



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

Feb 13, 2017 – 02:53 PM EST

PDB ID : 3JCD  
EMDB ID: : EMD-6549  
Title : Structure of Escherichia coli EF4 in posttranslocational ribosomes (Post EF4)  
Authors : Zhang, D.; Yan, K.; Liu, G.; Song, G.; Luo, J.; Shi, Y.; Cheng, E.; Wu, S.;  
Jiang, T.; Low, J.; Gao, N.; Qin, Y.  
Deposited on : 2015-12-01  
Resolution : 3.70 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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-20028442

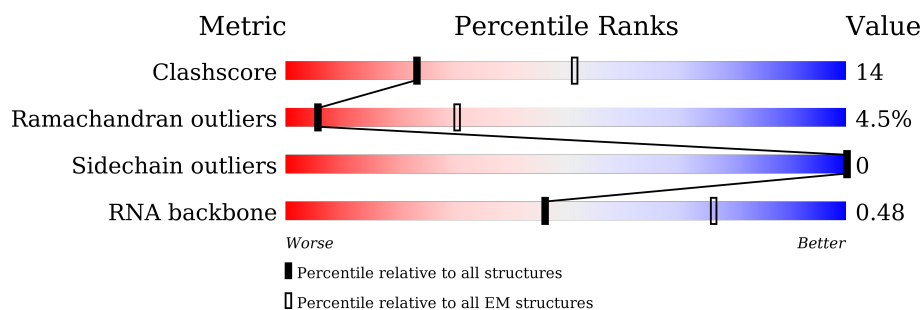
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.70 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.





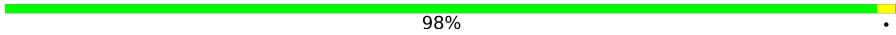
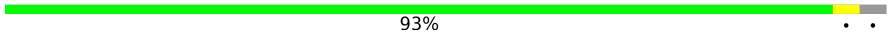

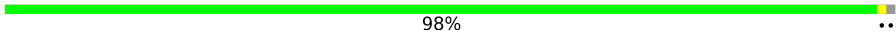
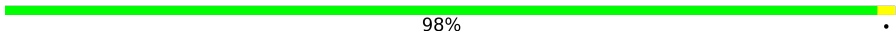



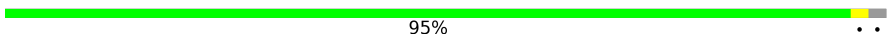


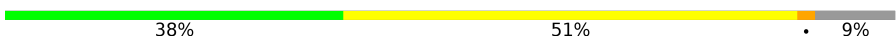











Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	b	241	85% 5% 10%
2	c	233	85% • 12%
3	d	206	95% •
4	e	167	87% • 10%
5	f	135	70% 6% 24%
6	g	179	81% • 16%
7	h	130	98% ••
8	i	130	95% ••


















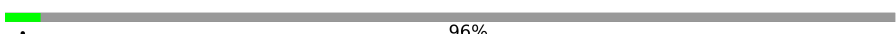






*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
9	j	103	 90% 5% 5%
10	k	129	 88% 9%
11	l	124	 98% ..
12	m	118	 93% ..
13	n	101	 88% 7% 5%
14	o	89	 98% ..
15	p	82	 98% .
16	q	84	 89% 6% 5%
17	r	75	 72% 27%
18	s	92	 83% 14%
19	t	87	 95% ..
20	u	71	 66% 6% 28%
21	0	57	 68% 30% .
22	1	55	 38% 51% 9%
23	2	46	 76% 22% .
24	3	64	 72% 27% .
25	4	38	 47% 45% 8%
26	5	234	 54% 46%
27	C	273	 59% 38% ..
28	D	209	 64% 33% .
29	E	201	 63% 35% .
30	F	179	 61% 35% ..
31	G	177	 62% 36% ..
32	H	149	 51% 46% .
33	I	142	 57% 41% ..

