



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Nov 16, 2017 – 06:38 PM EST

PDB ID : 5KPV
EMDB ID: : EMD-8280
Title : Structure of RelA bound to ribosome in presence of A/R tRNA (Structure II)
Authors : Loveland, A.B.; Bah, E.; Madireddy, R.; Zhang, Y.; Brilot, A.F.; Grigorieff, N.; Korostelev, A.A.
Deposited on : unknown
Resolution : 4.10 Å(reported)

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

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

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

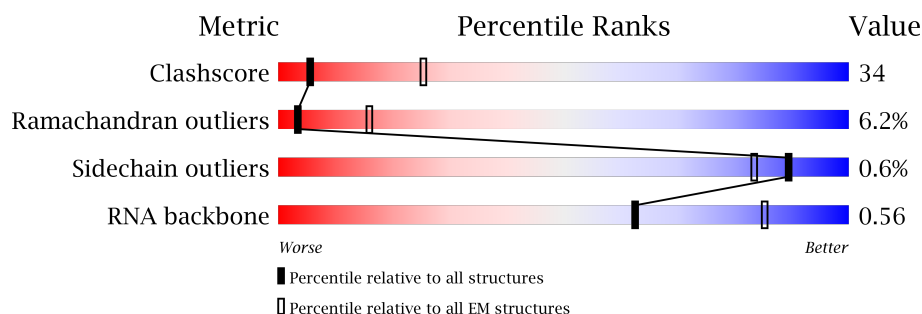
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 Å.

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




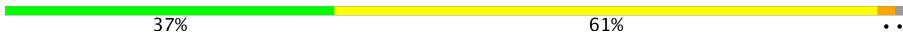
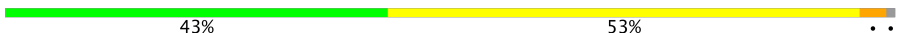


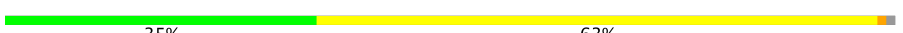
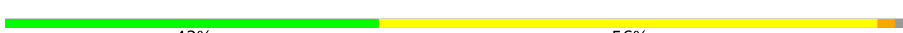




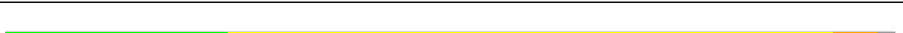













Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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

Mol	Chain	Length	Quality of chain
1	A	273	43% 53% ..
2	B	209	45% 53% .
3	C	201	39% 55% 6%
4	D	179	34% 62% ...
5	E	177	46% 52% ..
6	F	149	37% 54% 9%
7	G	165	21% 52% 6% 21%
8	H	142	27% 67% 5% ..

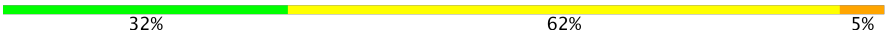


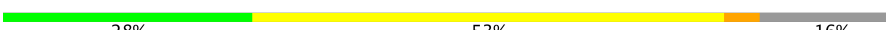
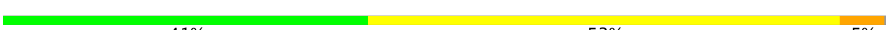
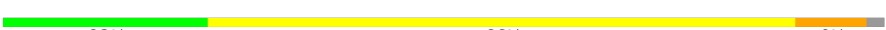




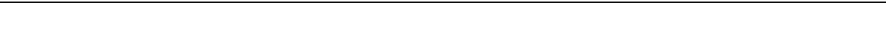

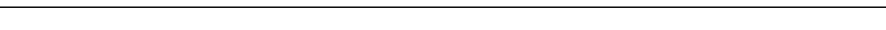
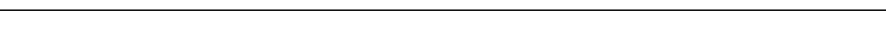

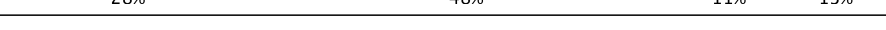








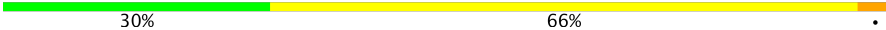
Continued on next page...

Continued from previous page...

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	

Continued on next page...

Continued from previous page...

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	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	33	750	<div><div></div><div>35%</div><div>48%</div><div>6%</div><div>10%</div></div>

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		

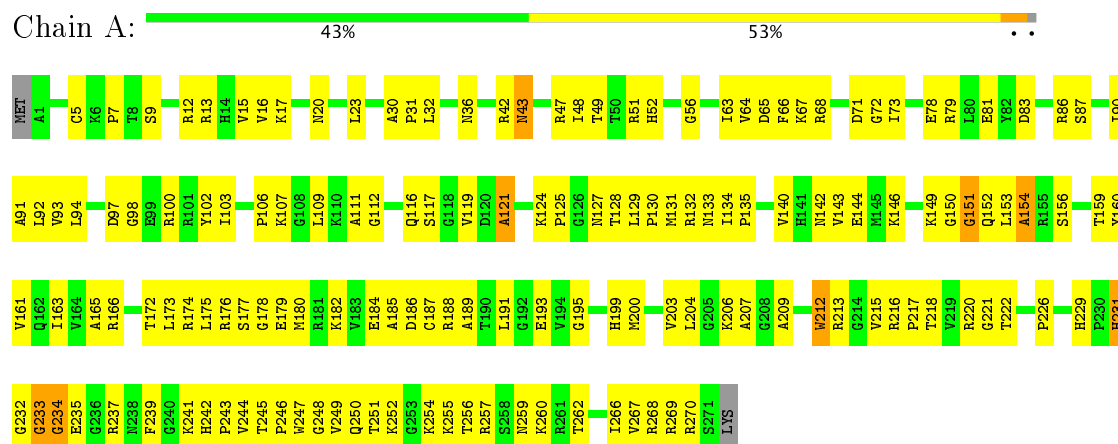
There are 7 discrepancies between the modelled and reference sequences:

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



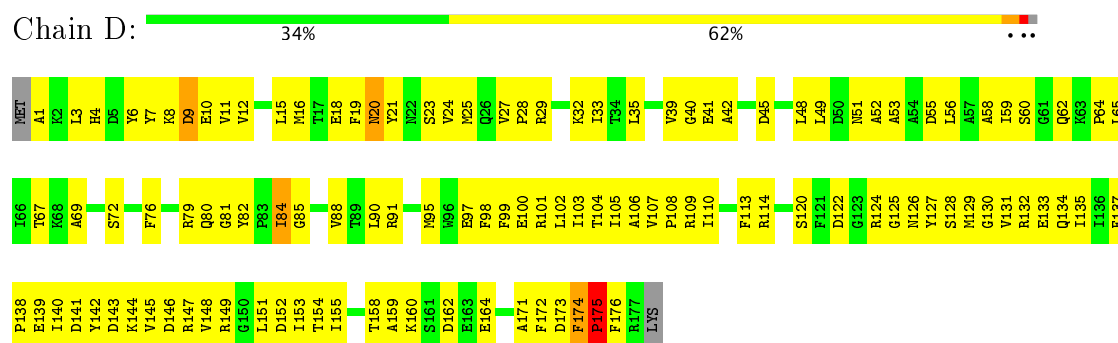
- Molecule 2: 50S ribosomal protein L3



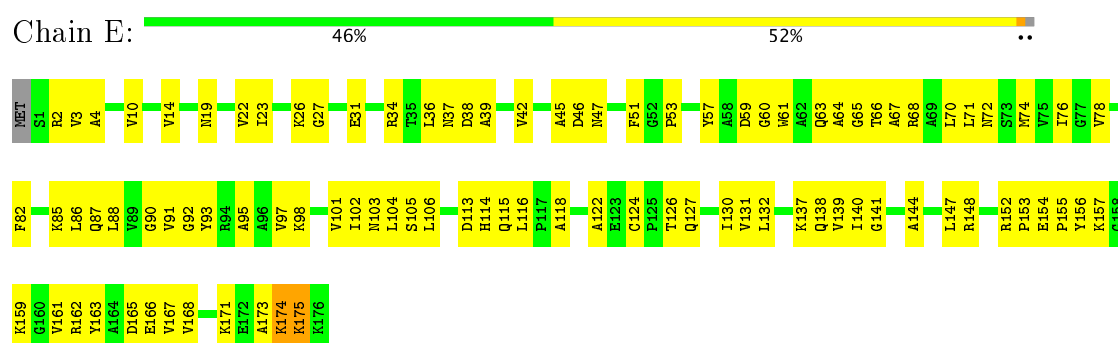
- Molecule 3: 50S ribosomal protein L4



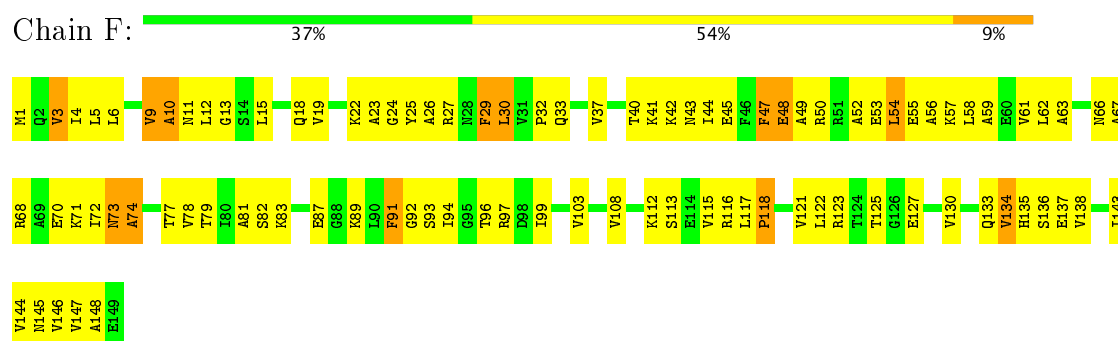
- Molecule 4: 50S ribosomal protein L5



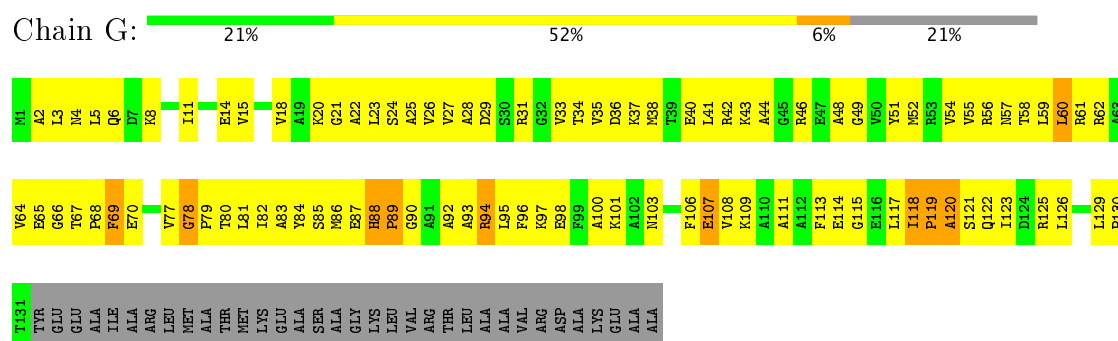
- Molecule 5: 50S ribosomal protein L6



- Molecule 6: 50S ribosomal protein L9

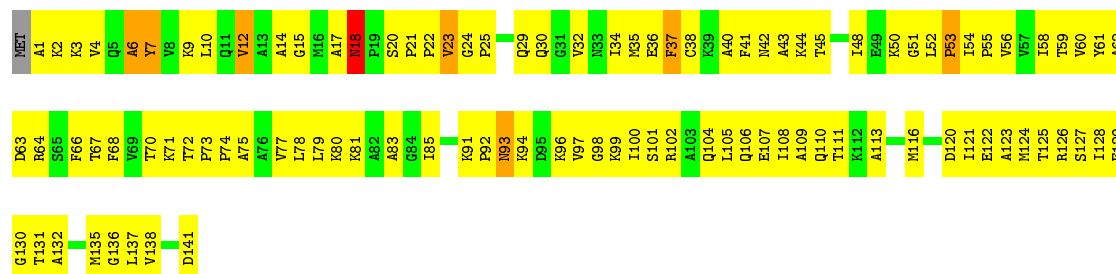


- Molecule 7: 50S ribosomal protein L10



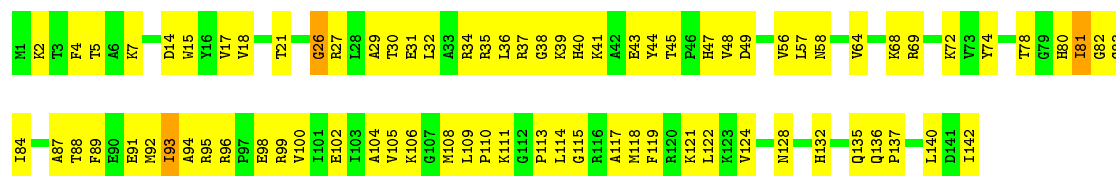
- Molecule 8: 50S ribosomal protein L11

Chain H:  27% 67% 5% ..



