210	C1139	U1065	C985	A911	U839	U755	C680	U606	C456
C1547	G1464	A1383	C1295	C1211	C1140	U1066	A911		C840	A756	G681	A529	C457
A1548	U1465	G1296	G1212	G1213	U1141		A988	G914	C915	G682	U607	G535	U464
A1549	U1466	A1385	C1297	A1213	A1142	A1069	G989	C915	C840	G758	U607	A608	G465
C1550		C1386	G1298	A1214	A1143	A1070	G990	G916		C759	G684	C610	A466
A1551	A1460	C1397	G1299	G1215	A1144		G991	U917	A844	G760	A685	C611	G467

A2799	C2723	G2638	C2573	A2497	A2418	U2348	G2277	G2186	C2124	A2052	G1980	U1899	U1818	U1744	C1656
A2800	U2724	A2639	G2574	C2496	U2419	G2349	A2278	U2189	G2125	G2053	A1981	U1898	A1821	A1745	U1657
G2801	A2725	G2640	A2577	C2499	C2420	C2350	A2281	U2188	G2126	A2054	U1982	A1901	A1821	A1746	C1658
U2804	U2728	G2641	G2578	G2502	U2423	G2351	G2282	C2196	C2127	C2055	G1989	G1902	G1824	U1747	U1662
G2805	G2729	G2642	C2579	A2503	C2424	G2352	C2283	C2197	C2128	G2056	G1990	G1903	G1825	C1748	G1663
C2806	G2730	C2643	U2580	U2504	A2425	G2353	A2284	A2198	C2129	A2059	U1991	G1904	G1826	A1749	A1664
U2807	G2732	C2644	G2581	G2505	A2426	G2354	C2285	A2199	U2130	A2060	U1992	C1905	U1827	A1665	A1665
C2808	A2733	G2645	G2582	U2506	G2428	G2355	C2286	C2200	U2131	A2061	G1993	G1907	G1828	G1666	G1667
A2809	U2734	G2646	U2583	C2507	G2429	G2356	A2287	U2203	U2132	A2062	C1996	C1908	A1829	A1668	A1668
G2810	G2737	A2657	U2584	G2508	A2430	G2357	G2288	G2204	A2134	C2063	G1997	G1909	G1836	A1669	A1669
G2811	U2738	C2658	U2585	U2509	A2435	G2358	G2289	G2204	A2135	C2064	C1998	G1910	C1837	U1765	U1670
A2812	A2739	G2659	U2586	G2509	A2436	G2359	G2290	U2204	A2136	C2065	C1999	U1911	C1838	G1766	U1671
A2813	U2740	C2660	A2587	C2512	A2437	G2360	U2291	C2208	U2137	C2066	C1999	U1911	C1838	G1766	U1671
C2814	A2741	G2661	G2588	A2513	A2438	G2361	G2292	C2209	G2138	G2067	C2000	A1912	G1842	G1770	A1672
G2815	U2742	A2673	A2589	U2514	C2440	G2362	G2293	G2210	U2139	U2068	C2001	A1913	G1843	C1771	G1673
U2816	G2743	G2674	A2590	C2515	U2441	G2363	G2294	A2211	G2140	G2069	G2008	C2008	C1844	C1772	G1674
G2817	U2744	A2675	A2591	A2516	C2442	G2364	C2295	C2215	G2141	A2070	C2009	A1916	G1845	A1773	A1676
C2818	G2745	G2676	G2592	C2517	C2443	G2365	U2296	G2216	A2142	A2071	G2010	U1917	G1846	C1774	A1679
G2819	A2746	G2677	U2593	A2518	G2444	G2366	A2297	G2216	C2143	C2072	G2011	U1917	G1847	U1775	A1679
A2820	U2747	C2678	G2594	U2519	G2445	G2367	G2298	C2216	G2144	C2073	G2012	G1921	G1848	C1776	G1680
G2821	G2748	A2679	U2595	C2520	A2446	G2368	U2299	G2221	C2145	U2074	G2013	G1922	A1849	G1776	G1681
C2822	C2752	U2680	G2596	C2521	A2447	G2369	C2300	G2222	C2146	U2075	A2014	G1923	G1850	U1779	G1682
A2823	U2756	C2681	G2599	G2529	A2448	G2370	U2301	G2222	A2147	C2075	A2015	U1923	G1851	A1780	U1683
G2824	A2757	A2682	A2600	G2529	U2449	G2371	U2302	G2224	U2148	A2080	U2016	C1925	U1852	U1781	G1684
