



wwPDB EM Map/Model Validation Report ⓘ

Sep 20, 2016 – 06:46 PM EDT

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 : 2016-07-05
Resolution : 4.10 Å(reported)

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

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027939

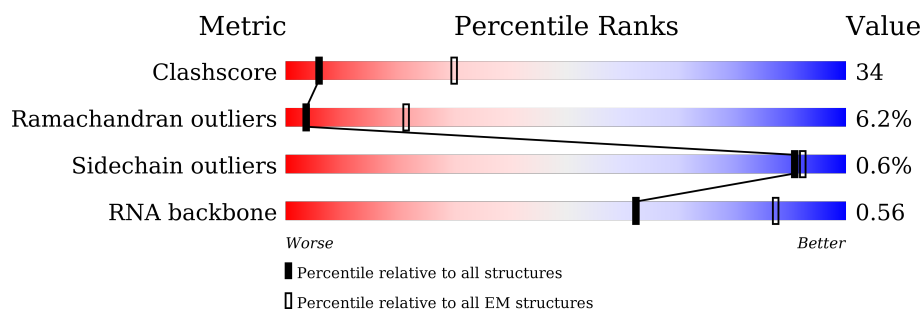
1 Overall quality at a glance

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.







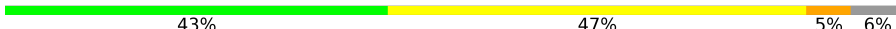
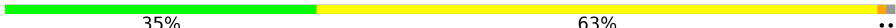
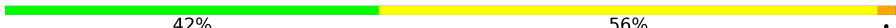


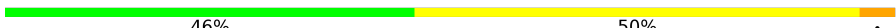
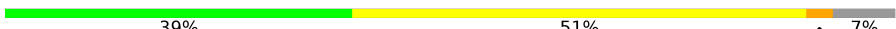
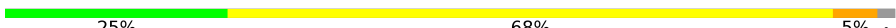




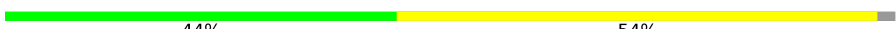
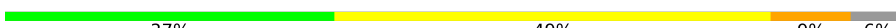

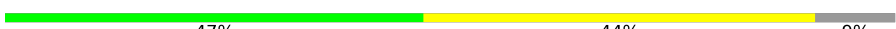
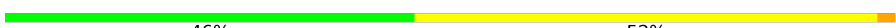

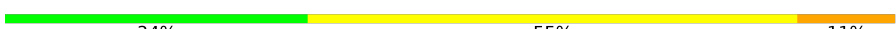


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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

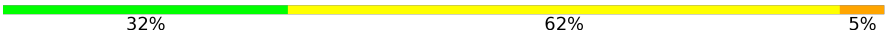

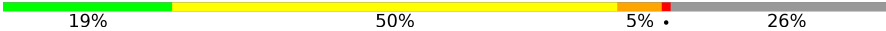








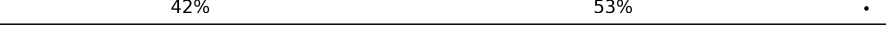


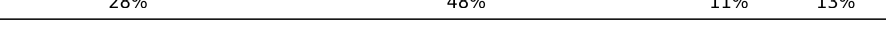




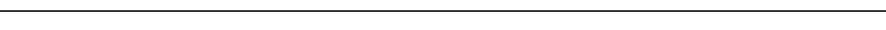

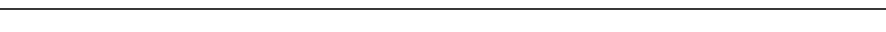
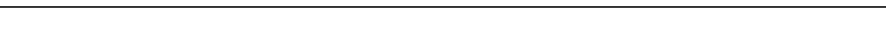


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Mol	Chain	Length	Quality of chain
9	I	142	
10	J	123	
11	K	144	
12	L	136	
13	M	127	
14	N	117	
15	O	115	
16	P	118	
17	Q	103	
18	R	110	
19	S	100	
20	T	104	
21	U	94	
22	V	85	
23	W	78	
24	X	63	
25	Y	59	
26	Z	70	
27	1	57	
28	2	55	
29	3	46	
30	4	65	
31	5	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	<div><div></div><div>35%</div><div>48%</div><div>6%</div><div>10%</div></div>

2 Entry composition

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		

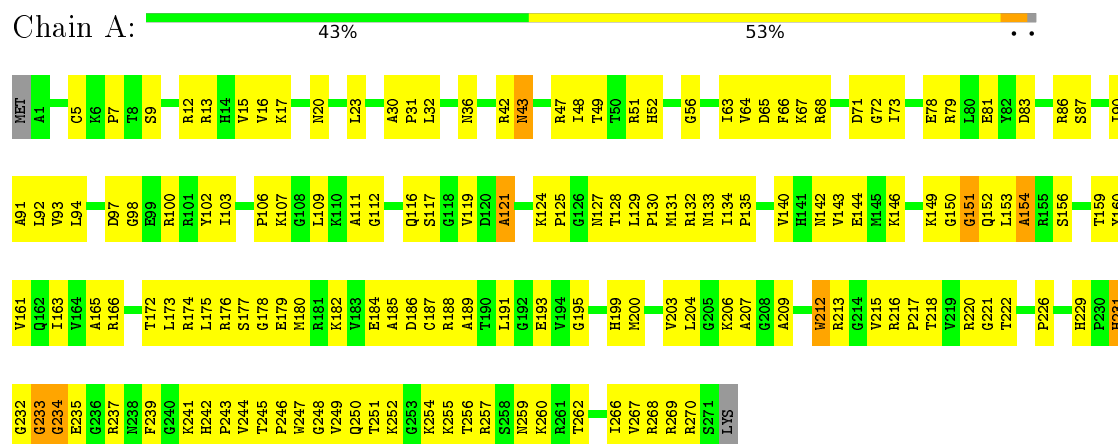
There are 7 discrepancies between the modelled and reference sequences:

