



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Nov 14, 2019 – 03:03 AM EST

PDB ID : 5KPW
EMDB ID: : EMD-8281
Title : Structure of RelA bound to ribosome in presence of A/R tRNA (Structure III)
Authors : Loveland, A.B.; Bah, E.; Madireddy, R.; Zhang, Y.; Brilot, A.F.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2016-07-05
Resolution : 3.90 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

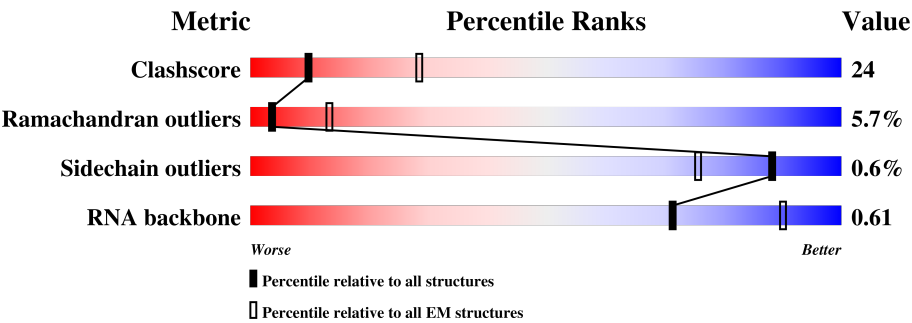
MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

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






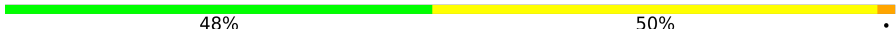
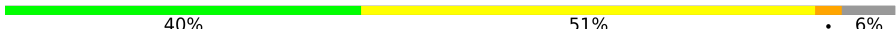





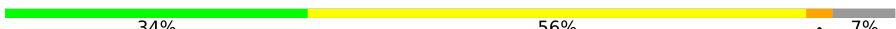
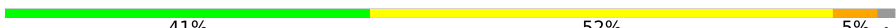





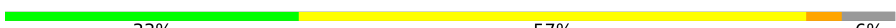


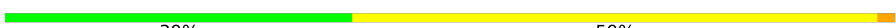

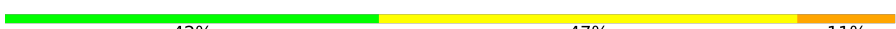


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

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

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



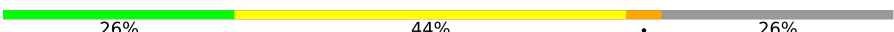


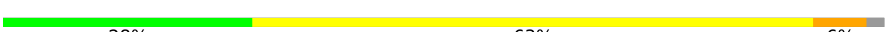
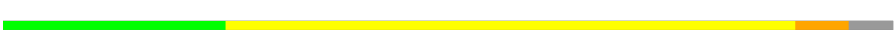





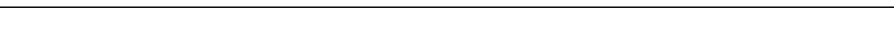

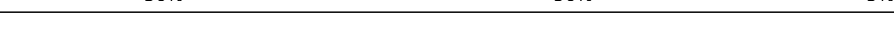

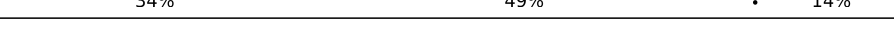






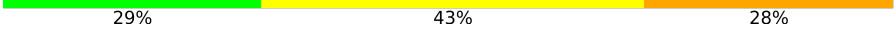

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Mol	Chain	Length	Quality of chain
9	I	142	
10	J	123	
11	K	144	
12	L	136	
13	M	127	
14	N	117	
15	O	115	
16	P	118	
17	Q	103	
18	R	110	
19	S	100	
20	T	104	
21	U	94	
22	V	85	
23	W	78	
24	X	63	
25	Y	59	
26	Z	70	
27	1	57	
28	2	55	
29	3	46	
30	4	65	
31	5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

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

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Mol	Chain	Length	Quality of chain
59	33	750	<div><div></div><div>38%</div><div>45%</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

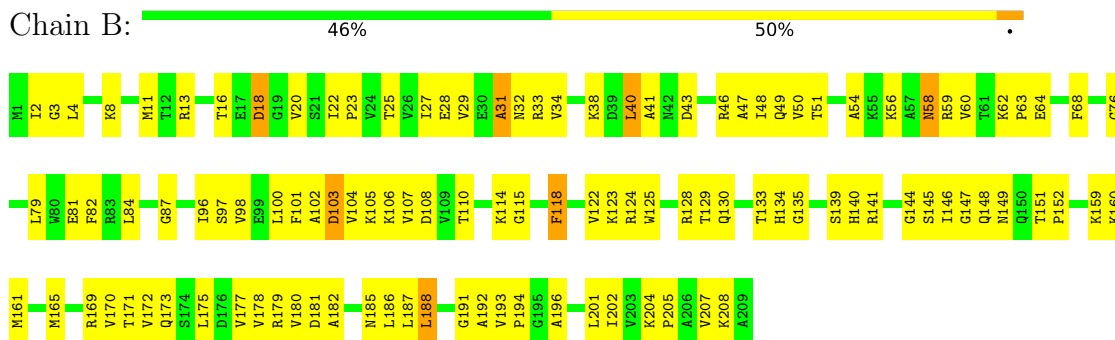
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