A2825	U2758	G2683	C2601	G2530	A2450	G2372	U2303	G2224	U2149	U2081	G2017	U1926	A1853	U1782	C1685
C2826	G2759	U2684	A2602	G2532	A2451	G2373	U2304	G2226	U2150	C2082	G2018	G1929	A1854	A1784	C1686
G2827	U2760	G2685	G2603	U2533	G2452	G2374	G2305	C2226	U2151	U2083	G2019	G1930	G1857	A1785	U1693
U2828	C2761	A2686	U2604	A2534	G2453	C2375	G2306	C2226	C2152	G2087	A2020	G1931	A1858	U1788	C1694
C2829	U2762	G2687	G2605	G2536	G2454	G2376	G2307	C2226	C2153	U2088	A2021	U1932	G1863	G1789	G1695
G2830	A2763	U2688	U2606	U2537	G2455	G2377	A2311	G2231	C2154	A2088	C2022	A1933	G1864	C1790	G1696
U2831	G2764	C2689	C2606	U2538	G2456	G2378	U2312	G2232	U2155	G2093	C2023	G1935	U1865	G1697	A1698
C2832	U2765	A2690	G2607	U2539	G2457	G2379	U2313	G2233	G2156	A2094	C2024	U1936	U1866	A1791	G1699
G2833	G2766	U2691	U2609	C2540	U2458	G2380	U2314	G2234	C2157	C2095	C2025	A1937	A1867	U1794	G1702
A2834	U2767	G2692	G2610	A2541	C2459	G2381	A2315	G2235	C2158	C2096	C2026	A1938	G1867	C1795	G1703
U2835	A2768	U2693	U2611	U2542	G2460	G2382	G2316	G2236	C2159	C2097	U2027	U1943	C1868	U1796	C1704
C2836	G2769	C2694	U2612	G2543	U2461	G2383	A2317	G2237	C2160	U2098	U2028	U1944	G1869	U1797	A1705
G2837	U2770	A2695	G2613	U2544	G2462	G2384	G2318	G2238	C2161	U2099	G2029	U1945	C1870	U1798	G1709
U2838	C2771	U2696	U2614	A2547	C2463	G2385	U2319	G2239	G2162	C2103	A2030	C1947	A1871	G1800	G1710
C2839	U2772	G2697	U2615	G2548	G2464	G2386	G2320	G2240	C2163	C2104	A2031	U1946	A1872	C1801	G1711
G2840	G2773	U2698	G2616	U2550	U2465	G2387	U2321	G2241	C2164	U2105	G2032	C1947	G1873	A1802	U1713
U2841	A2774	C2699	U2617	G2551	G2466	G2388	U2322	G2242	C2165	U2106	A2033	U1955	G1874	A1803	A1714
C2842	U2775	A2700	G2618	U2552	C2467	G2389	U2323	G2243	C2166	G2107	G2034	U1956	G1875	C1804	G1715
G2843	G2776	U2701	U2619	G2553	U2468	G2390	U2324	G2244	U2167	A2108	U2035	C1957	G1876	C1805	G1716
U2844	A2777	G2702	G2620	U2554	G2469	G2391	U2325	G2245	C2168	U2109	C2036	G1964	A1877	U1806	G1721
C2845	U2778	U2703	U2621	G2555	U2470	G2392	U2326	G2246	A2169	U2110	A2037	U1967	G1878	C1807	A1722
G2846	G2779	C2704	U2622	U2556	U2471	G2393	U2327	G2247	A2170	G2110	C2038	U1968	C1879	U1808	G1723
U2847	U2780	U2705	G2623	U2557	G2472	G2394	U2328	G2248	C2171	U2111	U2039	G1969	U1880	A1809	U1729
C2848	U2781	G2706	U2624	G2558	C2473	G2395	U2329	G2249	U2172	G2112	G2040	U1969	C1881	A1810	C1730
U2849	G2782	U2707	U2625	U2559	U2474	G2396	U2330	G2250	C2173	U2113	U2041	U1970	C1882	G1811	G1731
G2850	A2783	U2708	G2626	U2560	G2475	G2397	G2331	G2251	C2174	A2114	A2042	U1971	U1883	U1812	C1732
C2851	U2784	G2709	U2627	U2561	U2476	G2398	U2332	G2252	C2175	G2115	C2043	U1972	U1884	G1813	G1733
U2852	G2785	U2710	U2628	G2562	U2477	G2399	U2333	G2253	C2176	U2116	C2044	U1973	C1885	A1814	G1734
