



wwPDB EM Map/Model Validation Report ⓘ

Sep 20, 2016 – 07:42 PM EDT

PDB ID : 5KPX
EMDB ID: : EMD-8282
Title : Structure of RelA bound to ribosome in presence of A/R tRNA (Structure IV)
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 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

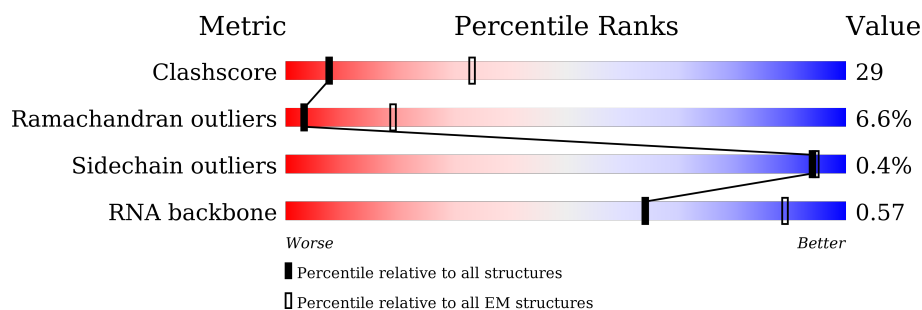
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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.




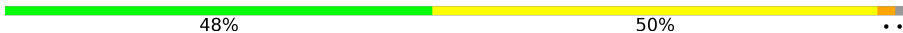



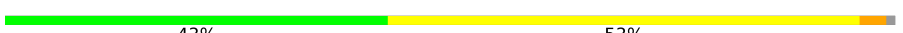
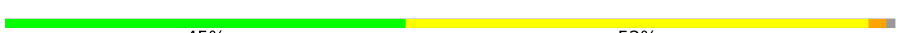




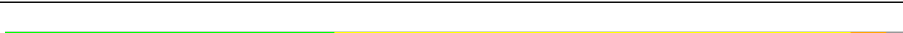













Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	44% 51% . .
2	B	209	44% 56% .
3	C	201	36% 58% 6%
4	D	179	39% 57% . .
5	E	177	45% 53% ..
6	F	149	38% 55% 7%
7	G	165	24% 50% . . 21%
8	H	142	34% 59% 6% .


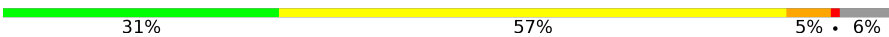
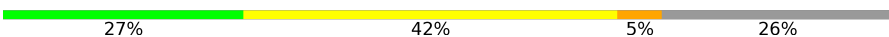


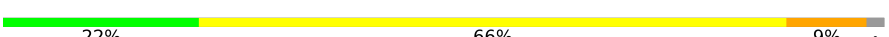
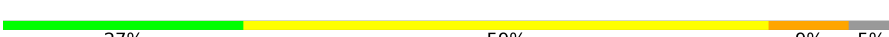
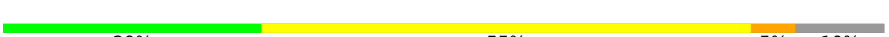
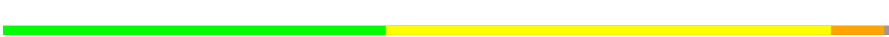

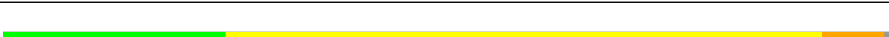


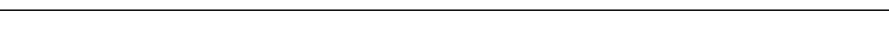
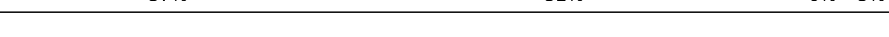
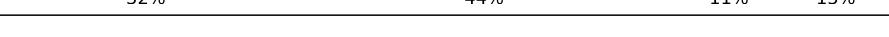


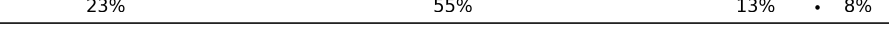
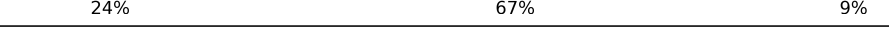


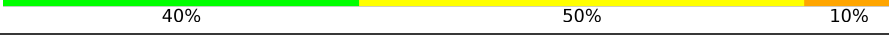
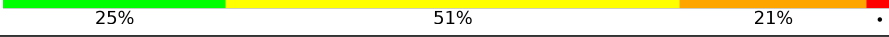

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	I	142	 49% 49% .
10	J	123	 48% 50% ..
11	K	144	 51% 39% 8% ..
12	L	136	 47% 47% 6%
13	M	127	 46% 45% . 6%
14	N	117	 43% 53% ..
15	O	115	 45% 52% ..
16	P	118	 49% 48% ..
17	Q	103	 31% 61% 8%
18	R	110	 53% 42% 5%
19	S	100	 43% 49% . 7%
20	T	104	 37% 58% . .
21	U	94	 47% 50% .
22	V	85	 42% 42% . 12%
23	W	78	 44% 53% ..
24	X	63	 38% 54% 8%
25	Y	59	 56% 36% 7% .
26	Z	70	 37% 50% 7% 6%
27	1	57	 39% 53% 7% .
28	2	55	 45% 44% . 9%
29	3	46	 50% 48% .
30	4	65	 43% 54% ..
31	5	38	 47% 50% .
32	6	241	 38% 49% . 10%
33	7	233	 39% 47% . 12%

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	33	750	<div><div></div><div>37%</div><div>46%</div><div>7%</div><div>10%</div></div>

2 Entry composition [i](#)

There are 59 unique types of molecules in this entry. The entry contains 154603 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L2.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 55 is a RNA chain called mRNA.

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

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

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

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

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

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

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

- Molecule 59 is a protein called GTP pyrophosphokinase.

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

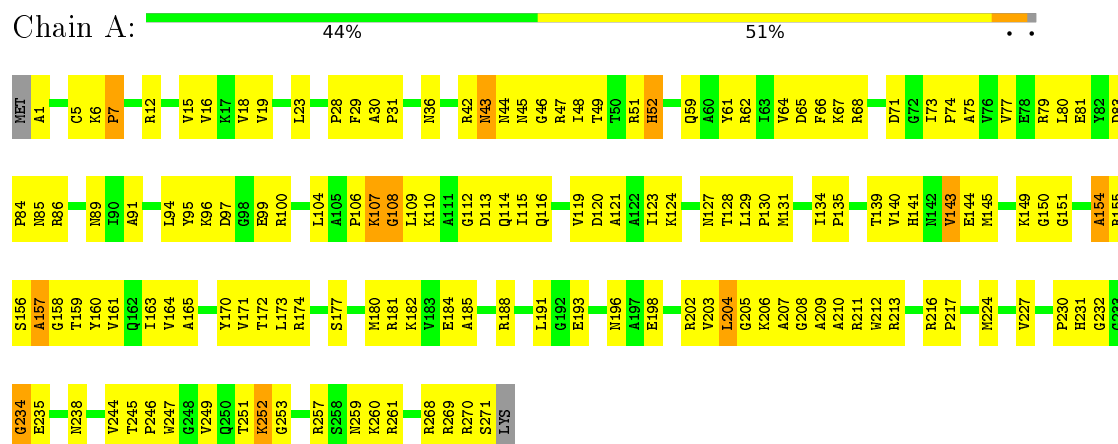
There are 7 discrepancies between the modelled and reference sequences:

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

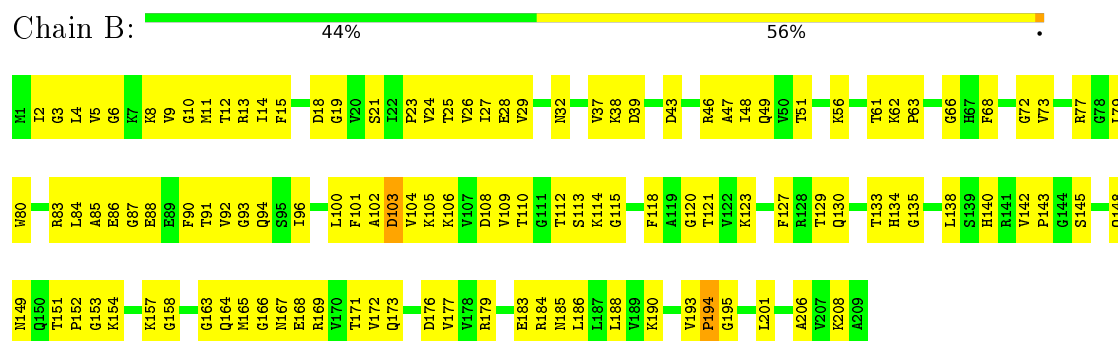
3 Residue-property plots

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



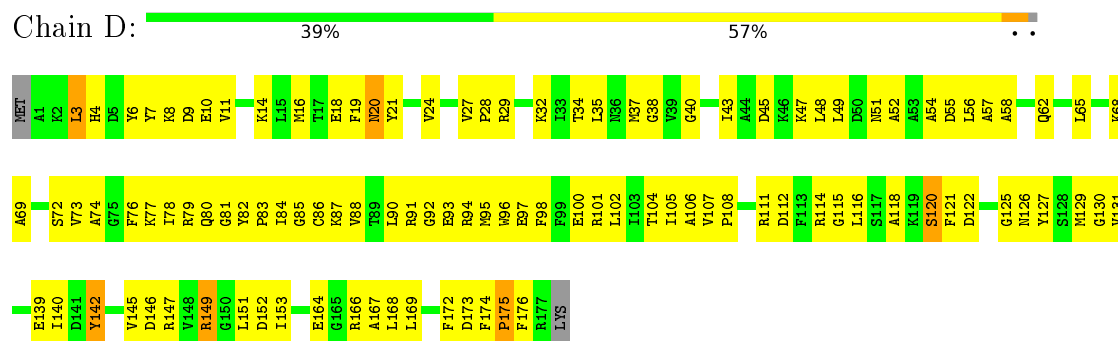
- Molecule 2: 50S ribosomal protein L3



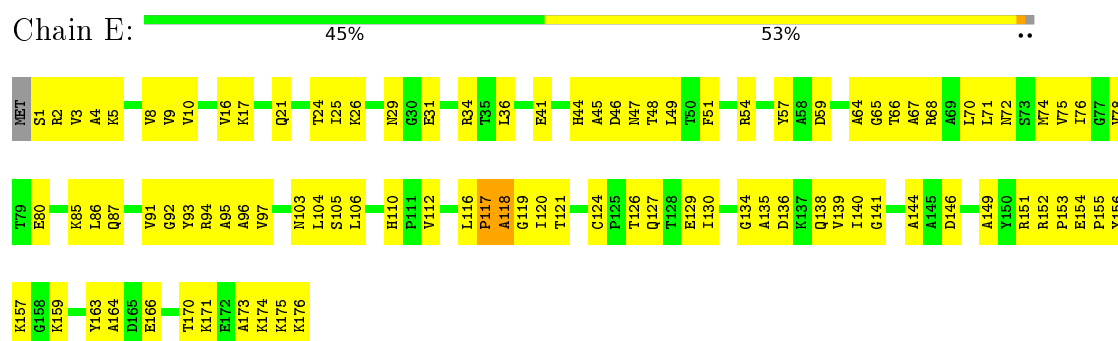
- Molecule 3: 50S ribosomal protein L4



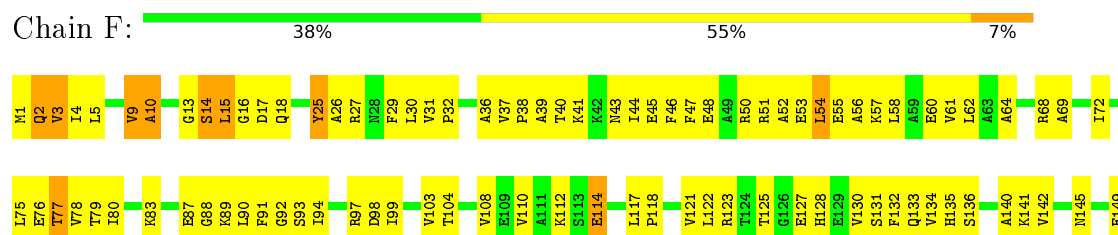
- Molecule 4: 50S ribosomal protein L5



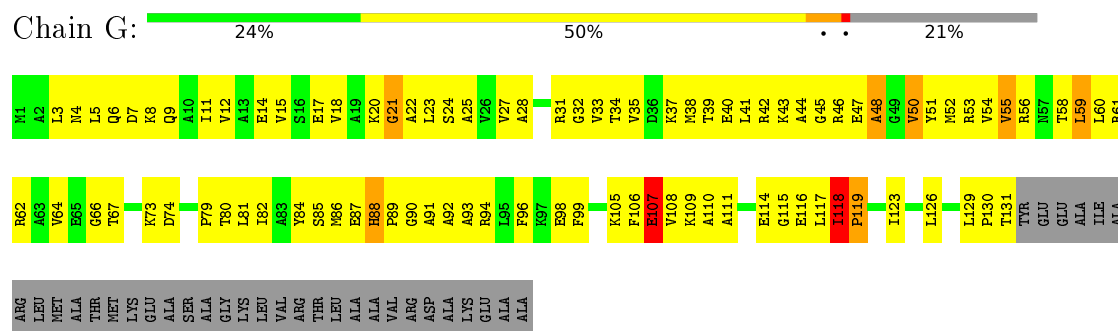
- Molecule 5: 50S ribosomal protein L6



- Molecule 6: 50S ribosomal protein L9



- Molecule 7: 50S ribosomal protein L10



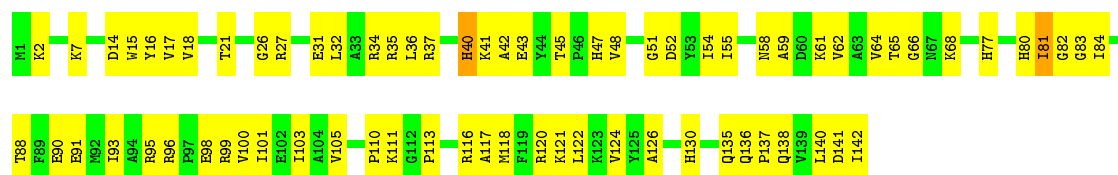
- Molecule 8: 50S ribosomal protein L11





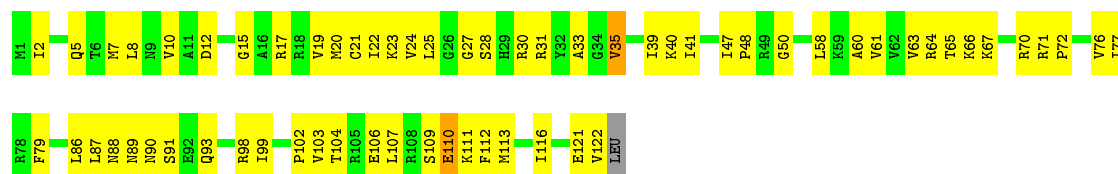
• Molecule 9: 50S ribosomal protein L13

Chain I: 49% 49%



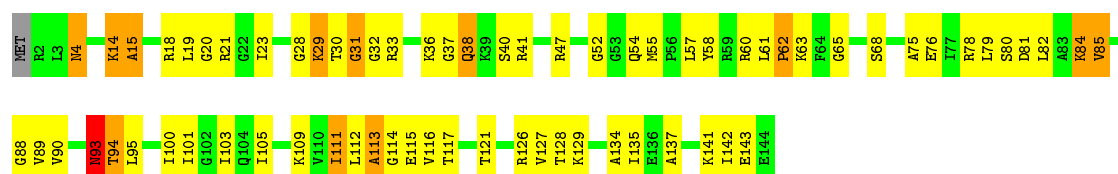
• Molecule 10: 50S ribosomal protein L14

Chain J: 48% 50%



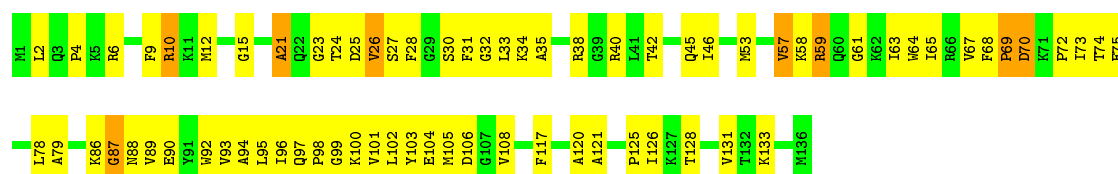
• Molecule 11: 50S ribosomal protein L15

Chain K: 51% 39% 8%

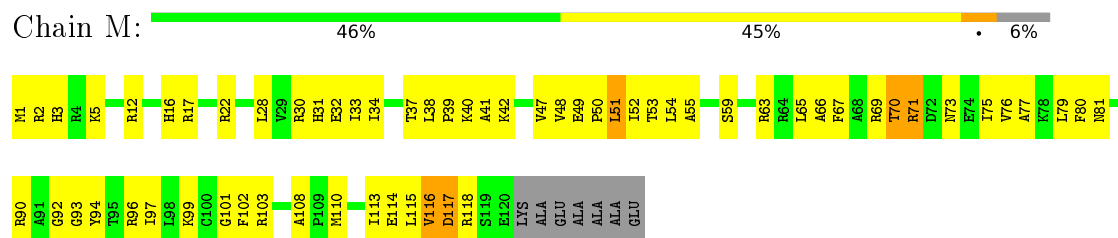


• Molecule 12: 50S ribosomal protein L16

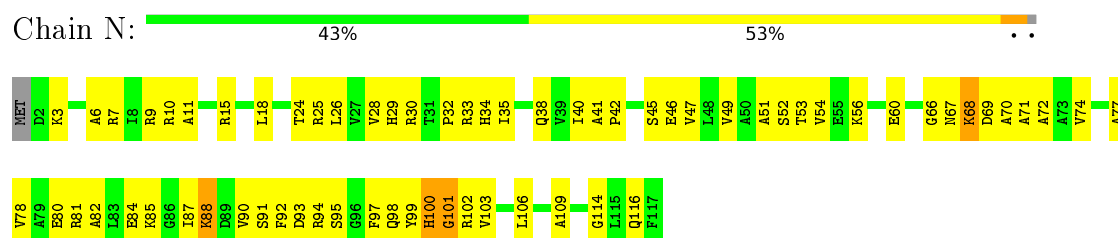
Chain L: 47% 47% 6%



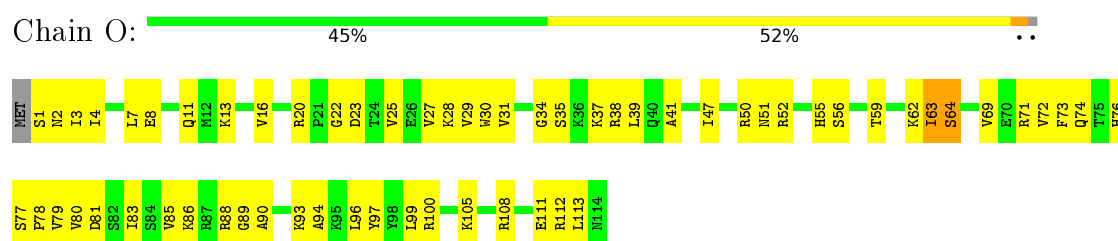
• Molecule 13: 50S ribosomal protein L17



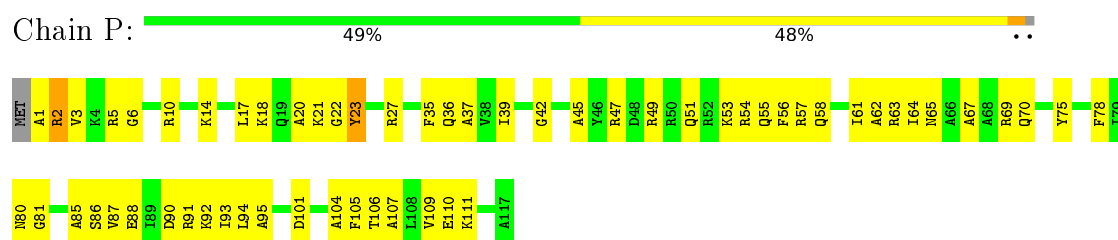
- Molecule 14: 50S ribosomal protein L18



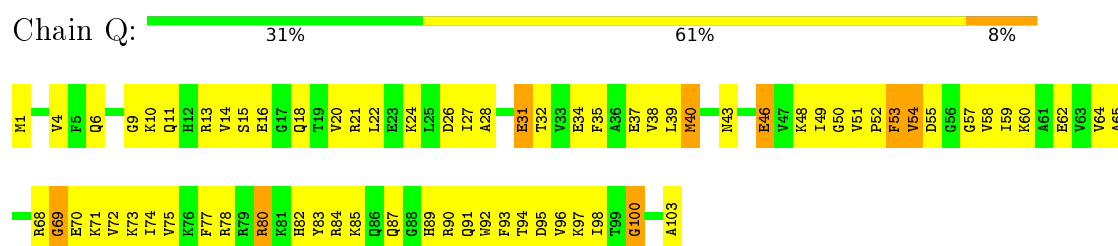
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20

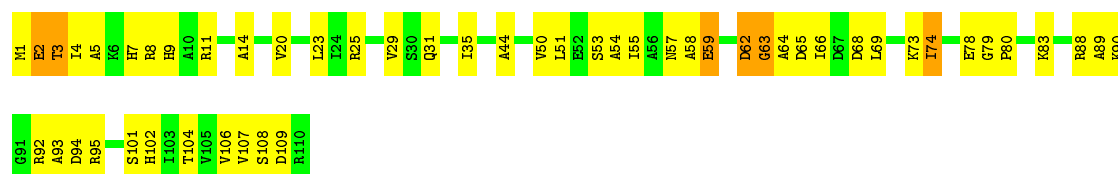


- Molecule 17: 50S ribosomal protein L21



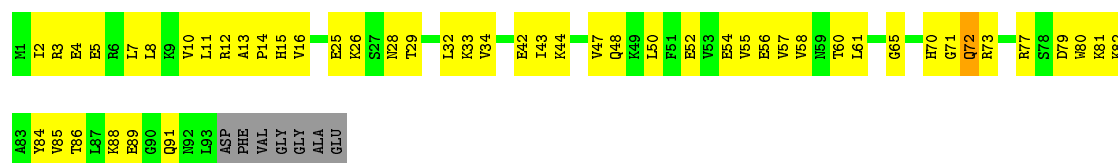
- Molecule 18: 50S ribosomal protein L22





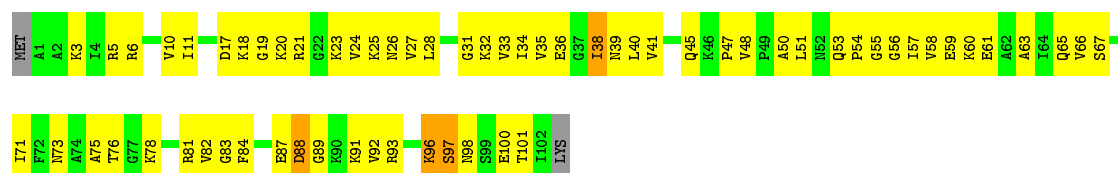
• Molecule 19: 50S ribosomal protein L23

Chain S: 43% 49% 7%



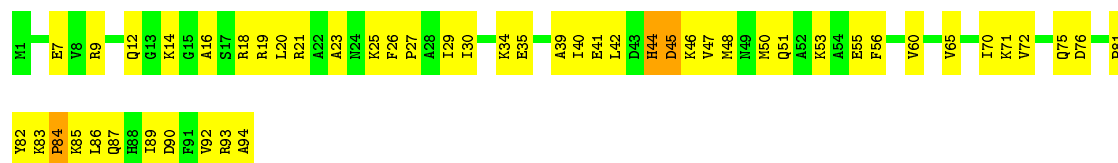
• Molecule 20: 50S ribosomal protein L24

Chain T: 37% 58% . .