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

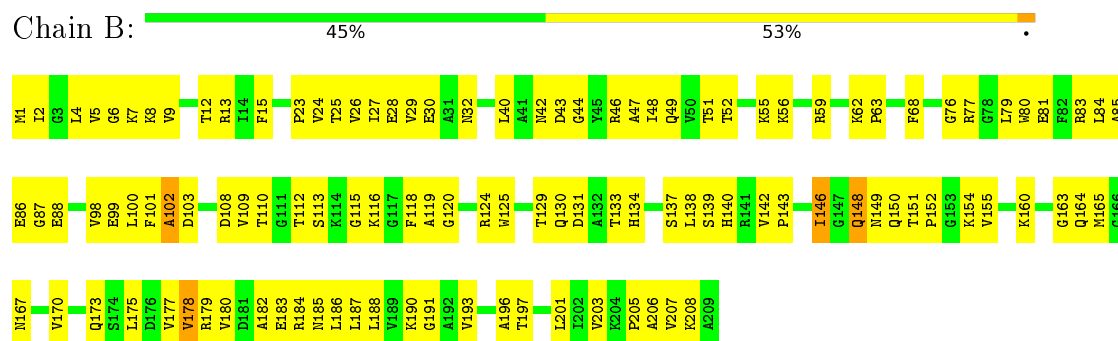
3 Residue-property plots

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

- Molecule 1: 50S ribosomal protein L2



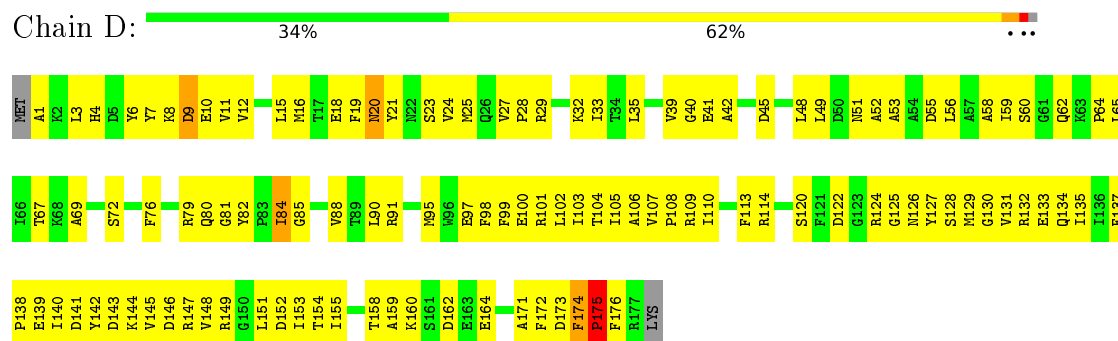
- Molecule 2: 50S ribosomal protein L3



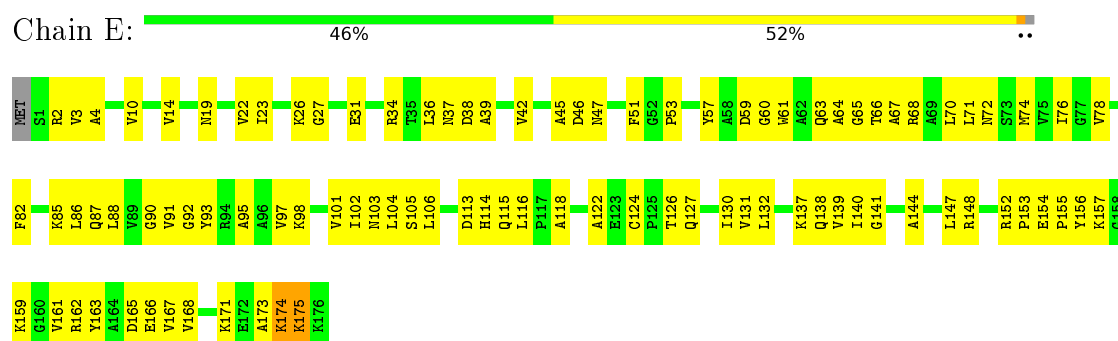
- Molecule 3: 50S ribosomal protein L4



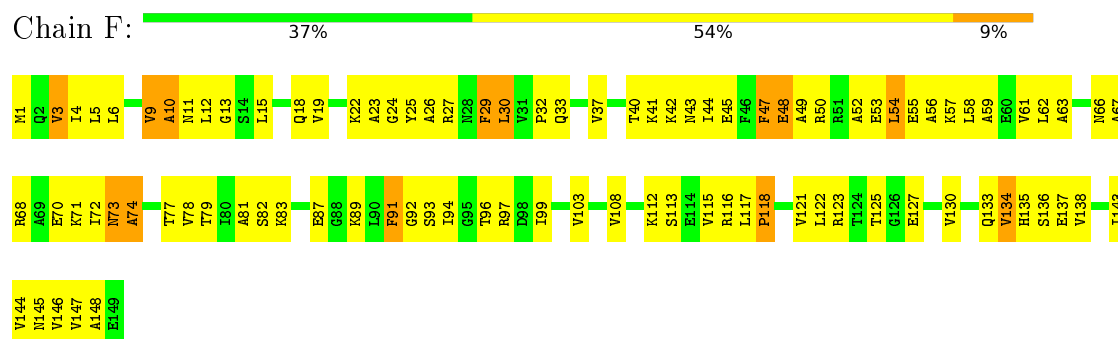
- Molecule 4: 50S ribosomal protein L5



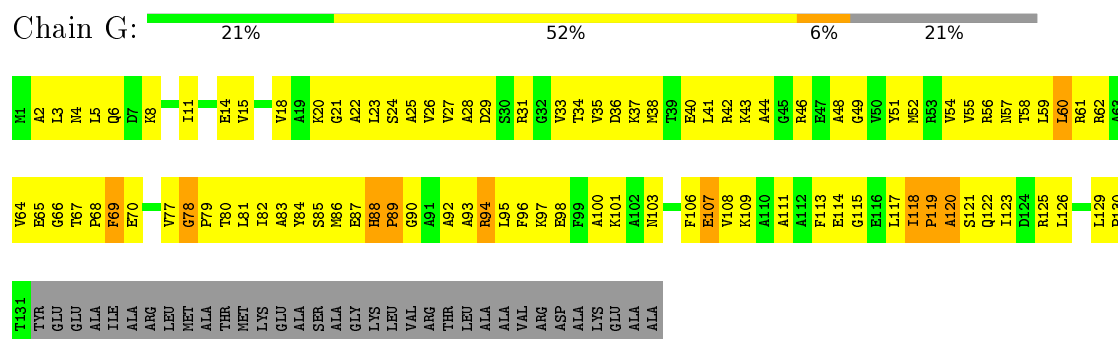
- Molecule 5: 50S ribosomal protein L6



- Molecule 6: 50S ribosomal protein L9

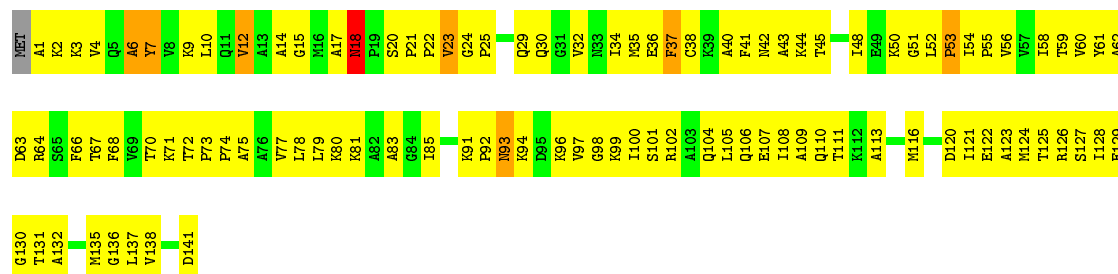


- Molecule 7: 50S ribosomal protein L10



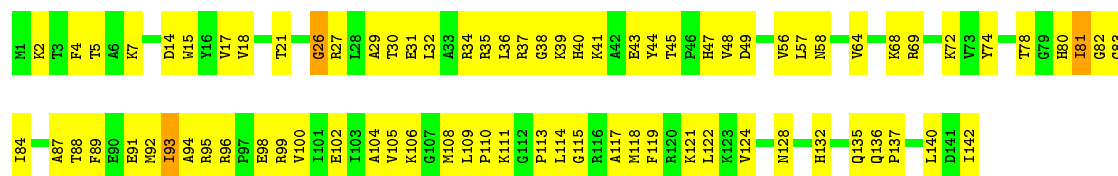
- Molecule 8: 50S ribosomal protein L11

Chain H:  27% 67% 5% ..



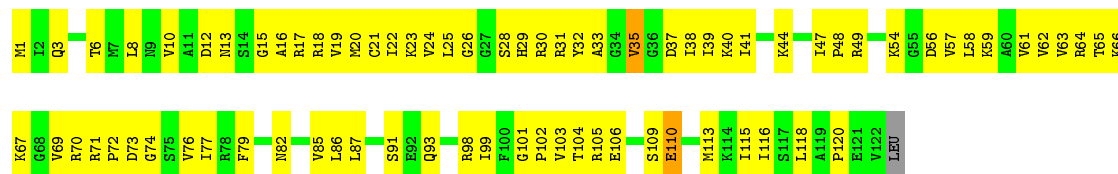
- Molecule 9: 50S ribosomal protein L13

Chain I:  44% 54% .



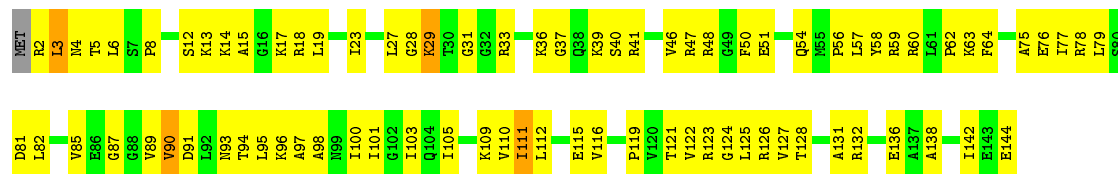
- Molecule 10: 50S ribosomal protein L14

Chain J:  37% 61% ..



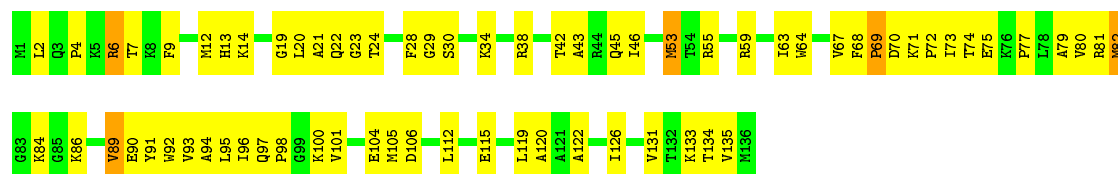
- Molecule 11: 50S ribosomal protein L15

Chain K:  43% 53% ..

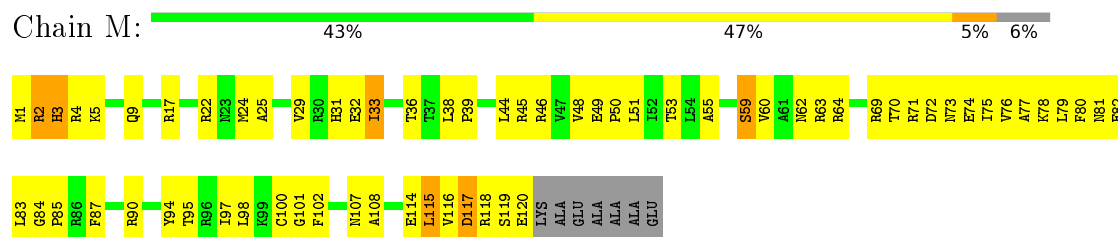


- Molecule 12: 50S ribosomal protein L16

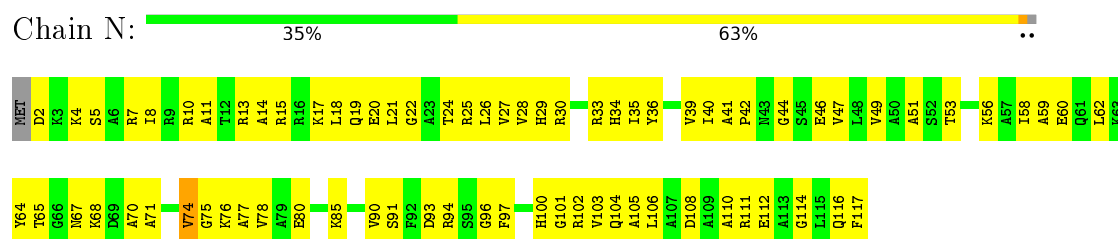
Chain L:  49% 47% .