C2853	U2786	G2711	G2629	U2563	U2478	G2400	U2334	G2254	U2177	A2117	G2045	U1974	G1886	A1815	G1735
G2854	U2787	U2712	U2630	U2564	U2479	G2401	U2335	G2255	U2178	U2118	G2046	U1975	G1887	C1816	A1738
U2855	G2788	C2713	U2631	G2565	U2480	G2402	U2336	G2256	C2179	A2119	C2047	U1976	C1888	A1817	A1739
C2856	U2789	U2714	G2632	U2566	U2481	G2403	U2337	G2257	C2180	U2120	G2048	U1977	G1889	G1817	G1740
U2857	G2790	G2715	U2633	U2567	U2482	G2404	U2338	G2258	U2181	A2121	G2049	U1978	C1890	C1818	G1741
G2858	U2791	U2716	A2634	G2568	G2483	G2405	U2339	G2259	U2182	U2122	G2050	U1979	C1891	A1819	G1742
C2859	G2792	C2717	G2634	U2569	C2484	G2406	U2340	G2260	U2183	U2123	G2051	U1980	C1892	A1820	G1743
U2860	U2793	U2718	A2635	U2570	U2485	G2407	U2341	G2261	U2184	A2124	G2052	U1981	C1893	G1821	G1744
C2861	G2794	G2719	G2635	U2571	U2486	G2408	U2342	G2262	U2185	U2125	G2053	U1982	C1894	A1822	G1745
G2862	U2795	U2720	A2636	G2572	U2487	G2409	U2343	G2263	U2186	U2126	G2054	U1983	C1895	A1823	G1746
U2863	C2796	G2721	G2636	U2573	U2488	G2410	U2344	G2264	U2187	A2127	G2055	U1984	C1896	A1824	G1747
C2864	U2797	U2722	A2637	U2574	U2489	G2411	U2345	G2265	U2188	U2128	G2056	U1985	C1897	A1825	G1748
U2865	G2798	G2723	G2637	U2575	U2490	G2412	U2346	G2266	U2189	U2129	G2057	U1986	C1898	A1826	G1749
G2866	U2799	U2724	A2638	G2576	U2491	G2413	U2347	G2267	U2190	A2130	G2058	U1987	C1899	A1827	G1750
C2867	C2799	G2725	G2638	U2577	U2492	G2414	U2348	G2268	U2191	U2131	G2059	U1988	C1900	A1828	G1751
U2868	U2800	U2726	A2639	G2578	U2493	G2415	U2349	G2269	U2192	A2132	G2060	U1989	C1901	A1829	G1752
G2869	C2801	G2727	G2640	U2579	U2494	G2416	U2350	G2270	U2193	U2133	G2061	U1990	C1902	A1830	G1753
U2870	U2802	U2728	A2641	G2580	U2495	G2417	U2351	G2271	U2194	U2134	G2062	U1991	C1903	A1831	G1754
C2871	G2803	U2729	G2642	U2581	U2496	G2418	U2352	G2272	U2195	U2135	G2063	U1992	C1904	A1832	G1755
U2872	U2804	U2730	G2643	G2582	U2497	G2419	U2353	G2273	U2196	U2136	G2064	U1993	C1905	A1833	G1756
G2873	C2805	G2731	C2644	U2583	U2498	G2420	U2354	G2274	U2197	U2137	G2065	U1994	C1906	A1834	G1757
C2874	U2806	U2732	G2645	U2584	U2499	G2421	U2355	G2275	U2198	U2138	G2066	U1995	C1907	A1835	G1758
U2875	G2807	U2733	G2646	U2585	U2500	G2422	U2356	G2276	U2199	U2139	G2067	U1996	C1908	A1836	G1759
C2876	U2808	U2734	A2647	U2586	U2501	G2423	U2357	G2277	U2200	U2140	G2068	U1997	C1909	A1837	G1760
G2877	G2809	U2735	G2648	U2587	U2502	G2424	U2358	G2278	U2201	U2141	G2069	U1998	C1910	A1838	G1761
U2878	C2810	U2736	G2649	U2588	U2503	G2425	U2359	G2279	U2202	U2142	G2070	U1999	C1911	A1839	G1762
C2879	A2811	G2737	A2657	U2589	U2504	G2426	U2360	G2280	U2203	U2143	G2071	U2000	C1912	A1840	G1763
G2880	U2812	U2738	C2658	U2590	U2505	G2427	U2361	G2281	U2204	U2144	G2072	U2001	C1913	A1841	G1764