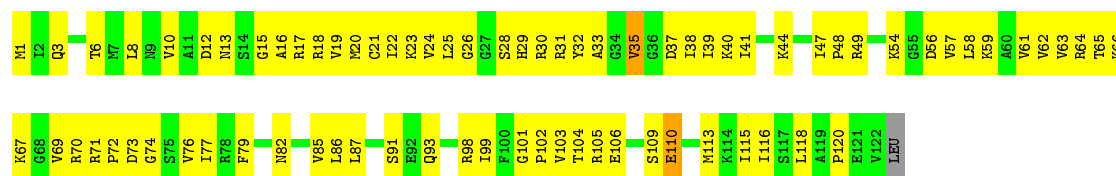
- Molecule 9: 50S ribosomal protein L13

Chain I:  44% 54% .



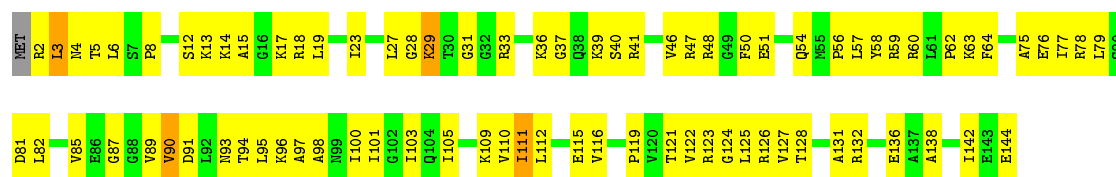
- Molecule 10: 50S ribosomal protein L14

Chain J:  37% 61% ..



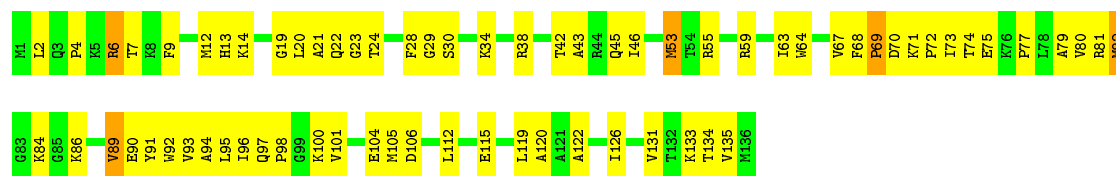
- Molecule 11: 50S ribosomal protein L15

Chain K:  43% 53% ..

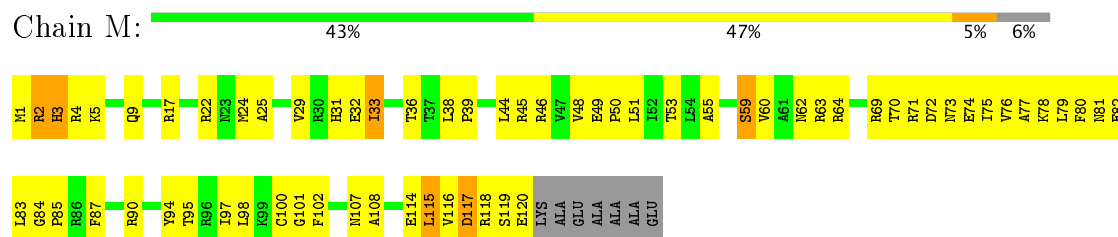


- Molecule 12: 50S ribosomal protein L16

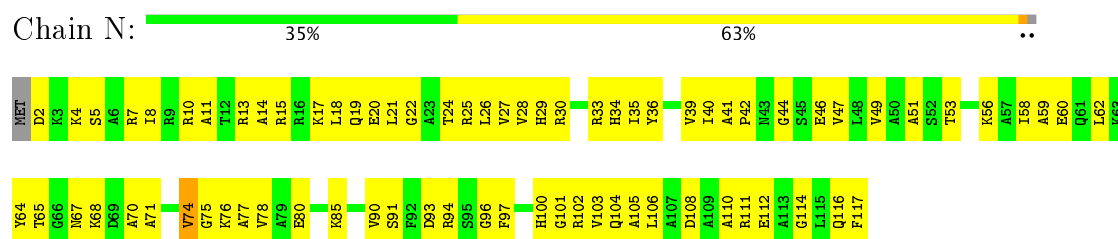
Chain L:  49% 47% .



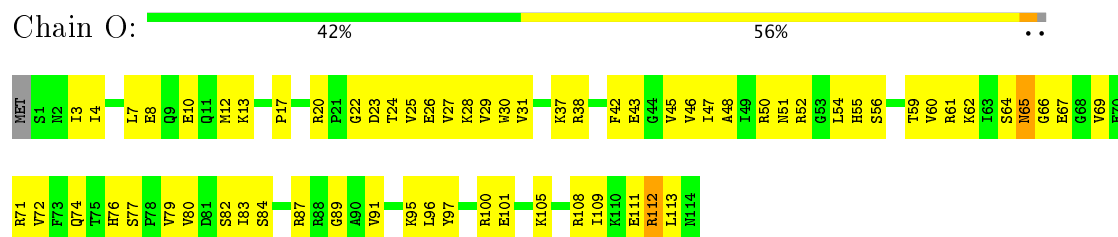
- Molecule 13: 50S ribosomal protein L17



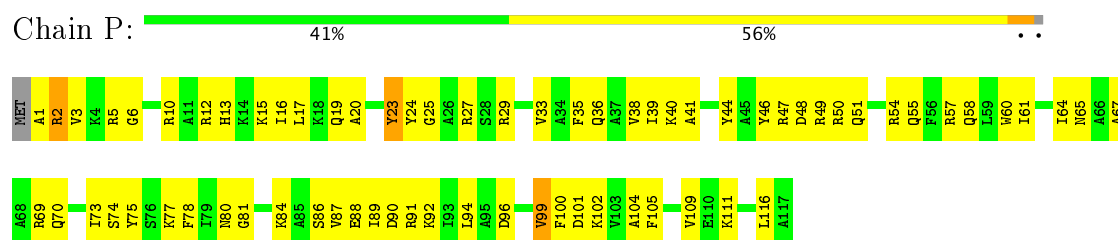
- Molecule 14: 50S ribosomal protein L18



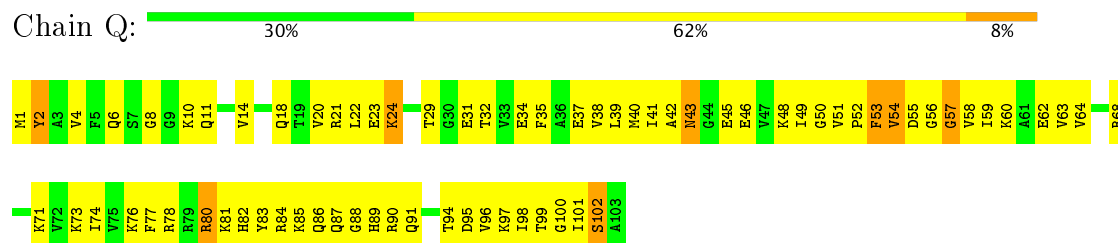
- Molecule 15: 50S ribosomal protein L19



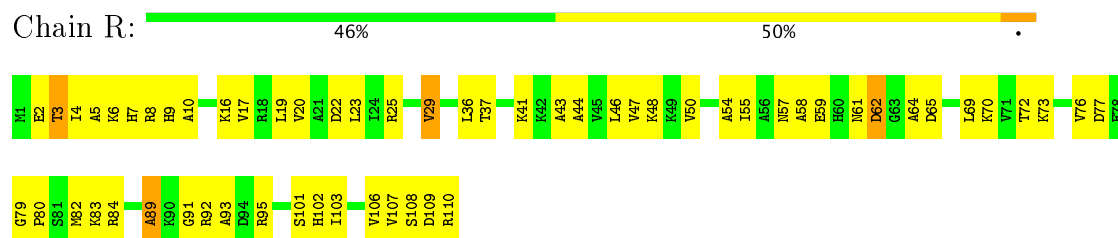
- Molecule 16: 50S ribosomal protein L20



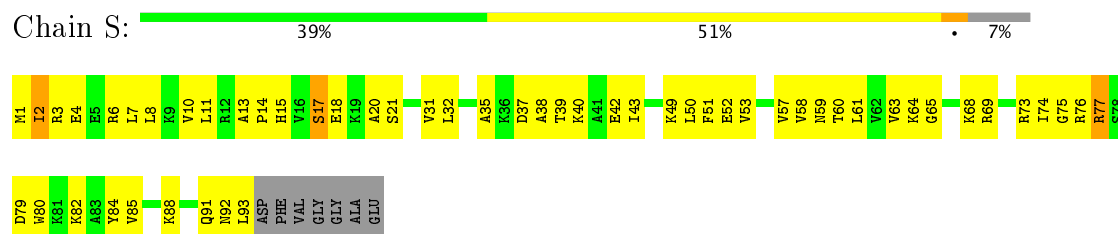
- Molecule 17: 50S ribosomal protein L21



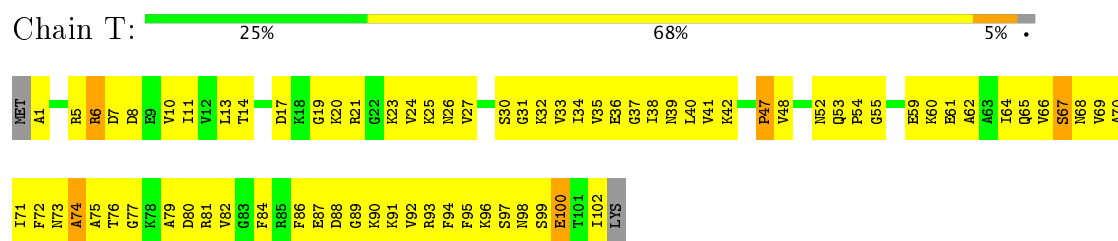
- Molecule 18: 50S ribosomal protein L22



• Molecule 19: 50S ribosomal protein L23



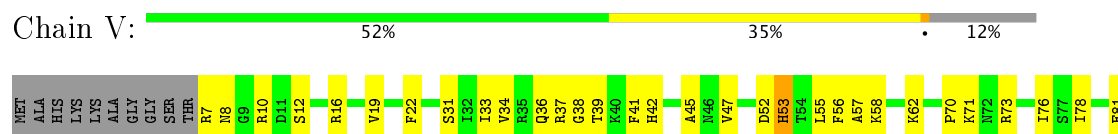
• Molecule 20: 50S ribosomal protein L24



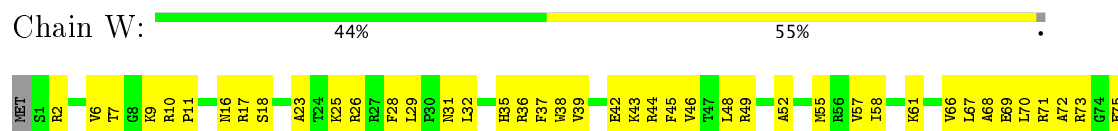
• Molecule 21: 50S ribosomal protein L25



• Molecule 22: 50S ribosomal protein L27



• Molecule 23: 50S ribosomal protein L28





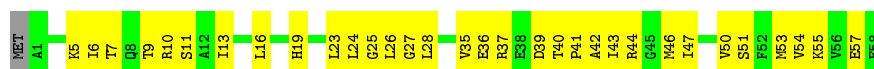
- Molecule 24: 50S ribosomal protein L29

Chain X: 29% 63% 8%



- Molecule 25: 50S ribosomal protein L30

Chain Y: 44% 54% .