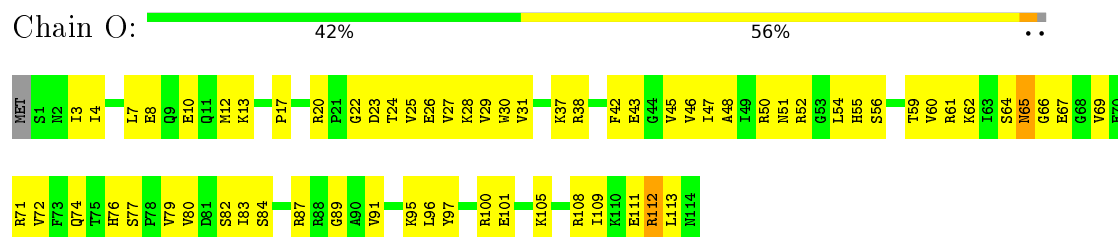
- Molecule 13: 50S ribosomal protein L17



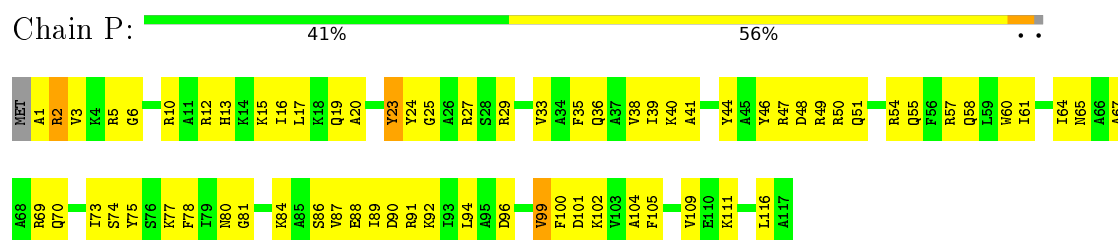
- Molecule 14: 50S ribosomal protein L18



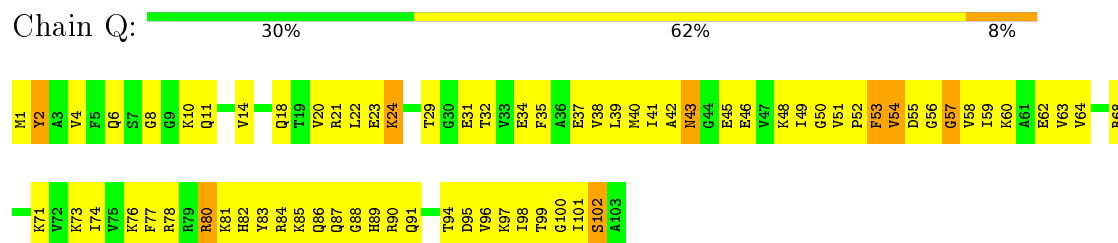
- Molecule 15: 50S ribosomal protein L19



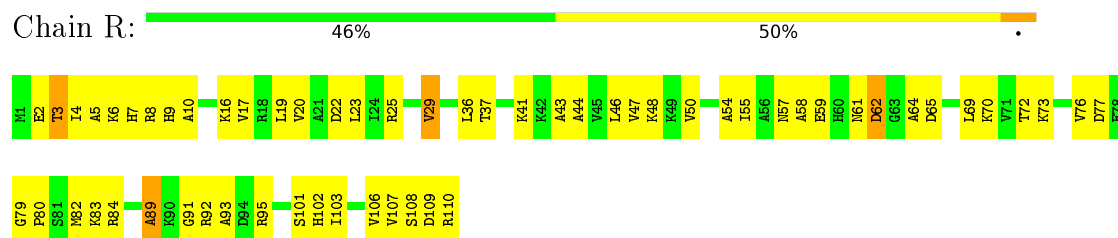
- Molecule 16: 50S ribosomal protein L20



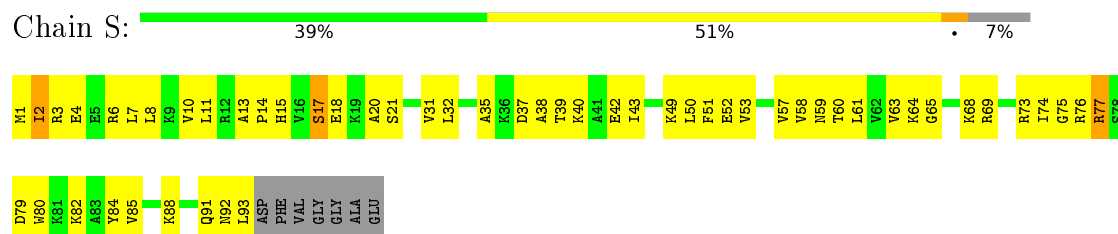
- Molecule 17: 50S ribosomal protein L21



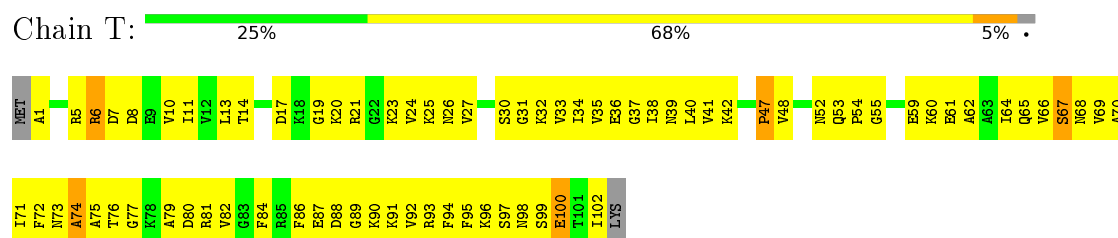
- Molecule 18: 50S ribosomal protein L22



• Molecule 19: 50S ribosomal protein L23



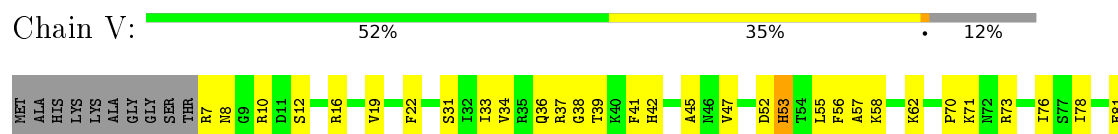
• Molecule 20: 50S ribosomal protein L24



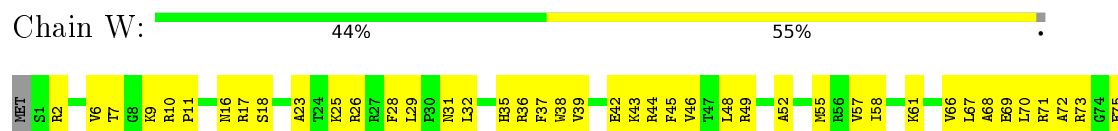
• Molecule 21: 50S ribosomal protein L25



• 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% .



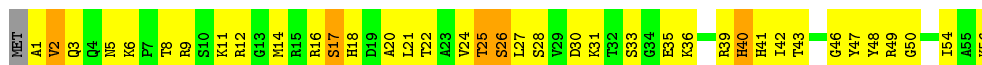
- Molecule 26: 50S ribosomal protein L31

Chain Z: 37% 49% 9% 6%



- Molecule 27: 50S ribosomal protein L32

Chain 1: 32% 58% 9% .



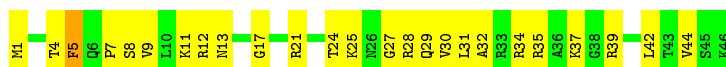
- Molecule 28: 50S ribosomal protein L33

Chain 2: 47% 44% 9%



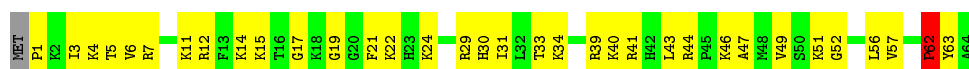
- Molecule 29: 50S ribosomal protein L34

Chain 3: 46% 52% .



- Molecule 30: 50S ribosomal protein L35

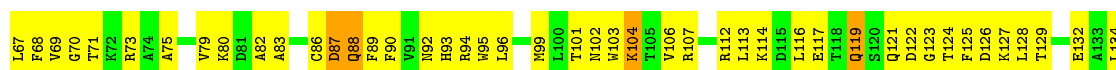
Chain 4: 46% 51% . .



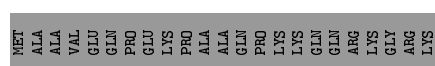
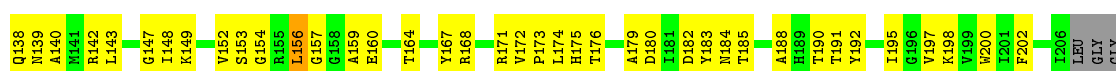
- Molecule 31: 50S ribosomal protein L36