- Molecule 54: 5S ribosomal RNA

Chain 28: 30% 62% 8%



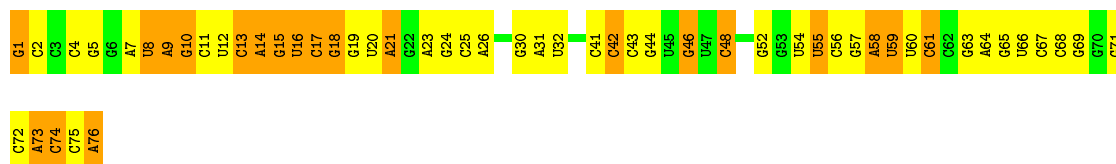
- Molecule 55: mRNA

Chain 29: 45% 45% 10%



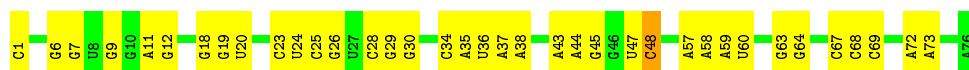
- Molecule 56: A-site tRNA<sup>Phe</sup>

Chain 30: 29% 43% 28%



- Molecule 57: P-site tRNA<sup>fMet</sup>

Chain 31: 52% 47%



- Molecule 58: E-site tRNA<sup>fMet</sup>

Chain 32: 22% 56% 22%



- Molecule 59: GTP pyrophosphokinase

Chain 33: 38% 45% 6% 10%

W35	SER	N594	Y407	K332	W260	R188	LYS	R58
I736	TTR	V483	Y408	T333	M263	I191	ALA	G59
D737	SER	T484	F409	V334	Q264		THR	V60
A738	ALA	T485	T410	E335			THR	E61
		S486	P411	I336	K287	L194	ASP	M62
L741		V487	K412	Q337	L288	K195	SER	V63
H742		V598		I338		W196	VAL	E64
L743	GLY	V599		R339	D271	E197	VAL	L65
SER		G601	V415	T340	E272	L198	SER	L66
		S667	E900	K341	L273	E199	SER	S67
		V668	D417	Q342	L274	L199	GLU	L68
		V669	L418	M343	F275	E200		V69
		R670	P419		C202	Y201	ALA	S70
		M671			F203	M71	ALA	M72
		V672	S422	E348	V276	R204	HIS	D73
		A673	T423	L349	D277	R204	ASN	I73
		H674	P424	G350	A278	Y205	LYS	V74
		D675	F427	V351	R280	L206		T75
		L506		ALA	L281	E210	GLY	L76
		R611		ALA	V282	Y211	GLU	R77
		C612		HIS	A283		PHE	A78
		G613	H430	TRP	E284	L214		D16
		Q614	I431	LYS	R285	A215		P17
		P615	S433	TTR	L286			E18
		I616	D434	LYS	Q287	L218		K19
		P617	D435	GLU	D288	E219		R82
		G618	G436		C289	E220		P83
		D619	H437			R221		L84
		E620	R438	S368	A292			A85
		I621	C439		L293	D224		D86
		V622		E371	G294	R225		A87
		Y534	A442		L295	E226		R88
		M535	K443	A375	V296	E155		V89
		V536	L444	K376	H297	E228		S91
				L377	T298	L229		E92
		B541	R447		H299	E230		S93
		S532	I448	A382	C231	E231		E94
		V633	Y453	TRP	R301	F232		R93
		H634	Q454	GLN	H302	V233		L95
		R635	L455	GLU	L303	E162		C34
		A636	L456	GLU	P304	V163		E33
		D637	Q456	MET	D305	L164		C32
		C638	M457	ALA	E306			E95
		S639	Q458	ASP	F307	A238		V94
		Q640	D459	SER	D308	E239		L96
		L641	Q460	GLY	D309	M240		R96
		P642	I461	GLU	Y310	K241		
		S643	E462	MET		A242		V99
		L644	E463	LEU	R315	E243		L100
		R645	Q466	ASP	P316	G244		K101
		S646	K467	GLU	V245	V245		S102
		H647	Q468	VAL	Y319	K246		V103
		A648	ARG	ARG		E177		V104
		P649	SER	SER		L178		M105
			GLN	GLN		A174		L106
			L470			E243		I107
			P470			V249		H108
			G581			V249		G109
		I652	GLN	VAL		K246		V110
		V653	LYS	PHE		E178		R111
		D654	SER	ASP		T179		
		A655	GLY	D404		M180		A114
		V656	T656			I181		ALA
		L720				V250		I182
						G251		ARG
						R252		L55
						G328		V156
						P320		L57

## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	77862	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	30488	Depositor
Image detector	GATAN K2 SUMMIT (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	A	0.29	0/2121	0.64	0/2852
10	J	0.30	0/947	0.63	0/1268
11	K	0.30	0/1054	0.66	0/1403
12	L	0.33	0/1093	0.59	0/1460
13	M	0.32	0/973	0.63	0/1301
14	N	0.28	0/902	0.57	0/1209
15	O	0.32	0/929	0.61	0/1242
16	P	0.32	0/960	0.56	0/1278
17	Q	0.35	0/829	0.67	1/1107 (0.1%)
18	R	0.27	0/864	0.65	0/1156
19	S	0.30	0/744	0.61	0/994
2	B	0.33	0/1586	0.62	0/2134
20	T	0.35	0/787	0.69	0/1051
21	U	0.32	0/766	0.58	0/1025
22	V	0.34	0/582	0.60	0/769
23	W	0.34	0/635	0.63	0/848
24	X	0.31	0/510	0.59	0/677
25	Y	0.30	0/453	0.55	0/605
26	Z	0.37	0/531	0.91	3/709 (0.4%)
27	1	0.28	0/450	0.56	0/599
28	2	0.32	0/416	0.57	0/554
29	3	0.35	0/380	0.58	0/498
3	C	0.34	0/1571	0.62	0/2113
30	4	0.32	0/513	0.61	0/676
31	5	0.29	0/303	0.63	0/397
32	6	0.37	0/1735	0.60	0/2338
33	7	0.32	0/1651	0.60	0/2225
34	8	0.32	0/1665	0.60	0/2227
35	9	0.31	0/1169	0.70	1/1573 (0.1%)
36	10	0.34	0/835	0.64	0/1128
37	11	0.29	0/1195	0.60	0/1602
38	12	0.31	0/989	0.60	0/1326
39	13	0.33	0/1034	0.66	0/1375
4	D	0.34	0/1434	0.58	0/1926



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
40	14	0.31	0/796	0.62	0/1077
41	15	0.33	0/885	0.68	0/1195
42	16	0.33	0/969	0.73	0/1300
43	17	0.28	0/892	0.63	0/1193
44	18	0.40	0/817	0.58	0/1088
45	19	0.28	0/722	0.55	0/964
46	20	0.35	0/659	0.64	1/884 (0.1%)
47	21	0.33	0/657	0.66	0/881
48	22	0.34	0/544	0.67	0/731
49	23	0.33	0/652	0.62	0/877
5	E	0.30	0/1343	0.62	0/1816
50	24	0.29	0/671	0.55	0/888
51	25	0.38	0/550	0.73	0/728
52	26	0.38	1/36967 (0.0%)	0.70	5/57666 (0.0%)
53	27	0.39	1/69801 (0.0%)	0.70	5/108894 (0.0%)
54	28	0.36	1/2876 (0.0%)	0.70	1/4483 (0.0%)
55	29	0.84	0/486	0.70	0/757
56	30	0.50	1/1813 (0.1%)	0.74	0/2823
57	31	0.37	1/1836 (0.1%)	0.68	0/2859
58	32	0.80	2/1835 (0.1%)	0.74	1/2857 (0.0%)
59	33	0.66	6/4985 (0.1%)	1.08	38/6770 (0.6%)
6	F	0.36	0/1122	0.68	0/1515
7	G	0.41	0/1001	0.74	1/1350 (0.1%)
8	H	0.38	0/1046	0.72	1/1410 (0.1%)
9	I	0.30	0/1152	0.61	0/1551
All	All	0.39	13/167683 (0.0%)	0.70	58/250202 (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
52	26	0	9
53	27	0	22
56	30	0	1
59	33	0	2
All	All	0	34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	33	156	ARG	CZ-NH2	-10.64	1.19	1.33
59	33	152	LYS	CD-CE	-7.75	1.31	1.51
59	33	17	PRO	CA-CB	-7.24	1.39	1.53
52	26	2	A	OP3-P	-7.10	1.52	1.61
58	32	1	C	OP3-P	-7.09	1.52	1.61