- Molecule 26: 50S ribosomal protein L31

Chain Z: 37% 49% 9% 6%



- Molecule 27: 50S ribosomal protein L32

Chain 1: 32% 58% 9% .



- Molecule 28: 50S ribosomal protein L33

Chain 2: 47% 44% 9%



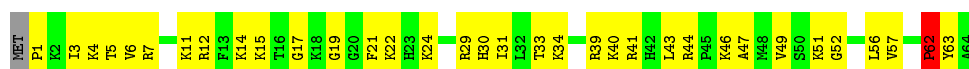
- Molecule 29: 50S ribosomal protein L34

Chain 3: 46% 52% .



- Molecule 30: 50S ribosomal protein L35

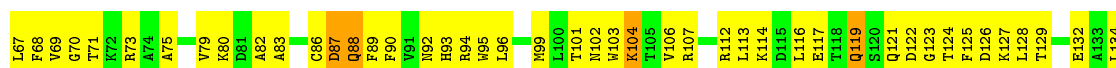
Chain 4: 46% 51% . .



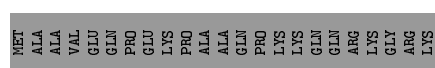
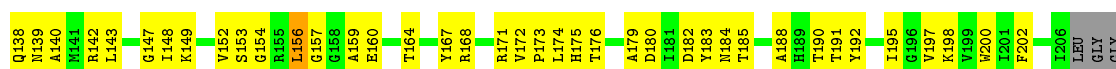
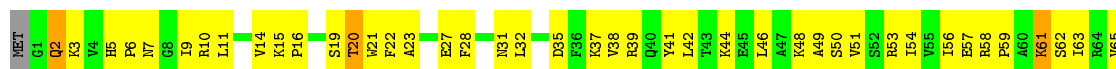
- Molecule 31: 50S ribosomal protein L36



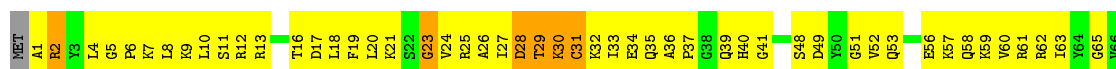
- Molecule 32: 30S ribosomal protein S2

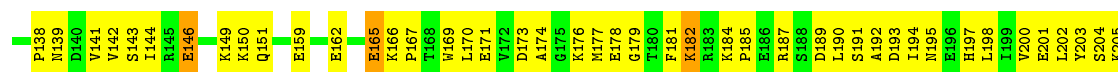


- Molecule 33: 30S ribosomal protein S3



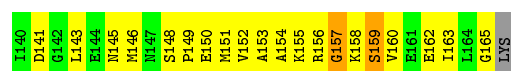
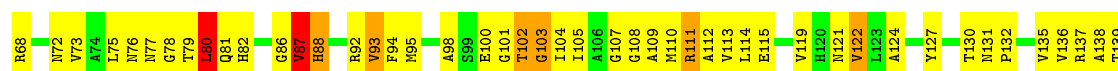
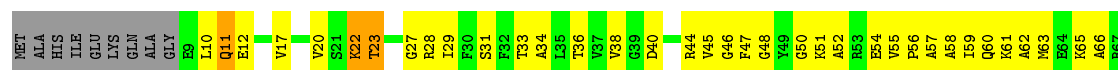
- Molecule 34: 30S ribosomal protein S4





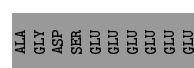
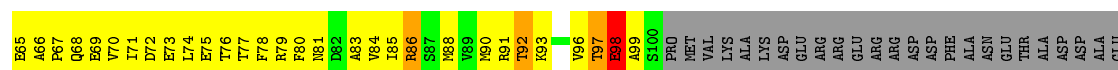
• Molecule 35: 30S ribosomal protein S5

Chain 9: 32% 54% 7% 6%



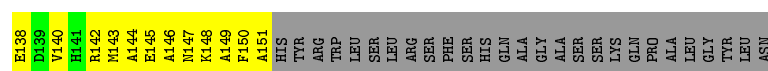
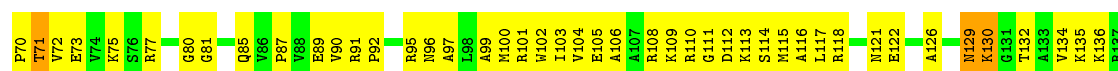
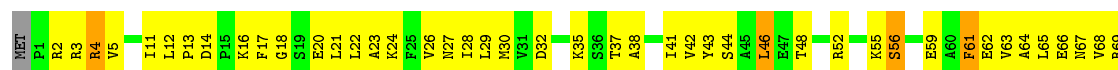
• Molecule 36: 30S ribosomal protein S6

Chain 10: 19% 50% 5% 26%



• Molecule 37: 30S ribosomal protein S7

Chain 11: 28% 53% 16%

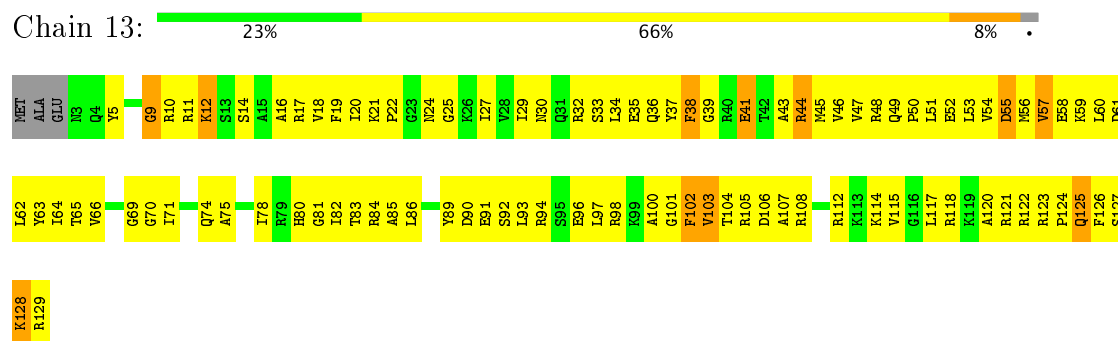


• Molecule 38: 30S ribosomal protein S8

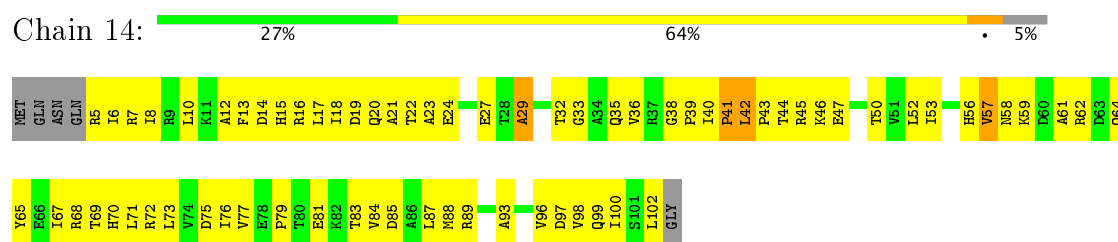
Chain 12: 41% 53% 5%



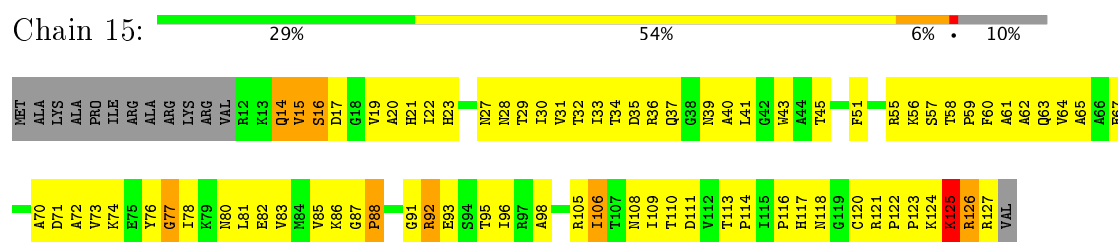
- Molecule 39: 30S ribosomal protein S9



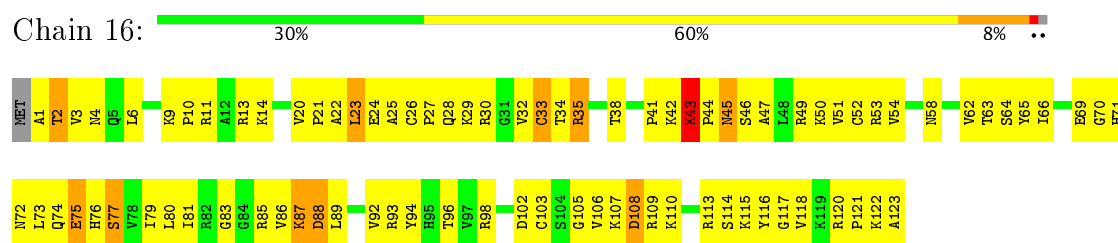
- Molecule 40: 30S ribosomal protein S10



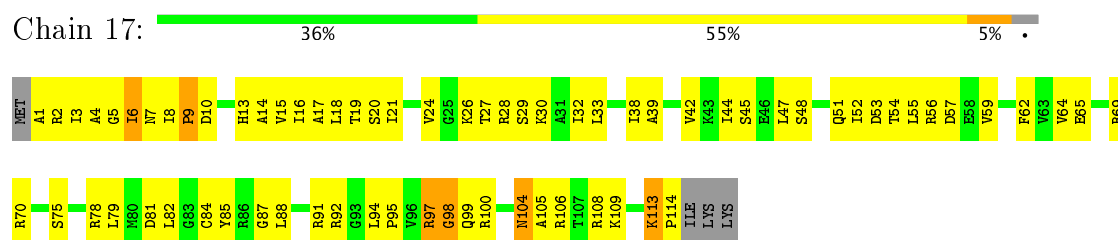
- Molecule 41: 30S ribosomal protein S11



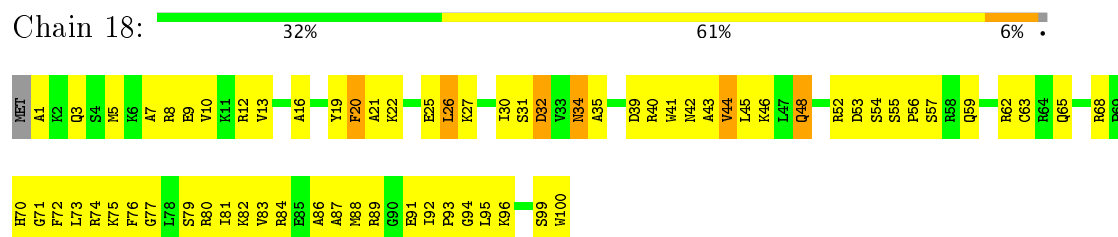
- Molecule 42: 30S ribosomal protein S12