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	J	142	
35	K	123	
36	L	144	
37	M	136	
38	N	127	
39	O	117	
40	P	115	
41	Q	118	
42	R	103	
43	S	110	
44	T	100	
45	U	104	
46	V	94	
47	W	85	
48	X	78	
49	Y	63	
50	Z	59	
51	x	599	
52	a	1533	
53	A	2904	
54	B	120	
55	7	15	
56	8	76	
56	9	76	

## 2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 147815 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 30S ribosomal protein S2.

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

- Molecule 2 is a protein called 30S ribosomal protein S3.

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

- Molecule 3 is a protein called 30S ribosomal protein S4.

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

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	102	Total	C	N	O	S	0	0
			832	525	150	150	7		

- Molecule 6 is a protein called 30S ribosomal protein S7.

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

- Molecule 7 is a protein called 30S ribosomal protein S8.

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

- Molecule 8 is a protein called 30S ribosomal protein S9.

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

- Molecule 9 is a protein called 30S ribosomal protein S10.

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

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 11 is a protein called 30S ribosomal protein S12.

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

- Molecule 12 is a protein called 30S ribosomal protein S13.

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

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

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

- Molecule 15 is a protein called 30S ribosomal protein S16.

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

- Molecule 16 is a protein called 30S ribosomal protein S17.

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

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	r	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 18 is a protein called 30S ribosomal protein S19.

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

- Molecule 19 is a protein called 30S ribosomal protein S20.

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

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	u	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 22 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 23 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 24 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 25 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 26 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	5	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	270	Total	C	N	O	S	0	0
			2076	1285	422	362	7		

- Molecule 28 is a protein called 50S ribosomal protein L3.



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

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

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

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

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

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

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

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

- Molecule 51 is a protein called Elongation factor 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	26	Total	C	N	O	S	0	0
			214	134	43	35	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	1533	Total	C	N	O	P	0	0
			32895	14671	6036	10655	1533		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	2903	Total	C	N	O	P	0	0
			62320	27801	11467	20149	2903		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 55 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	9	Total	C	N	O	P	0	0
			191	86	34	62	9		

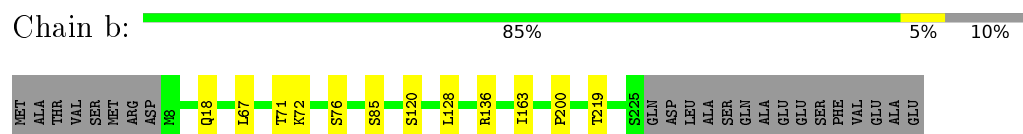
- Molecule 56 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	8	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		
56	9	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

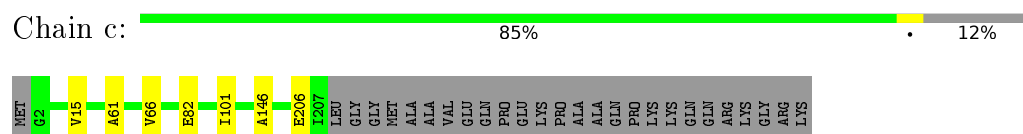
### 3 Residue-property plots [i](#)

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.