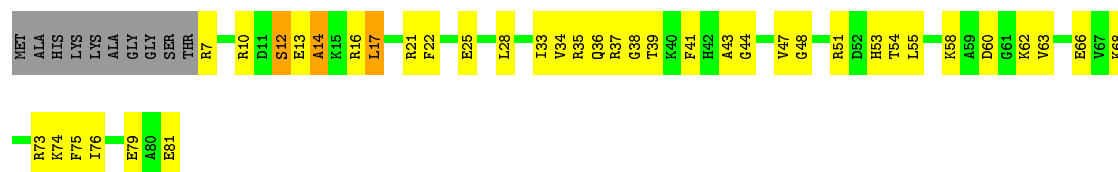
• Molecule 21: 50S ribosomal protein L25

Chain U: 47% 50% .



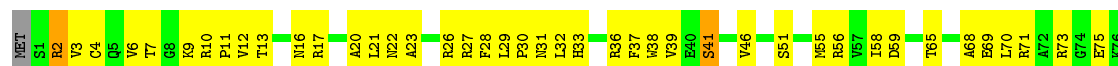
• Molecule 22: 50S ribosomal protein L27

Chain V: 42% 42% 12%



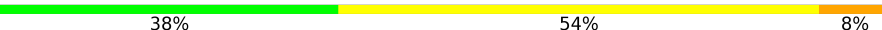
• Molecule 23: 50S ribosomal protein L28

Chain W: 44% 53% . .



Y77

- Molecule 24: 50S ribosomal protein L29

Chain X: 



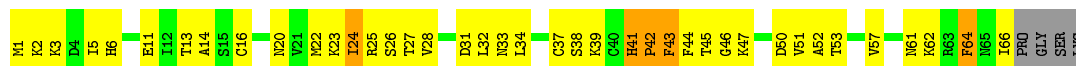
- Molecule 25: 50S ribosomal protein L30

Chain Y: 



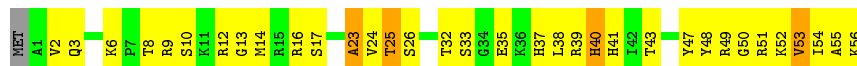
- Molecule 26: 50S ribosomal protein L31

Chain Z: 



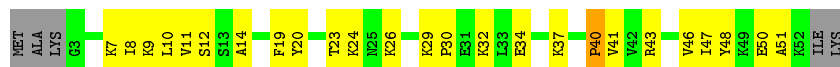
- Molecule 27: 50S ribosomal protein L32

Chain 1: 



- Molecule 28: 50S ribosomal protein L33

Chain 2: 



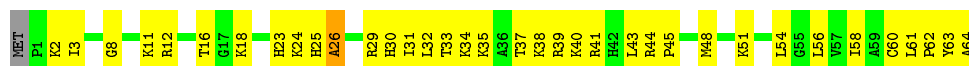
- Molecule 29: 50S ribosomal protein L34

Chain 3: 



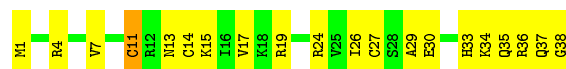
- Molecule 30: 50S ribosomal protein L35

Chain 4: 



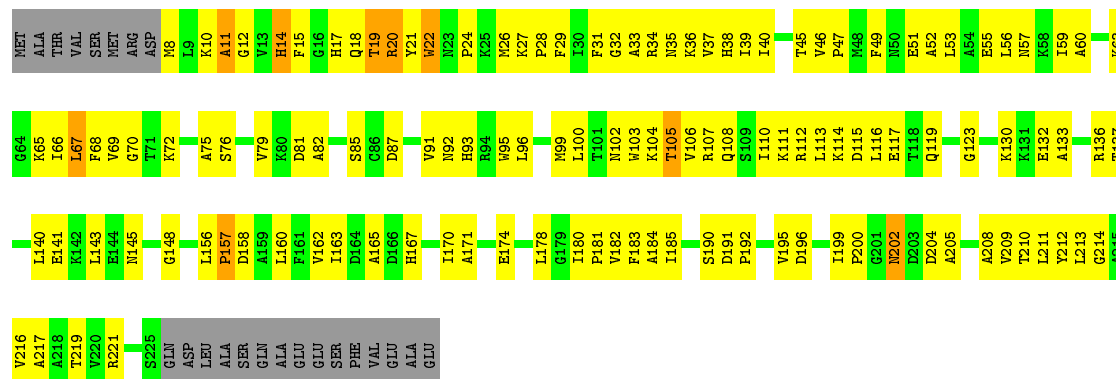
- Molecule 31: 50S ribosomal protein L36

Chain 5: 47% 50%



- Molecule 32: 30S ribosomal protein S2

Chain 6:  38% 49% 10%



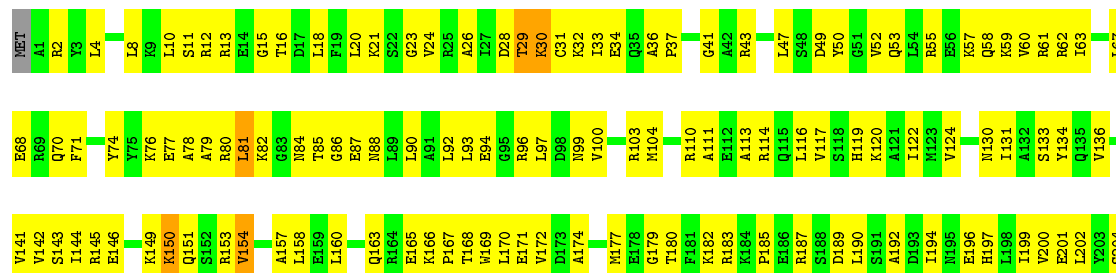
- Molecule 33: 30S ribosomal protein S3

Chain 7:  39% 47% 12%



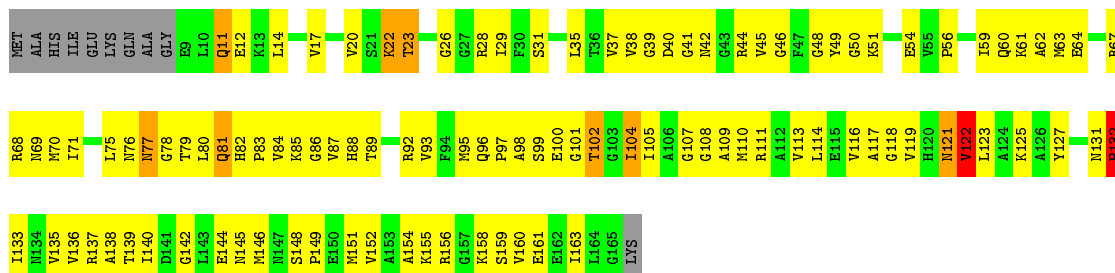
- Molecule 34: 30S ribosomal protein S4

Chain 8: 39% 58% .