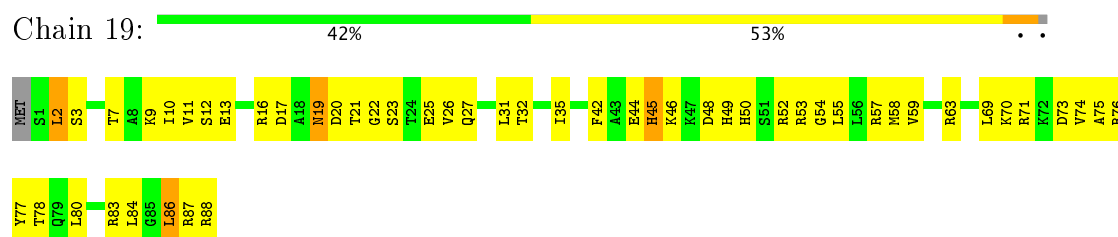
- Molecule 43: 30S ribosomal protein S13



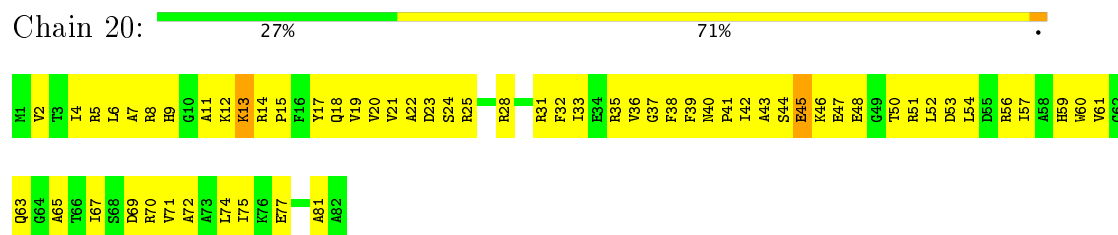
- Molecule 44: 30S ribosomal protein S14



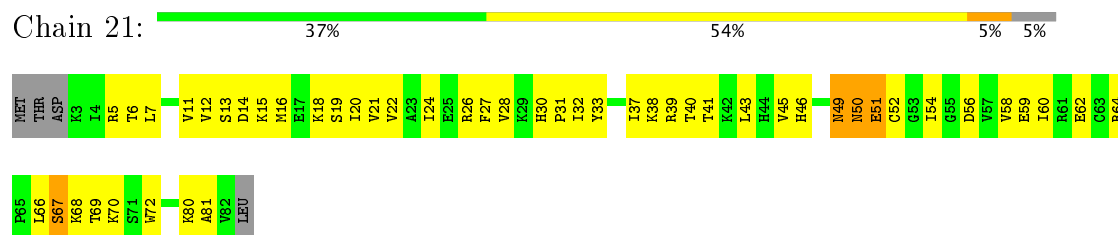
- Molecule 45: 30S ribosomal protein S15



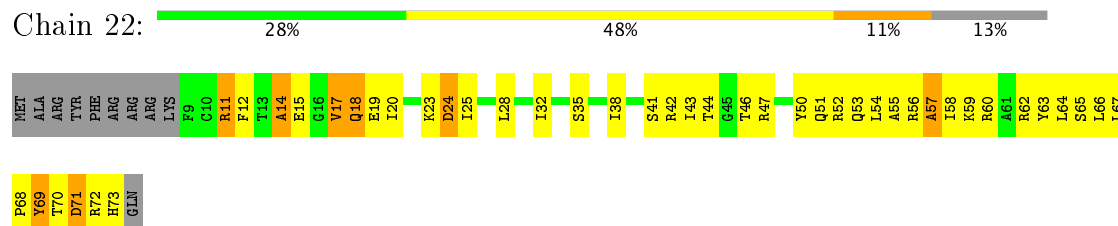
- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17

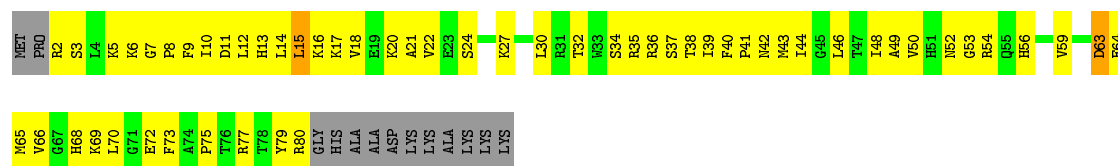


- Molecule 48: 30S ribosomal protein S18



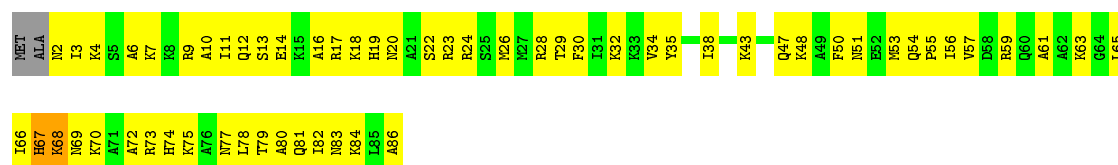
- Molecule 49: 30S ribosomal protein S19

Chain 23: 25% 59% 14%



- Molecule 50: 30S ribosomal protein S20

Chain 24: 30% 66% ..



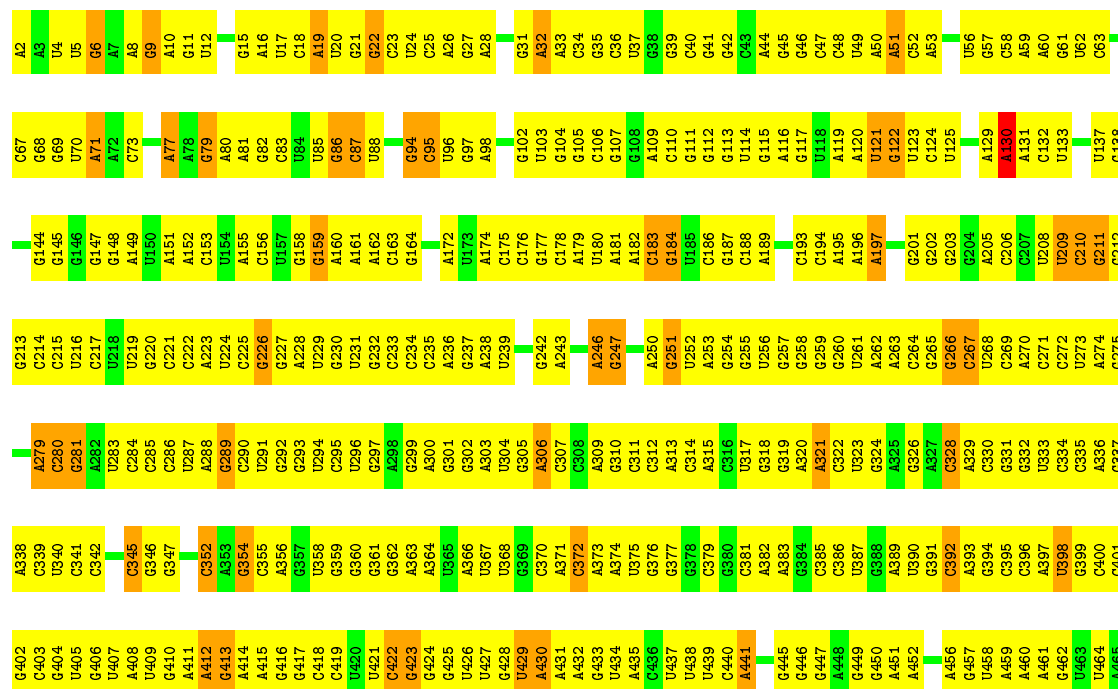
- Molecule 51: 30S ribosomal protein S21