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	33	156	ARG	NE-CZ-NH1	19.60	130.10	120.30
59	33	156	ARG	NH1-CZ-NH2	-13.76	104.26	119.40
59	33	17	PRO	N-CA-CB	-11.19	89.87	103.30
59	33	17	PRO	CA-CB-CG	10.30	124.37	104.80
59	33	63	VAL	CG1-CB-CG2	-9.24	96.11	110.90

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	26	159	G	Sidechain
52	26	380	G	Sidechain
52	26	820	U	Sidechain
52	26	898	G	Sidechain
52	26	938	A	Sidechain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2082	0	2157	111	0
2	B	1565	0	1616	100	0
3	C	1552	0	1619	102	0
4	D	1410	0	1447	120	0
5	E	1323	0	1374	77	0
6	F	1111	0	1148	93	0
7	G	988	0	1025	135	0
8	H	1032	0	1088	109	0
9	I	1129	0	1162	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	938	0	1012	64	0
11	K	1045	0	1117	88	0
12	L	1074	0	1157	62	0
13	M	960	0	1000	65	0
14	N	892	0	923	51	0
15	O	917	0	965	61	0
16	P	947	0	1022	72	0
17	Q	816	0	839	54	0
18	R	857	0	922	45	0
19	S	738	0	807	51	0
20	T	779	0	834	55	0
21	U	753	0	780	37	0
22	V	575	0	592	31	0
23	W	625	0	655	32	0
24	X	509	0	543	40	0
25	Y	449	0	491	25	0
26	Z	522	0	521	41	0
27	1	444	0	461	36	0
28	2	409	0	440	17	0
29	3	377	0	418	35	0
30	4	504	0	574	32	0
31	5	302	0	343	28	0
32	6	1704	0	1732	100	0
33	7	1624	0	1699	126	0
34	8	1643	0	1710	136	0
35	9	1156	0	1199	80	0
36	10	817	0	808	68	0
37	11	1181	0	1240	65	0
38	12	979	0	1034	59	0
39	13	1022	0	1070	118	0
40	14	786	0	828	83	0
41	15	869	0	878	65	0
42	16	955	0	1019	65	0
43	17	883	0	944	85	0
44	18	805	0	847	62	0
45	19	714	0	737	26	0
46	20	649	0	666	62	0
47	21	648	0	691	50	0
48	22	535	0	552	40	0
49	23	637	0	665	52	0
50	24	665	0	714	42	0
51	25	544	0	579	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	26	33016	0	16617	892	0
53	27	62322	0	31345	1639	0
54	28	2572	0	1302	90	0
55	29	432	0	218	13	0
56	30	1623	0	821	66	0
57	31	1644	0	836	26	0
58	32	1643	0	836	76	0
59	33	4911	0	4550	616	0
All	All	154603	0	105189	6144	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 24.

The worst 5 of 6144 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)
59:33:17:PRO:HB3	59:33:39:TRP:NE1	1.57	1.18
52:26:484:G:H4'	52:26:485:U:H5'	1.23	1.18
51:25:20:ARG:HH22	52:26:1538:C:H1'	1.05	1.13
59:33:65:ILE:HG21	59:33:157:ILE:HD11	1.31	1.11
59:33:188:ARG:HH12	59:33:377:LEU:HA	1.08	1.11