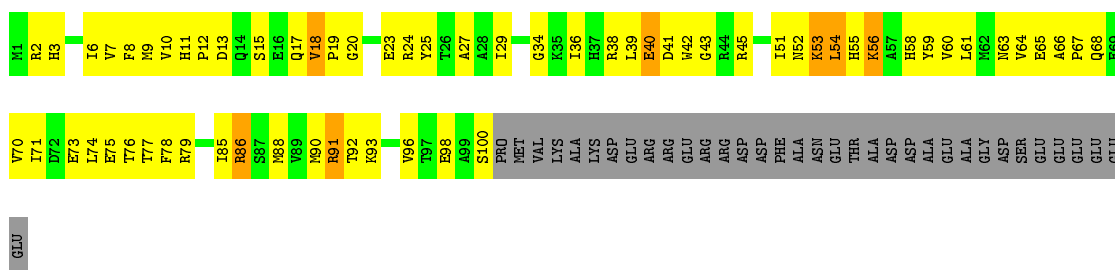


K205

- Molecule 35: 30S ribosomal protein S5

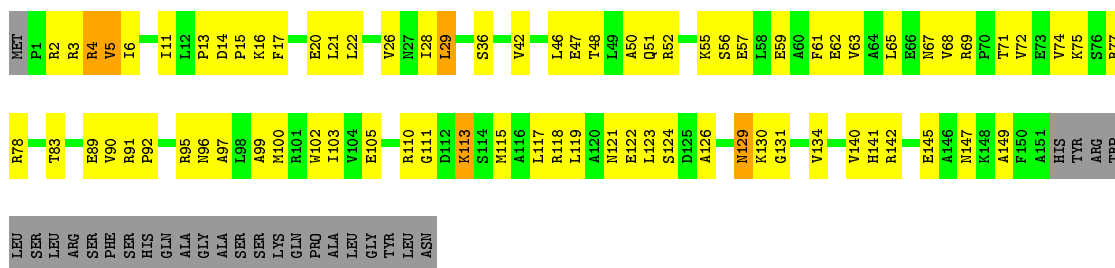
Chain 9:  31% 57% 5% • 6%

- Molecule 36: 30S ribosomal protein S6

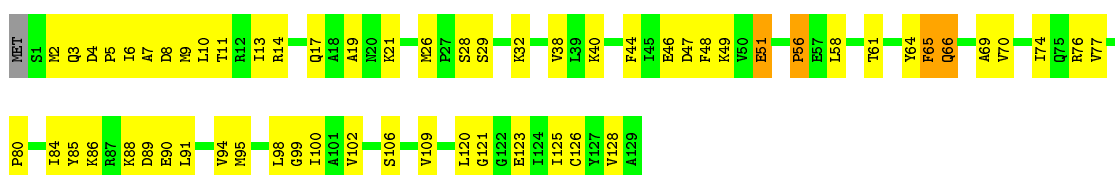
Chain 10:  27% 42% 5% 26%

GLU

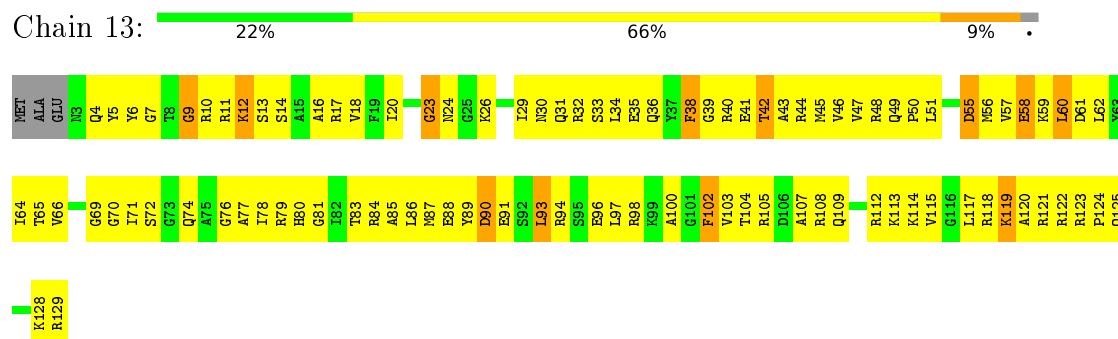
- Molecule 37: 30S ribosomal protein S7

Chain 11:  41% 40% • 16%

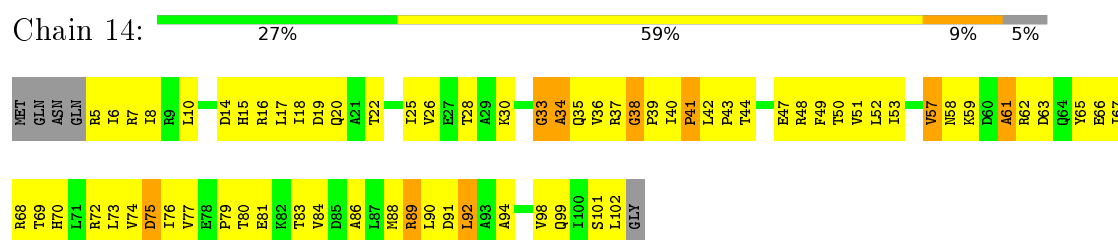
- Molecule 38: 30S ribosomal protein S8

Chain 12:  53% 43% • •

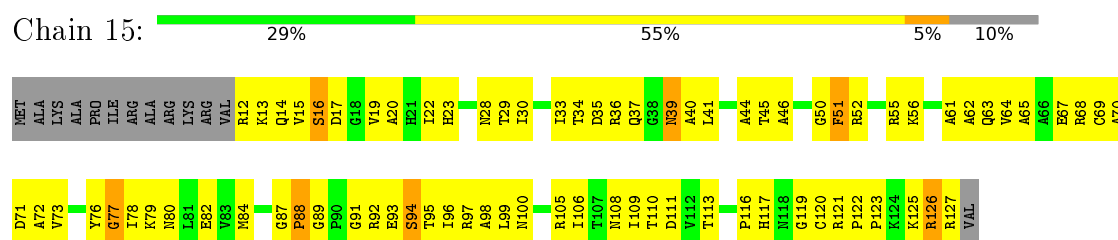
- Molecule 39: 30S ribosomal protein S9



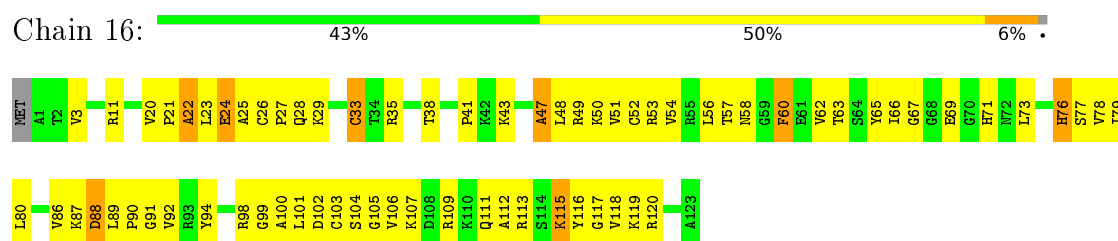
- Molecule 40: 30S ribosomal protein S10



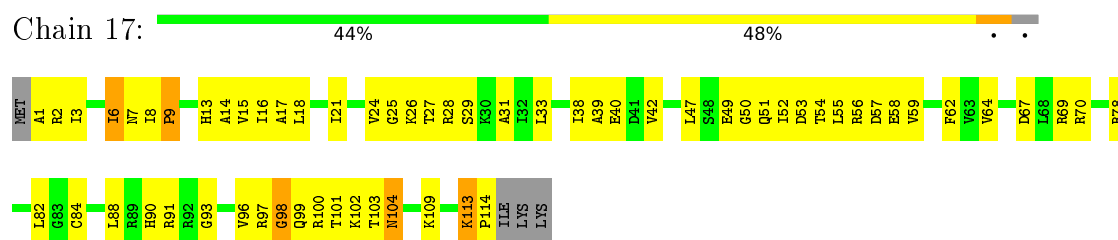
- Molecule 41: 30S ribosomal protein S11



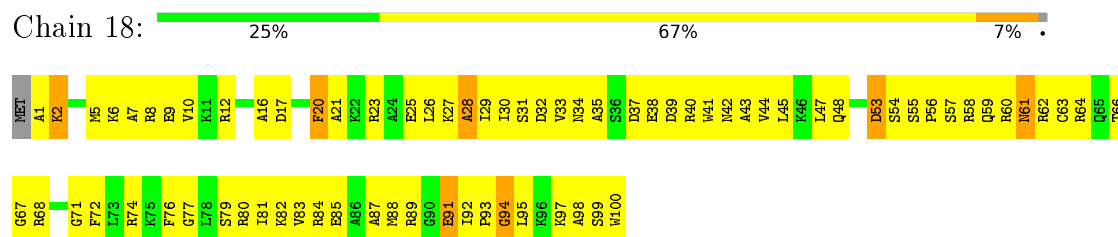
- Molecule 42: 30S ribosomal protein S12



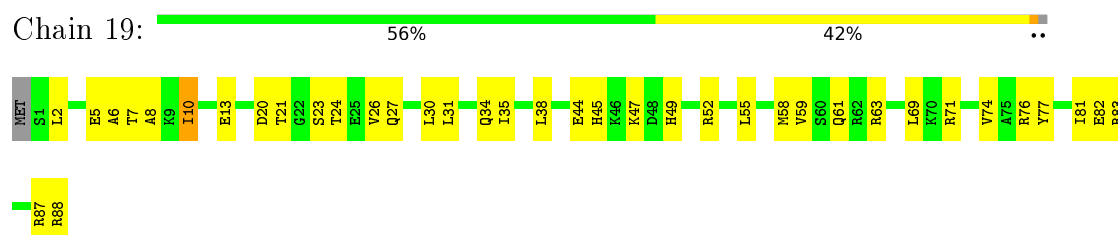
- Molecule 43: 30S ribosomal protein S13



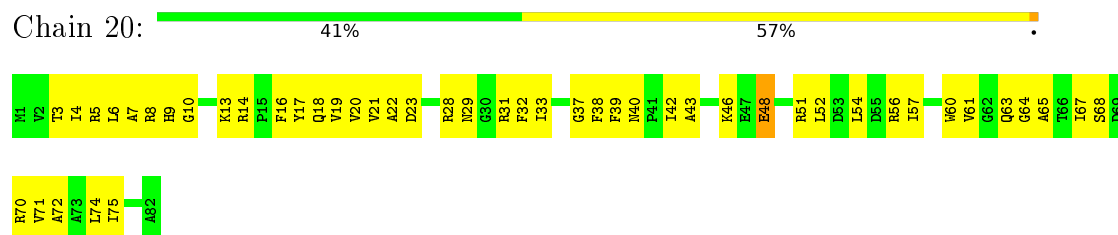
- Molecule 44: 30S ribosomal protein S14



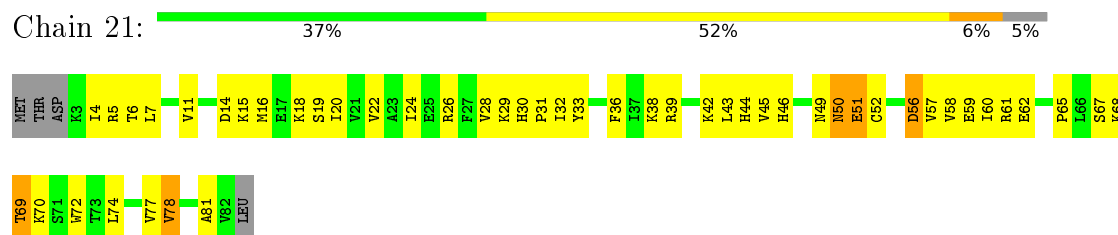
- Molecule 45: 30S ribosomal protein S15



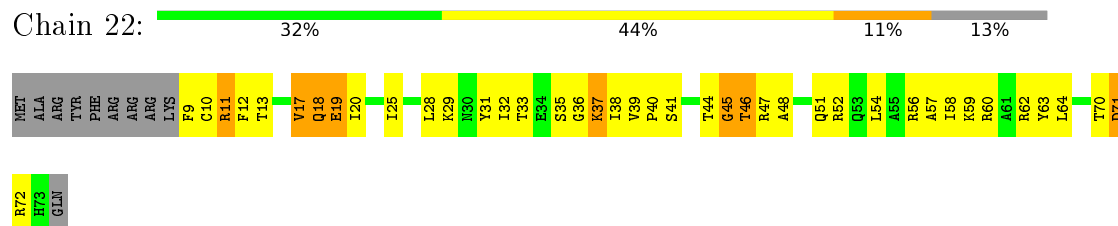
- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17

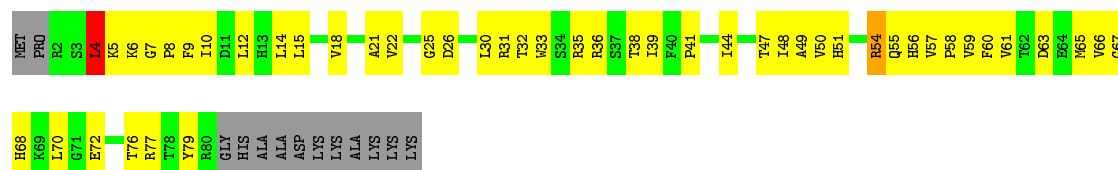


- Molecule 48: 30S ribosomal protein S18



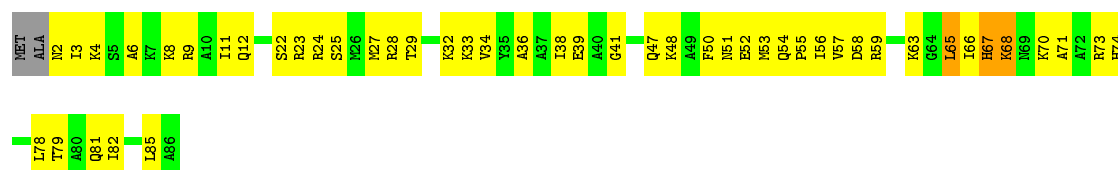
- Molecule 49: 30S ribosomal protein S19

Chain 23: 



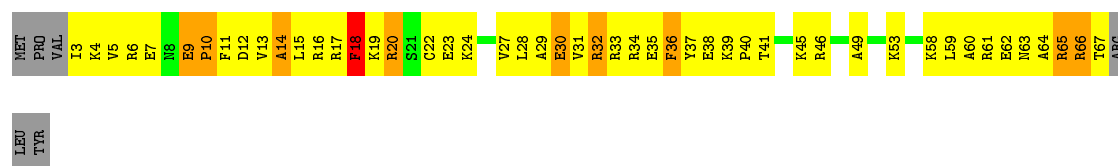
- Molecule 50: 30S ribosomal protein S20

Chain 24: 