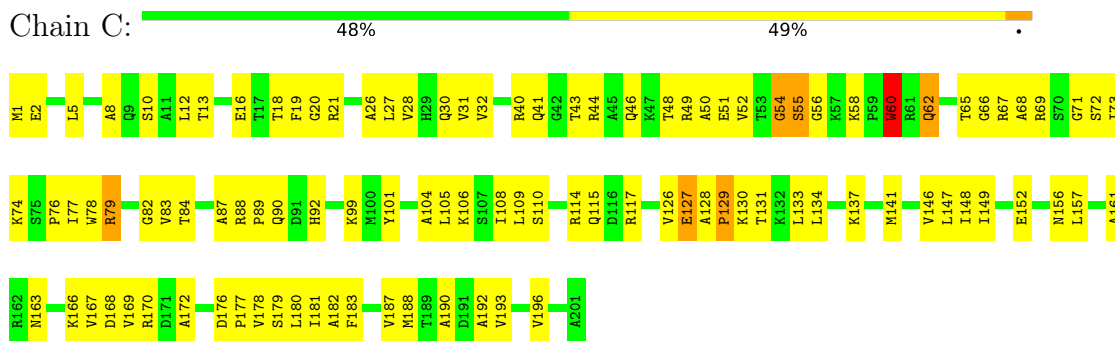
• Molecule 1: 50S ribosomal protein L2



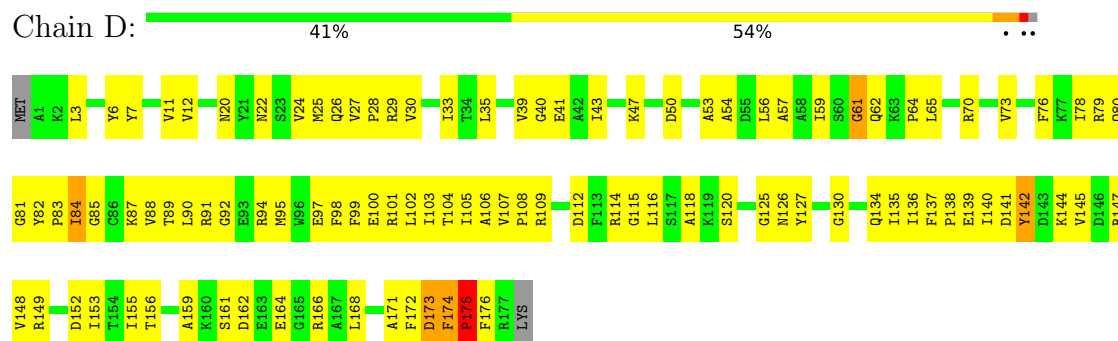
• Molecule 2: 50S ribosomal protein L3



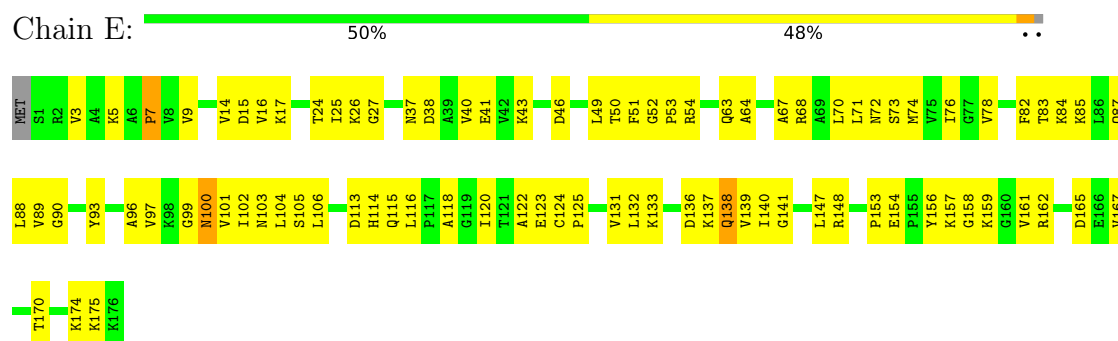
• Molecule 3: 50S ribosomal protein L4



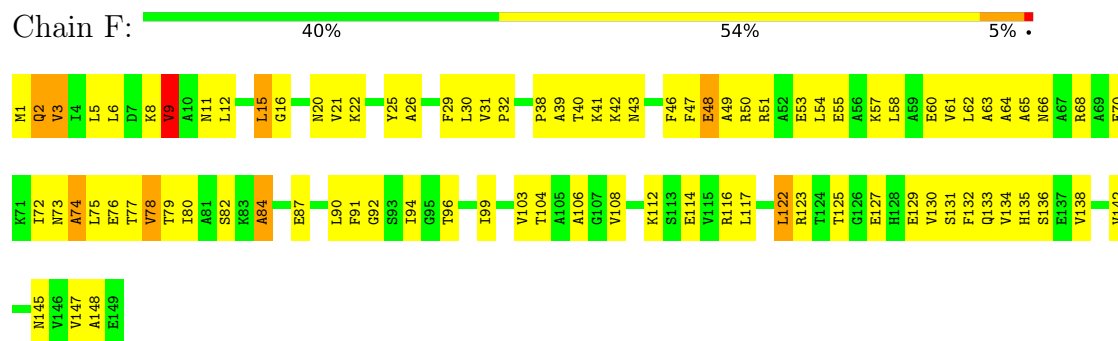
• Molecule 4: 50S ribosomal protein L5



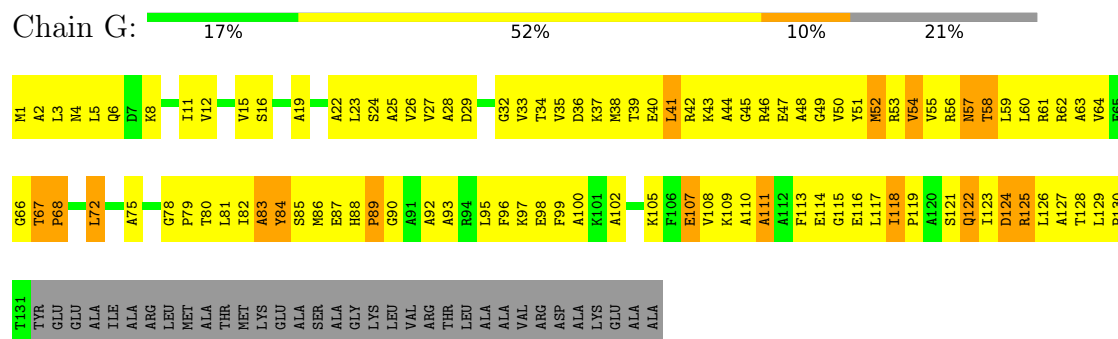
- Molecule 5: 50S ribosomal protein L6



- Molecule 6: 50S ribosomal protein L9

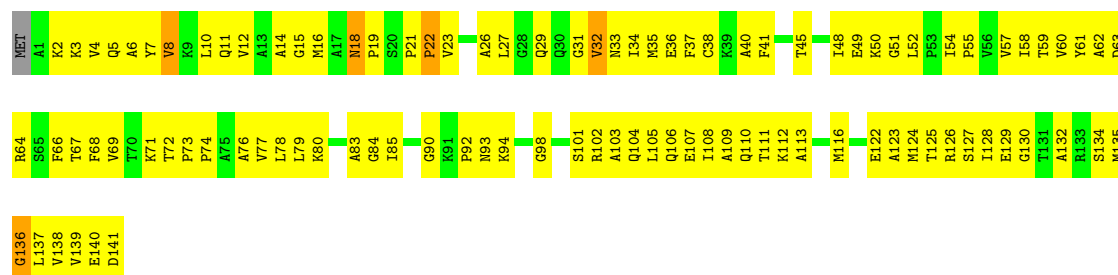


- Molecule 7: 50S ribosomal protein L10



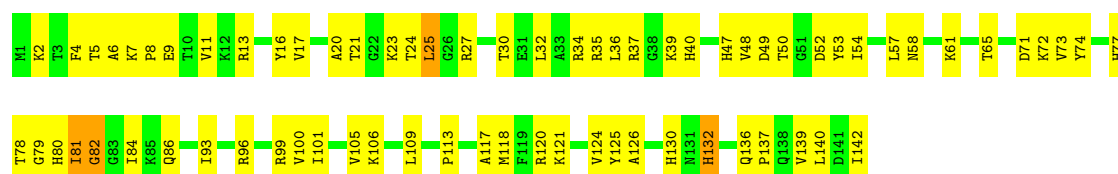
- Molecule 8: 50S ribosomal protein L11

Chain H:  29% 67%



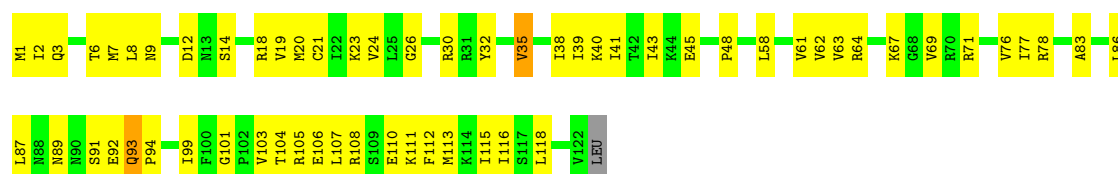
- Molecule 9: 50S ribosomal protein L13

Chain I:  50% 47%



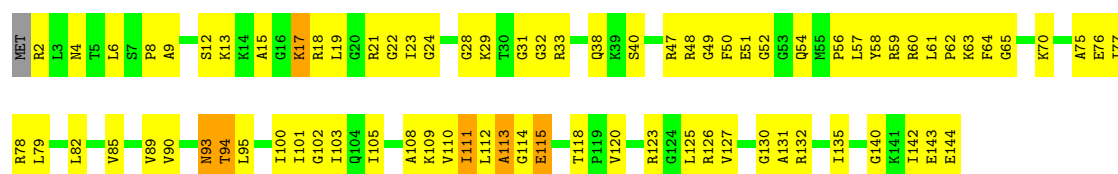
- Molecule 10: 50S ribosomal protein L14

Chain J:  50% 47%



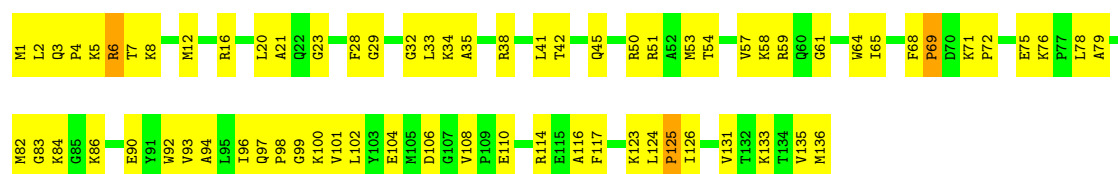
- Molecule 11: 50S ribosomal protein L15

Chain K:  44% 51%

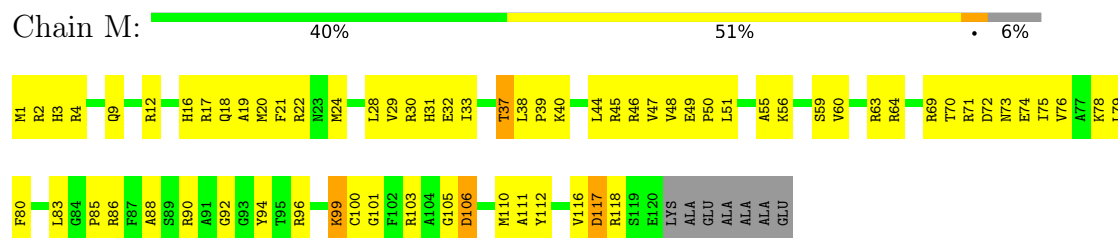


- Molecule 12: 50S ribosomal protein L16

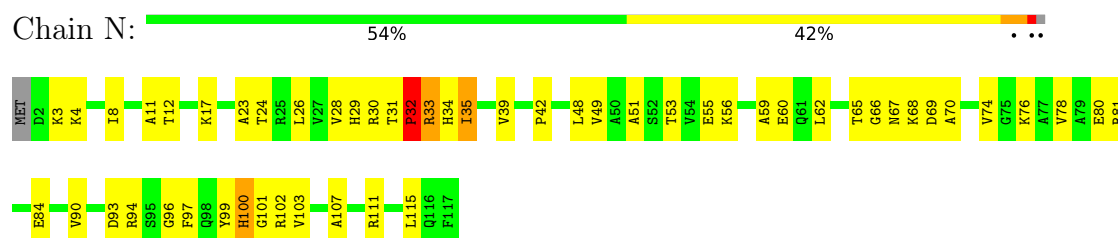
Chain L:  48% 50%



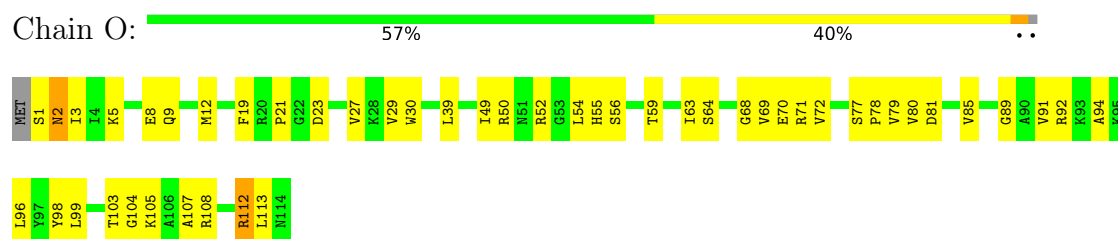
- Molecule 13: 50S ribosomal protein L17