Chain 25: 23% 62% 7% 8%

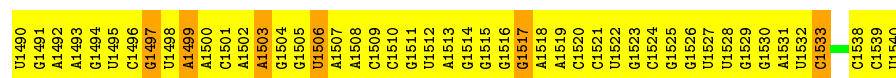


- Molecule 52: 16S ribosomal RNA

Chain 26: 20% 70% 10%

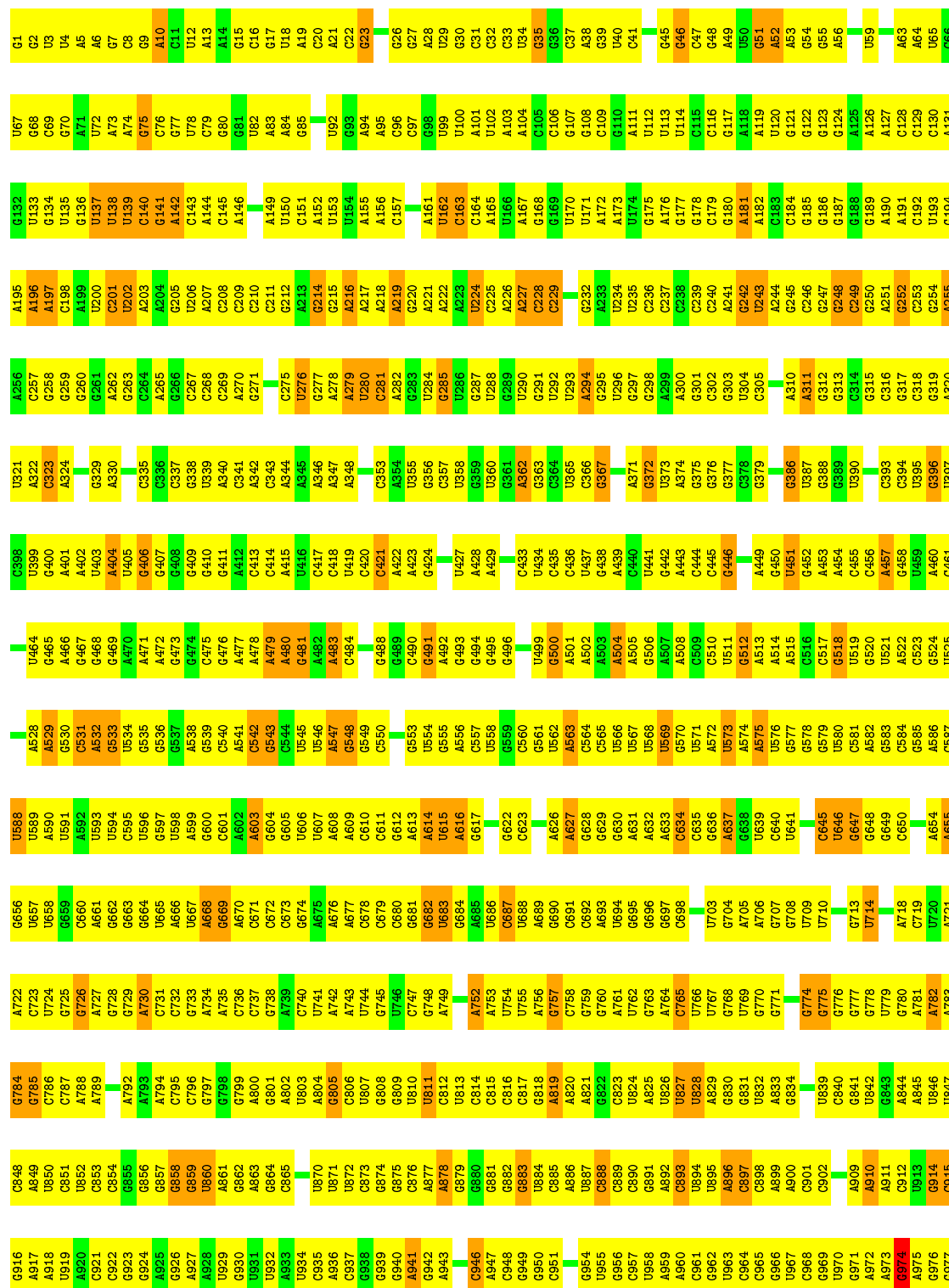


A1430	A1367	A1306	U1235	A1170	G1108	C1045	A978	U916	C956	U788	C726	A663	U593	G530	A466
A1431	A1368	U1307	A1236	A1171	C1109	A1046	C979	G917	C957	U789	G727	G664	U594	U531	U467
A1432	A1369	U1308	A1237		A1110	G1047	G980	A918	G958	A790	A728	A665	A729	A532	A468
A1433	G1370	A1309	A1238	G1174	A1111	G1048	U981	A919	G959	G791	A729	G666	A596	A533	C469
A1434	G1371	G1310	A1239	G1175	C1112	U1049	U982	U920	A860	A792	G730	G667	G597	U534	C470
A1435	A1372	A1311	U1240		C1113	G1050		U921	G661	U793	G731	G668	U598	A535	U471
U1436	G1373	G1312	G1241	A1180	C1114	C1051	U986	G922	C962	A794	C732	G669	C599	C536	U472
A1437	U1313	U1314	G1242	G1181	U1115	U1052	G987	A923	U963	G795		G670	A600	G537	U473
G1438	C1314	C1243	G1243	G1182	U1116	G1053	G988	C924	A864	G796	C735	G671	G601	G538	G474
A1439	U1315	U1316	G1244	U1183	A1117	C1054	U989	G925	A865	G797	C736	U672		A539	C475
U1440	G1316	G1245	C1245	U1184	C1118	A1055	C990	G926	C966	U798	C737	A673	G604	G540	U476
A1441	C1317	A1246	A1246	G1185	C1119	U1056	U991	G927	G667	G799	C738	G674	U605	G541	C477
G1442	G1318	G1186		G1186	C1120	G1057	U992	G928	C968	G800	C739	A675	G606	G542	A478
C1443	A1318	G1187		G1187	U1121	G1058	G993	G929	G969	U801	U740	A676	A607	U543	
U1444	C1320	A1250	A1250		U1122	C1059	A994		U870	A802	G741	U677	A608	G544	C483
U1445	U1321	A1251	A1251	G1190	U1123	C1060	G995	C932	U871	G803	G742	U678	A609	C545	G484
A1446	C1322	G1253	C1253	A1191		G1061	A996	G933	A872	A807	A743	C679	U610	A546	U485
A1447	G1386	A1254	A1254	C1192	U1126	U1062	U997	C934	A873	C808	C744	C680		A547	U486
C1448	G1387	G1255	G1255	G1193	G1127	C1063	C998	A935	G874	G809	G745	A681	C613	G548	A487
C1449	C1388	A1256	A1256	U1194	G1128	U1064	C999	C936	U875		A746	G682	C549	C549	C488
U1450	C1389	A1257	A1257	G1195	C1129	U1065	A1000	A937	C976	G811	A747	G683		G550	C489
U1451	U1391	C1327	G1258	A1196	A1130	U1066	C1001	A938	G877	C812	A748	U684	C617	U551	G490
C1452	G1392	C1328	C1259	A1197	G1131	A1067		G939	A878	G812	A749	G685	C618	U552	G491
G1453	U1393	A1329	G1260	G1198	C1132		A1004	C940	C979		C750	U686	U619	A553	C492
U1454	U1330	A1261	A1261	U1199	G1133	U1070	A1005	G941	C980	A815	C751	A687	C620	A554	A493
G1455	G1331	C1262	C1262	C1200	G1134	C1071	G1006	G942	G881	A816	G752	G688	A621	U555	C494
A1456	A1332	G1263	G1263	A1201	U1135	U1072	U1007	U943	C982	C817	A753	C689	A622	C556	A495
G1457	C1333	U1264	U1264	U1202	C1136	U1073	U1008	G944	C983	G818	A754	G690	C623	C557	A496
A1458	A1334	C1265	C1265	C1203	G1137	G1074	U1009	G945	U884	A819	G755	G691	C624	G558	G497
G1459	U1335			A1204	G1138	U1075	U1010	A946	G885	U820	C756	U692	U625	A559	A498
C1460	C1336	C1273	C1273	U1205	G1139	U1076	C1011	G947	G886	G821	U757	G693	G626	A560	A499
G1461	G1337	A1274	A1274	U1206	C1140	U1077	A1012	C948	G887	U822	C758	A694	G627	U561	G500
C1462	U1338	A1275	A1275	G1207	G1141	U1078	G1013	A949	G888	C823	A759	A695	C628	U562	C501
U1463	A1339	G1276	G1276	C1208	G1142	U1079	A1014	U950	A889	G824	G760	A696	A629	A563	A502
C1464	C1404	C1277	C1277	C1209	G1143	A1080	G1015	G951	G890	A825	G761	U697	C563	C564	C503
A1465	G1405	G1278	G1278	U1210	G1144	A1081	A1016	U952	U891	C826	U762	G698	C631	U565	C504
C1466	U1406	G1279	G1279	U1211	A1145	A1082		G953	A892	U827	G763	G699	U632	G566	G505
C1467	C1407	A1280	A1280	U1212	A1146	U1083	A1019	G954	C993	U828	C764		G633	G567	G506
A1468	A1408	C1281	C1281	A1213	C1147	G1084	G1020	U955	G994	G829	C765	G703	C634	G568	C507
C1469	C1409	U1282	U1282	G1214	U1148	U1085		U956	G995	G830	A766	A704	A635	G569	U508
U1470	A1410	U1283	U1283	G1215	C1149	U1086	U1023	U957	C996	A831	A767	G705	U636	G570	A509
U1471	C1411	C1284	C1284	A1216	A1150	G1087	G1024	A958	C997	G832	A768	A706	C637	U571	A510
U1472	A1412	U1285	U1285	C1217	A1151	G1088	U1025	A959	G998	G833	G769	U707	U638	A572	C511
C1473	C1413	A1286	A1286	C1218		G1089	G1026	U960	C999	U834	C770	C708		A573	U512
G1474	U1414	A1287	A1287	A1219	G1154	U1090	C1027	U961	A900	U835	G771	U709	A642	A574	C513
A1475	U1351			G1220	A1155	U1091	C1028	C962	A901	G836	U772	G710	C643	G575	C514
G1476	C1352	G1292	G1292	G1221	G1156	A1092	U1029	G963	G902	U837	G773	G711	U644	C576	G515
U1477	G1353	C1293	C1293	G1222	A1157	A1093	U1030	A964	G903	G838		A712	G645	G577	U516
A1478	A1418	G1294	G1294	C1223	C1158	G1094	C1031	U965	U904	C839	G776	G713	G646	C578	G517
C1479	G1419	U1295	U1295	C1224	U1159	U1095	G1032	G966	U905	C840	A777	G714	C647	A579	
A1480	G1356	C1296	C1296	A1225	G1160	C1096	G1033		A906	C841	G778	A715	A648	C580	A520
U1481	U1420	G1297	G1297	C1226	C1161	C1097	G1034	A969	A907	U842	C779	A716	A649	G581	G521
G1482	G1421	U1298	U1298	A1227	C1162	U1098	U1037	C970	A908	U843	C780	U717		C522	C522
A1483	G1423	C1299	C1299	C1228	A1163	G1099	C1038	G971	A909	G844	A781	A718		G584	A523
C1484	U1424	G1300	G1300	C1229	A1164	C1100	G1039	C972	C910	A845	A782	U657		G585	G524
U1485	U1425	U1301	U1301	C1230	U1165	A1101	G1039	G973	U911	G846	C783	G721	U658	C586	C525
G1486	G1426	C1302	C1302	G1231	G1166	A1102	U1040	A974	C912	G847	A784	G722	U659	G587	C526
A1487	U1364	C1303	C1303	U1232	A1167	C1103	G1041	A975	A913		G785	G723	C660	G588	G527
G1488	G1428	G1304	G1304	C1233	U1168	C1104	A1044	G976	A914	U854	G786	G724	G661		G528
G1489	C1366			C1234	A1169	C1107		A977	A915	U855	A787	G725	U662	G592	G529