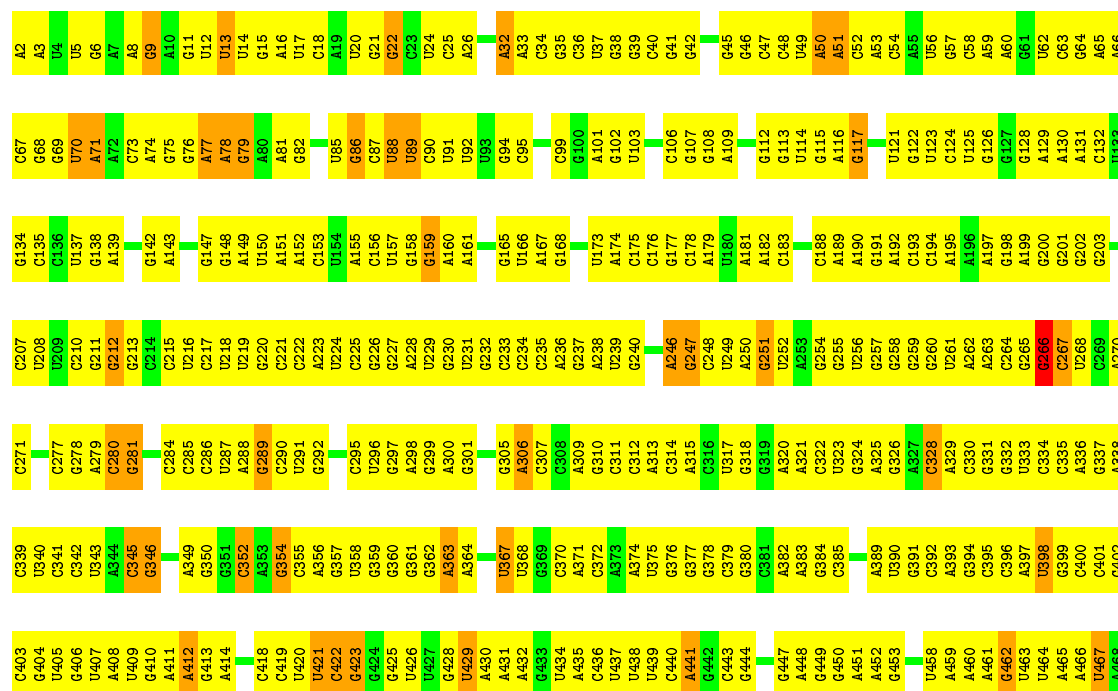
- Molecule 51: 30S ribosomal protein S21

Chain 25: 



- Molecule 52: 16S ribosomal RNA

Chain 26: 



G1458	A1394	A1333	U1264	G1203	G1139	G1074	A1005	A937	U875	C811	C744	A675	A596	A532	C469
G1459	C1395	G1334	C1265	A1204	C1140	U1075	G1006	G942	C876	G812	G745	A676	A597	A533	C470
G1460	A1396	U1335	G1268	U1205	C1141	U1076	U1007	G943	A877	A815	A746	U677	U598	U534	C471
G1461	C1397	C1336	G1269	G1206	G1142	G1077	U1008	U943	A878	A816	A747	U678	C599	A535	U472
C1462	A1398	A1269	G1207	G1207	G1143	U1078	U1009	G944	C879	A817	G748	C679	A600	C536	U473
U1463	C1399	C1273	C1208	C1208	G1144	U1079	U1010	G945	C880	C816	A749	G679	G601	G537	U474
U1464	C1400	A1274	C1209	C1209	A1145	A1080	C1011	A946	G881	G818	C750	A681	A602	G538	C475
G1465	G1401	A1275	C1210	C1210	A1146	A1081	A1014	G947	C882	G820	U751	G682	U603	A539	U476
A1468	C1402	C1342	A1276	U1211	C1147	G1084	G1015	C948	C883	U820	A752	G683	G604	G540	C477
C1469	C1403	G1343	G1278	A1212	U1148	U1085	G1018	A949	U884	G821	A753	U684	U605	G541	A478
C1470	C1404	C1344	G1279	U1212	U1149	U1085	G1019	U950	G885	G822	C754	U685	G606	G542	U479
U1470	U1405	U1345	A1280	G1214	A1151	G1088	G1018	G951	G886	G824	G755	U686	A607	U543	U480
U1471	U1406	A1346	G1281	G1215	A1152	G1089	A1019	U952	G889	G825	C756	A608	A608	G544	U481
C1472	C1407	G1347	C1282	A1216	A1152	U1090	G1024	G953	A889	C826	C757	C689	A609	C545	A482
G1473	A1408	U1348	C1282	C1217	A1155	U1091	G1025	G954	G890	U827	C758	G690	C613	A546	C483
U1474	C1409	C1349	U1283	C1218	A1156	U1091	G1026	U955	U891	U828	A759	G691	G614	A547	G484
G1475	A1410	A1350	G1284	A1219	G1157	A1092	G1027	U956	A892	G829	U762	U692	G615	G548	U485
A1476	C1411	U1351	A1285	G1220	A1157	A1093	C1027	U957	C893	G830	U763	G692	G616	C549	U486
U1477	C1412	C1352	U1286	G1221	C1158	G1094	C1028	A958	G894	A831	G763	A694	G617	G550	A487
C1478	C1413	G1353	A1287	G1222	U1159	U1095	U1029	A959	G895	G832	C764	A695	G618	U551	C488
A1482	U1414	C1354	A1288	C1223	U1160	C1096	U1030	U960	C896	G833	G765	A696	C619	U552	C489
G1483	G1415	G1355	A1289	U1224	C1161	C1097	G1031	U961	C897	U834	A766	U697	A621	A553	C490
U1484	G1416	C1356	A1225	A1225	C1162	C1098	G1032	C962	G898	U835	A767	A698	A622	A554	C491
C1485	G1417	A1357	C1226	C1226	A1163	G1099	G1033	G963	C899	G836	G768	G703	G623	U555	C492
U1486	A1418	U1358	A1227	A1227	A1163	G1100	G1034	A964	A900	U837	C770	G705	G624	C556	A493
G1487	G1419	C1359	G1294	C1228	G1166	A1101	C1037	U965	A901	G838	C771	G706	U625	G557	G494
U1488	U1420	A1360	U1295	A1229	A1167	A1102	G1038	G966	G902	U839	A772	A706	U626	G558	A495
C1489	G1421	C1361	C1230	C1230	U1168	C1103	G1039	C967	G903	C840	U772	U707	G626	A559	A496
U1490	G1422	A1362	G1297	G1231	A1169	U1094	G1039	A968	U904	C841	G773	G708	G627	A560	G497
C1491	G1423	C1363	U1298	U1232	A1170	G1106	U1040	A969	U905	U842	G774	U709	G628	U561	A498
U1492	U1424	A1364	A1299	G1233	A1171	C1107	G1041	C970	A906	U843	G775	G710	A629	U562	C499
U1493	G1425	G1365	G1300	C1234	C1172	G1108	C1045	G971	A907	C844	G776	G711	A630	A563	G500
A1496	U1426	C1366	U1301	U1235	C1172	C1109	G1046	C972	A908	A845	A777	A712	C631	C563	C501
C1497	C1427	C1367	C1302	A1236	G1175	A1110	G1047	G973	A909	G846	C778	G713	U632	U565	A502
U1498	A1428	A1368	C1303	C1237	A1176	A1111	G1048	A974	C910	G847	C779	G714	G633	G566	C503
A1499	G1429	C1369	G1304	A1238	G1177	C1112	U1049	A975	U911	C848	A780	A715	C634	G567	C504
U1500	C1430	C1370	A1305	G1239	G1178	C1113	G1050	G976	C912	G849	A781	A635	A635	G568	G505
C1501	U1432	G1371	U1307	G1241	A1179	C1114	G1051	A977	A913	U850	A782	A716	U636	C569	
A1502	G1433	U1372	U1308	G1242	A1180	U1115	C1052	A978	A914	G851	C783	C720	A642	A572	A510
C1503	A1434	A1373	G1309	G1243	G1181	U1116	U1053	C979	A915	G852	A784	G721	C643	A573	C511
G1504	U1435	C1374	G1310	C1244	G1182	A1117	C1054	U980	U916	C853	G785	G722	U644	A574	C512
U1505	A1436	U1376	G1313	G1245	U1183	U1118	C1055	U981	G917	U854	G786	U723	U645	G575	C514
C1506	G1437	A1377	U1313	C1245	G1184	C1119	U1056	U982	A918	U855	A787	G725	G645	C576	C515
U1507	G1438	C1378	G1316	A1248	G1187	U1121	G1057	A983	A919	C856	A792	C726	G656	G577	U516
A1508	C1439	G1379	G1317	C1249	A1188	U1122	G1058	C984	U920	G858	U793	G727	U657	C578	C517
C1509	U1440	U1380	C1317	A1250	U1189	U1123	C1059	G988	U921	G859	A794	A728	C658	A579	C518
G1510	A1441	A1381	A1318	A1251	G1190	G1124	U1060	U992	C924	A864	C796	G731	U659	C580	A520
U1511	C1382	C1382	A1319	A1252	A1191	U1125	G1061	G993	G925	A865	C797	G732	C660	G581	G521
C1512	C1383	C1383	G1323	G1253	G1192	U1126	U1062	A994	G926	A866	C798	G733	G661	G584	C522
A1513	G1384	G1384	A1324	A1254	G1193	G1127	C1063	G994	G927	A867	U798	G734	G664	G585	A523
G1514	C1385	G1385	G1325	G1255	U1194	C1128	G1064	G995	G928	C866	C799	C735	A665	C586	C524
U1515	C1386	C1386	A1256	A1257	C1195	U1065	U1065	A996	G929	G867	A802	C737	G666	G587	C525
G1516	U1451	G1387	U1326	A1257	A1196	A1130	C1066	U997	G929	C868	C806	C738	G667	G588	C526
C1517	C1452	C1388	C1327	G1258	A1197	G1131	G1067	C998	C930	G869	C807	C739	G668	U589	G527
U1518	G1453	U1390	A1328	C1259	G1198	C1132	U1069	C999	G933	U870	U740	G669	G689	U590	C528
A1519	C1454	C1391	A1329	G1260	U1199	G1133	U1070	G1001	G933	U871	A807	U741	G690	U591	C529
C1520	A1456	G1392	U1330	C1261	C1200	G1133	C1071	G1002	C934	A872	C808	G742	A673	G592	G530
C1521	G1457	U1393	A1332	C1263	A1201	C1137	U1073	G1003	A935	G874	C910	A743	G674	G591	U531