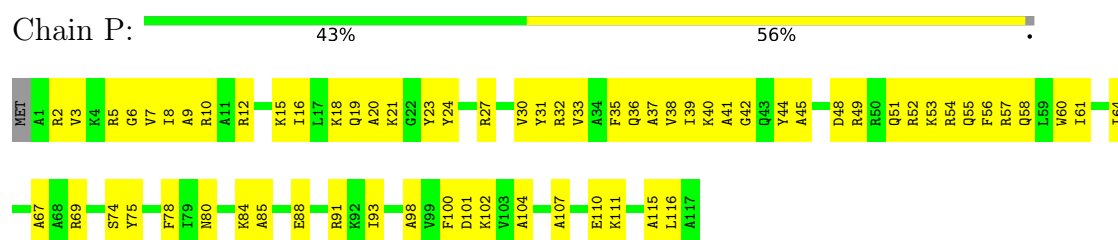
- Molecule 14: 50S ribosomal protein L18



- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20

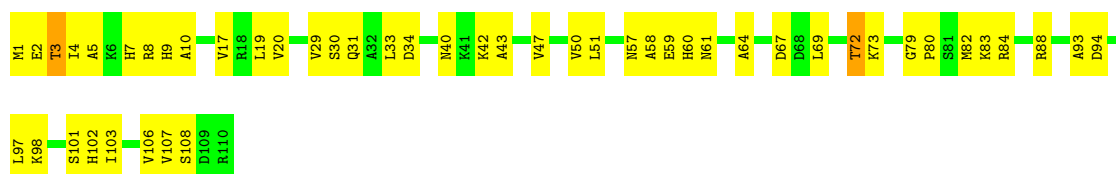


- Molecule 17: 50S ribosomal protein L21



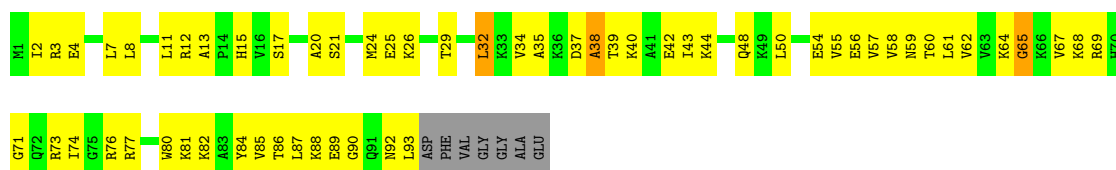
- Molecule 18: 50S ribosomal protein L22





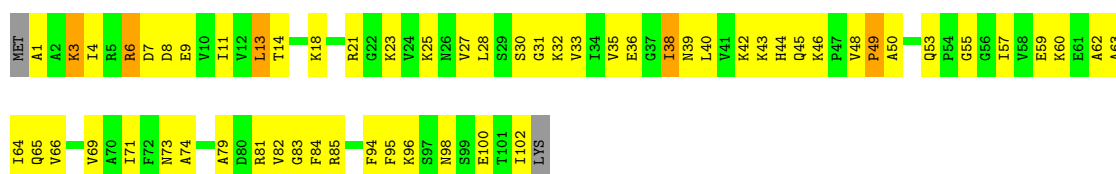
- Molecule 19: 50S ribosomal protein L23

Chain S: 34% 56% 7%



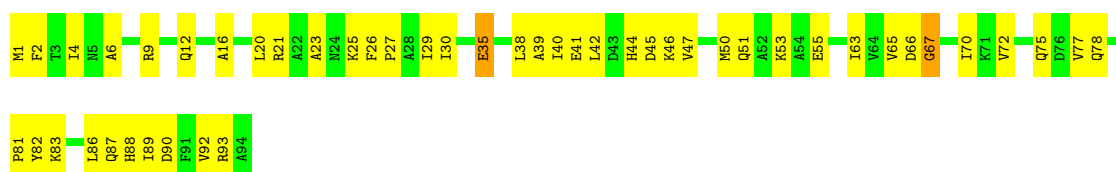
- Molecule 20: 50S ribosomal protein L24

Chain T: 41% 52% 5%



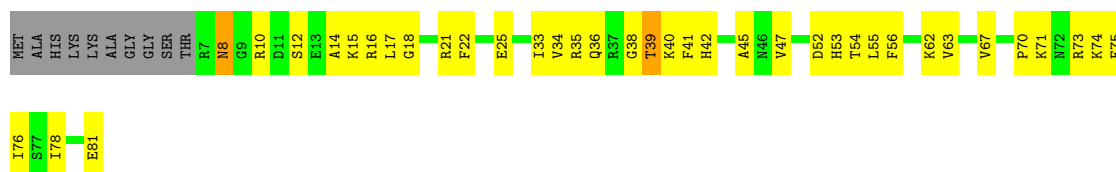
- Molecule 21: 50S ribosomal protein L25

Chain U: 49% 49% 2%



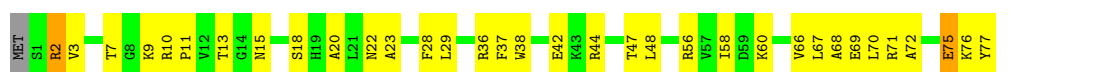
- Molecule 22: 50S ribosomal protein L27

Chain V: 44% 42% 12%



- Molecule 23: 50S ribosomal protein L28

Chain W: 55% 41% 4%



- [illegible]

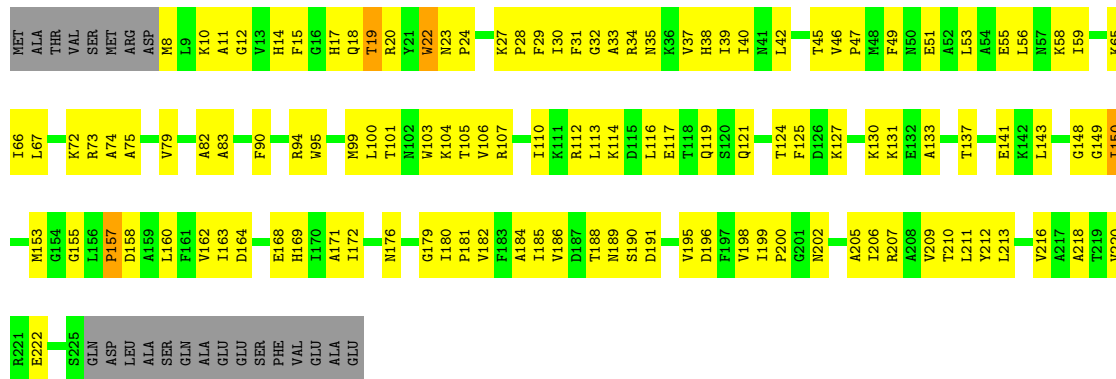
- Molecule 31: 50S ribosomal protein L36