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	A	269/273 (98%)	226 (84%)	34 (13%)	9 (3%)	4	39
2	B	207/209 (99%)	165 (80%)	29 (14%)	13 (6%)	1	24
3	C	199/201 (99%)	164 (82%)	23 (12%)	12 (6%)	2	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	175/179 (98%)	140 (80%)	27 (15%)	8 (5%)	3	30
5	E	174/177 (98%)	145 (83%)	22 (13%)	7 (4%)	3	34
6	F	147/149 (99%)	119 (81%)	16 (11%)	12 (8%)	1	17
7	G	129/165 (78%)	92 (71%)	17 (13%)	20 (16%)	0	4
8	H	139/142 (98%)	106 (76%)	27 (19%)	6 (4%)	3	32
9	I	140/142 (99%)	127 (91%)	7 (5%)	6 (4%)	3	32
10	J	120/123 (98%)	101 (84%)	14 (12%)	5 (4%)	3	32
11	K	141/144 (98%)	116 (82%)	16 (11%)	9 (6%)	1	24
12	L	134/136 (98%)	110 (82%)	20 (15%)	4 (3%)	5	41
13	M	118/127 (93%)	99 (84%)	14 (12%)	5 (4%)	3	32
14	N	114/117 (97%)	92 (81%)	16 (14%)	6 (5%)	2	28
15	O	112/115 (97%)	88 (79%)	20 (18%)	4 (4%)	4	37
16	P	115/118 (98%)	108 (94%)	5 (4%)	2 (2%)	11	52
17	Q	101/103 (98%)	82 (81%)	16 (16%)	3 (3%)	5	41
18	R	108/110 (98%)	85 (79%)	19 (18%)	4 (4%)	4	36
19	S	91/100 (91%)	73 (80%)	13 (14%)	5 (6%)	2	27
20	T	100/104 (96%)	80 (80%)	13 (13%)	7 (7%)	1	21
21	U	92/94 (98%)	76 (83%)	13 (14%)	3 (3%)	4	39
22	V	73/85 (86%)	64 (88%)	7 (10%)	2 (3%)	6	43
23	W	75/78 (96%)	67 (89%)	6 (8%)	2 (3%)	6	43
24	X	61/63 (97%)	52 (85%)	5 (8%)	4 (7%)	1	23
25	Y	56/59 (95%)	50 (89%)	4 (7%)	2 (4%)	4	37
26	Z	64/70 (91%)	50 (78%)	9 (14%)	5 (8%)	1	18
27	1	54/57 (95%)	42 (78%)	6 (11%)	6 (11%)	0	10
28	2	48/55 (87%)	41 (85%)	6 (12%)	1 (2%)	8	48
29	3	44/46 (96%)	35 (80%)	7 (16%)	2 (4%)	3	31
30	4	62/65 (95%)	51 (82%)	6 (10%)	5 (8%)	1	17
31	5	36/38 (95%)	26 (72%)	6 (17%)	4 (11%)	0	10
32	6	216/241 (90%)	177 (82%)	31 (14%)	8 (4%)	4	36
33	7	204/233 (88%)	172 (84%)	26 (13%)	6 (3%)	5	42
34	8	203/206 (98%)	158 (78%)	30 (15%)	15 (7%)	1	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	9	155/167 (93%)	116 (75%)	25 (16%)	14 (9%)	1	15
36	10	98/135 (73%)	76 (78%)	15 (15%)	7 (7%)	1	21
37	11	149/179 (83%)	123 (83%)	17 (11%)	9 (6%)	2	25
38	12	127/130 (98%)	112 (88%)	13 (10%)	2 (2%)	11	53
39	13	125/130 (96%)	98 (78%)	17 (14%)	10 (8%)	1	17
40	14	96/103 (93%)	77 (80%)	11 (12%)	8 (8%)	1	16
41	15	114/129 (88%)	92 (81%)	18 (16%)	4 (4%)	4	38
42	16	121/124 (98%)	98 (81%)	11 (9%)	12 (10%)	1	12
43	17	112/118 (95%)	90 (80%)	11 (10%)	11 (10%)	1	13
44	18	98/101 (97%)	71 (72%)	20 (20%)	7 (7%)	1	21
45	19	86/89 (97%)	73 (85%)	8 (9%)	5 (6%)	2	26
46	20	80/82 (98%)	64 (80%)	12 (15%)	4 (5%)	2	29
47	21	78/84 (93%)	53 (68%)	19 (24%)	6 (8%)	1	19
48	22	63/75 (84%)	48 (76%)	9 (14%)	6 (10%)	1	14
49	23	77/92 (84%)	60 (78%)	13 (17%)	4 (5%)	2	28
50	24	83/87 (95%)	75 (90%)	5 (6%)	3 (4%)	4	37
51	25	63/71 (89%)	44 (70%)	9 (14%)	10 (16%)	0	4
59	33	663/750 (88%)	550 (83%)	78 (12%)	35 (5%)	2	28
All	All	6509/6970 (93%)	5299 (81%)	841 (13%)	369 (6%)	4	26

5 of 369 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	18	ASP
2	B	181	ASP
2	B	188	LEU
3	C	55	SER
3	C	127	GLU