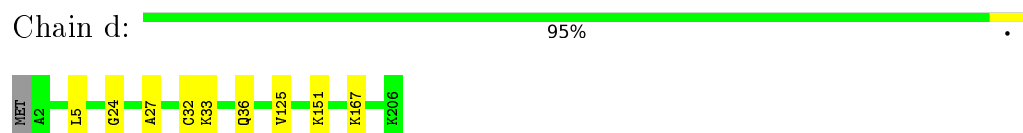
- Molecule 1: 30S ribosomal protein S2



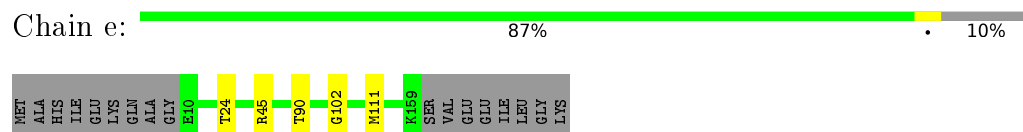
- Molecule 2: 30S ribosomal protein S3



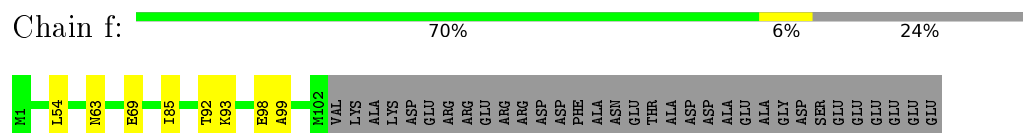
- Molecule 3: 30S ribosomal protein S4



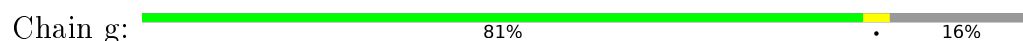
- Molecule 4: 30S ribosomal protein S5

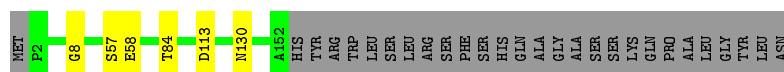


- Molecule 5: 30S ribosomal protein S6



- Molecule 6: 30S ribosomal protein S7





- Molecule 7: 30S ribosomal protein S8

Chain h:  98%

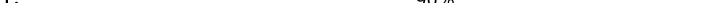


- Molecule 8: 30S ribosomal protein S9

Chain i:  95% ..

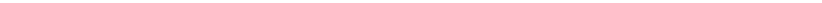


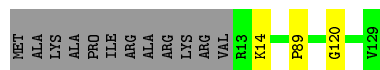
- Molecule 9: 30S ribosomal protein S10

Chain j:  90% 5% 5%



- Molecule 10: 30S ribosomal protein S11

Chain k:  88% 9%



- Molecule 11: 30S ribosomal protein S12

Chain 1:  98%

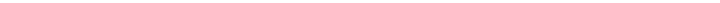


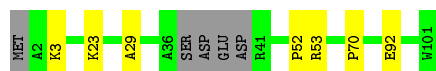
- Molecule 12: 30S ribosomal protein S13

Chain m:  93% ..



- Molecule 13: 30S ribosomal protein S14

Chain n:  88% 7% 5%



- Molecule 14: 30S ribosomal protein S15

Chain o:  98% ..




- Molecule 15: 30S ribosomal protein S16

Chain p:  98% .



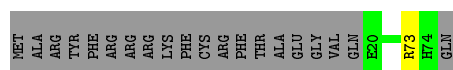
- Molecule 16: 30S ribosomal protein S17

Chain q:  89% 6% 5%




- Molecule 17: 30S ribosomal protein S18

Chain r:  72% 27%



- Molecule 18: 30S ribosomal protein S19

Chain s:  83% 14%



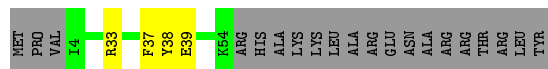
- Molecule 19: 30S ribosomal protein S20

Chain t:  95% ..



- Molecule 20: 30S ribosomal protein S21

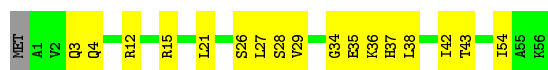
Chain u:  66% 6% 28%



- Molecule 21: 50S ribosomal protein L32

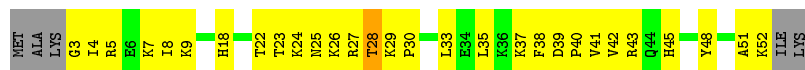


Chain 0: 




- Molecule 22: 50S ribosomal protein L33

Chain 1: 



- Molecule 23: 50S ribosomal protein L34

Chain 2: 



- Molecule 24: 50S ribosomal protein L35

Chain 3: 