• Molecule 53: 23S ribosomal RNA

Chain 27: 19% 68% 12%

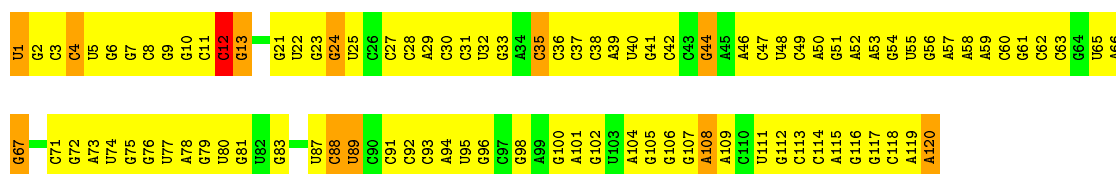


G1949	A1885	U1820	C1760	U1692	C1564	A1496	G1432	A1365	G1299	U1234	A1169	C1104	C1043	G978
G1950	G1888	A1821	C1761	U1693	C1565	U1497	A1433	A1366	G1300	G1235	C1170	U1105	C1044	A979
G1951	G1889	A1822	A1762	C1694	A1566	C1498	A1434	A1367	A1301	G1236	C1171	G1106	C1045	A980
A1952	A1890	G1823	G1763	G1695	G1567	C1499	G1435	G1368	A1302	G1237	C1172	G1107	C1046	A981
G1953	G1891	A1824	C1764	G1696	G1568	G1501	G1436	G1369	G1303	A1237	U1173	A1111	C1047	C982
G1954	A1892	G1825	U1765	G1697	A1569	A1502	A1437	G1370	G1306	G1238	U1174	G1112	A1048	A983
G1955	G1893	G1826	G1766	A1698	A1570	A1503	A1438	G1371	A1307	G1239	A1175	U1113	C1049	A984
G1956	C1894	A1827	C1767	G1699	A1571	A1504	A1439	U1372	G1308	U1240	U1176	U1114	A1050	C985
G1957	G1894	G1828	G1768	A1700	A1572	A1505	U1440	A1373	A1308	A1241	U1177	G1115	G1051	A988
G1958	C1895	A1829	U1769	G1701	G1573	A1506	G1441	G1374	A1309	U1242	C1178	C1114	C1052	G989
G1959	G1896	G1830	G1770	G1702	A1574	U1507	A1442	U1375	G1307	C1243	G1179	G1115	C1053	A990
A1960	G1897	G1831	C1771	G1703	C1575	A1508	U1443	G1376	U1312	A1244	U1180	U1119	A1054	A991
C1961	A1898	G1832	A1772	C1704	U1576	A1509	G1444	G1377	U1313		U1181	G1120	G1055	C992
C1962	A1899	G1833	A1773	A1705	C1577	A1509	G1445	A1378	C1314		U1182	C1121	G1056	G993
G1963	C1900					G1510	G1446	U1379		G1248	U1183	U1129	U1058	C994
G1964	A1901	C1837	U1774	G1706	U1578	G1511	C1447		C1315	U1249	U1184	C1122	A1057	G995
C1965	G1902	G1838	U1775	G1707	A1579	G1512	U1448	A1383	C1316	G1250	U1185	C1123	G1059	C996
A1966	G1903	A1839	G1776	C1708	A1580	U1513	G1449	A1384	G1317	G1251	G1186	G1124	U1060	A996
C1967	G1904	G1840	U1777	U1709	G1581	G1514	G1449	A1385	C1318	A1252	G1187	G1125	G1061	G997
C1968	C1905	U1841	U1778	G1710	C1582	G1514	G1450	A1386	C1319	A1253	U1188	A1126	G1062	C998
A1969	G1906	G1842	U1779	A1711	G1585	A1515	C1451	C1387	C1320	U1254	U1189	A1127	G1063	U999
U1970	G1907	G1843	U1780	U1712	C1586	G1516	G1452	A1388	A1321	G1255	U1190	G1128	G1064	G1003
G1971		C1844	U1781		G1587	C1517	A1453	G1389		G1256	G1191	A1129	U1065	U1004
G1972	G1911	G1845	U1782	G1715	U1588	G1518	C1454	G1390	U1326	C1257	G1192	U1130	U1066	C1005
G1973	A1912	A1846	A1783	U1716	G1589	G1519	G1455		A1327	U1258	G1193	G1131	A1067	C1006
C1974	A1913	G1847	A1784	A1717	A1590	U1520		U1394	A1328	A1260	G1194	U1132	G1068	C1007
G1975	A1914	C1848	U1785	G1718	A1591	G1521	C1461	A1395	U1329	C1261	G1195	A1133	G1069	A1008
U1976	G1915	G1849	A1786	U1719	C1592	A1522	C1462		C1330	A1262	C1196	A1134	A1070	A1009
A1977	G1916	A1850	A1787	G1720	A1593	U1523	C1463	C1398	G1331	G1263	G1197	G1136	G1071	G1010
U1978	U1917	G1851	G1788	G1721	A1594	A1524	G1464	C1399	G1332	A1264	G1198	G1137	G1072	G1011
U1979	A1918	U1852	A1789	A1722	C1595	G1526	U1466	U1400	G1334	A1265	U1199	G1138	G1073	U1012
A1980	A1919	G1853	C1790	A1723	A1596	G1527	U1467	G1401	C1335	G1266	C1200	G1139	G1074	C1013
G1981	U1920	C1854	A1791	C1728	U1597	U1528	U1468	U1402	A1336	C1267	U1201	C1140	G1075	U1014
U1982	G1921	G1857	G1792	U1729	A1598	G1529	A1469	A1403		A1268		A1142	A1076	U1015
G1983	C1922	C1858	C1793	C1730	U1599	G1530	A1470	C1404	U1340	C1270	A1204	A1143	U1078	U1018
G1984	U1923	A1859	A1794	G1731	A1600	A1531	G1471	U1405	G1341	G1271	A1205	A1144	A1080	U1019
C1985	C1924	G1860	C1795	C1732	G1601	A1532	C1472	U1406	A1342	A1272		C1145	U1081	A1020
C1986	C1925	G1861	U1796	G1733	U1602	C1533	C1473	G1407	G1343		G1208	C1146	U1082	A1021
A1987	U1926	G1862	U1797	U1736	A1603	U1534	U1474		G1344		G1209	C1147	U1083	G1022
G1988	A1927		G1737	G1737	C1604	A1535	G1475	U1411	C1345	C1278	G1210	U1148	U1084	U1023
G1989	C1928	A1866	U1738	G1738	C1605	C1536	U1476	U1412	C1346	G1279	G1211	G1149	A1085	G1024
U1991	G1930	G1867	A1739	A1739	G1606	G1537	A1477	A1413	A1347	G1280	A1213	C1150	A1086	G1025
G1992	U1931	C1868	G1740	G1740	C1607	U1542	G1478		C1348	G1281	A1214	A1151	A1087	G1026
U1993	A1932	A1869	C1741	C1741	A1608	G1543	C1479	G1416	C1349	U1282	G1215	C1152	A1088	A1027
C1994	G1933	G1870	U1742	G1743	A1609	U1544	U1481	C1417	C1350	G1283	G1216	C1153	A1089	A1028
U1995	C1934	A1871	G1743	G1743	A1610	A1548	G1482	G1418	C1351	G1284	U1217	G1154	A1090	A1029
C1996	G1935	G1872	A1744	A1744	C1611	A1549	A1483	A1419	U1352	A1285	G1218	A1155	G1091	C1030
C1997	A1936	A1873	U1745	A1745	G1612	C1550	U1484	A1420	A1353	A1286	U1219	A1156	G1092	G1031
A1998	A1937	G1874	G1746	U1747	A1614	A1551	U1485	G1421	A1354	A1287	G1220	G1157	G1093	A1032
G1999	C1938	C1875	U1747	C1748	C1615	A1552	U1486	G1422	G1355	G1288		C1158	U1094	U1033
C2000	U1939	A1876	G1752		A1616	A1553	U1487	G1423	G1356	C1289	G1223	U1159	A1095	G1036
C2001	U1940	G1684	C1753		C1617	G1555	C1488	G1424	C1357	C1290	U1224	G1160	A1096	G1037
C2002	G2002	C1685	G1753		A1618	C1489	G1489	G1425	G1358		G1225	C1161	U1097	A1039
A2003	U1943	G1686	A1754		G1619	U1556	A1490	G1426	A1359	U1294	A1226	G1162		G1040
G2004	U1944	G1687	U1755		G1620	U1559	G1491	A1427	G1360	C1295	G1228	A1165	C1100	U1101
A2005	G1945	U1688	G1756		U1621	G1560	G1492	C1428	G1361	G1296	G1229	G1166	C1101	G1041
C2006	U1946	A1689	U1757		G1622	C1561	G1493	G1429	C1362	C1297	A1230	C1167	C1102	U1102
U2007	G1947	U1690	A1758		G1623	U1562	A1494	G1430	C1363	C1297	U1231	G1168	A1103	G1042
C2008	G1948	G1691	A1759			U1563	A1495	A1431	G1364	C1298				

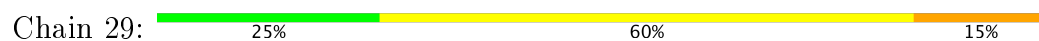
A2899	A2900	C2901	U2903	G2834	A2835	U2836	A2837	G2838	A2839	C2840	G2841	A2842	G2843	A2844	G2845	U2846	G2847	A2848	G2849	A2850	G2851	A2852	G2853	A2854	C2855	G2859	A2860	U2861	G2862	G2863	G2864	G2867	A2868	G2869	U2870	A2871	G2872	A2873	G2874	C2875	G2876	A2879	C2880	U2881	A2882	U2883	A2884	G2885	C2888	C2889	U2890	G2891	A2892	G2893	A2894	G2895	U2896	G2897	A2898			
C2771	C2772	C2773	C2774	G2708	G2709	C2710	A2711	C2712	G2713	C2714	C2715	C2716	C2717	G2718	C2719	U2720	A2721	C2722	C2723	U2724	A2725	C2726	A2727	U2728	C2729	C2730	C2731	G2732	A2733	A2734	G2735	A2736	C2737	A2738	U2739	C2805	C2806	U2807	G2808	A2809	A2810	G2811	G2812	A2813	A2814	C2815	U2816	U2817	U2818	G2819	A2820	A2821	G2822	A2823	C2824	C2827	G2828	A2829	G2830	G2831	U2832	U2833
G2641	G2642	G2643	G2644	G2645	G2646	U2647	G2648	G2649	U2650	C2651	A2654	G2655	U2656	G2659	A2661	A2662	G2663	A2665	G2671	U2672	G2673	A2674	A2675	G2676	G2677	C2678	A2679	U2680	G2681	A2682	C2683	U2684	G2685	U2686	G2687	G2688	U2689	U2690	C2691	G2692	G2693	G2694	U2695	U2696	G2697	U2698	A2700	A2701	G2702	C2703	C2704	A2705										
C2579	U2580	G2581	G2582	U2583	U2584	U2585	U2586	G2587	G2588	A2589	C2590	G2591	G2592	A2593	G2594	U2595	G2596	G2597	A2598	G2599	A2600	C2601	A2602	G2603	U2604	U2605	G2606	G2607	A2608	U2609	G2610	C2611	G2612	U2613	A2614	C2615	G2616	U2617	G2618	C2619	C2620		G2623	C2626	G2627	G2628	U2629	G2630	G2631	A2632	A2633	A2634	A2635	U2636	G2637	G2638	A2639	A2640				
G2452	A2453	G2454	U2455	C2456	U2457	G2458	A2459	U2460	G2461	A2462	C2463	U2464	C2465	C2466	A2467	A2468	A2469	G2470	A2471	A2472		C2475	A2476	U2477	A2478	U2479	C2480	A2481	A2482		G2485	A2486	G2487	U2488	A2489	G2490	U2491	U2492	G2493	G2494	A2495		C2498	C2499	U2500	G2501	G2502	A2503	U2504	G2505	U2506	C2507	A2508	G2509		C2512	A2513	U2514	A2515			
U2390	G2391	A2392	U2393	C2394	C2395	U2396	G2397	U2398	G2399	C2400	U2401	U2402	C2403	U2404	G2405	A2406	A2407	U2408	G2409	A2410	A2411	A2412	C2413	G2414	G2415	C2416	C2417	A2418	C2419	C2420	G2421	C2422	U2423	G2424	A2425	A2426	C2427	G2428	G2429	A2430	U2431	A2432		A2435	G2436	G2437	U2438	A2439	U2440	U2441	C2442	C2443	G2444		G2447	A2448	U2449	A2450	A2451			
U2329	G2330	G2331	C2332	A2333	U2334	A2335	G2336	U2337	C2338	C2339	U2340	C2341	C2342	U2343	U2344	C2345	A2346	C2347	U2348	C2349	C2350	C2351	A2352		G2355	U2356	C2357	A2358	C2359	G2360	G2361	C2362	U2363	G2364	G2365	A2366	G2367	C2368	A2369	G2370	U2371	U2372	U2373	C2374	G2375	A2376	U2377	A2378	G2379	C2380	A2381	U2382	C2383	U2384	C2385	A2386	U2387	G2388	G2389			
A2199	C2200	G2132	U2202	U2203	G2204		C2208	U2209	U2210	C2211	A2212	U2213	C2214	C2215	G2216	C2217	U2218	U2219	C2220	G2221	C2222	G2223	C2224	A2225	C2226	A2227	G2228	U2229	G2230	C2231	C2232	U2233	G2234	G2235		G2238	U2239	U2240	A2241	G2242	U2243	U2244	U2245	G2246	A2247	C2248	U2249	G2250	C2251	G2252	U2253	A2254	C2255	G2256	U2257	C2258	U2259	C2261				
U2132	G2133	A2134	U2135	G2136	U2137		G2144	C2145	C2146	A2147	G2148	U2149		G2152	C2153	U2154	A2155	G2156	G2157	A2158	C2159	C2160	C2161	G2162	A2163	C2164	G2165	U2166	U2167	C2168	A2169	A2170	U2171	U2172	A2173	C2174	C2175	U2176	C2177	C2178	C2179		U2182	A2183	A2184	U2185	G2186	U2187	U2188	U2189	G2190	A2191	U2192	G2193	U2194	U2195	U2196	U2197	A2198			
A2070	A2071	C2072	G2073	U2074	U2075		C2078	U2079	A2080	U2081	A2082	G2083	C2084	U2085	G2086	C2087	U2088	C2089	U2090	A2101	G2102	C2103	U2104	U2105	U2106		U2109	G2110	U2111	G2112	U2113	A2114	A2115	G2116	U2118	A2119	G2120	G2121	U2122	G2123	A2124	G2125	A2126	G2127	U2128	C2129	U2130	U2131														
A2009	G2010	U2011	G2012	A2013	G2014	A2015	U2016	U2017	G2018	A2019	A2020	C2021	U2022	C2023	G2024	C2025	U2026	G2027	U2028	G2029	A2030	A2031		U2034	G2035	C2036	A2037	G2038	U2039	G2040	U2041	A2042	C2043	G2044	C2045	G2046	C2047	G2048	C2049	G2050	A2051	A2052	G2053	A2054	C2055	G2056	G2057	A2058	A2059	U2060	G2061	A2062	C2063	G2064	C2065	G2066	G2067	U2068	G2069			