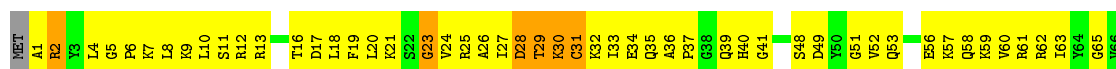
- Molecule 32: 30S ribosomal protein S2

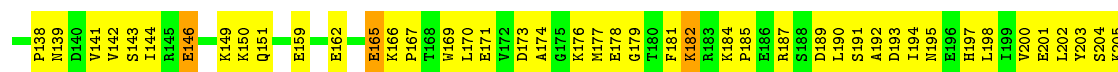


- Molecule 33: 30S ribosomal protein S3



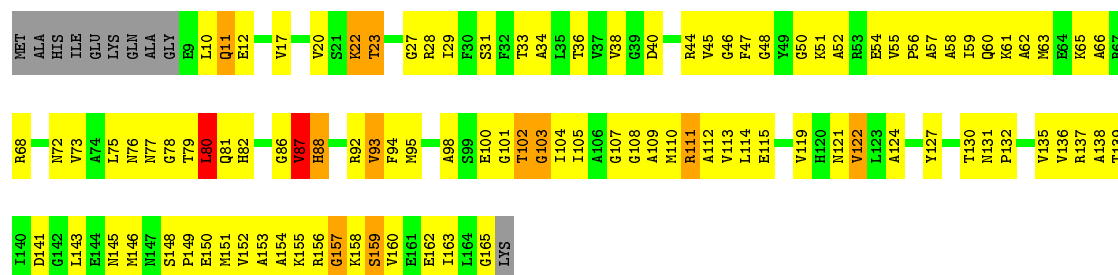
- Molecule 34: 30S ribosomal protein S4





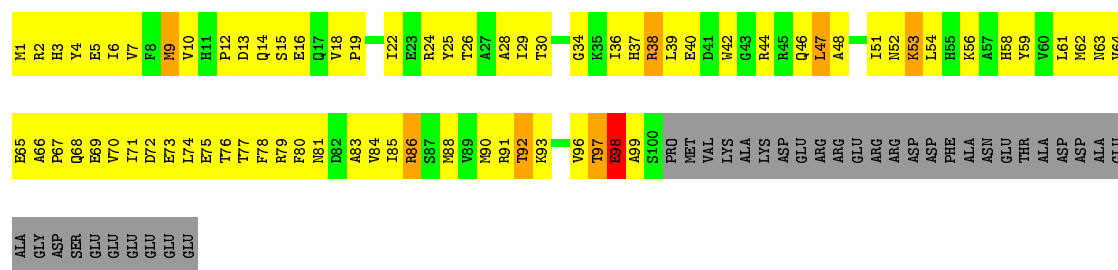
• Molecule 35: 30S ribosomal protein S5

Chain 9: 32% 54% 7% 6%



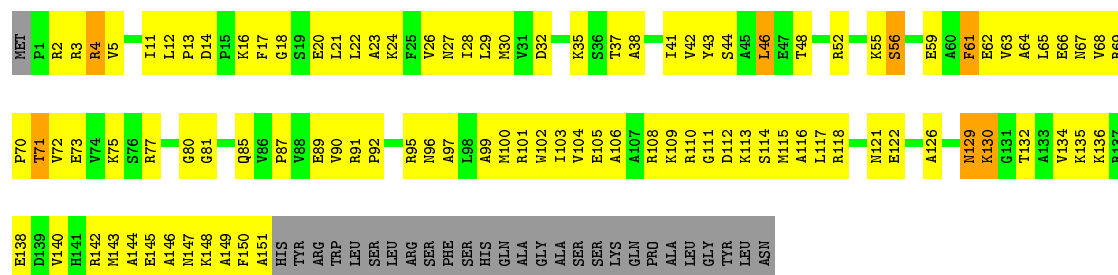
• Molecule 36: 30S ribosomal protein S6

Chain 10: 19% 50% 5% 26%



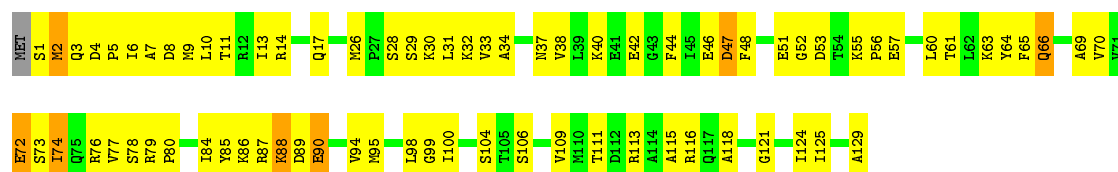
• Molecule 37: 30S ribosomal protein S7

Chain 11: 28% 53% 16%

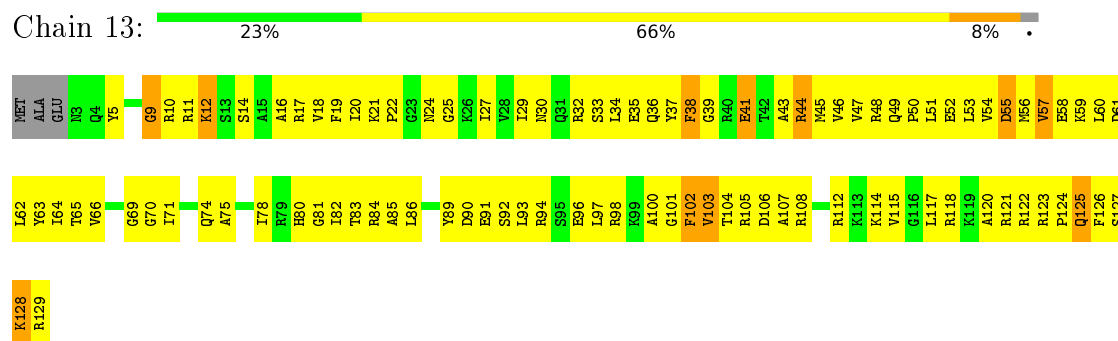


• Molecule 38: 30S ribosomal protein S8

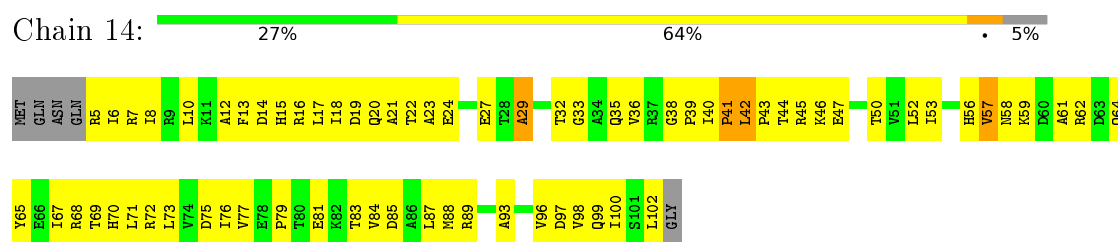
Chain 12: 41% 53% 5%



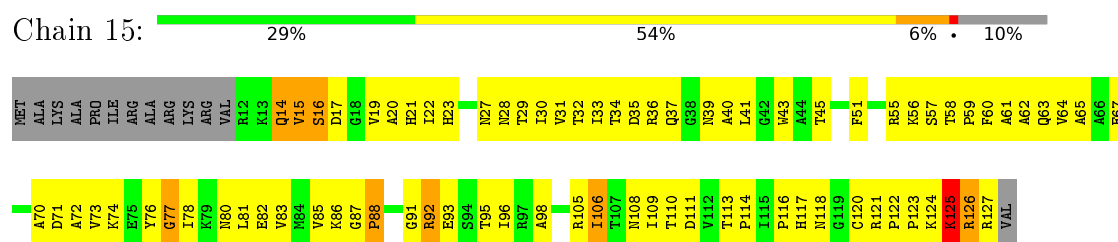
- Molecule 39: 30S ribosomal protein S9



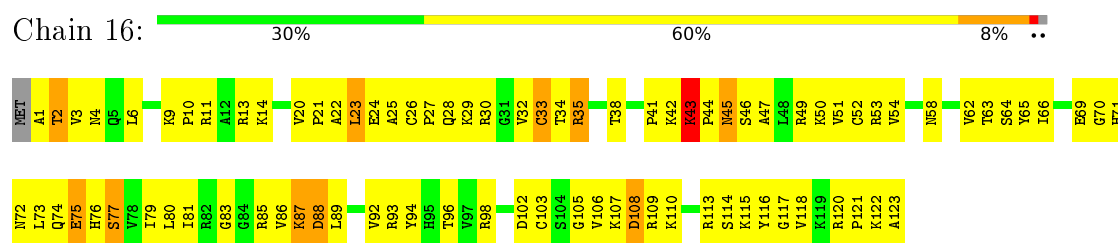
- Molecule 40: 30S ribosomal protein S10



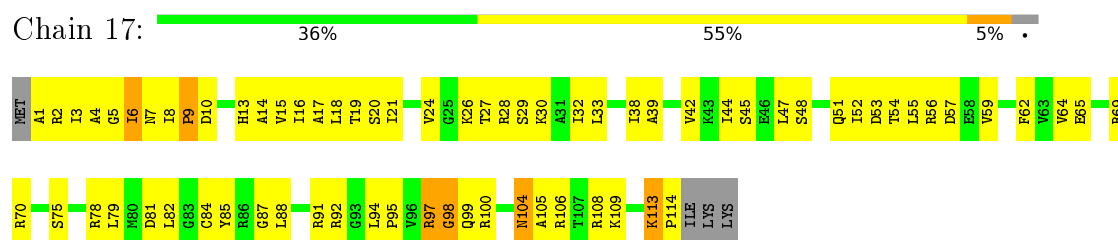
- Molecule 41: 30S ribosomal protein S11



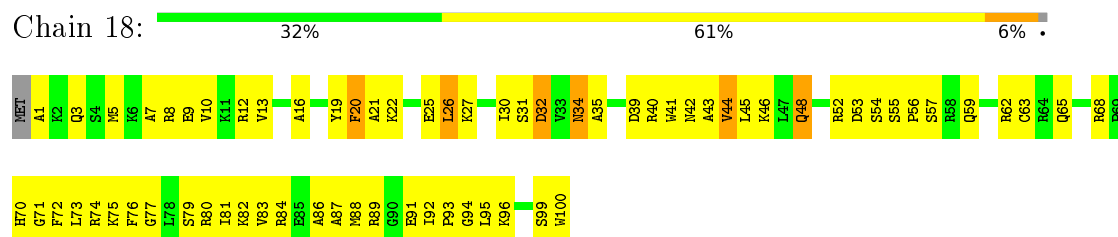
- Molecule 42: 30S ribosomal protein S12



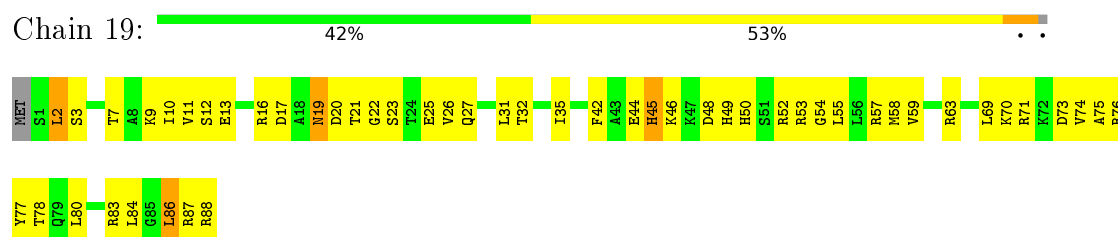
- Molecule 43: 30S ribosomal protein S13