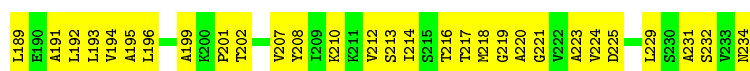
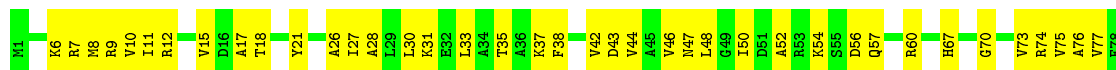
- Molecule 25: 50S ribosomal protein L36

Chain 4: 



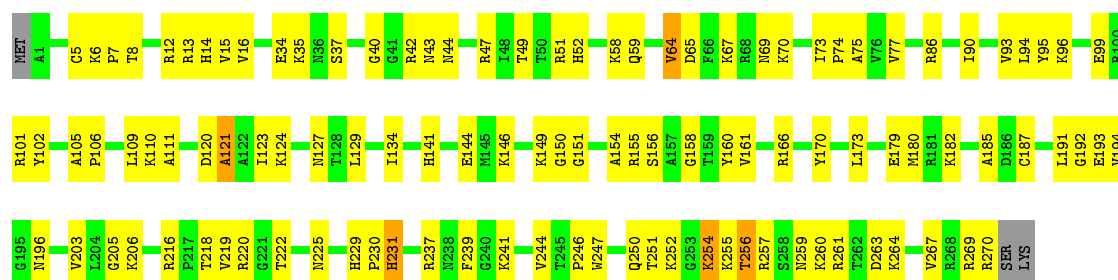
- Molecule 26: 50S ribosomal protein L1

Chain 5: 



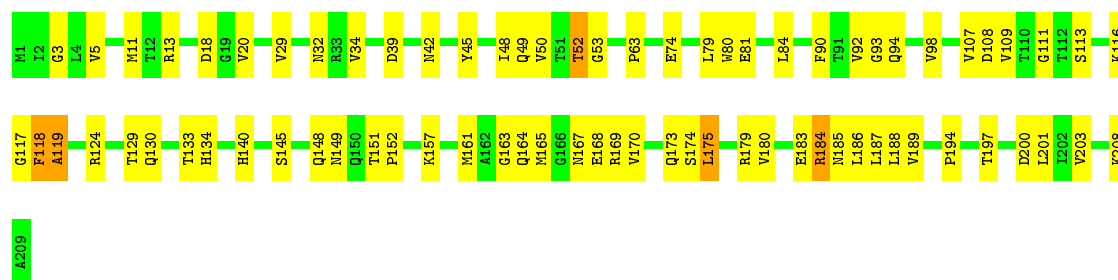
- Molecule 27: 50S ribosomal protein L2

Chain C: 