U1522
G1523
C1524
G1525
G1526
U1527
U1528
G1529
G1530
A1534
C1538
G1539
U1540

• Molecule 53: 23S ribosomal RNA

Chain 27: 26% 62% 11%

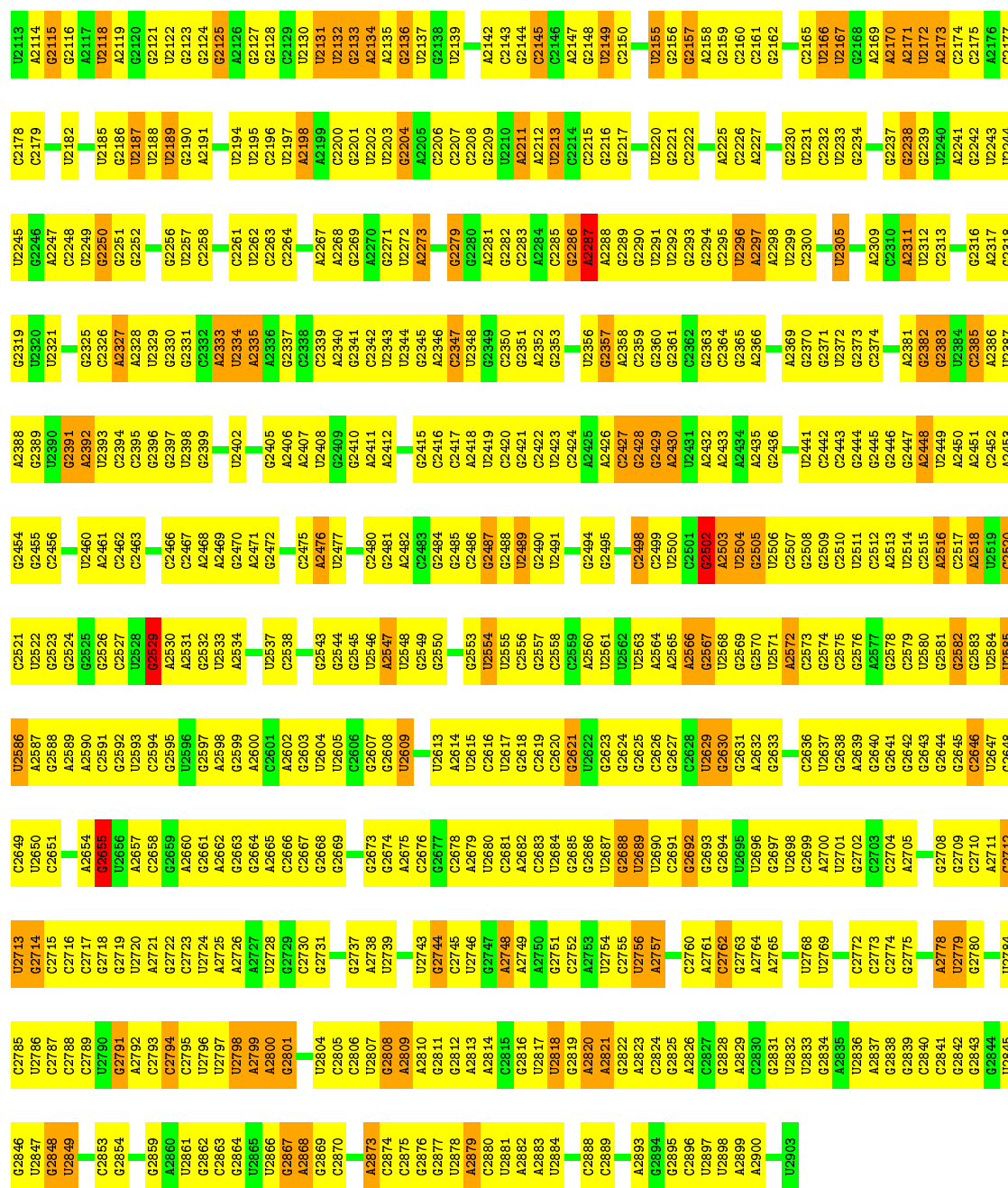
G1
A5
A6
A7
G7
C8
G9
A10
C11
U12
A13
A14
G15
C16
G17
U18
A19
C20
G21
A22
C23
G24
U25
G26
C27
A28
U29
G30
C31
U34
G35
A38
G39
U40
G45
G46
C47
G48
A49
U50
G51
A52
G53
A54
G55
A56
C57
G61
U62
A63
G64
U65
C66
G67
A68
C69

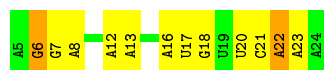
G70
A71
U72
G73
A74
G75
G80
G81
U82
A83
G84
A85
G86
G87
G88
G89
G90
A91
U92
A93
G94
U95
A96
G97
U98
A99
G100
C101
G102
A103
U104
G105
C106
G107
U108
G109
A110
U111
G112
A113
U114
G115
C116
G117
A118
U119
G120
A121
U122
G123
A124
G125
A126
G127
C128
U129
A130
G131
U132
A133
G134
U135
A136
G137
U138
A139
G140
U141
G142
A143
U144

G145
A146
C147
U148
A149
G150
C151
A152
U153
G154
A155
U156
C157
G158
G159
A160
U161
G162
A163
C164
G165
U166
A167
G168
U169
A170
G171
U172
A173
G174
U175
A176
G177
A181
U182
G183
A184
G185
U186
A187
G188
U189
G190
A191
U192
G193
A194
U195
G196
A197
U198
G199
A200
U201
G202
A203
U204
G205
A206
U207

C208
G209
C210
G211
A212
U213
G214
A215
U216
G217
A218
U219
G220
A221
U222
A223
G224
U225
A226
G227
C228
A229
G230
U231
A232
G233
C234
U235
A236
G237
C238
U239
A240
G241
U242
A243
G244
U245
A246
G247
C248
A249
G250
U251
G252
A253
U254
G255
A256
U257
G258
A259
U260
G261
A262
U263
G264
A265
U266
G267
A268
U269
G270
A271
U272
G273
A274
U275
G276
A277
U278
G279
A280
U281
G282
A283
U284
G285
A286
U287
G288
A289
U290
G291
A292
U293
G294
A295
U296
G297
A298
U299
G300
A301
U302
G303
A304
U305
G306
A307
U308
G309
A310
U311
G312
A313
U314
G315
A316
U317
G318
A319
U320
G321
A322
U323
G324
A325
U326
G327
A328
U329
G330
A331
U332
G333
A334
U335
G336
A337
U338
G339
A340
U341
G342
A343
U344
G345
A346
U347
G348
A349
U350
G351
A352
U353
G354
A355
U356
G357
A358
U359
G360
A361
U362
G363
A364
U365
G366
A367
G368
A369
U370
G371
A372
U373
G374
A375
U376
G377
A378
U379
G380
A381
U382
G383
A384
U385
G386
A387
U388
G389
A390
U391
G392
A393
U394
G395
A396
U397
G398
A399
U400
G401
A402
U403
G404
A405
U406
G407
A408
U409
G410
A411
U412
G413
A414
U415
G416
A417
U418
G419
A420
U421
G422
A423
U424
G425
A426
U427
G428
A429
U430
G431
A432
U433
G434
A435
U436
G437
A438
U439
G440
A441
U442
G443
A444
U445
G446
A447
U448
G449
A450
U451
G452
A453
U454
G455
A456
U457
G458
A459
U460
G461
A462
U463
G464
A465
U466
G467
A468
U469
G470
A471
U472
G473
A474
U475
G476
A477
U478
G479
A480
U481
G482
A483
U484
G485
A486
U487
G488
A489
U490
G491
A492
U493
G494
A495
U496
G497
A498
U499
G500
A501
U502
G503
A504
U505
G506
A507
U508
G509
A510
U511
G512
A513
U514
G515
A516
U517
G518
A519
U520
G521
A522
U523
G524
A525
U526
G527
A528
U529
G530
A531
U532
G533
A534
U535
G536
A537
U538
G539
A540
U541
G542
A543
U544
G545
A546
U547
G548
A549
U550
G551
A552
U553
G554
A555
U556
G557
A558
U559
G560
A561
U562
G563
A564
U565
G566
A567
U568
G569
A570
U571
G572
A573
U574
G575
A576
U577
G578
A579
U580
G581
A582
U583
G584
A585
U586
G587
A588
U589
G590
A591
U592
G593
A594
U595
G596
A597
U598
G599
A600
U601
G602
A603
U604
G605
A606
U607
G608
A609
U610
G611
A612
U613
G614
A615
U616
G617
A618
U619
G620
A621
U622
G623
A624
U625
G626
A627
U628
G629
A630
U631
G632
A633
U634
G635
A636
U637
G638
A639
U640
G641
A642
U643
G644
A645
U646
G647
A648
U649
G650
A651
U652
G653
A654
U655
G656
A657
U658
G659
A660
U661
G662
A663
U664
G665
A666
U667
A668
G669
A670
U671
G672
A673
U674
G675
A676
U677
G678
A679
U680
G681
A682
U683
G684
A685
U686
G687
A688
U689
G690
A691
U692
G693
A694
U695
G696
A697
U698
G699
A700
U701
G702
A703
U704
G705
A706
U707
G708
A709
U710
G711
A712
U713
G714
A715
U716
G717
A718
U719
G720
A721
U722
G723
A724
U725
G726
A727
U728
G729
A730
U731
G732
A733
U734
G735
A736
U737
G738
A739
U740
G741
A742
U743
G744
A745
U746
G747
A748
U749
G750
A751
U752
G753
A754
U755
G756
A757
U758
G759
A760
U761
G762
A763
U764
G765
A766
U767
G768
A769
U770
G771
A772
U773
G774
A775
U776
G777
A778
U779
G780
A781
U782
G783
A784
U785
G786
A787
U788
G789
A790
U791
G792
A793
U794
G795
A796
U797
G798
A799
U800
G801
A802
U803
G804
A805
U806
G807
A808
U809
G810
A811
U812
G813
A814
U815
G816
A817
U818
G819
A820
U821
G822
A823
U824
G825
A826
U827
G828
A829
U830
G831
A832
U833
G834
A835
U836
G837
A838
U839
G840
A841
U842
G843
A844
U845
G846
A847
U848
G849
A850
U851
G852
A853
U854
G855
A856
U857
G858
A859
U860
G861
A862
U863
G864
A865
U866
G867
A868
U869
G870
A871
U872
G873
A874
U875
G876
A877
U878
G879
A880
U881
G882
A883
U884
G885
A886
U887
G888
A889
U890
G891
A892
U893
G894
A895
U896
G897
A898
U899
G900
A901
U902
G903
A904
U905
G906
A907
U908
G909
A910
U911
G912
A913
U914
G915
A916
U917
G918
A919
U920
G921
A922
U923
G924
A925
U926
G927
A928
U929
G930
A931
U932
G933
A934
U935
G936
A937
U938
G939
A940
U941
G942
A943
U944
G945
A946
U947
G948
A949
U950
G951
A952
U953
G954
A955
U956
G957
A958
U959
G960
A961
U962
G963
A964
U965
G966
A967
U968
G969
A970
U971
G972
A973
U974
G975
A976
U977
G978
A979
U980
G981
A982
U983
G984
A985
U986
G987
A988
U989
G990
A991
U992
G993
A994
U995
G996
A997
U998
G999
A1000
U1001