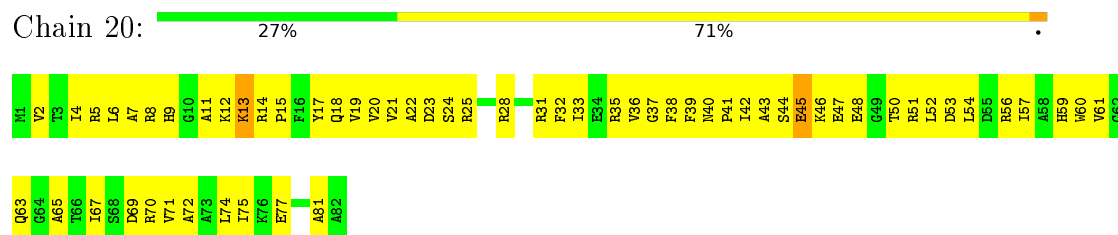
- Molecule 44: 30S ribosomal protein S14



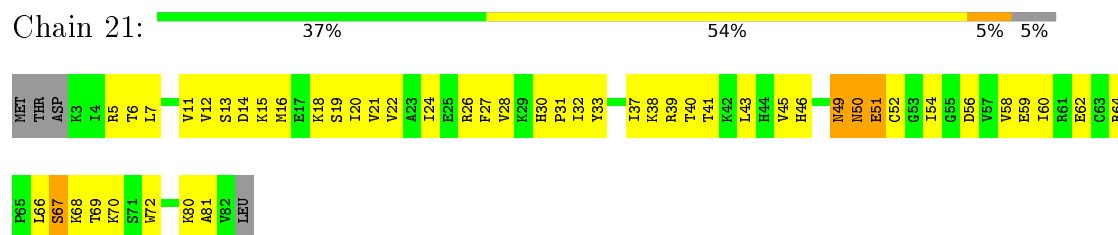
- Molecule 45: 30S ribosomal protein S15



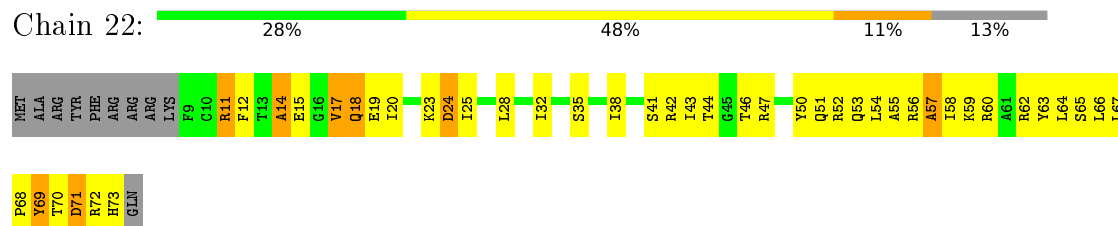
- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17

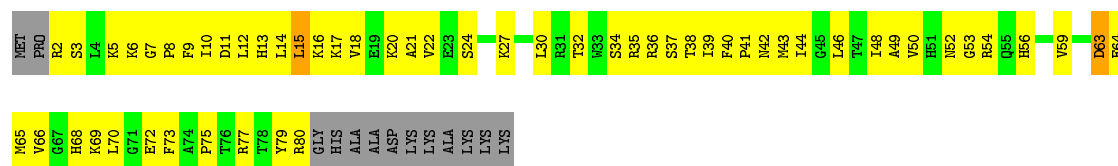


- Molecule 48: 30S ribosomal protein S18



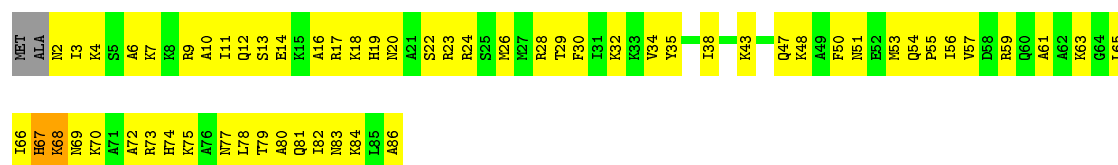
- Molecule 49: 30S ribosomal protein S19

Chain 23: 25% 59% 14%



- Molecule 50: 30S ribosomal protein S20

Chain 24: 30% 66% ..



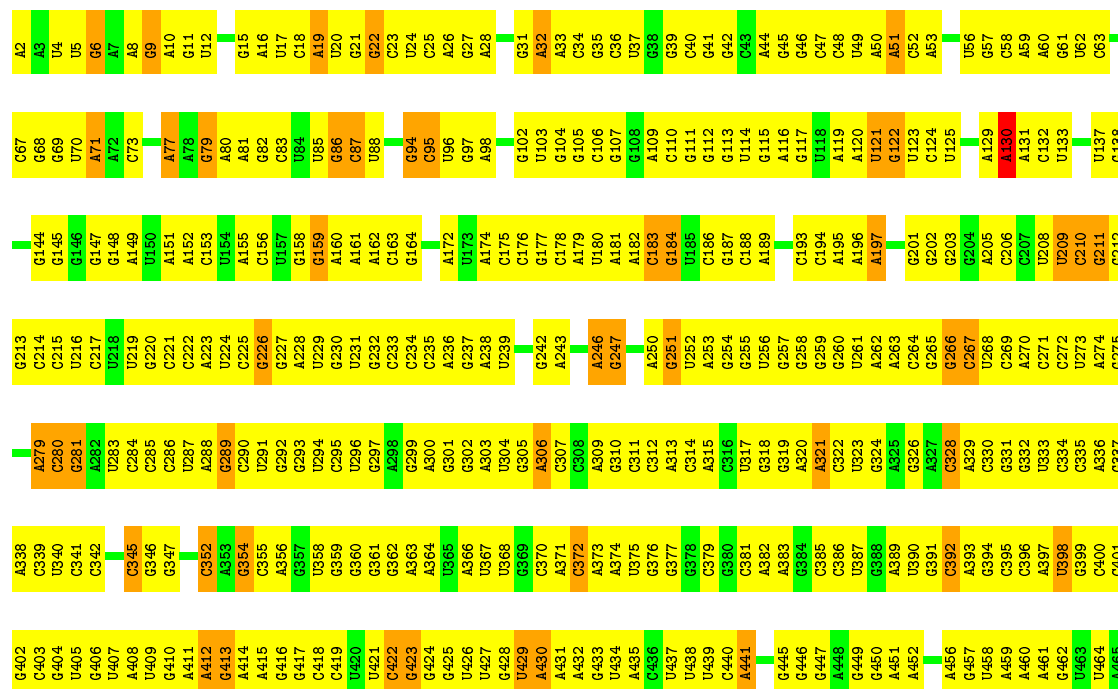
- Molecule 51: 30S ribosomal protein S21