### 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	A	216/218 (99%)	215 (100%)	1 (0%)	91	96
2	B	164/164 (100%)	163 (99%)	1 (1%)	89	95
3	C	165/165 (100%)	164 (99%)	1 (1%)	89	95
4	D	148/150 (99%)	146 (99%)	2 (1%)	71	87
5	E	137/138 (99%)	136 (99%)	1 (1%)	87	94
6	F	114/114 (100%)	113 (99%)	1 (1%)	82	92
7	G	100/123 (81%)	99 (99%)	1 (1%)	80	90
8	H	109/110 (99%)	109 (100%)	0	100	100
9	I	116/116 (100%)	116 (100%)	0	100	100
10	J	103/104 (99%)	103 (100%)	0	100	100
11	K	102/103 (99%)	102 (100%)	0	100	100
12	L	109/109 (100%)	109 (100%)	0	100	100
13	M	100/103 (97%)	99 (99%)	1 (1%)	80	90
14	N	86/87 (99%)	84 (98%)	2 (2%)	56	80
15	O	99/100 (99%)	99 (100%)	0	100	100
16	P	89/90 (99%)	89 (100%)	0	100	100
17	Q	84/84 (100%)	84 (100%)	0	100	100
18	R	93/93 (100%)	93 (100%)	0	100	100
19	S	80/84 (95%)	79 (99%)	1 (1%)	73	88
20	T	83/85 (98%)	82 (99%)	1 (1%)	75	89
21	U	78/78 (100%)	78 (100%)	0	100	100
22	V	57/63 (90%)	57 (100%)	0	100	100
23	W	67/68 (98%)	67 (100%)	0	100	100
24	X	55/55 (100%)	55 (100%)	0	100	100
25	Y	48/49 (98%)	48 (100%)	0	100	100
26	Z	59/62 (95%)	58 (98%)	1 (2%)	66	86
27	1	47/48 (98%)	47 (100%)	0	100	100
28	2	45/49 (92%)	45 (100%)	0	100	100
29	3	38/38 (100%)	38 (100%)	0	100	100
30	4	51/52 (98%)	51 (100%)	0	100	100
31	5	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	6	180/199 (90%)	179 (99%)	1 (1%)	89	95
33	7	170/190 (90%)	168 (99%)	2 (1%)	75	89
34	8	172/173 (99%)	171 (99%)	1 (1%)	89	95
35	9	119/126 (94%)	117 (98%)	2 (2%)	66	86
36	10	87/116 (75%)	86 (99%)	1 (1%)	78	89
37	11	124/147 (84%)	124 (100%)	0	100	100
38	12	104/105 (99%)	104 (100%)	0	100	100
39	13	105/107 (98%)	103 (98%)	2 (2%)	62	84
40	14	86/90 (96%)	86 (100%)	0	100	100
41	15	89/99 (90%)	89 (100%)	0	100	100
42	16	103/104 (99%)	103 (100%)	0	100	100
43	17	92/96 (96%)	91 (99%)	1 (1%)	78	89
44	18	83/84 (99%)	81 (98%)	2 (2%)	54	79
45	19	76/77 (99%)	76 (100%)	0	100	100
46	20	65/65 (100%)	65 (100%)	0	100	100
47	21	74/78 (95%)	74 (100%)	0	100	100
48	22	56/65 (86%)	55 (98%)	1 (2%)	64	85
49	23	70/79 (89%)	70 (100%)	0	100	100
50	24	65/66 (98%)	65 (100%)	0	100	100
51	25	55/61 (90%)	55 (100%)	0	100	100
59	33	452/635 (71%)	449 (99%)	3 (1%)	87	94
All	All	5303/5698 (93%)	5273 (99%)	30 (1%)	89	95

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	Z	37	CYS
33	7	101	ASN
59	33	267	ASN
33	7	100	ILE
34	8	170	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:



Mol	Chain	Res	Type
24	X	58	ASN
32	6	177	ASN
59	33	264	GLN
26	Z	61	ASN
31	5	37	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	26	1538/1539 (99%)	178 (11%)	5 (0%)
53	27	2902/2903 (99%)	379 (13%)	17 (0%)
54	28	119/120 (99%)	15 (12%)	1 (0%)
55	29	19/20 (95%)	3 (15%)	0
56	30	75/76 (98%)	22 (29%)	1 (1%)
57	31	76/77 (98%)	5 (6%)	0
58	32	76/77 (98%)	16 (21%)	0
All	All	4805/4812 (99%)	618 (12%)	24 (0%)

5 of 618 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	26	4	U
52	26	9	G
52	26	13	U
52	26	22	G
52	26	32	A

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	27	1020	A
53	27	1694	C
54	28	66	A
53	27	1130	U
53	27	1378	A

## 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.