Chain 5: 42% 47% 11%



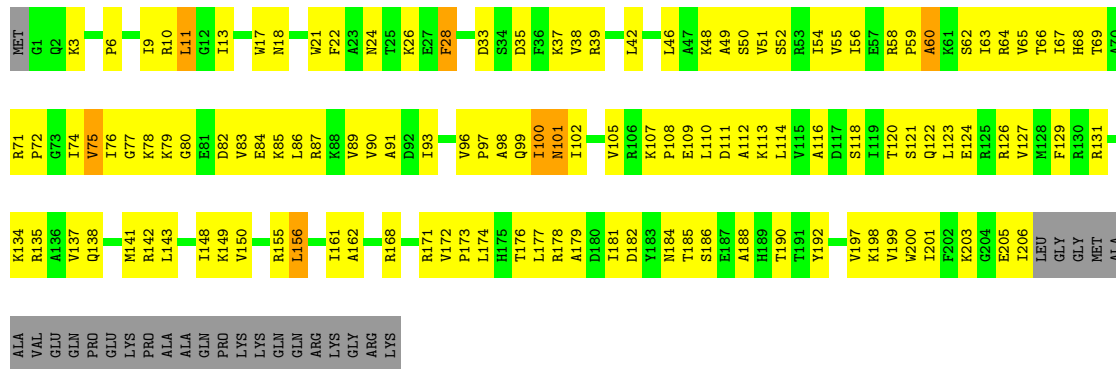
- Molecule 32: 30S ribosomal protein S2

Chain 6: 41% 48% 10%

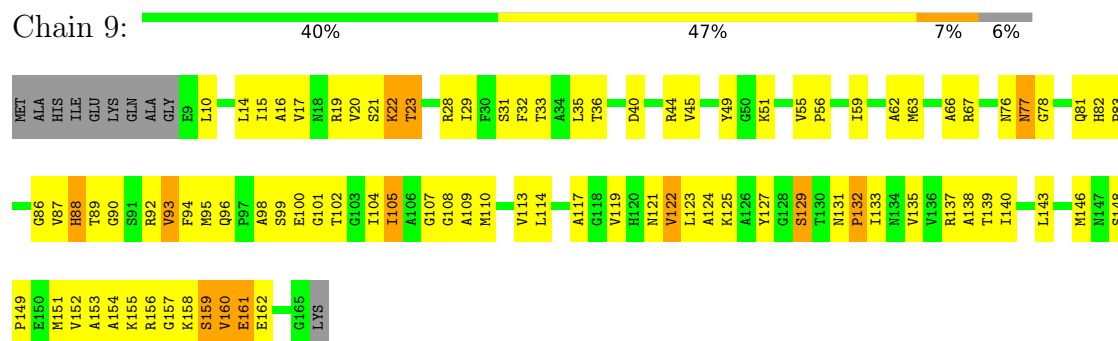


- Molecule 33: 30S ribosomal protein S3

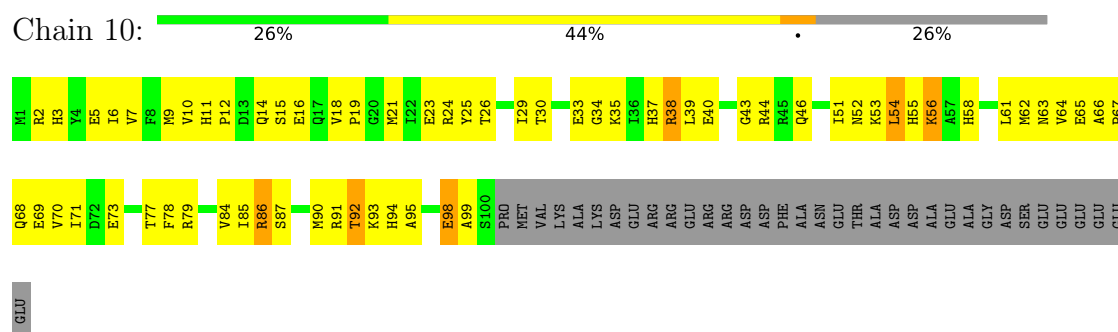
Chain 7: 35% 50% 12%



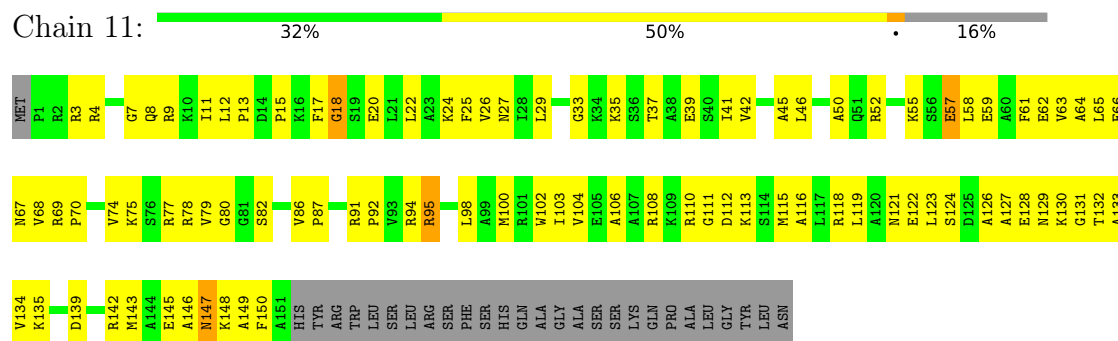
- Molecule 35: 30S ribosomal protein S5



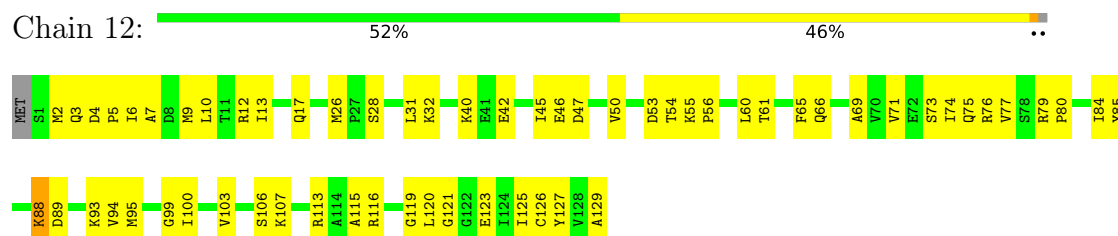
- Molecule 36: 30S ribosomal protein S6



- Molecule 37: 30S ribosomal protein S7

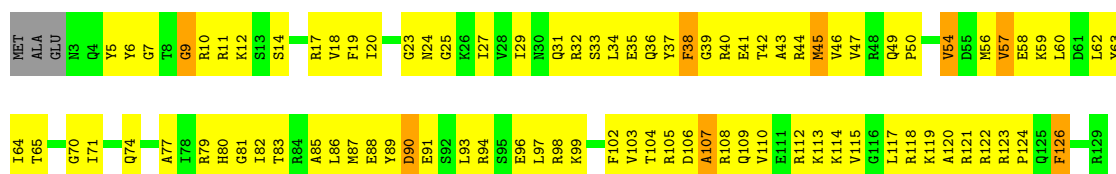


- Molecule 38: 30S ribosomal protein S8



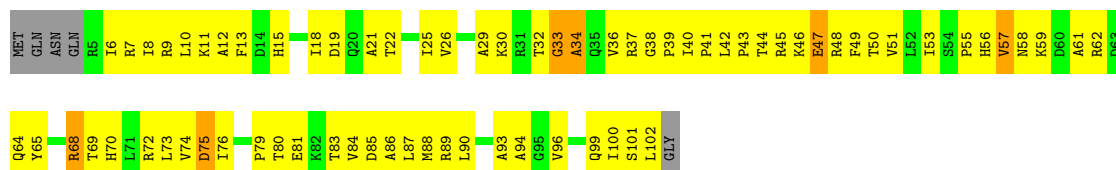
- Molecule 39: 30S ribosomal protein S9

Chain 13:  28% 63% 6%



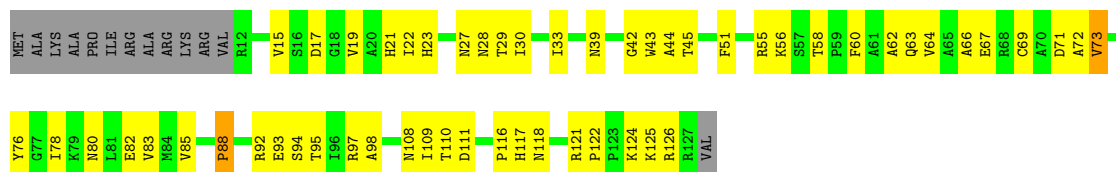
• Molecule 40: 30S ribosomal protein S10

Chain 14: 25% 64% 6% 5%



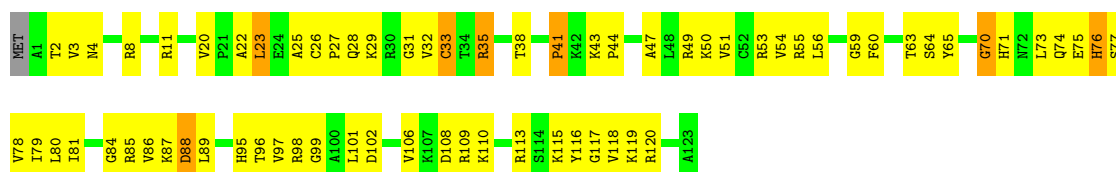
• Molecule 41: 30S ribosomal protein S11

Chain 15: 47% 41% 10%



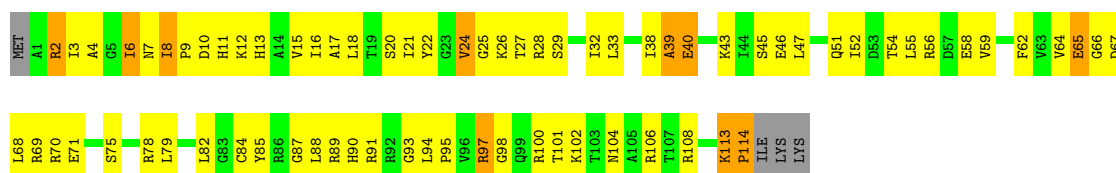
• Molecule 42: 30S ribosomal protein S12

Chain 16: 44% 50% 6%



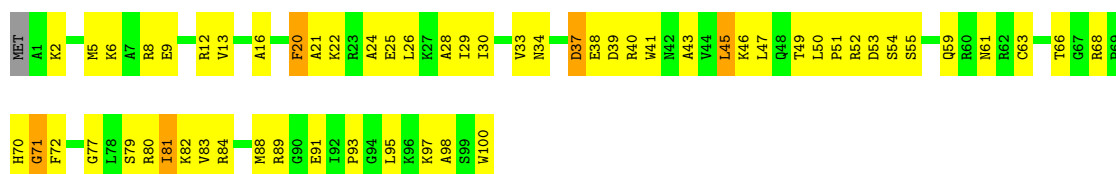
• Molecule 43: 30S ribosomal protein S13

Chain 17: 35% 53% 8%



• Molecule 44: 30S ribosomal protein S14

Chain 18: 42% 52% 5%



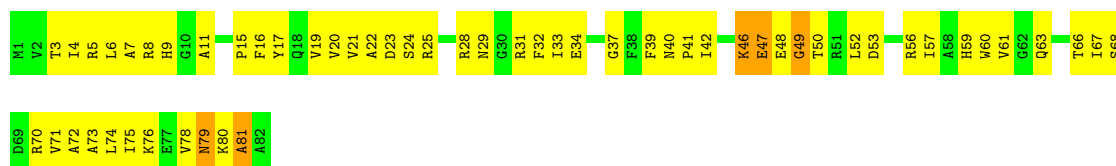
- Molecule 45: 30S ribosomal protein S15

Chain 19: 63% 34% ..