● Molecule 54: 5S ribosomal RNA

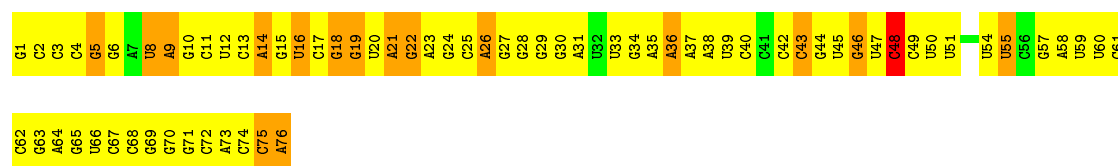
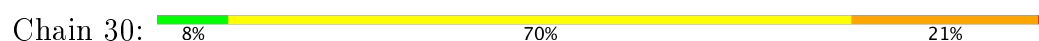
Chain 28:  20% 70% 90%



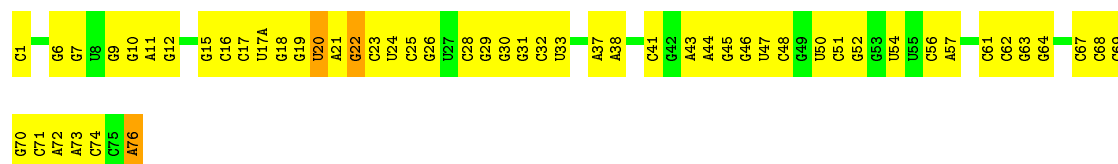
- Molecule 55: mRNA



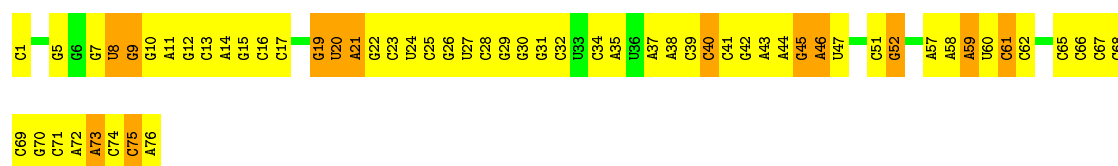
- Molecule 56: A-site tRNA^{Phe}



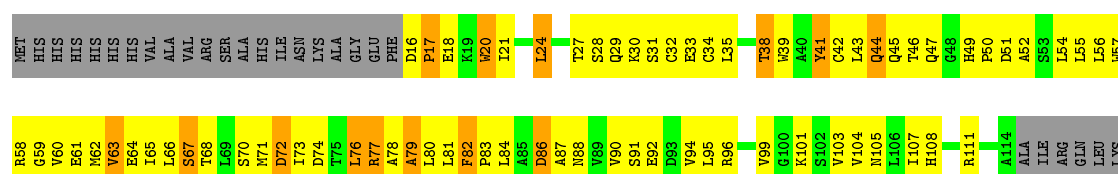
- Molecule 57: P-site tRNA^{Met}



- Molecule 58: E-site tRNA^{Met}



- Molecule 59: GTP pyrophosphokinase



G723	R724	W725	L726	G727	K728	L729	W730	Q731	V732	P733	D734	W735	I736	D737	A738	R739	R740	L741	H742	GLY	SER																																																																																																
SER	ALA	G664	Y665	S666	L605	L606	H607	H608	L609	A610	R611	G612	C613	D614	P615	L616	P617	G618	D619	E620	I621	Y634	I681	D682	I683	T684	T685	I686	L687	A688	N689	E690	K691	V694	L695	G696	V697	A698	S699	R700	S701	D702	T703	K704	Q705	Q706	L707	A708	T709	I710	D711	K712	T713	I714	E715	I716	Y717	N718	L719	Q720	V721	L722																																																							
E600	G601	N604	L605	L606	H607	H608	L609	A610	R611	G612	C613	D614	P615	L616	P617	G618	D619	E620	I621	Y634	I681	D682	I683	T684	T685	I686	L687	A688	N689	E690	K691	V694	L695	G696	V697	A698	S699	R700	S701	D702	T703	K704	Q705	Q706	L707	A708	T709	I710	D711	K712	T713	I714	E715	I716	Y717	N718	L719	Q720	V721	L722																																																									
K491	A494	W495	F496	R497	R501	D514	I521	S522	E527	L531	P532	R533	D540	A544	I551	N554	N565	K566	A569	Q572	D573	A576	L577	L580	Q581	GLN	LYS	SER	Y585	T586	P587	R590	R596	V597	V598	V599	V600	G601	N604	L605	L606	H607	H608	L609	A610	R611	G612	C613	D614	P615	L616	P617	G618	D619	E620	I621	Y634	I681	D682	I683	T684	T685	I686	L687	A688	N689	E690	K691	V694	L695	G696	V697	A698	S699	R700	S701	D702	T703	K704	Q705	Q706	L707	A708	T709	I710	D711	K712	T713	I714	E715	I716	Y717	N718	L719	Q720	V721	L722																				
P419	A420	G421	S422	T423	P424	F427	A428	Y429	H430	I431	H432	S433	D434	V435	G436	H437	R438	Q439	A442	K443	T444	G445	G446	R447	T448	F451	T452	Y453	G458	D459	Q460	T461	E462	I463	T464	Q466	Q467	Q468	P469	M470	S471	S472	R473	M477	P478	M479	Y482	Y483	T484	T485	R486	V487	P491	D494	R405	V406	Y407	V408	F409	T410	P411	D417	L418																																																						
E335	I336	Q337	I338	T339	T340	K341	Q342	M343	V351	ALA	ALA	HIS	TRP	LYS	TYR	LYS	GLU	G360	S368	E371	I374	A382	TRP	GLN	GLU	GLU	MET	ALA	ASP	SER	GLY	GLU	MET	E306	F307	D308	D309	Y310	K315	P316	V319	I322	V325	V326	L327	G328	P329	K332	T333	V334	E335	I336	Q337	I338	T339	T340	K341	Q342	M343	V351	ALA	ALA	HIS	TRP	LYS	TYR	LYS	GLU	G360	S368	E371	I374	A382	TRP	GLN	GLU	GLU	MET	ALA	ASP	SER	GLY	GLU	MET	E306	F307	D308	D309	Y310	K315	P316	V319	I322	V325	V326	L327	G328	P329	K332	T333	V334																
L194	K195	W196	L197	L198	E199	D200	F201	C202	GLU	Q131	V132	D133	H134	V135	R136	Y137	M138	I214	A215	L218	H219	F146	R147	C148	V149	I150	I151	K152	L153	H227	Y228	I229	E230	E231	F232	V233	G234	H235	L236	R237	A238	E239	M240	K241	A242	E243	G244	V245	K246	A247	E248	V249	Y250	G251	R252	I259	W260	M263	L194	K195	W196	L197	L198	E199	D200	F201	C202	GLU	Q131	V132	D133	H134	V135	R136	Y137	M138	I214	A215	L218	H219	F146	R147	C148	V149	I150	I151	K152	L153	H227	Y228	I229	E230	E231	F232	V233	G234	H235	L236	R237	A238	E239	M240	K241	A242	E243	G244	V245	K246	A247	E248	V249	Y250	G251	R252	I259	W260	M263
ALA	THR	HIS	THR	ASP	SER	VAL	SER	SER	GLU	Q131	V132	D133	H134	V135	R136	Y137	M138	I214	A215	L218	H219	F146	R147	C148	V149	I150	I151	K152	L153	H227	Y228	I229	E230	E231	F232	V233	G234	H235	L236	R237	A238	E239	M240	K241	A242	E243	G244	V245	K246	A247	E248	V249	Y250	G251	R252	I259	W260	M263	ALA	THR	HIS	THR	ASP	SER	VAL	SER	SER	GLU	Q131	V132	D133	H134	V135	R136	Y137	M138	I214	A215	L218	H219	F146	R147	C148	V149	I150	I151	K152	L153	H227	Y228	I229	E230	E231	F232	V233	G234	H235	L236	R237	A238	E239	M240	K241	A242	E243	G244	V245	K246	A247	E248	V249	Y250	G251	R252	I259	W260	M263

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	46935	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	0.34	0/2121	0.71	0/2852
10	J	0.32	0/947	0.68	0/1268
11	K	0.34	0/1054	0.71	1/1403 (0.1%)
12	L	0.36	0/1093	0.64	0/1460
13	M	0.35	0/973	0.65	1/1301 (0.1%)
14	N	0.33	0/902	0.63	0/1209
15	O	0.35	0/929	0.67	0/1242
16	P	0.38	0/960	0.60	0/1278
17	Q	0.36	0/829	0.79	1/1107 (0.1%)
18	R	0.32	0/864	0.67	0/1156
19	S	0.34	0/744	0.76	0/994
2	B	0.37	0/1586	0.70	0/2134
20	T	0.35	0/787	0.68	0/1051
21	U	0.35	0/766	0.66	1/1025 (0.1%)
22	V	0.39	0/582	0.68	0/769
23	W	0.34	0/635	0.65	0/848
24	X	0.32	0/510	0.62	0/677
25	Y	0.33	0/453	0.68	0/605
26	Z	0.40	0/531	0.76	0/709
27	1	0.31	0/450	0.71	0/599
28	2	0.38	0/416	0.68	0/554
29	3	0.39	0/380	0.67	0/498
3	C	0.39	0/1571	0.70	0/2113
30	4	0.35	0/513	0.62	0/676
31	5	0.33	0/303	0.74	0/397
32	6	0.40	0/1735	0.67	1/2338 (0.0%)
33	7	0.35	0/1651	0.64	0/2225
34	8	0.33	0/1665	0.68	2/2227 (0.1%)
35	9	0.33	0/1169	0.67	0/1573
36	10	0.35	0/835	0.75	1/1128 (0.1%)
37	11	0.32	0/1195	0.62	0/1602
38	12	0.35	0/989	0.70	0/1326
39	13	0.35	0/1034	0.71	0/1375
4	D	0.35	0/1434	0.62	0/1926

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	14	0.35	0/796	0.71	1/1077 (0.1%)
41	15	0.36	0/885	0.73	1/1195 (0.1%)
42	16	0.36	0/969	0.76	1/1300 (0.1%)
43	17	0.31	0/892	0.70	0/1193
44	18	0.46	0/817	0.61	0/1088
45	19	0.32	0/722	0.58	0/964
46	20	0.37	0/659	0.71	0/884
47	21	0.35	0/657	0.72	0/881
48	22	0.38	0/544	0.62	0/731
49	23	0.36	0/652	0.72	0/877
5	E	0.32	0/1343	0.65	0/1816
50	24	0.33	0/671	0.55	0/888
51	25	0.41	0/550	0.73	1/728 (0.1%)
52	26	0.51	1/36967 (0.0%)	0.72	4/57666 (0.0%)
53	27	0.54	3/69801 (0.0%)	0.72	7/108894 (0.0%)
54	28	0.41	1/2876 (0.0%)	0.71	1/4483 (0.0%)
55	29	0.97	0/486	0.74	0/757
56	30	0.65	1/1813 (0.1%)	0.77	0/2823
57	31	0.44	1/1836 (0.1%)	0.70	0/2859
58	32	0.89	2/1835 (0.1%)	0.77	1/2857 (0.0%)
59	33	0.65	6/4985 (0.1%)	1.09	37/6770 (0.5%)
6	F	0.40	0/1122	0.66	0/1515
7	G	0.45	0/1001	0.79	3/1350 (0.2%)
8	H	0.42	0/1046	0.79	1/1410 (0.1%)
9	I	0.33	0/1152	0.64	0/1551
All	All	0.50	15/167683 (0.0%)	0.72	66/250202 (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	13
53	27	0	34
56	30	0	1
59	33	0	3
All	All	0	51

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	33	156	ARG	CZ-NH2	-10.66	1.19	1.33
59	33	152	LYS	CD-CE	-7.76	1.31	1.51
53	27	1379	U	O3'-P	-7.76	1.51	1.61
59	33	17	PRO	CA-CB	-7.25	1.39	1.53
52	26	2	A	OP3-P	-7.00	1.52	1.61

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	33	156	ARG	NE-CZ-NH1	19.76	130.18	120.30
59	33	156	ARG	NH1-CZ-NH2	-13.83	104.19	119.40
59	33	17	PRO	N-CA-CB	-11.16	89.90	103.30
59	33	17	PRO	CA-CB-CG	10.28	124.33	104.80
59	33	63	VAL	CG1-CB-CG2	-9.25	96.11	110.90

There are no chirality outliers.