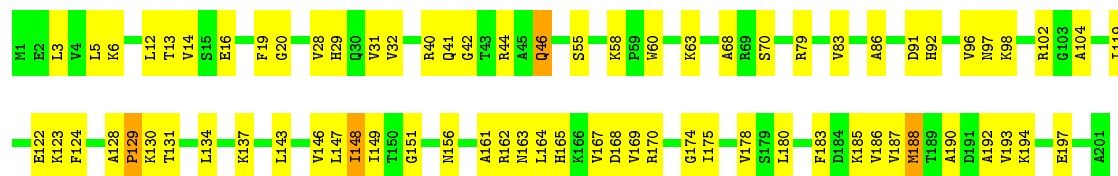
• Molecule 28: 50S ribosomal protein L3

Chain D: 64% 33%



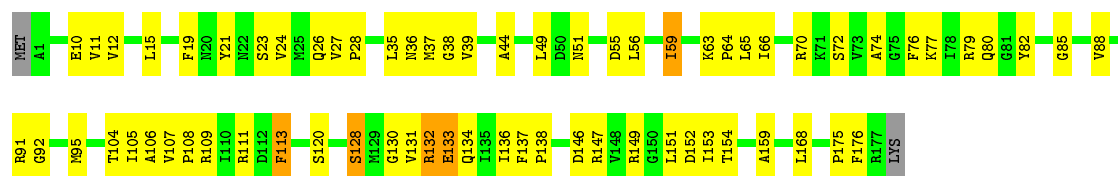
• Molecule 29: 50S ribosomal protein L4

Chain E: 63% 35%



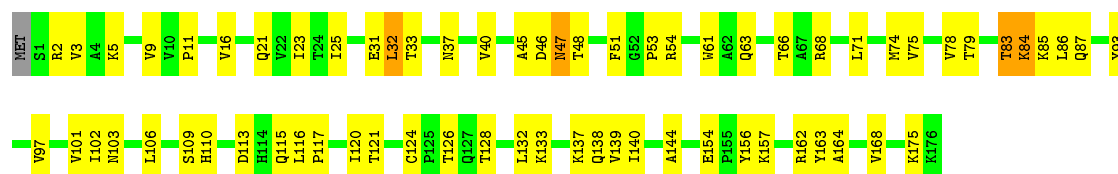
• Molecule 30: 50S ribosomal protein L5

Chain F: 61% 35%

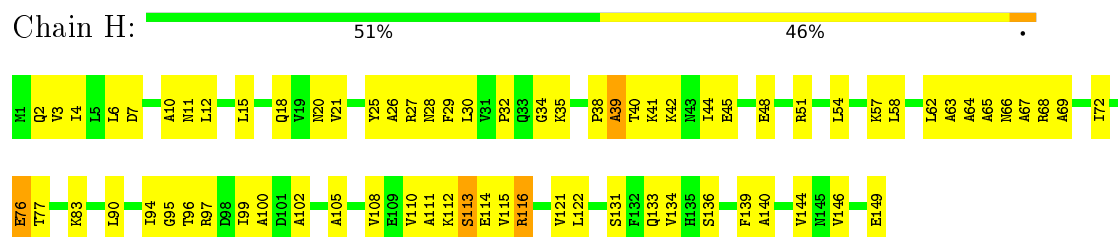


• Molecule 31: 50S ribosomal protein L6

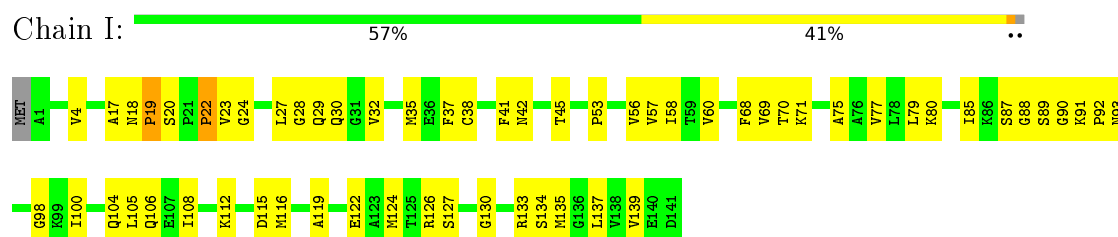