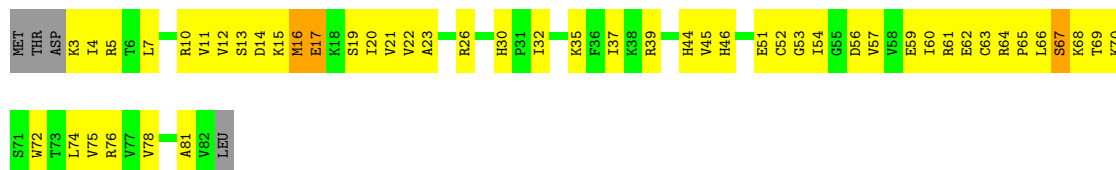
- Molecule 46: 30S ribosomal protein S16

Chain 20: 32% 62% 6%



- Molecule 47: 30S ribosomal protein S17

Chain 21: 36% 56% 5%



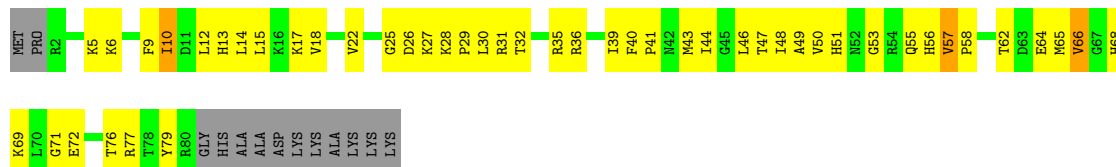
- Molecule 48: 30S ribosomal protein S18

Chain 22: 41% 36% 9% 13%



- Molecule 49: 30S ribosomal protein S19

Chain 23: 34% 49% 14%



- Molecule 50: 30S ribosomal protein S20

Chain 24:  51% 46% ..



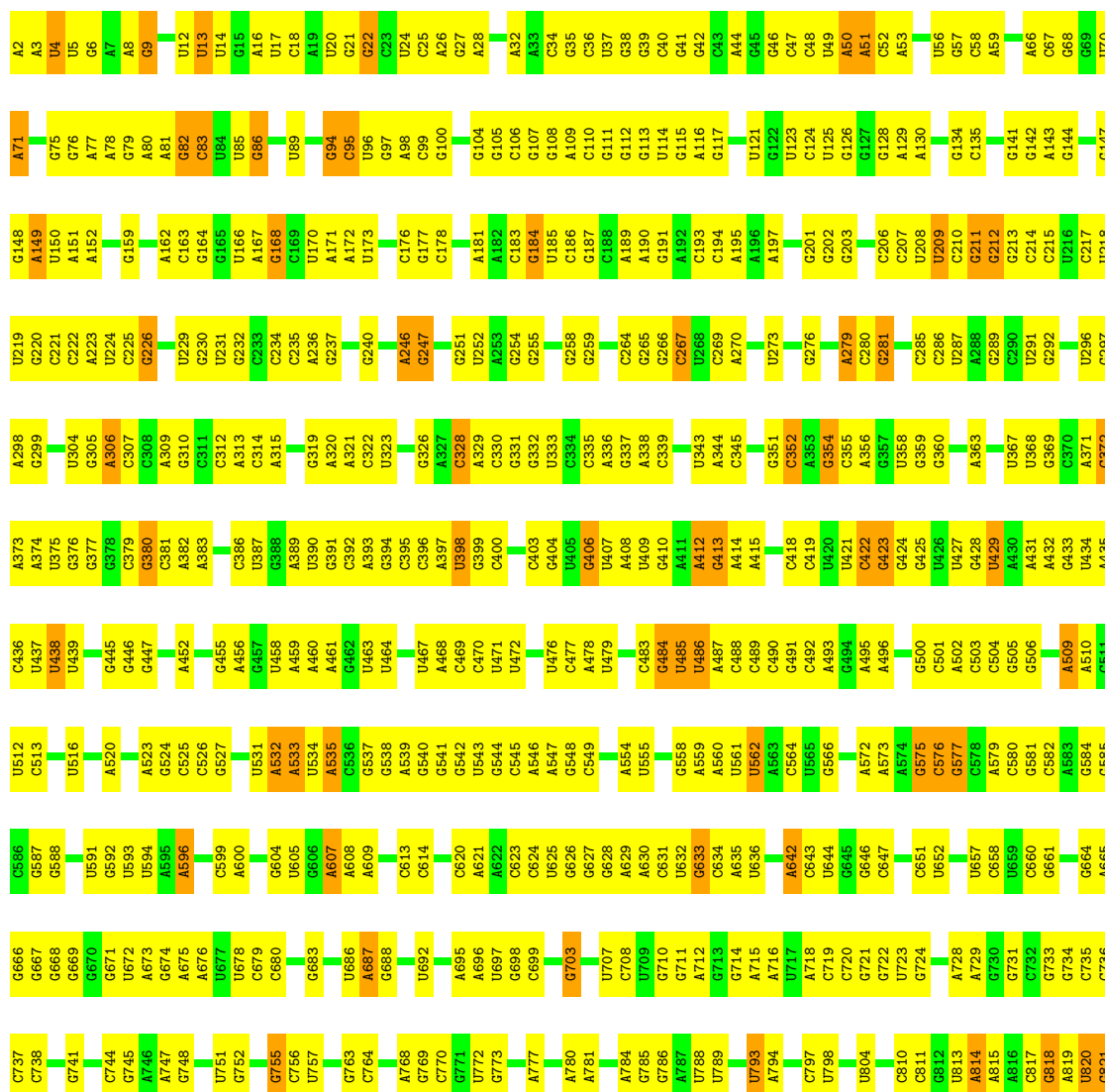
- Molecule 51: 30S ribosomal protein S21