Chain 25: 23% 62% 7% 8%



- Molecule 52: 16S ribosomal RNA

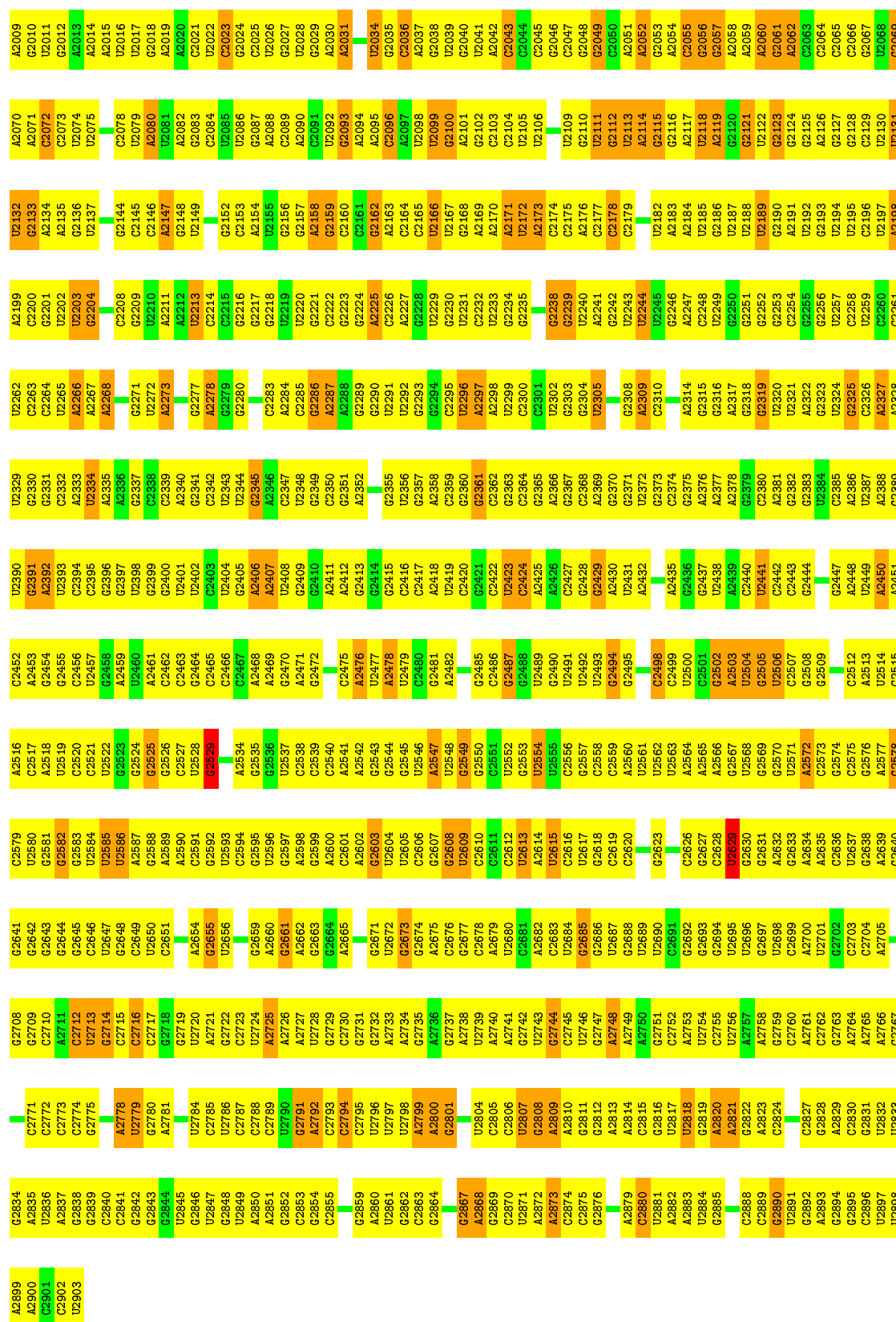
Chain 26: 20% 70% 10%



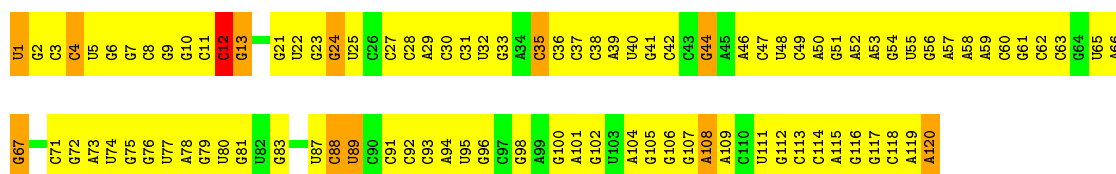
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A1431	A1368	U1307	A1236	A1171	C1109	A1046	C979	G917	C957	U789	G727	G664	U594	U531	U467
A1432	A1369	U1308	A1237		A1110	G1047	G980	A918	G958	A790	A728	A665	A596	A532	A468
A1433	G1370	A1309	A1238	G1174	A1111	G1048	U981	A919	G959	G791	A729	G666	A596	A533	C469
A1434	G1371	G1310	A1239	G1175	C1112	U1049	U982	U920	A860	A792	G730	G667	U598	U534	C470
A1435	A1372	A1311	U1240		C1113	G1050		U921	G661	G793	G731	G668	U598	A535	U471
U1436	G1373	G1312	G1241	A1180	C1114	C1051	U986	G922	C962	A794	C732	G669	C599	C536	U472
A1437		U1313	G1242	G1181	U1116	U1052	G987	A923	U963	G795		G670	A600	G537	U473
G1438		C1314	C1243	A1182	U1115	G1053	G988	C924	A864	G796	C735	G671	G601	G538	G474
A1439	U1380	U1315	U1183	U1183	A1117	C1054	U989	G925	A865	G797	C736	U672		A539	C475
U1440	G1316	G1316	C1244	U1184	A1118	A1055	C990	G926	C966	G798	C737	U673	G604	G540	U476
A1441	U1381	C1317	A1246	G1185	C1119	U1056	U991	G927	G667	G799	C738	G674	U605	G541	C477
G1442	G1382	A1318		G1186	C1120	G1057	U992	G928	C968	G800	C739	U675	G606	G542	A478
C1443	C1383	A1319	A1260	G1187	U1121	G1058	G993	G929	G969	U801	U740	U676	A607	U543	
U1444		U1320	A1251		U1122	C1059	A994		U870	A802	G741	U677	A608	G544	C483
U1445	G1384	C1321	A1252	G1190	U1123	U1060	G995	G933	U871	G803	G742	U678	A609	C545	G484
A1446	G1385	U1321	A1253	A1191		G1061	A996	A938	A872	A807	A743	C679		A546	U485
A1447	G1386	C1322	G1253	C1192	U1126	U1062	U997	A935	A873	C808	G744	C680	G613	A547	U486
A1448	G1387	G1323	A1254	G1193	G1127	C1063	C998	A936	G874	G809	G745	A681		G548	A487
C1449	C1388	A1324	G1255	G1194	G1128	U1064	C999	C936	U875		A746	G682	C549	C549	C488
U1450	C1389	C1325	A1256	U1195	C1129	U1065	A1000	A937	C976	G811	A747	G683	G550	G550	C489
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G1453	U1393	A1329	G1260	G1198	C1132		A1004	C940	C979	U815	C750	U686	U619	A553	C492
U1454	U1394	U1330	A1261	U1199	G1133	U1070	A1005	G941	C980	A816	C751	A687	C620	A554	A493
G1455	C1395	G1331	C1262	C1200	G1134	C1071	G1006	G942	G881	A817	G752	G688	A621	U555	C494
A1456	A1396	A1332	G1263	A1201	U1135	U1072	U1007	U943	C982	C817	A753	C689	A622	C566	A495
G1457	G1397	A1333	U1264	U1202	C1136	U1073	U1008	G944	C983	G818	A754	C690	C623	C567	A496
A1458	A1398	G1334	C1265	C1203	G1137	G1074	U1009	G945	U884	A819	G755	G691	C624	G558	G497
G1459	U1335	U1335		A1204	G1138	U1075	U1010	A946	G885	U820	C756	U692	U625	A559	A498
C1460	C1400	C1336	C1273	U1205	G1139	U1076	C1011	G947	G886	G821	U757	G693	G626	A560	A499
G1461	G1401	G1337	A1274	U1206	C1140	U1077	A1012	C948	G887	U822	C758	A694	G627	U561	G500
A1462	C1402	G1338	A1275	G1207	G1141	U1078	G1013	A949	G888	C823	A759	A695	C627	U562	C501
U1463	A1403	A1339	G1276	C1208	G1142	G1079	A1014	U950	A889	G824	G760	A696	A629	A563	A502
C1464	C1404	A1340	G1277	C1209	G1143	A1080	G1015	G951	G890	A825	G761	U697	C563	C564	C503
A1465	G1405	U1341	G1278	G1210	G1144	A1081	A1016	U952	U891	C826	U762	G698	C631	U565	C504
C1466	U1406	C1342	G1279	U1211	A1145	A1082		G953	A892	U827	G763	G699	U632	G566	G505
C1467	C1407	G1343	A1280	U1212	A1146	U1083	A1019	G954	C993	U828	C764		G633	G567	G506
A1468	A1408	C1344	C1281	U1213	C1147	G1084	G1020	U955	G994	G829	C765	G703	C634	G568	C507
C1469	C1409	U1345	C1282	A1214	U1148	U1085		U956	G995	G830	A766	A704	A635	G569	U508
U1470	A1410	A1346	U1283	G1215	C1149	U1086	U1023	U957	C996	A831	A767	G705	U636	G570	A509
U1471	C1411	G1347	C1284	A1216	A1150	G1087	G1024	A958	C997	G832	A768	A706	C637	U571	A510
U1472	C1412	U1348	A1285	C1217	A1151	G1088	U1025	A959	G998	G833	G769	U707	U638	A572	C511
C1473	A1413	A1349	U1286	C1218		G1089	G1026	U960	C999	U834	C770	C708		A573	U512
G1475	U1414	A1350	A1287	A1219	G1154	U1090	C1027	U961	A900	U835	G771	U709	A642	A574	C513
A1476	G1415	U1351		G1220	A1155	U1091	C1028	C962	A901	G836	U772	G710	C643	G575	C514
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U1478	G1353	G1353	C1293	G1222	A1157	A1093	U1030	A964	G903	G838		A712	G645	G577	U516
C1479	U1354	U1354	G1294	C1223	C1158	G1094	C1031	U965	U904	C839	G776	G713	G646	C578	G517
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U1481	U1420	A1357	G1297	C1226	C1161	C1097	G1034	A969	A907	U842	C779	A716	A648	G581	G521
G1482	G1422		U1298	A1227	U1162	U1098	U1037	C970	A908	U843	C780	U717	U653	C522	C522
A1483	G1423	A1360	U1299	C1228	A1163	G1099	C1037	G971	A909	G844	A781	A718		G584	A523
C1484	U1424	G1361	G1300	C1229	A1164	C1100	U1038	G972	A845	A845	A782	U657	G658	G585	G524
U1485	U1425	A1362	U1301	C1230	U1165	A1101	G1039	G973	U911	G846	C783	G721	U659	C586	C525
G1486	G1426	A1363	C1302	G1231	G1166	A1102	U1040	A974	C912	G847	A784	G722	U659	G587	C526
U1487	U1364		C1303	U1232	A1167	C1103	G1041	A975	A913		G785	G723	C660	G588	G527
G1488	A1428	G1365	G1304	C1233	U1168	C1103		G976	A914	U854	G786	G724	G661		C528
G1489	A1429	C1366	G1305	C1234	A1169	C1107	A1044	A977	A915	U855	A787	G725	U662	G592	G529