Chain G: 62% 36%



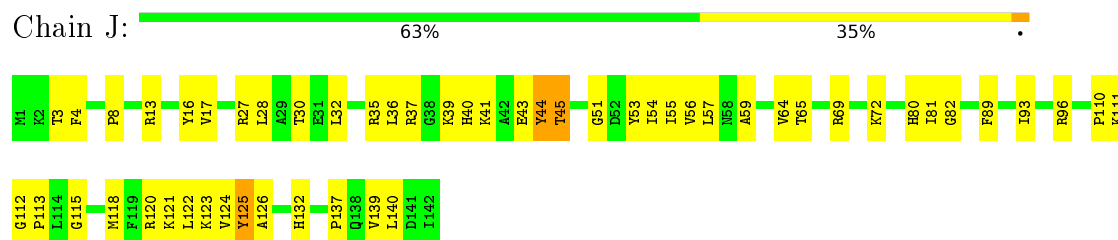
- Molecule 32: 50S ribosomal protein L9



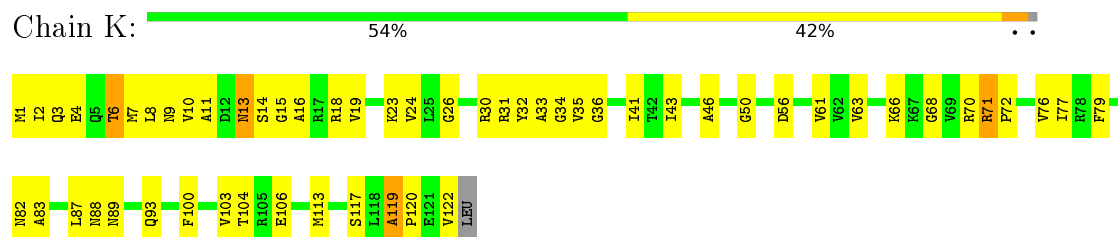
- Molecule 33: 50S ribosomal protein L11



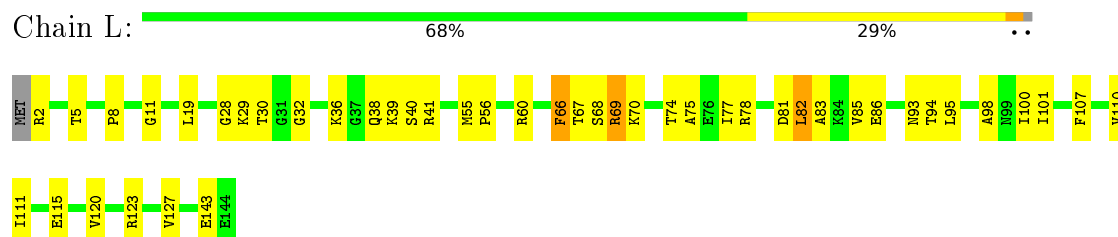
- Molecule 34: 50S ribosomal protein L13



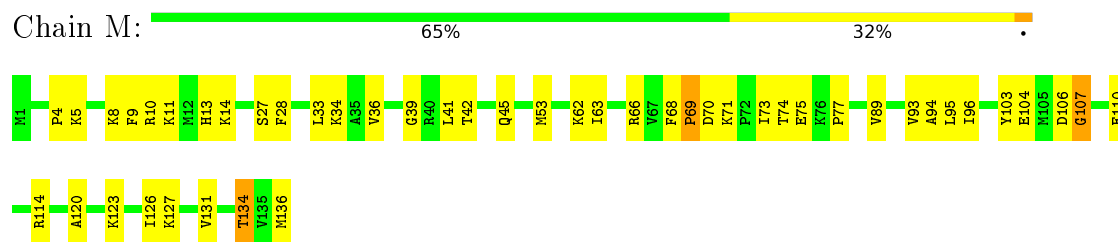
- Molecule 35: 50S ribosomal protein L14



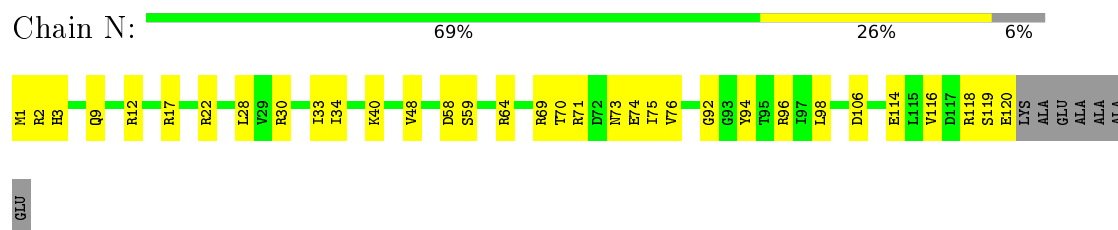
- Molecule 36: 50S ribosomal protein L15