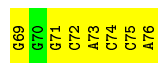
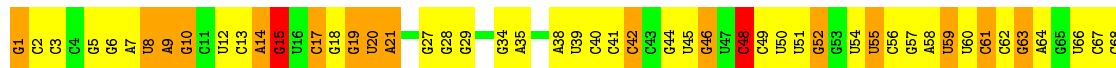
G2048	A1977	G1906	C1836	A1773	G1697	A1632	G1585	G1482	G1408	G1337	G1266	G1195	U1130	A1069	G1002
G2049	A1978	G1907	C1837	C1774	A1698	G1633	G1586	G1483	U1409	G1338	U1267	C1196	G1131	A1070	G1003
G2050	U1978	C1908	G1838	G1776	G1699	G1633	G1561	U1484	G1416	G1339	A1268	U1197	U1132	C1072	C1006
A2051	G1980	C1909	G1839	G1775	A1705	U1636	U1562	U1485	C1417	U1340	A1269	U1198	U1133	C1073	C1007
A2052	A1981	U1911	G1842	U1778	C1706	A1637	U1563	U1486	G1418	G1341	C1270	U1199	C1135	G1074	A1008
G2053	U1982	A1912	C1843	U1779	G1707	G1638	C1564	U1487	A1419	C1345	G1271	C1200	G1138	G1075	A1009
A2054	G1983	G1913	G1844	U1780	C1708	G1639	C1565	A1490	G1421	C1351	U1272	U1201	G1139	C1076	A1010
G2055	G1984	C1914	G1845	U1781	U1709	A1640	G1567	G1491	G1422	A1274	A1275	A1205	G1140	A1077	G1011
G2056	G1985	U1915	G1846	U1782	G1710	A1641	G1568	C1498	G1423	C1352	A1276	G1206	U1141	U1078	U1012
G2057	C1986	U1916	G1847	A1783	G1711	U1647	A1569	C1500	G1426	A1353	G1277	C1207	U1142	C1079	C1013
A2058	U1917	G1917	G1848	U1784	U1712	U1648	A1570	G1501	A1427	A1354	C1278	U1209	A1143	A1080	A1014
A2059	U1918	A1784	A1849	A1785	U1713	U1649	A1571	A1502	G1428	A1356	G1279	G1210	A1144	U1081	U1015
A2060	G1922	U1919	G1850	U1786	G1715	U1651	A1572	A1503	G1429	C1357	G1280	C1211	C1145	U1082	G1016
G2061	U1993	C1924	A1853	U1787	U1720	G1651	A1573	A1504	G1430	C1358	G1281	G1212	G1149	U1083	U1019
A2062	C1994	C1925	A1854	A1789	G1721	G1652	A1574	A1505	G1431	A1359	A1284	A1213	C1150	A1084	A1020
C2063	U1995	G1926	G1857	C1790	U1725	G1653	U1576	A1506	A1431	G1360	A1285	G1216	A1151	A1085	A1021
C2064	C1996	U1930	A1858	A1791	C1726	A1654	U1577	U1507	G1432	G1361	A1286	G1217	C1152	G1087	G1022
C2065	C1997	U1931	G1859	G1792	C1727	A1655	U1578	C1507	A1433	G1362	A1287	U1218	C1153	A1088	U1023
C2066	A1998	A1932	G1863	U1793	C1728	G1656	U1584	A1508	A1434	C1363	G1288	U1219	C1154	A1089	G1024
G2067	C2000	G1933	U1864	C1795	U1729	C1658	C1585	A1509	G1435	G1364	G1290	G1220	A1155	A1090	G1025
U2068	C2001	G1934	U1865	U1796	G1730	G1659	A1586	G1510	G1436	A1365	G1293	C1221	A1156	G1091	G1026
G2069	G1935	U1936	A1866	G1797	G1731	G1661	G1587	A1515	C1437	C1370	U1294	C1222	G1157	C1092	A1027
A2070	A1936	A1936	G1867	U1798	C1732	U1662	G1587	G1516	U1438	G1371	U1294	G1223	G1160	G1093	A1028
A2071	U2007	U1937	C1868	G1799	G1733	G1663	A1591	U1520	A1439	U1372	C1297	G1227	C1161	U1094	A1029
C2072	C2008	A1938	G1869	C1800	G1734	A1664	C1592	G1521	G1441	U1373	C1298	G1227	C1162	A1095	C1030
C2073	A2009	A1938	C1869	G1734	A1665	A1665	U1593	G1522	U1442	G1374	C1299	G1228	C1163	A1096	G1031
U2074	U2011	C1941	U1870	A1801	A1735	G1666	U1594	A1522	U1443	U1375	G1300	C1229	C1164	C1104	G1041
U2075	G2012	U1942	A1871	A1802	U1736	G1667	C1595	U1523	G1444	G1376	A1301	U1230	C1165	A1098	U1033
A2013	A2013	U1943	A1872	A1803	G1737	G1668	A1596	G1524	G1445	G1377	A1302	U1234	G1166	G1100	G1036
U2078	U2016	U1946	G1873	A1804	G1738	A1669	A1597	A1525	C1446	A1378	G1303	U1235	G1167	U1101	G1037
A2080	U2017	C1947	G1874	A1805	A1744	A1670	A1598	G1526	G1447	U1379	C1304	G1236	G1168	C1102	U1037
U2081	G2018	G1948	G1875	C1806	A1745	A1671	A1599	G1527	U1448	G1380	C1305	U1242	A1169	A1103	G1041
A2082	A2019	G1949	A1876	G1807	A1746	A1672	C1600	U1528	G1449	G1381	C1306	C1237	C1170	A1097	G1042
G2083	A2020	G1950	G1877	A1808	U1747	A1673	U1529	G1537	G1450	G1382	A1307	G1238	G1171	U1105	U1045
C2084	A2021	U1951	C1878	A1810	C1748	G1674	A1603	G1538	C1451	A1383	A1308	A1241	C1172	G1106	C1045
U2085	U2022	A1952	G1879	A1811	A1749	C1675	C1604	C1533	G1452	A1384	G1309	U1242	U1173	G1107	A1046
U2086	A1953	C1953	G1880	G1812	G1750	A1676	C1605	U1534	A1453	A1385	G1310	U1242	U1174	U1108	G1047
G2087	G2023	G1954	C1881	G1813	U1751	A1677	C1606	U1535	C1454	C1386	G1311	C1243	A1175	C1109	A1048
A2088	G2024	G1955	U1882	G1814	G1751	A1678	C1607	A1536	G1455	A1387	U1312	U1243	U1176	G1110	C1049
C2089	C2025	U1956	U1883	G1814	A1754	G1679	A1608	G1537	G1461	G1388	U1313	U1248	G1177	A1111	U1057
A2090	U2026	C1957	G1884	A1815	A1755	U1680	A1609	U1538	C1462	C1389	G1314	U1249	C1178	G1112	G1052
C2091	G2027	C1957	A1885	G1816	A1756	G1681	A1610	G1538	C1463	U1390	C1315	G1250	G1179	U1113	C1053
U2092	U2028	U1958	G1886	G1817	G1756	G1682	C1611	U1539	G1464	U1391	U1316	C1251	U1180	C1114	A1054
A2093	G2029	G1959	A1889	U1818	U1757	U1683	C1612	G1540	G1465	U1394	U1318	G1252	U1181	G1115	G1055
A2094	A2030	C1960	G1890	A1819	U1758	G1684	G1613	C1541	G1466	A1395	C1319	A1253	U1182	G1116	G1056
U2095	A2031	C1961	G1891	U1820	A1759	G1685	A1614	U1542	U1468	A1396	C1320	U1255	U1183	C1117	U1057
A2097	G2032	C1962	C1892	A1821	C1760	C1686	A1615	G1543	U1469	U1397	A1321	G1256	U1184	C1118	U1058
U2098	A2033	U1963	C1893	C1822	C1761	G1687	C1616	G1544	A1468	U1400	A1322	C1257	G1185	U1119	G1059
U2099	U2034	G1964	C1894	G1823	A1762	U1688	A1617	A1545	A1470	U1401	U1326	U1258	G1186	G1122	U1060
C2104	C2035	U1965	C1895	G1824	G1763	U1689	C1618	U1546	U1474	U1402	U1327	U1259	U1187	G1123	U1061
U2105	G2036	C1967	G1896	U1825	C1764	A1689	G1619	C1547	U1475	G1403	A1327	G1260	U1188	G1124	G1062
U2106	A2037	G1968	U1897	G1826	U1765	G1691	U1620	A1548	U1476	C1404	G1331	A1262	U1189	G1125	C1063
G2107	G2038	A1969	A1900	U1827	G1766	U1692	U1621	A1549	U1477	U1405	G1332	U1263	G1190	G1126	C1064
U2108	U2039	U1970	A1901	G1828	G1767	U1693	G1622	C1550	G1479	U1406	G1333	U1264	G1191	A1126	U1065
U2109	G2040	U1971	C1902	A1829	U1769	U1694	G1623	A1551	G1480	U1407	G1334	A1265	G1192	A1127	U1066
G2110	U2041	G1972	G1903	C1830	G1770	U1695	C1694	A1552	G1481	U1408	G1335	U1265	G1193	G1128	A1067
U2111	A2042	G1973	G1904	G1831	C1771	G1696	G1696	U1629						A1129	
G2112	C2043	C1974	G1905		A1772										





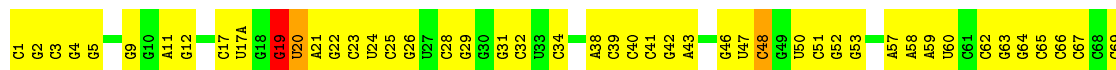
• Molecule 56: A-site tRNA^{Phe}

Chain 30: 25% 51% 21% .



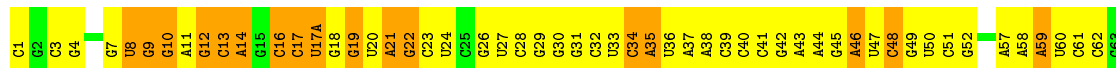
• Molecule 57: P-site tRNA^{fMet}

Chain 31: 35% 60% . .



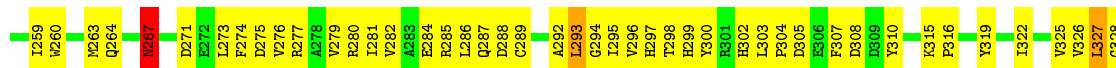
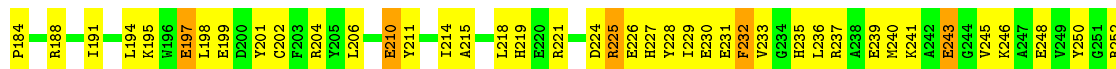
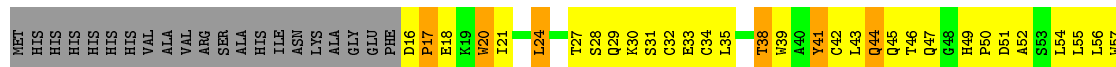
• Molecule 58: E-site tRNA^{fMet}

Chain 32: 17% 60% 23%



• Molecule 59: GTP pyrophosphokinase

Chain 33: 37% 46% 7% 10%





4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	57430	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	0.70	0/2852
10	J	0.35	0/947	0.68	0/1268
11	K	0.36	0/1054	0.71	1/1403 (0.1%)
12	L	0.35	0/1093	0.64	0/1460
13	M	0.33	0/973	0.64	0/1301
14	N	0.32	0/902	0.63	0/1209
15	O	0.34	0/929	0.73	1/1242 (0.1%)
16	P	0.37	0/960	0.57	0/1278
17	Q	0.39	0/829	0.77	1/1107 (0.1%)
18	R	0.33	0/864	0.68	0/1156
19	S	0.34	0/744	0.66	0/994
2	B	0.37	0/1586	0.67	0/2134
20	T	0.35	0/787	0.76	1/1051 (0.1%)
21	U	0.36	0/766	0.63	0/1025
22	V	0.37	0/582	0.62	0/769
23	W	0.37	0/635	0.70	0/848
24	X	0.36	0/510	0.62	0/677
25	Y	0.34	0/453	0.62	0/605
26	Z	0.42	0/531	0.71	1/709 (0.1%)
27	1	0.35	0/450	0.72	0/599
28	2	0.37	0/416	0.60	0/554
29	3	0.41	0/380	0.64	0/498
3	C	0.39	0/1571	0.71	1/2113 (0.0%)
30	4	0.35	0/513	0.70	0/676
31	5	0.33	0/303	0.68	0/397
32	6	0.42	0/1735	0.68	1/2338 (0.0%)
33	7	0.35	0/1651	0.63	1/2225 (0.0%)
34	8	0.36	0/1665	0.64	0/2227
35	9	0.35	0/1169	0.69	0/1573
36	10	0.38	0/835	0.69	0/1128
37	11	0.34	0/1195	0.65	0/1602
38	12	0.34	0/989	0.68	0/1326
39	13	0.36	0/1034	0.72	0/1375
4	D	0.36	0/1434	0.66	0/1926