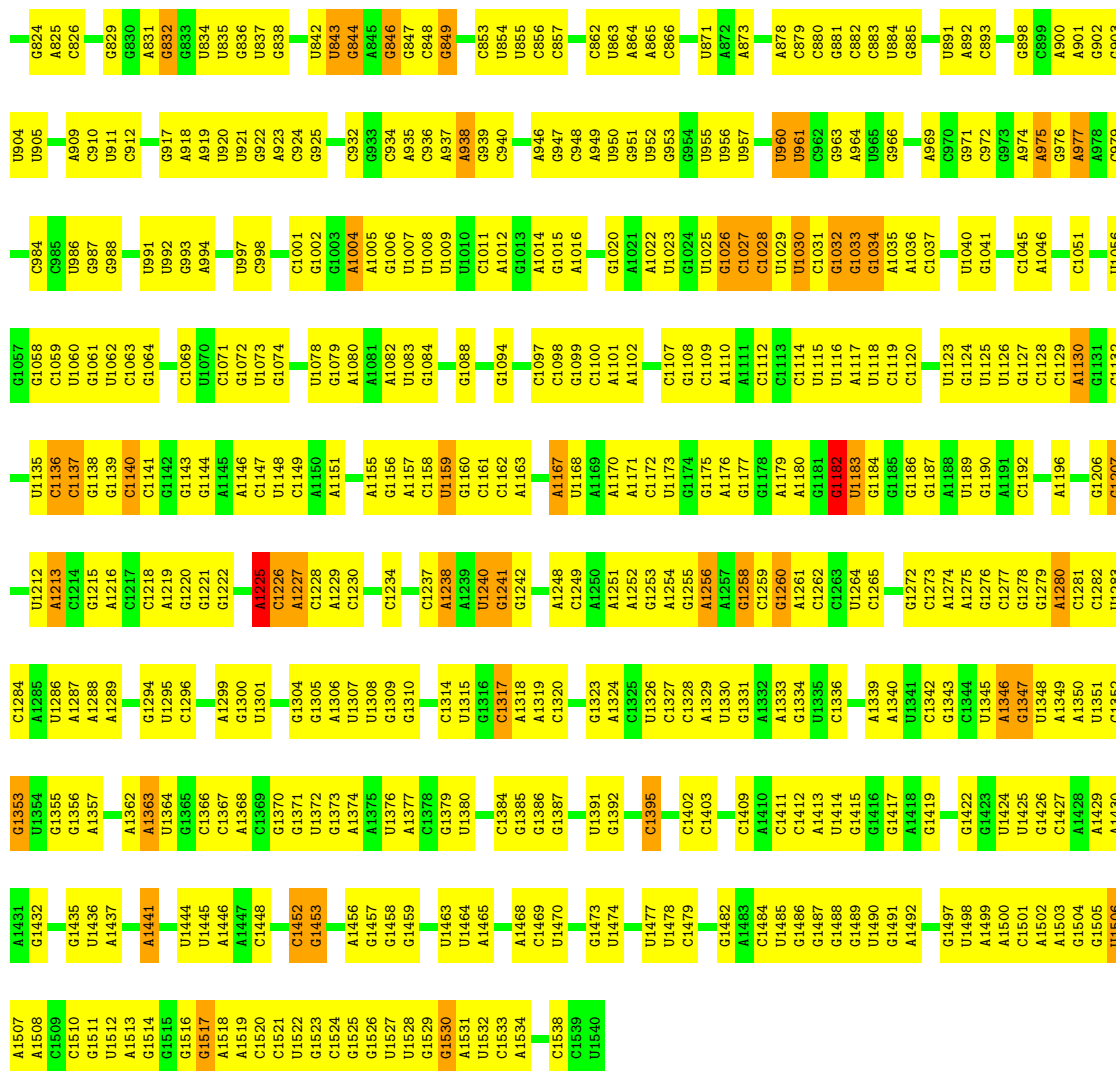
Chain 25:  34% 46% 11% 8%



- Molecule 52: 16S ribosomal RNA

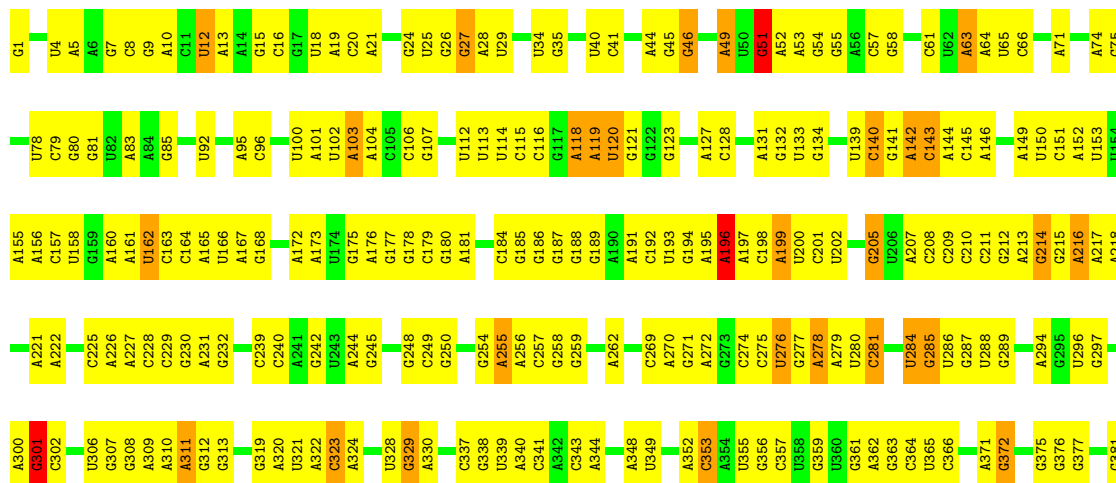
Chain 26:  38% 55% 7%





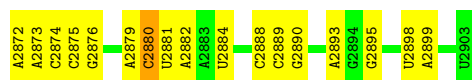
• Molecule 53: 23S ribosomal RNA

Chain 27:



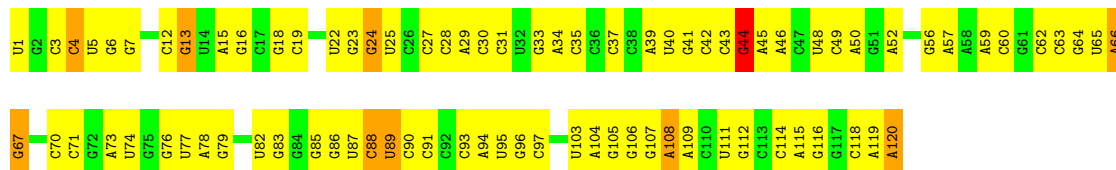
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C1388	U1394	A1395	U1396	C1399	U1400	C1487	C1488	A1403	C1404	U1405	U1406	U1411	A1495	A1496	U1497	C1498	C1499	G1500	G1501	A1502	A1503	A1504	A1505	U1506	C1507	A1508	A1509	G1510	U1511	A1512	U1513	G1514	A1515	G1516	U1520	G1521	A1508	G1524	A1528	G1529	A1535	C1536	U1539	G1540	C1541	U1542	G1543	A1544	A1545	C1546	U1547	U1548	A1549	C1550	A1554																																																																																																																																																																																																																																																																																																																																																																																																																													
G1300	A1301	A1304	C1305	U1316	U1317	U1324	U1325	U1331	C1332	C1320	A1321	U1326	U1327	C1243	A1244	U1329	C1330	G1331	G1332	G1333	G1334	C1335	A1253	A1254	U1340	G1343	U1344	C1345	C1351	U1352	A1262	U1353	A1354	A1355	A1356	A1357	G1361	C1362	A1385	C1446	C1447	C1448	U1372	A1373	C1374	U1375	A1378	U1379	G1459	U1460	C1461	C1464	A1465	A1466	A1467	A1468	A1469																																																																																																																																																																																																																																																																																																																																																																																																																											
G1225	C1229	A1230	C1233	U1234	U1235	U1236	C1239	U1240	C1243	A1244	G1245	C1248	U1249	C1250	C1251	C1252	C1253	A1254	U1340	G1343	U1344	C1345	C1351	U1352	A1262	U1353	A1354	A1355	A1356	A1357	G1361	C1362	A1385	C1446	C1447	C1448	U1372	A1373	C1374	U1375	A1378	U1379	G1459	U1460	C1461	C1464	A1465	A1466	A1467	A1468	A1469																																																																																																																																																																																																																																																																																																																																																																																																																																	
C1145	C1147	U1148	C1149	C1150	C1151	U1234	U1235	U1236	C1239	U1240	C1243	A1244	G1245	C1248	U1249	C1250	C1251	C1252	C1253	A1254	U1340	G1343	U1344	C1345	C1351	U1352	A1262	U1353	A1354	A1355	A1356	A1357	G1361	C1362	A1385	C1446	C1447	C1448	U1372	A1373	C1374	U1375	A1378	U1379	G1459	U1460	C1461	C1464	A1465	A1466	A1467	A1468	A1469																																																																																																																																																																																																																																																																																																																																																																																																																															
C1076	A1077	U1078	C1079	A1080	U1081	U1082	U1083	A1084	U1085	A1086	U1087	A1088	A1089	A1090	G1091	C1092	G1093	A1096	U1097	A1098	A1099	A1100	A1103	C1104	U1105	U1174	G1106	C1110	A1111	U1112	U1113	C1114	G1115	C1118	U1119	G1120	A1046	G1047	C1123	C1124	G1125	A1126	A1127	G1128	A1054	A1055	A1056	A1057	A1058	U1059	U1060	U1061	A1134	C1135	C1138	C1139	C1140	U1141	A1142	A1143	C1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155	C1156	C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201	C1202	C1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455	C1456	C1457	C1458	C1459	C1460	C1461	C1462	C1463	C1464	C1465	C1466	C1467	C1468	C1469	C1470	C1471	C1472	C1473	C1474	C1475	C1476	C1477	C1478	C1479	C1480	C1481	C1482	C1483	C1484	C1485	C1486	C1487	C1488	C1489	C1490	C1491	C1492	C1493	C1494	C1495	C1496	C1497	C1498	C1499	C1500	C1501	C1502	C1503	C1504	C1505	C1506	C1507	C1508	C1509	C1510	C1511	C1512	C1513	C1514	C1515	C1516	C1517	C1518	C1519	C1520	C1521	C1522	C1523	C1524	C1525	C1526	C1527	C1528	C1529	C1530	C1531	C1532	C1533	C1534	C1535	C1536	C1537	C1538	C1539	C1540	C1541	C1542	C1543	C1544	C1545	C1546	C1547	C1548	C1549	C1550	C1551
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A614	U615	C620	A621	C622	C623	C624	A627	A633	C634	C635	C636	C637	A637	C638	C639	C640	C641	C642	C643	C644	C645	C646	C647	C648	C649	C650	C651	C652	C653	C654	C655	C656	C657	C658	C659	C660	C661	C662	C663	C664	C665	C666	C667	C668	C669	C670	C671	C672	C673	C674	C675	C676	C677	C678	C679	C680	C681	C682	C683	C684	C685	C686	C687	C688	C689	C690	C691	C692	C693	C694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	C712	C713	C714	C715	C716	C717	C718	C719	C720	C721	C722	C723	C724	C725	C726	C727	C728	C729	C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835	C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000	C1001	C1002	C1003	C1004	C1005	C1006	C1007	C1008	C1009	C1010	C1011	C1012	C1013	C1014	C1015	C1016	C1017	C1018	C1019	C1020	C1021	C1022	C1023	C1024	C1025	C1026	C1027	C1028	C1029	C1030	C1031	C1032	C1033	C1034	C1035	C1036	C1037	C1038	C1039	C1040	C1041	C1042	C1043	C1044	C1045	C1046	C1047	C1048	C10																																											