5 of 51 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	26	130	A	Sidechain
52	26	159	G	Sidechain
52	26	266	G	Sidechain
52	26	820	U	Sidechain
52	26	88	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	A	2082	0	2157	183	0
2	B	1565	0	1616	121	0
3	C	1552	0	1619	137	0
4	D	1410	0	1447	150	0
5	E	1323	0	1374	88	0
6	F	1111	0	1148	83	0
7	G	988	0	1025	124	0
8	H	1032	0	1088	136	0
9	I	1129	0	1162	89	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	938	0	1012	90	0
11	K	1045	0	1117	89	0
12	L	1074	0	1157	70	0
13	M	960	0	1000	75	0
14	N	892	0	923	73	0
15	O	917	0	965	78	0
16	P	947	0	1022	94	0
17	Q	816	0	839	90	0
18	R	857	0	922	52	0
19	S	738	0	807	55	0
20	T	779	0	834	79	0
21	U	753	0	780	71	0
22	V	575	0	592	29	0
23	W	625	0	655	45	0
24	X	509	0	543	60	0
25	Y	449	0	491	41	0
26	Z	522	0	521	52	0
27	1	444	0	461	52	0
28	2	409	0	440	20	0
29	3	377	0	418	33	0
30	4	504	0	574	33	0
31	5	302	0	343	30	0
32	6	1704	0	1732	124	0
33	7	1624	0	1699	111	0
34	8	1643	0	1710	168	0
35	9	1156	0	1199	110	0
36	10	817	0	808	98	0
37	11	1181	0	1240	97	0
38	12	979	0	1034	84	0
39	13	1022	0	1070	130	0
40	14	786	0	828	92	0
41	15	869	0	878	89	0
42	16	955	0	1019	118	0
43	17	883	0	944	97	0
44	18	805	0	847	95	0
45	19	714	0	737	54	0
46	20	649	0	666	87	0
47	21	648	0	691	52	0
48	22	535	0	552	54	0
49	23	637	0	665	71	0
50	24	665	0	714	67	0
51	25	544	0	579	80	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	26	33016	0	16617	1573	0
53	27	62322	0	31345	2882	0
54	28	2572	0	1302	116	0
55	29	432	0	218	14	0
56	30	1623	0	821	75	0
57	31	1644	0	836	46	0
58	32	1643	0	836	66	0
59	33	4911	0	4550	655	0
All	All	154603	0	105189	8829	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 34.

The worst 5 of 8829 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)
53:27:45:G:H5''	53:27:46:G:H5'	1.22	1.18
59:33:17:PRO:HB3	59:33:39:TRP:NE1	1.57	1.17
7:G:55:VAL:HA	53:27:1084:A:H5'	1.26	1.15
53:27:1702:G:H2'	53:27:1703:G:H5''	1.15	1.14
59:33:24:LEU:HD21	59:33:70:SER:HA	1.19	1.12

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%)	218 (81%)	41 (15%)	10 (4%)	4	35
2	B	207/209 (99%)	172 (83%)	28 (14%)	7 (3%)	4	37
3	C	199/201 (99%)	147 (74%)	32 (16%)	20 (10%)	1	12

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	175/179 (98%)	143 (82%)	27 (15%)	5 (3%)	5	40
5	E	174/177 (98%)	149 (86%)	20 (12%)	5 (3%)	5	40
6	F	147/149 (99%)	108 (74%)	20 (14%)	19 (13%)	0	6
7	G	129/165 (78%)	93 (72%)	25 (19%)	11 (8%)	1	16
8	H	139/142 (98%)	104 (75%)	25 (18%)	10 (7%)	1	20
9	I	140/142 (99%)	120 (86%)	14 (10%)	6 (4%)	3	31
10	J	120/123 (98%)	97 (81%)	16 (13%)	7 (6%)	2	25
11	K	141/144 (98%)	110 (78%)	20 (14%)	11 (8%)	1	18
12	L	134/136 (98%)	113 (84%)	15 (11%)	6 (4%)	3	30
13	M	118/127 (93%)	91 (77%)	22 (19%)	5 (4%)	3	32
14	N	114/117 (97%)	98 (86%)	15 (13%)	1 (1%)	20	62
15	O	112/115 (97%)	93 (83%)	15 (13%)	4 (4%)	4	36
16	P	115/118 (98%)	103 (90%)	7 (6%)	5 (4%)	3	31
17	Q	101/103 (98%)	77 (76%)	16 (16%)	8 (8%)	1	18
18	R	108/110 (98%)	87 (81%)	15 (14%)	6 (6%)	2	26
19	S	91/100 (91%)	71 (78%)	16 (18%)	4 (4%)	3	31
20	T	100/104 (96%)	79 (79%)	14 (14%)	7 (7%)	1	20
21	U	92/94 (98%)	76 (83%)	11 (12%)	5 (5%)	2	27
22	V	73/85 (86%)	65 (89%)	7 (10%)	1 (1%)	13	54
23	W	75/78 (96%)	67 (89%)	6 (8%)	2 (3%)	6	42
24	X	61/63 (97%)	49 (80%)	7 (12%)	5 (8%)	1	17
25	Y	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
26	Z	64/70 (91%)	47 (73%)	7 (11%)	10 (16%)	0	4
27	1	54/57 (95%)	43 (80%)	6 (11%)	5 (9%)	1	15
28	2	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
29	3	44/46 (96%)	32 (73%)	11 (25%)	1 (2%)	7	45
30	4	62/65 (95%)	51 (82%)	8 (13%)	3 (5%)	2	29
31	5	36/38 (95%)	26 (72%)	5 (14%)	5 (14%)	0	5
32	6	216/241 (90%)	170 (79%)	32 (15%)	14 (6%)	1	23
33	7	204/233 (88%)	175 (86%)	22 (11%)	7 (3%)	4	37
34	8	203/206 (98%)	157 (77%)	30 (15%)	16 (8%)	1	18

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	9	155/167 (93%)	109 (70%)	33 (21%)	13 (8%)	1	16
36	10	98/135 (73%)	77 (79%)	14 (14%)	7 (7%)	1	20
37	11	149/179 (83%)	123 (83%)	14 (9%)	12 (8%)	1	17
38	12	127/130 (98%)	110 (87%)	8 (6%)	9 (7%)	1	20
39	13	125/130 (96%)	93 (74%)	19 (15%)	13 (10%)	0	11
40	14	96/103 (93%)	76 (79%)	15 (16%)	5 (5%)	2	27
41	15	114/129 (88%)	90 (79%)	13 (11%)	11 (10%)	1	13
42	16	121/124 (98%)	95 (78%)	13 (11%)	13 (11%)	0	10
43	17	112/118 (95%)	88 (79%)	14 (12%)	10 (9%)	1	15
44	18	98/101 (97%)	72 (74%)	21 (21%)	5 (5%)	2	28
45	19	86/89 (97%)	70 (81%)	11 (13%)	5 (6%)	2	25
46	20	80/82 (98%)	59 (74%)	18 (22%)	3 (4%)	4	34
47	21	78/84 (93%)	54 (69%)	19 (24%)	5 (6%)	1	23
48	22	63/75 (84%)	50 (79%)	5 (8%)	8 (13%)	0	7
49	23	77/92 (84%)	64 (83%)	11 (14%)	2 (3%)	6	42
50	24	83/87 (95%)	75 (90%)	6 (7%)	2 (2%)	7	44
51	25	63/71 (89%)	40 (64%)	19 (30%)	4 (6%)	1	24
59	33	663/750 (88%)	557 (84%)	60 (9%)	46 (7%)	1	21
All	All	6509/6970 (93%)	5226 (80%)	879 (14%)	404 (6%)	3	24

5 of 404 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	86	GLU
2	B	102	ALA
3	C	6	LYS
3	C	11	ALA
3	C	57	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	A	216/218 (99%)	215 (100%)	1 (0%)	91	96
2	B	164/164 (100%)	164 (100%)	0	100	100
3	C	165/165 (100%)	165 (100%)	0	100	100
4	D	148/150 (99%)	146 (99%)	2 (1%)	71	87
5	E	137/138 (99%)	137 (100%)	0	100	100
6	F	114/114 (100%)	114 (100%)	0	100	100
7	G	100/123 (81%)	100 (100%)	0	100	100
8	H	109/110 (99%)	107 (98%)	2 (2%)	64	85
9	I	116/116 (100%)	116 (100%)	0	100	100
10	J	103/104 (99%)	102 (99%)	1 (1%)	80	90
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%)	86 (100%)	0	100	100
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%)	83 (99%)	1 (1%)	75	88
18	R	93/93 (100%)	93 (100%)	0	100	100
19	S	80/84 (95%)	80 (100%)	0	100	100
20	T	83/85 (98%)	82 (99%)	1 (1%)	75	88
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%)	50 (98%)	1 (2%)	60	83
31	5	34/34 (100%)	34 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	6	180/199 (90%)	178 (99%)	2 (1%)	78	89
33	7	170/190 (90%)	169 (99%)	1 (1%)	89	95
34	8	172/173 (99%)	172 (100%)	0	100	100
35	9	119/126 (94%)	117 (98%)	2 (2%)	66	86
36	10	87/116 (75%)	85 (98%)	2 (2%)	56	80
37	11	124/147 (84%)	123 (99%)	1 (1%)	85	92
38	12	104/105 (99%)	103 (99%)	1 (1%)	80	90
39	13	105/107 (98%)	104 (99%)	1 (1%)	80	90
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%)	92 (100%)	0	100	100
44	18	83/84 (99%)	80 (96%)	3 (4%)	40	72
45	19	76/77 (99%)	75 (99%)	1 (1%)	73	88
46	20	65/65 (100%)	65 (100%)	0	100	100
47	21	74/78 (95%)	73 (99%)	1 (1%)	71	87
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%)	54 (98%)	1 (2%)	64	85
59	33	452/635 (71%)	449 (99%)	3 (1%)	87	94
All	All	5303/5698 (93%)	5272 (99%)	31 (1%)	89	95

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	9	80	LEU
36	10	47	LEU
59	33	267	ASN
35	9	87	VAL
37	11	61	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
21	U	24	ASN
32	6	177	ASN
51	25	63	ASN
22	V	8	ASN
29	3	29	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	26	1538/1539 (99%)	205 (13%)	9 (0%)
53	27	2902/2903 (99%)	447 (15%)	24 (0%)
54	28	119/120 (99%)	14 (11%)	1 (0%)
55	29	19/20 (95%)	5 (26%)	1 (5%)
56	30	75/76 (98%)	19 (25%)	0
57	31	76/77 (98%)	8 (10%)	0
58	32	76/77 (98%)	19 (25%)	1 (1%)
All	All	4805/4812 (99%)	717 (14%)	36 (0%)

5 of 717 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	26	4	U
52	26	6	G
52	26	9	G
52	26	19	A
52	26	22	G

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	27	859	G
53	27	1801	A
54	28	88	C
53	27	1130	U
53	27	1818	U

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.