G1949	A1885	U1820	C1760	U1692	A1630	C1564	A1496	G1432	A1365	G1299	U1234	A1169	C1104	C1043	G978	
G1950	G1888	A1821	C1761	U1693	G1631	C1565	U1497	A1433	A1366	G1300	G1235	C1170	U1105	C1044	A979	
U1951	G1889	A1822	A1762	C1694	A1632	A1566	C1498	A1434	A1367	A1301	G1236	C1171	G1106	C1045	A980	
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A1953	G1891	G1824	C1764	G1696	A1634	G1568	G1501	G1436	G1369	G1303	A1237	U1174	A1111	G1047	C982	
G1954	G1892	G1825	U1765	G1697	A1635	A1569	G1502	C1437	C1370	U1175	G1238	U1175	A1112	A1048	A983	
U1955	C1893	G1826	G1766	A1698	U1636	A1570	A1503	U1438	G1371	C1306	G1239	A1176	G1113	C1049	A984	
G1956	G1894	A1827	C1767	G1699	A1637	A1571	A1504	A1439	U1372	A1307	U1240	U1177	U1113	A1050	C985	
U1957	C1894	G1828	G1768	A1700	C1638	A1572	A1505	U1440	A1373	A1308	A1241	G1177	C1114	C1051	A988	
G1958	C1895	A1829	U1769	G1701	G1639	G1573	A1506	G1441	G1374	G1309	U1242	C1178	G1115	C1052	G989	
G1959	G1896	G1830	G1770	G1702	A1640	C1574	U1506	U1442	U1375	G1309	C1243	G1179	G1115	C1053	A990	
A1960	G1897	G1831	C1771	G1703	A1641	C1575	C1507	U1443	C1376	U1312	A1244	U1180	U1119	A1054	A991	
C1961	U1898	G1832	A1772	C1704	G1642	U1576	A1508	G1444	G1377	U1313	U1245	U1181	G1120	G1055	C992	
U1962	A1899	C1833	C1773	A1705	C1646	U1577	A1509	G1445	U1378	C1314	G1248	G1182	C1121	A1057	G993	
G1963	G1900	A1837	C1774	C1706	C1646	U1578	G1510	G1446	U1379	U1315	U1249	U1183	G1122	G1058	C994	
U1964	A1901	G1838	U1775	G1707	U1647	A1579	G1511	C1447	A1383	G1316	G1250	U1184	C1123	U1059	C995	
C1965	G1902	G1839	G1776	C1708	U1648	A1580	C1512	G1448	A1384	G1317	G1251	G1185	G1124	G1060	A996	
A1966	G1903	G1839	U1777	U1709	G1649	G1581	U1513	G1449	A1384	U1318	G1252	G1186	G1125	U1060	A996	
C1967	G1904	G1840	U1778	G1710	A1650	C1582	G1514	G1450	A1385	C1319	A1253	G1187	A1126	U1061	G997	
G1968	C1905	U1841	U1779	A1711	G1651	C1583	A1515	C1451	C1386	C1320	A1254	U1188	A1127	G1062	C998	
A1969	G1906	G1842	U1780	U1712	A1652	U1584	A1516	G1452	A1387	A1321	U1255	U1189	G1128	G1063	U999	
U1970	G1907	C1843	U1781	U1713	G1653	A1586	G1517	A1453	G1388	U1326	G1256	G1190	A1129	C1064	G1003	
G1971	U1911	C1844	U1782	G1715	A1654	G1587	C1518	C1454	G1389	U1326	G1257	G1191	U1130	U1065	U1004	
U1972	G1912	G1845	A1783	U1716	C1655	U1588	G1519	G1455	U1390	A1327	U1258	G1192	G1131	U1066	C1005	
C1973	A1913	G1846	A1784	A1717	A1656	U1589	U1520	C1461	U1394	U1328	G1259	G1193	U1132	A1067	C1006	
G1974	G1914	G1847	A1785	G1718	U1657	A1590	G1521	C1462	U1394	U1329	A1260	A1194	A1133	G1068	C1007	
U1975	A1915	A1848	U1786	G1719	C1658	A1591	A1522	C1463	A1395	C1330	G1261	G1195	A1134	A1068	A1008	
U1976	G1916	G1849	A1787	U1720	G1659	C1592	U1523	G1463	U1396	G1331	A1262	G1196	C1135	A1070	A1009	
A1977	G1916	G1850	C1788	G1721	G1660	A1593	G1524	G1464	C1398	G1332	U1263	G1197	G1136	G1071	A1010	
U1978	U1917	U1851	A1789	A1722	G1661	U1594	A1525	U1465	C1399	G1333	A1264	U1198	G1137	C1072	G1011	
U1979	A1918	U1852	C1790	U1722	U1662	C1595	C1526	U1466	U1400	G1334	A1265	U1199	G1138	A1073	U1012	
U1980	A1919	A1853	G1791	C1728	G1663	A1596	G1527	U1467	G1401	G1335	G1266	C1200	G1139	G1074	C1013	
C1981	G1920	A1854	U1792	U1729	A1664	A1597	A1528	U1468	U1402	A1336	U1267	U1201	C1140	C1075	A1014	
U1982	G1921	G1857	C1793	C1730	A1665	A1598	G1529	A1469	A1403	G1337	A1268	A1204	U1141	C1076	U1015	
G1983	G1922	A1858	A1794	G1731	G1666	U1599	U1530	A1470	C1404	U1340	C1270	A1205	A1143	U1078	U1018	
U1984	C1923	G1859	C1795	C1732	G1667	C1600	C1531	C1471	U1405	G1341	G1271	A1206	A1144	A1080	U1019	
C1985	U1924	U1859	G1796	G1733	A1668	G1601	A1532	C1472	U1406	A1342	A1272	G1208	C1145	A1081	A1020	
G1986	C1925	G1860	G1797	U1736	A1669	U1602	C1533	G1473	G1407	G1343	U1273	U1209	C1146	U1082	A1021	
A1987	U1926	G1861	U1798	U1737	C1670	A1603	U1534	U1474	U1411	G1344	U1278	G1210	A1147	U1083	G1022	
G1988	A1927	G1862	G1799	U1738	U1671	C1604	A1535	G1475	G1410	C1345	C1279	G1211	U1148	U1084	U1023	
U1989	G1928	U1866	C1800	G1738	A1672	G1605	G1536	U1476	U1412	G1346	G1279	G1212	G1149	A1085	G1024	
C1990	G1929	A1866	A1801	A1739	G1673	C1606	G1537	A1477	A1413	A1347	G1280	G1213	C1150	A1086	G1025	
U1991	U1930	G1867	A1802	G1740	C1674	A1607	U1542	G1478	U1413	C1348	U1281	A1213	C1151	A1086	G1026	
G1992	A1931	C1868	A1803	C1741	C1675	A1608	G1543	G1479	G1416	C1349	G1282	G1214	C1152	G1087	A1027	
U1993	A1932	G1869	C1804	U1742	A1676	U1609	A1544	U1480	C1417	C1350	G1283	G1215	C1153	A1088	A1028	
C1994	G1933	A1870	A1805	G1743	A1677	A1610	A1548	U1481	G1418	C1351	U1284	U1217	G1154	A1089	A1029	
U1995	G1934	A1871	C1806	A1744	A1678	C1611	A1549	G1482	G1418	U1352	A1284	G1218	A1155	A1090	A1030	
C1996	G1935	A1872	G1807	U1745	A1679	G1612	C1550	U1483	A1419	U1352	A1285	G1219	A1156	G1091	G1031	
U1997	A1936	G1873	A1808	A1746	U1680	G1613	A1551	U1484	A1420	A1353	A1286	U1219	C1157	C1092	U1032	
A1998	A1937	C1874	G1809	U1747	G1681	A1614	A1552	U1485	G1421	A1354	A1287	G1220	C1158	G1093	A1033	
G1999	U1938	G1875	A1810	C1748	G1682	C1615	A1553	U1486	G1422	G1355	G1288	G1223	U1159	U1094	U1033	
C2000	U1939	A1876	G1811	U1748	U1683	A1616	G1555	U1487	G1423	C1356	C1289	U1224	G1160	A1095	G1036	
C2001	U1940	A1877	U1812	G1752	C1684	C1617	U1556	G1488	G1424	G1357	C1290	G1225	C1161	A1096	G1037	
G2002	G1941	G1878	G1813	A1753	C1685	A1618	C1557	C1489	G1425	G1358	U1293	A1226	G1162	U1097	A1038	
A2003	U1943	C1879	A1814	G1754	G1686	G1619	U1558	A1490	G1426	A1359	U1294	G1227	G1163	C1100	G1038	
G2004	U1944	U1880	A1815	A1755	G1687	G1620	U1559	G1491	A1427	C1360	C1295	G1228	A1165	U1101	A1039	
U2005	G1945	A1881	G1816	G1756	U1688	U1621	G1560	G1492	C1428	G1361	G1296	C1229	G1166	A1040	A1040	
C2006	U1946	U1882	A1817	A1757	A1689	G1622	C1561	G1493	G1429	C1362	G1297	A1230	C1167	C1102	G1041	
U2007	G1947	U1883	U1818	U1758	A1690	G1623	U1562	A1494	G1430	C1363	C1297	U1231	G1168	A1103	G1042	
C2008	A1948	G1884	A1819	A1759	C1691											



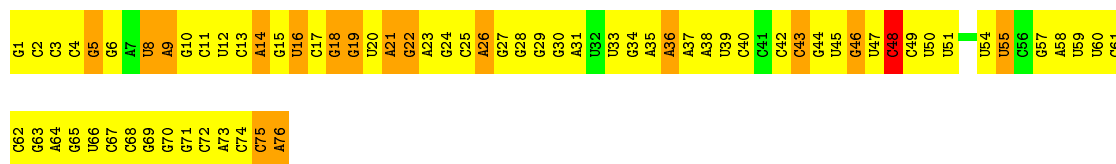
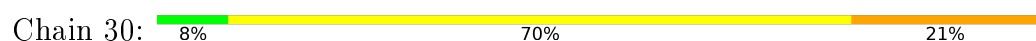
• Molecule 54: 5S ribosomal RNA