A2799	C9723	G2638	C9573	A2497	A2418	U2348	G2277	G2186	G2124	A2062	G1980	U1898	U1818	U1744	C1656
A2800	U2724	A2639	G2574	C2496	U2419	G2349	A2278	U2189	G2125	G2063	A1981	U1899	A1821	A1745	U1657
G2801	A2725	G2640	A2577	C2499	C2420	G2350	A2281	U2197	G2126	C2065	U1982	A1901	A1821	A1746	C1658
G2804	U2728	G2641	G2578	G2502	U2423	A2352	G2282	C2196	G2128	G2066	G1989	G1902	G1824	U1747	U1662
G2805	G2729	G2642	C2579	A2503	C2424	G2353	C2283	U2197	C2129	U2067	G1990	G1903	G1825	C1748	G1663
G2806			U2580	U2504	A2425	G2354	A2284	A2198	U2130	A2069	U1991	G1904	G1826	A1749	A1664
U2807	G2732	U2647	G2581	G2506	G2428	G2355	C2285	A2199	U2131	A2069	G1992	C1905	U1827	A1685	A1685
G2808	A2733	G2648	G2582	U2506	G2429	G2356	C2286	C2200	G2132	A2061	U1993	G1906	G1828	G1666	G1666
A2809	G2737	G2649	G2583	C2507	A2430	G2357	A2287	U2203	G2133	A2062	G1997	G1907	A1829	G1667	A1667
G2810			U2584	G2508	A2430	G2358	A2288	G2204	A2134	C2063	G1996	C1908		A1668	A1668
G2811	U2738	A2657	U2585	G2509	A2435	G2359	G2289	U2203	A2135	C2064	G1997	G1909	C1836	G1764	A1669
G2812	U2739	G2658	U2586			G2360	G2290	G2204	A2136	C2065	G1998	G1910	C1837	U1765	G1670
A2813	A2740	G2659	A2587			G2361	U2291	C2208	U2137	C2066	C1999	U1911	C1838	G1766	U1671
A2814			G2588	C2512		G2362	G2292	G2209	G2138	G2067	C2000	A1912			A1672
G2815	A2741		A2513	A2513	A2439	G2363	G2293	G2210	U2139	U2068	A1913	A1913	G1770	G1770	G1673
	G2742	G2673	A2589	G2514	C2440	G2364	U2210	A2211	G2140	G2069	C2001	C2001	C1843	C1771	G1674
	U2743	A2674	C2515	G2515	U2441	G2365	G2294	A2211	G2141	A2070	G1914	G1914	C1844	A1772	G1675
U2818	G2744	A2675	A2516	A2516	C2442	G2366	G2295		G2142	A2071	U1915	U1915	G1845	A1773	A1676
G2819	A2748	G2676	G2517	C2517	C2443	G2367	U2296	C2215	A2143	C2071	A2009	A1916	G1846	C1774	
A2820			A2518	A2518	G2444	G2368	A2297	G2216	C2144	C2072	G2010	U1917			A1679
A2821	G2751	G2677	G2519	G2519		G2369	A2298		G2145	C2073	U2011	G1921	U1775	U1775	A1680
G2822	C2752	A2679	G2520	C2520	A2448	G2370	U2299	G2221	C2146	U2074	G1922	G1922	A1848	G1776	G1681
A2823			C2521			G2371	C2300	G2222	C2147	U2075	A2013	U1923	G1850	G1779	G1682
						G2372	C2301	G2223	G2148	C2078	A2014	U1924	G1851	U1780	U1683
G2828	U2756	G2681	G2599	G2529	A2450	G2373	U2302	G2224	U2149	U2079	U2016	C1925	U1852	U1781	G1684
A2829	A2757	G2682	A2600			G2374	U2305	A2226	U2150	A2080	G2017	U1926	A1853	U1782	C1685
G2830	U2758	G2683	C2601					C2226	U2151	C2081	G2018	U1926	A1854	G1783	C1686
G2831	G2759	G2684	A2602	G2532	A2453	C2380	G2308		G2152	C2087	A2019	G1929	G1857	A1784	U1693
G2832	G2760	G2685	G2603	U2533	G2454	A2381	A2309	U2229	C2153	G2087	A2020	U1930	A1858	A1785	C1694
U2833	U2687	G2686	U2604	A2534	G2455	G2382	C2310	G2230	A2154	A2088	C2021	U1931			G1695
G2834	G2688	G2687	G2605	G2535	G2456	G2383	A2311	G2231	U2155		U2022	G1935	G1788	G1788	G1696
U2835	U2689	G2688	C2606	G2536	G2457	G2384	U2312	G2232	G2156	A2094	G2024	U1936	U1789	C1790	G1697
U2836	G2690	G2689	G2607	U2537	A2459	G2385	U2313	G2233	G2157	A2095	C2025	A1936	U1864	A1698	A1698
A2837	U2691	G2690	U2609	G2538	U2460	G2386	A2314	G2234	A2158	C2096	U2026	A1937	A1866	A1791	G1699
G2838	G2692	G2691	C2609	G2539	A2461	G2387	G2315	G2235	A2159	C2097	G2027	A1938	G1867	U1794	G1702
G2839	G2693	U2690	U2613	G2540	C2462	G2388	G2316	G2236	C2160	U2098	U2028	U1943	G1868	C1795	G1702
C2840			U2614	A2541	G2463	G2389	G2317	G2237	G2161	U2099	G2029	U1943	G1869	U1796	G1703
C2841	A2764	U2690	G2615	G2542	G2464	G2390	A2317	U2240	G2162		A2030	U1946	C1870	U1797	C1704
G2842	A2765	G2691	C2616	G2543	G2465	G2391	G2318	A2241	A2163	C2103	A2031	C1947	A1871	U1798	A1705
G2843	A2766	G2692	U2617	G2544		G2392	G2319	G2242	C2164	C2104	G2032	U1947	A1872	G1799	
G2844	C2771	U2693	G2618		G2472	C2393	U2320	U2243	C2165	U2105	A2033	U1955	G1873	C1800	U1709
U2845	A2778	A2700	C2619	A2547		C2394	U2321	U2244	C2166	U2106	G2034	U1956	G1874	A1801	G1710
G2846	U2779	G2702	G2620	U2552	C2476	U2401	A2322	U2245	U2167	U2107	G2035	U1957	G1875	A1802	
U2847	G2780	G2703	G2621	G2553	U2477	U2402	A2323	G2246	A2168	A2108	C2036	C1957	A1876	A1803	A1713
G2848		C2704	U2622	G2554	U2478	U2403	G2325	A2247	A2169	U2109	A2037	G1964	A1877	C1804	U1714
U2849	U2783	G2705	G2623	U2555	A2479	U2404	C2326	C2248	A2170	G2110	G2038	G1964	G1878	G1715	G1715
A2850	U2784	G2706	G2624	U2556	U2479	U2405	A2327	C2249	A2171	U2111	U2039	G1967	C1879	C1806	G1721
G2853	G2785	G2707	G2625	C2557	C2480	G2406	A2328	U2249	U2172	G2112	G2040	C1967	U1880	A1808	A1722
G2854	U2786	G2708	G2626	G2558	G2481	U2407	U2329	C2261	A2173	U2113	U2041	G1968	C1881	U1809	
	C2787	A2711	C2627		A2482	U2408	G2330	U2262	C2174	U2114	A2042	A1969	U1882	A1809	U1729
	G2788	G2712	C2628	U2561	C2483	G2409	U2334	A2266	C2175	A2114	C2043	A1970	U1883	G1810	C1730
G2859	U2789	U2713	G2629	U2562	G2488	G2410	U2334	A2267	A2176	G2115	C2043	A1971	U1884	G1811	U1730
A2860	U2790	G2714	G2630	U2563	U2489	A2411	G2342	A2268	U2180	A2117	G2046	G1972	U1885	G1813	C1732
U2861	G2791	G2715	G2631	U2564	G2490	A2412	U2343	U2272	U2181	A2118	G2047	U1976	G1888	G1814	
G2862	U2792	C2716	A2632	A2565	G2491	G2413	U2344	U2273	U2182	A2119	G2048	A1977	C1893	A1815	G1738
	C2793	U2717	G2633	A2566	U2492	G2414	U2345	A2274	A2183	A2119	G2049	A1978	C1894	A1739	G1740
U2866	G2794	G2719	A2634	A2567	U2493	G2415	A2346		U2185		C2050	U1979			
G2867	C2795	U2720	G2635	G2568	G2494	G2416	A2346								
A2868		G2722	U2637	A2572	G2494	G2417	C2347								



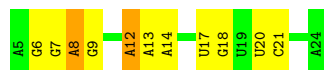
• Molecule 54: 5S ribosomal RNA

Chain 28: 30% 62% 8%



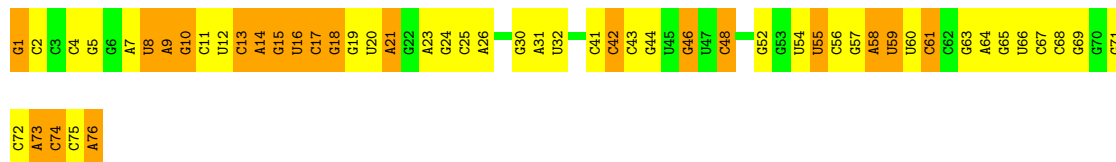
• Molecule 55: mRNA

Chain 29: 45% 45% 10%



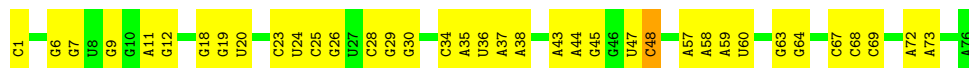
• Molecule 56: A-site tRNAPhe

Chain 30: 29% 43% 28%



• Molecule 57: P-site tRNAfMet

Chain 31: 52% 47% 1%



• Molecule 58: E-site tRNAfMet

Chain 32: 22% 56% 22%



• Molecule 59: GTP pyrophosphokinase

Chain 33: 38% 45% 6% 10%

[illegible]

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	77862	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	30488	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.29	0/2121	0.64	0/2852
10	J	0.30	0/947	0.63	0/1268
11	K	0.30	0/1054	0.66	0/1403
12	L	0.33	0/1093	0.59	0/1460
13	M	0.32	0/973	0.63	0/1301
14	N	0.28	0/902	0.57	0/1209
15	O	0.32	0/929	0.61	0/1242
16	P	0.32	0/960	0.56	0/1278
17	Q	0.35	0/829	0.67	1/1107 (0.1%)
18	R	0.27	0/864	0.65	0/1156
19	S	0.30	0/744	0.61	0/994
2	B	0.33	0/1586	0.62	0/2134
20	T	0.35	0/787	0.69	0/1051
21	U	0.32	0/766	0.58	0/1025
22	V	0.34	0/582	0.60	0/769
23	W	0.34	0/635	0.63	0/848
24	X	0.31	0/510	0.59	0/677
25	Y	0.30	0/453	0.55	0/605
26	Z	0.37	0/531	0.91	3/709 (0.4%)
27	1	0.28	0/450	0.56	0/599
28	2	0.32	0/416	0.57	0/554
29	3	0.35	0/380	0.58	0/498
3	C	0.34	0/1571	0.62	0/2113
30	4	0.32	0/513	0.61	0/676
31	5	0.29	0/303	0.63	0/397
32	6	0.37	0/1735	0.60	0/2338
33	7	0.32	0/1651	0.60	0/2225
34	8	0.32	0/1665	0.60	0/2227
35	9	0.31	0/1169	0.70	1/1573 (0.1%)
36	10	0.34	0/835	0.64	0/1128
37	11	0.29	0/1195	0.60	0/1602
38	12	0.31	0/989	0.60	0/1326
39	13	0.33	0/1034	0.66	0/1375
4	D	0.34	0/1434	0.58	0/1926