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	14	0.38	0/796	0.72	1/1077 (0.1%)
41	15	0.36	0/885	0.75	0/1195
42	16	0.36	0/969	0.76	3/1300 (0.2%)
43	17	0.32	0/892	0.62	0/1193
44	18	0.33	0/817	0.58	0/1088
45	19	0.33	0/722	0.60	0/964
46	20	0.39	0/659	0.67	0/884
47	21	0.36	0/657	0.71	0/881
48	22	0.38	0/544	0.73	0/731
49	23	0.37	0/652	0.70	1/877 (0.1%)
5	E	0.35	0/1343	0.69	0/1816
50	24	0.32	0/671	0.56	0/888
51	25	0.42	0/550	0.73	1/728 (0.1%)
52	26	0.55	1/36967 (0.0%)	0.71	3/57666 (0.0%)
53	27	0.60	1/69801 (0.0%)	0.72	10/108894 (0.0%)
54	28	0.45	1/2876 (0.0%)	0.69	1/4483 (0.0%)
55	29	0.63	0/486	0.67	0/757
56	30	0.67	1/1813 (0.1%)	0.78	1/2823 (0.0%)
57	31	0.49	1/1836 (0.1%)	0.69	1/2859 (0.0%)
58	32	0.87	1/1835 (0.1%)	0.78	0/2857
59	33	0.67	6/4985 (0.1%)	1.09	37/6770 (0.5%)
6	F	0.44	0/1122	0.64	0/1515
7	G	0.50	0/1001	0.79	2/1350 (0.1%)
8	H	0.49	0/1046	0.69	1/1410 (0.1%)
9	I	0.33	0/1152	0.63	0/1551
All	All	0.54	12/167683 (0.0%)	0.72	70/250202 (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	16
53	27	0	37
56	30	0	2
58	32	0	1
59	33	0	2
All	All	0	58

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	33	156	ARG	CZ-NH2	-10.57	1.19	1.33
59	33	152	LYS	CD-CE	-7.77	1.31	1.51
59	33	17	PRO	CA-CB	-7.25	1.39	1.53
57	31	1	C	OP3-P	-6.97	1.52	1.61
56	30	1	G	OP3-P	-6.93	1.52	1.61

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	33	156	ARG	NE-CZ-NH1	19.92	130.26	120.30
59	33	156	ARG	NH1-CZ-NH2	-13.88	104.13	119.40
59	33	17	PRO	N-CA-CB	-11.14	89.93	103.30
59	33	17	PRO	CA-CB-CG	10.28	124.33	104.80
59	33	63	VAL	CG1-CB-CG2	-9.24	96.12	110.90

There are no chirality outliers.

5 of 58 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	26	117	G	Sidechain
52	26	159	G	Sidechain
52	26	239	U	Sidechain
52	26	266	G	Sidechain
52	26	438	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	166	0
2	B	1565	0	1616	126	0
3	C	1552	0	1619	123	0
4	D	1410	0	1447	111	0
5	E	1323	0	1374	81	0
6	F	1111	0	1148	85	0
7	G	988	0	1025	114	0
8	H	1032	0	1088	101	0
9	I	1129	0	1162	73	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	938	0	1012	59	0
11	K	1045	0	1117	85	0
12	L	1074	0	1157	67	0
13	M	960	0	1000	65	0
14	N	892	0	923	68	0
15	O	917	0	965	75	0
16	P	947	0	1022	82	0
17	Q	816	0	839	86	0
18	R	857	0	922	47	0
19	S	738	0	807	48	0
20	T	779	0	834	50	0
21	U	753	0	780	49	0
22	V	575	0	592	35	0
23	W	625	0	655	39	0
24	X	509	0	543	33	0
25	Y	449	0	491	18	0
26	Z	522	0	521	46	0
27	1	444	0	461	39	0
28	2	409	0	440	25	0
29	3	377	0	418	35	0
30	4	504	0	574	41	0
31	5	302	0	343	33	0
32	6	1704	0	1732	105	0
33	7	1624	0	1699	111	0
34	8	1643	0	1710	145	0
35	9	1156	0	1199	122	0
36	10	817	0	808	74	0
37	11	1181	0	1240	74	0
38	12	979	0	1034	70	0
39	13	1022	0	1070	109	0
40	14	786	0	828	82	0
41	15	869	0	878	90	0
42	16	955	0	1019	97	0
43	17	883	0	944	77	0
44	18	805	0	847	104	0
45	19	714	0	737	31	0
46	20	649	0	666	70	0
47	21	648	0	691	64	0
48	22	535	0	552	51	0
49	23	637	0	665	55	0
50	24	665	0	714	60	0
51	25	544	0	579	72	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	26	33016	0	16617	1357	0
53	27	62322	0	31345	2394	0
54	28	2572	0	1302	112	0
55	29	432	0	218	15	0
56	30	1623	0	821	58	0
57	31	1644	0	836	33	0
58	32	1643	0	836	78	0
59	33	4911	0	4550	627	0
All	All	154603	0	105189	7602	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 29.

The worst 5 of 7602 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)
59:33:188:ARG:NH1	59:33:377:LEU:HA	1.23	1.40
59:33:24:LEU:HD21	59:33:70:SER:HA	1.19	1.16
59:33:17:PRO:HB3	59:33:39:TRP:NE1	1.58	1.15
34:8:84:ASN:HD22	34:8:87:GLU:HG3	0.98	1.15
59:33:188:ARG:NH1	59:33:377:LEU:CA	2.09	1.14

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%)	34 (13%)	17 (6%)	2	26
2	B	207/209 (99%)	175 (84%)	25 (12%)	7 (3%)	5	42
3	C	199/201 (99%)	157 (79%)	23 (12%)	19 (10%)	1	15

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	175/179 (98%)	143 (82%)	23 (13%)	9 (5%)	2	31
5	E	174/177 (98%)	148 (85%)	19 (11%)	7 (4%)	4	37
6	F	147/149 (99%)	116 (79%)	20 (14%)	11 (8%)	1	21
7	G	129/165 (78%)	91 (70%)	27 (21%)	11 (8%)	1	17
8	H	139/142 (98%)	107 (77%)	21 (15%)	11 (8%)	1	19
9	I	140/142 (99%)	120 (86%)	16 (11%)	4 (3%)	6	45
10	J	120/123 (98%)	94 (78%)	19 (16%)	7 (6%)	2	28
11	K	141/144 (98%)	108 (77%)	18 (13%)	15 (11%)	0	11
12	L	134/136 (98%)	104 (78%)	17 (13%)	13 (10%)	1	14
13	M	118/127 (93%)	95 (80%)	18 (15%)	5 (4%)	3	35
14	N	114/117 (97%)	92 (81%)	16 (14%)	6 (5%)	2	30
15	O	112/115 (97%)	96 (86%)	13 (12%)	3 (3%)	6	46
16	P	115/118 (98%)	99 (86%)	13 (11%)	3 (3%)	7	47
17	Q	101/103 (98%)	74 (73%)	19 (19%)	8 (8%)	1	19
18	R	108/110 (98%)	84 (78%)	17 (16%)	7 (6%)	1	26
19	S	91/100 (91%)	76 (84%)	13 (14%)	2 (2%)	8	50
20	T	100/104 (96%)	81 (81%)	11 (11%)	8 (8%)	1	19
21	U	92/94 (98%)	75 (82%)	13 (14%)	4 (4%)	3	35
22	V	73/85 (86%)	64 (88%)	5 (7%)	4 (6%)	2	30
23	W	75/78 (96%)	65 (87%)	7 (9%)	3 (4%)	4	37
24	X	61/63 (97%)	53 (87%)	2 (3%)	6 (10%)	1	14
25	Y	56/59 (95%)	48 (86%)	4 (7%)	4 (7%)	1	23
26	Z	64/70 (91%)	49 (77%)	8 (12%)	7 (11%)	0	10
27	1	54/57 (95%)	39 (72%)	9 (17%)	6 (11%)	0	10
28	2	48/55 (87%)	39 (81%)	8 (17%)	1 (2%)	9	51
29	3	44/46 (96%)	38 (86%)	4 (9%)	2 (4%)	3	33
30	4	62/65 (95%)	49 (79%)	11 (18%)	2 (3%)	5	43
31	5	36/38 (95%)	28 (78%)	5 (14%)	3 (8%)	1	18
32	6	216/241 (90%)	158 (73%)	40 (18%)	18 (8%)	1	18
33	7	204/233 (88%)	174 (85%)	24 (12%)	6 (3%)	6	45
34	8	203/206 (98%)	166 (82%)	27 (13%)	10 (5%)	3	32

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	9	155/167 (93%)	119 (77%)	20 (13%)	16 (10%)	1	12
36	10	98/135 (73%)	71 (72%)	18 (18%)	9 (9%)	1	16
37	11	149/179 (83%)	125 (84%)	16 (11%)	8 (5%)	2	30
38	12	127/130 (98%)	109 (86%)	14 (11%)	4 (3%)	5	44
39	13	125/130 (96%)	93 (74%)	16 (13%)	16 (13%)	0	7
40	14	96/103 (93%)	74 (77%)	10 (10%)	12 (12%)	0	8
41	15	114/129 (88%)	89 (78%)	15 (13%)	10 (9%)	1	17
42	16	121/124 (98%)	90 (74%)	21 (17%)	10 (8%)	1	18
43	17	112/118 (95%)	89 (80%)	15 (13%)	8 (7%)	1	23
44	18	98/101 (97%)	74 (76%)	16 (16%)	8 (8%)	1	18
45	19	86/89 (97%)	73 (85%)	10 (12%)	3 (4%)	4	41
46	20	80/82 (98%)	59 (74%)	20 (25%)	1 (1%)	15	59
47	21	78/84 (93%)	57 (73%)	14 (18%)	7 (9%)	1	16
48	22	63/75 (84%)	44 (70%)	11 (18%)	8 (13%)	0	7
49	23	77/92 (84%)	62 (80%)	11 (14%)	4 (5%)	2	31
50	24	83/87 (95%)	71 (86%)	9 (11%)	3 (4%)	4	40
51	25	63/71 (89%)	36 (57%)	14 (22%)	13 (21%)	0	2
59	33	663/750 (88%)	559 (84%)	61 (9%)	43 (6%)	1	26
All	All	6509/6970 (93%)	5217 (80%)	860 (13%)	432 (7%)	3	25

5 of 432 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	97	ASP
1	A	107	LYS
1	A	121	ALA
1	A	143	VAL
1	A	154	ALA

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%)	163 (99%)	2 (1%)	78	90
4	D	148/150 (99%)	147 (99%)	1 (1%)	88	94
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%)	99 (99%)	1 (1%)	82	91
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%)	101 (99%)	1 (1%)	82	91
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%)	84 (100%)	0	100	100
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%)	83 (100%)	0	100	100
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%)	57 (97%)	2 (3%)	44	77
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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	6	180/199 (90%)	179 (99%)	1 (1%)	90	95
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%)	87 (100%)	0	100	100
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%)	65	86
40	14	86/90 (96%)	86 (100%)	0	100	100
41	15	89/99 (90%)	87 (98%)	2 (2%)	60	84
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%)	83 (100%)	0	100	100
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%)	73 (99%)	1 (1%)	74	89
48	22	56/65 (86%)	56 (100%)	0	100	100
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%)	448 (99%)	4 (1%)	84	92
All	All	5303/5698 (93%)	5280 (100%)	23 (0%)	94	97

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	7	102	ILE
35	9	132	PRO
59	33	425	LEU
35	9	122	VAL
39	13	60	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
22	V	72	ASN
32	6	57	ASN
59	33	88	ASN
23	W	16	ASN
26	Z	20	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	26	1538/1539 (99%)	190 (12%)	8 (0%)
53	27	2902/2903 (99%)	410 (14%)	22 (0%)
54	28	119/120 (99%)	9 (7%)	1 (0%)
55	29	19/20 (95%)	4 (21%)	0
56	30	75/76 (98%)	20 (26%)	1 (1%)
57	31	76/77 (98%)	6 (7%)	0
58	32	76/77 (98%)	22 (28%)	1 (1%)
All	All	4805/4812 (99%)	661 (13%)	33 (0%)

5 of 661 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	26	9	G
52	26	13	U
52	26	22	G
52	26	32	A
52	26	39	G

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	27	1020	A
53	27	1730	C
54	28	88	C
53	27	1111	A
53	27	1130	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.