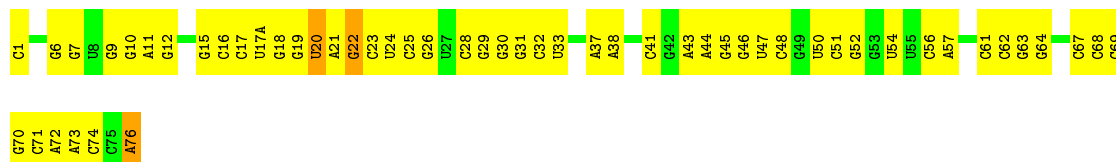
- Molecule 55: mRNA



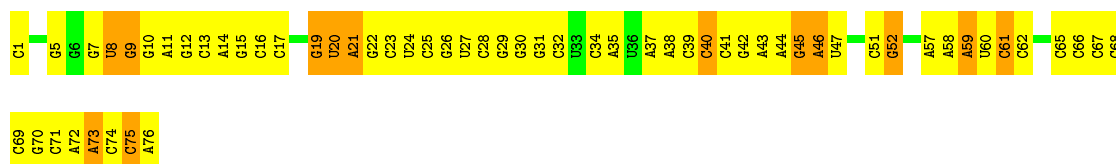
- Molecule 56: A-site tRNA^{Phe}



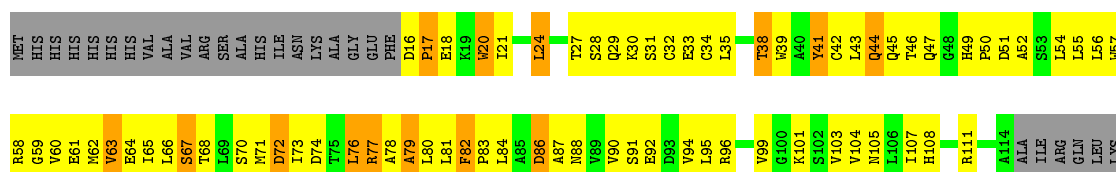
- Molecule 57: P-site tRNA^{Met}



- 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	N606	H607	H608	I609	A610	R611	G612	C613	Q614	P615	I616	P617	G618	D619	E620	I621	Y622	I623	V624	G625	P626	T627	R629	G630	I631	S632	H633	H634	R635	A636	D637	C638	E639	Q640	L641	E642	B643	L644	R645	S646	H647	A648	P649	B650	R651	I652	V653	D654	A655	V656	H657	G658	E659	SER	TYR			
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																											
P419	A420	G421	S422	T423	P424	F427	A428	Y429	H430	I431	H432	S433	D434	V435	G436	H437	R438	Q439	A442	K443	I444	G445	G446	R447	T448	F451	T452	Y453	G458	D459	Q460	SER	GLY	GLU	MET	ALA	ASP	L302	L303	P304	D305	E306	F307	D308	GLU	VAL	ARG	SER	GLN	VAL	PHE	ASP	D404	R405	V406	Y407	V408	F409	G328	P329	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	MET	ASP	GLY	GLU	MET	LEU	ASP	GLU	VAL	ARG	SER	GLN	VAL	PHE	ASP	D404	R405	V406	Y407	V408	F409	G328	P329	P411	D417	L418												
Q264	L194	K195	W196	L197	L198	E199	D200	F201	C202	GLU	Q131	R204	V132	D133	H134	V135	R136	Y137	M138	I214	A215	L218	F146	R147	C148	V149	V150	I151	K152	L153	H227	Y228	I229	E230	E231	F232	V233	G234	H235	L236	R237	A238	E239	M240	K241	A242	E243	G244	L173	V245	K246	A247	E248	V249	Y250	G251	R252	I259	W260	M263			
Q264	L194	K195	W196	L197	L198	E199	D200	F201	C202	GLU	Q131	R204	V132	D133	H134	V135	R136	Y137	M138	I214	A215	L218	F146	R147	C148	V149	V150	I151	K152	L153	H227	Y228	I229	E230	E231	F232	V233	G234	H235	L236	R237	A238	E239	M240	K241	A242	E243	G244	L173	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	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	30488	Depositor
Image detector	Not provided	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

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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

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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	40
2	B	207/209 (99%)	172 (83%)	28 (14%)	7 (3%)	5	42
3	C	199/201 (99%)	147 (74%)	32 (16%)	20 (10%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	175/179 (98%)	143 (82%)	27 (15%)	5 (3%)	6	45
5	E	174/177 (98%)	149 (86%)	20 (12%)	5 (3%)	6	45
6	F	147/149 (99%)	108 (74%)	20 (14%)	19 (13%)	0	7
7	G	129/165 (78%)	93 (72%)	25 (19%)	11 (8%)	1	17
8	H	139/142 (98%)	104 (75%)	25 (18%)	10 (7%)	1	23
9	I	140/142 (99%)	120 (86%)	14 (10%)	6 (4%)	3	35
10	J	120/123 (98%)	97 (81%)	16 (13%)	7 (6%)	2	28
11	K	141/144 (98%)	110 (78%)	20 (14%)	11 (8%)	1	20
12	L	134/136 (98%)	113 (84%)	15 (11%)	6 (4%)	3	34
13	M	118/127 (93%)	91 (77%)	22 (19%)	5 (4%)	3	36
14	N	114/117 (97%)	98 (86%)	15 (13%)	1 (1%)	21	67
15	O	112/115 (97%)	93 (83%)	15 (13%)	4 (4%)	4	41
16	P	115/118 (98%)	103 (90%)	7 (6%)	5 (4%)	3	35
17	Q	101/103 (98%)	77 (76%)	16 (16%)	8 (8%)	1	19
18	R	108/110 (98%)	87 (81%)	15 (14%)	6 (6%)	2	29
19	S	91/100 (91%)	71 (78%)	16 (18%)	4 (4%)	3	35
20	T	100/104 (96%)	79 (79%)	14 (14%)	7 (7%)	1	23
21	U	92/94 (98%)	76 (83%)	11 (12%)	5 (5%)	2	30
22	V	73/85 (86%)	65 (89%)	7 (10%)	1 (1%)	14	59
23	W	75/78 (96%)	67 (89%)	6 (8%)	2 (3%)	6	47
24	X	61/63 (97%)	49 (80%)	7 (12%)	5 (8%)	1	18
25	Y	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
26	Z	64/70 (91%)	47 (73%)	7 (11%)	10 (16%)	0	5
27	1	54/57 (95%)	43 (80%)	6 (11%)	5 (9%)	1	16
28	2	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
29	3	44/46 (96%)	32 (73%)	11 (25%)	1 (2%)	8	50
30	4	62/65 (95%)	51 (82%)	8 (13%)	3 (5%)	3	32
31	5	36/38 (95%)	26 (72%)	5 (14%)	5 (14%)	0	6
32	6	216/241 (90%)	170 (79%)	32 (15%)	14 (6%)	1	26
33	7	204/233 (88%)	175 (86%)	22 (11%)	7 (3%)	5	42
34	8	203/206 (98%)	157 (77%)	30 (15%)	16 (8%)	1	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	9	155/167 (93%)	109 (70%)	33 (21%)	13 (8%)	1	17
36	10	98/135 (73%)	77 (79%)	14 (14%)	7 (7%)	1	23
37	11	149/179 (83%)	123 (83%)	14 (9%)	12 (8%)	1	19
38	12	127/130 (98%)	110 (87%)	8 (6%)	9 (7%)	1	23
39	13	125/130 (96%)	93 (74%)	19 (15%)	13 (10%)	1	12
40	14	96/103 (93%)	76 (79%)	15 (16%)	5 (5%)	2	31
41	15	114/129 (88%)	90 (79%)	13 (11%)	11 (10%)	1	14
42	16	121/124 (98%)	95 (78%)	13 (11%)	13 (11%)	0	11
43	17	112/118 (95%)	88 (79%)	14 (12%)	10 (9%)	1	17
44	18	98/101 (97%)	72 (74%)	21 (21%)	5 (5%)	2	31
45	19	86/89 (97%)	70 (81%)	11 (13%)	5 (6%)	2	28
46	20	80/82 (98%)	59 (74%)	18 (22%)	3 (4%)	4	39
47	21	78/84 (93%)	54 (69%)	19 (24%)	5 (6%)	2	26
48	22	63/75 (84%)	50 (79%)	5 (8%)	8 (13%)	0	8
49	23	77/92 (84%)	64 (83%)	11 (14%)	2 (3%)	7	48
50	24	83/87 (95%)	75 (90%)	6 (7%)	2 (2%)	7	49
51	25	63/71 (89%)	40 (64%)	19 (30%)	4 (6%)	2	27
59	33	663/750 (88%)	557 (84%)	60 (9%)	46 (7%)	1	24
All	All	6509/6970 (93%)	5226 (80%)	879 (14%)	404 (6%)	4	27

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%)	92	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%)	74	89
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%)	66	87
9	I	116/116 (100%)	116 (100%)	0	100	100
10	J	103/104 (99%)	102 (99%)	1 (1%)	82	91
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%)	82	91
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%)	78	90
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%)	78	90
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%)	68	88
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%)	63	86
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%)	178 (99%)	2 (1%)	80	90
33	7	170/190 (90%)	169 (99%)	1 (1%)	90	95
34	8	172/173 (99%)	172 (100%)	0	100	100
35	9	119/126 (94%)	117 (98%)	2 (2%)	68	88
36	10	87/116 (75%)	85 (98%)	2 (2%)	58	83
37	11	124/147 (84%)	123 (99%)	1 (1%)	86	93
38	12	104/105 (99%)	103 (99%)	1 (1%)	82	91
39	13	105/107 (98%)	104 (99%)	1 (1%)	82	91
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%)	42	76
45	19	76/77 (99%)	75 (99%)	1 (1%)	76	89
46	20	65/65 (100%)	65 (100%)	0	100	100
47	21	74/78 (95%)	73 (99%)	1 (1%)	74	89
48	22	56/65 (86%)	55 (98%)	1 (2%)	66	87
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%)	66	87
59	33	452/635 (71%)	449 (99%)	3 (1%)	88	94
All	All	5303/5698 (93%)	5272 (99%)	31 (1%)	91	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.