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

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

Mol	Chain	#Chirality outliers	#Planarity outliers
52	26	0	9
53	27	0	22
56	30	0	1
59	33	0	2
All	All	0	34

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

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

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

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

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

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

5.2 Too-close contacts

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

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

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

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

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

The worst 5 of 6144 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:33:17:PRO:HB3	59:33:39:TRP:NE1	1.57	1.18
52:26:484:G:H4'	52:26:485:U:H5'	1.23	1.18
51:25:20:ARG:HH22	52:26:1538:C:H1'	1.05	1.13
59:33:65:ILE:HG21	59:33:157:ILE:HD11	1.31	1.11
59:33:188:ARG:HH12	59:33:377:LEU:HA	1.08	1.11

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	269/273 (98%)	226 (84%)	34 (13%)	9 (3%)	4	36
2	B	207/209 (99%)	165 (80%)	29 (14%)	13 (6%)	1	22
3	C	199/201 (99%)	164 (82%)	23 (12%)	12 (6%)	2	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	175/179 (98%)	140 (80%)	27 (15%)	8 (5%)	2	28
5	E	174/177 (98%)	145 (83%)	22 (13%)	7 (4%)	3	31
6	F	147/149 (99%)	119 (81%)	16 (11%)	12 (8%)	1	15
7	G	129/165 (78%)	92 (71%)	17 (13%)	20 (16%)	0	4
8	H	139/142 (98%)	106 (76%)	27 (19%)	6 (4%)	3	29
9	I	140/142 (99%)	127 (91%)	7 (5%)	6 (4%)	3	29
10	J	120/123 (98%)	101 (84%)	14 (12%)	5 (4%)	3	29
11	K	141/144 (98%)	116 (82%)	16 (11%)	9 (6%)	1	22
12	L	134/136 (98%)	110 (82%)	20 (15%)	4 (3%)	5	38
13	M	118/127 (93%)	99 (84%)	14 (12%)	5 (4%)	3	29
14	N	114/117 (97%)	92 (81%)	16 (14%)	6 (5%)	2	25
15	O	112/115 (97%)	88 (79%)	20 (18%)	4 (4%)	4	34
16	P	115/118 (98%)	108 (94%)	5 (4%)	2 (2%)	10	48
17	Q	101/103 (98%)	82 (81%)	16 (16%)	3 (3%)	5	38
18	R	108/110 (98%)	85 (79%)	19 (18%)	4 (4%)	4	33
19	S	91/100 (91%)	73 (80%)	13 (14%)	5 (6%)	2	25
20	T	100/104 (96%)	80 (80%)	13 (13%)	7 (7%)	1	19
21	U	92/94 (98%)	76 (83%)	13 (14%)	3 (3%)	4	36
22	V	73/85 (86%)	64 (88%)	7 (10%)	2 (3%)	5	40
23	W	75/78 (96%)	67 (89%)	6 (8%)	2 (3%)	5	40
24	X	61/63 (97%)	52 (85%)	5 (8%)	4 (7%)	1	21
25	Y	56/59 (95%)	50 (89%)	4 (7%)	2 (4%)	4	34
26	Z	64/70 (91%)	50 (78%)	9 (14%)	5 (8%)	1	16
27	1	54/57 (95%)	42 (78%)	6 (11%)	6 (11%)	0	9
28	2	48/55 (87%)	41 (85%)	6 (12%)	1 (2%)	8	44
29	3	44/46 (96%)	35 (80%)	7 (16%)	2 (4%)	3	28
30	4	62/65 (95%)	51 (82%)	6 (10%)	5 (8%)	1	15
31	5	36/38 (95%)	26 (72%)	6 (17%)	4 (11%)	0	9
32	6	216/241 (90%)	177 (82%)	31 (14%)	8 (4%)	4	33
33	7	204/233 (88%)	172 (84%)	26 (13%)	6 (3%)	5	38
34	8	203/206 (98%)	158 (78%)	30 (15%)	15 (7%)	1	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	9	155/167 (93%)	116 (75%)	25 (16%)	14 (9%)	1	14
36	10	98/135 (73%)	76 (78%)	15 (15%)	7 (7%)	1	19
37	11	149/179 (83%)	123 (83%)	17 (11%)	9 (6%)	2	22
38	12	127/130 (98%)	112 (88%)	13 (10%)	2 (2%)	11	49
39	13	125/130 (96%)	98 (78%)	17 (14%)	10 (8%)	1	16
40	14	96/103 (93%)	77 (80%)	11 (12%)	8 (8%)	1	15
41	15	114/129 (88%)	92 (81%)	18 (16%)	4 (4%)	4	35
42	16	121/124 (98%)	98 (81%)	11 (9%)	12 (10%)	1	11
43	17	112/118 (95%)	90 (80%)	11 (10%)	11 (10%)	1	12
44	18	98/101 (97%)	71 (72%)	20 (20%)	7 (7%)	1	19
45	19	86/89 (97%)	73 (85%)	8 (9%)	5 (6%)	2	23
46	20	80/82 (98%)	64 (80%)	12 (15%)	4 (5%)	2	26
47	21	78/84 (93%)	53 (68%)	19 (24%)	6 (8%)	1	17
48	22	63/75 (84%)	48 (76%)	9 (14%)	6 (10%)	1	12
49	23	77/92 (84%)	60 (78%)	13 (17%)	4 (5%)	2	26
50	24	83/87 (95%)	75 (90%)	5 (6%)	3 (4%)	4	34
51	25	63/71 (89%)	44 (70%)	9 (14%)	10 (16%)	0	4
59	33	663/750 (88%)	550 (83%)	78 (12%)	35 (5%)	2	25
All	All	6509/6970 (93%)	5299 (81%)	841 (13%)	369 (6%)	4	23

5 of 369 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	216/218 (99%)	215 (100%)	1 (0%)	90	95
2	B	164/164 (100%)	163 (99%)	1 (1%)	87	94
3	C	165/165 (100%)	164 (99%)	1 (1%)	87	94
4	D	148/150 (99%)	146 (99%)	2 (1%)	69	86
5	E	137/138 (99%)	136 (99%)	1 (1%)	85	93
6	F	114/114 (100%)	113 (99%)	1 (1%)	81	90
7	G	100/123 (81%)	99 (99%)	1 (1%)	78	89
8	H	109/110 (99%)	109 (100%)	0	100	100
9	I	116/116 (100%)	116 (100%)	0	100	100
10	J	103/104 (99%)	103 (100%)	0	100	100
11	K	102/103 (99%)	102 (100%)	0	100	100
12	L	109/109 (100%)	109 (100%)	0	100	100
13	M	100/103 (97%)	99 (99%)	1 (1%)	78	89
14	N	86/87 (99%)	84 (98%)	2 (2%)	53	77
15	O	99/100 (99%)	99 (100%)	0	100	100
16	P	89/90 (99%)	89 (100%)	0	100	100
17	Q	84/84 (100%)	84 (100%)	0	100	100
18	R	93/93 (100%)	93 (100%)	0	100	100
19	S	80/84 (95%)	79 (99%)	1 (1%)	71	86
20	T	83/85 (98%)	82 (99%)	1 (1%)	74	87
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%)	63	83
27	1	47/48 (98%)	47 (100%)	0	100	100
28	2	45/49 (92%)	45 (100%)	0	100	100
29	3	38/38 (100%)	38 (100%)	0	100	100
30	4	51/52 (98%)	51 (100%)	0	100	100
31	5	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	6	180/199 (90%)	179 (99%)	1 (1%)	87	94
33	7	170/190 (90%)	168 (99%)	2 (1%)	74	87
34	8	172/173 (99%)	171 (99%)	1 (1%)	87	94
35	9	119/126 (94%)	117 (98%)	2 (2%)	63	83
36	10	87/116 (75%)	86 (99%)	1 (1%)	76	88
37	11	124/147 (84%)	124 (100%)	0	100	100
38	12	104/105 (99%)	104 (100%)	0	100	100
39	13	105/107 (98%)	103 (98%)	2 (2%)	60	81
40	14	86/90 (96%)	86 (100%)	0	100	100
41	15	89/99 (90%)	89 (100%)	0	100	100
42	16	103/104 (99%)	103 (100%)	0	100	100
43	17	92/96 (96%)	91 (99%)	1 (1%)	76	88
44	18	83/84 (99%)	81 (98%)	2 (2%)	52	76
45	19	76/77 (99%)	76 (100%)	0	100	100
46	20	65/65 (100%)	65 (100%)	0	100	100
47	21	74/78 (95%)	74 (100%)	0	100	100
48	22	56/65 (86%)	55 (98%)	1 (2%)	62	83
49	23	70/79 (89%)	70 (100%)	0	100	100
50	24	65/66 (98%)	65 (100%)	0	100	100
51	25	55/61 (90%)	55 (100%)	0	100	100
59	33	452/635 (71%)	449 (99%)	3 (1%)	85	93
All	All	5303/5698 (93%)	5273 (99%)	30 (1%)	88	94

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

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

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

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

5.3.3 RNA ⓘ

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

5 of 618 RNA backbone outliers are listed below:

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

5 of 24 RNA pucker outliers are listed below:

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

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.