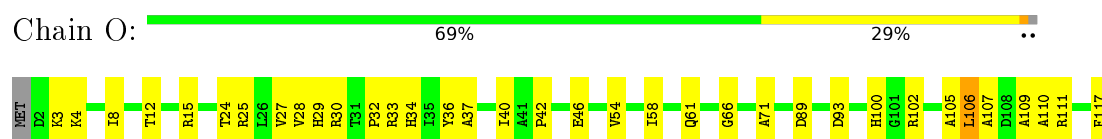
- Molecule 37: 50S ribosomal protein L16



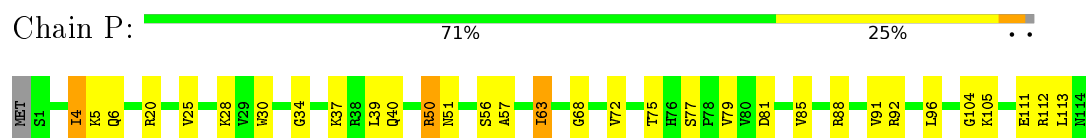
- Molecule 38: 50S ribosomal protein L17



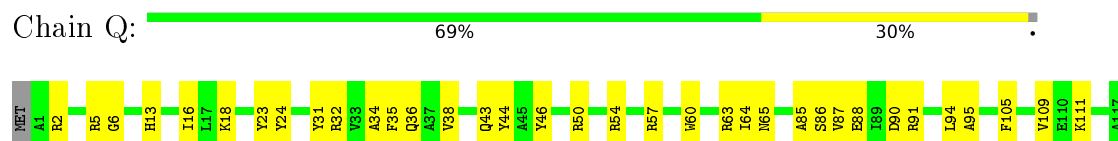
- Molecule 39: 50S ribosomal protein L18



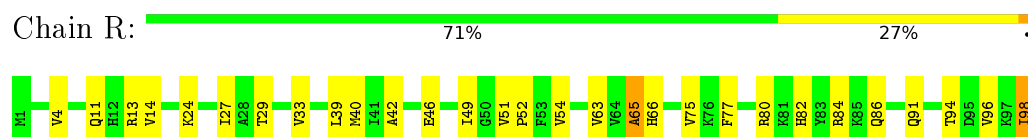
- Molecule 40: 50S ribosomal protein L19



- Molecule 41: 50S ribosomal protein L20



- Molecule 42: 50S ribosomal protein L21



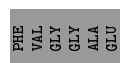
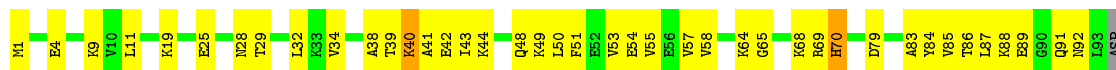
- Molecule 43: 50S ribosomal protein L22





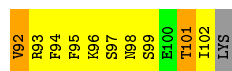
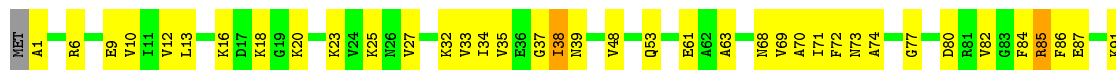
• Molecule 44: 50S ribosomal protein L23

Chain T: 52% 39% 7%



• Molecule 45: 50S ribosomal protein L24

Chain U: 52% 42% 6%



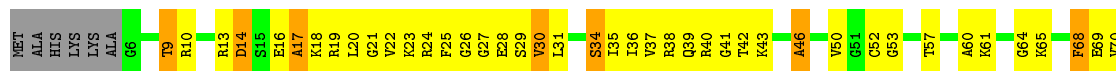
• Molecule 46: 50S ribosomal protein L25

Chain V: 69% 29% 2%



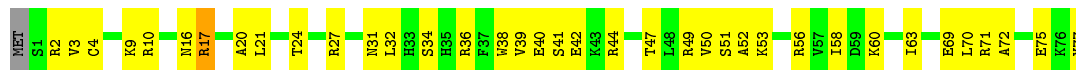
• Molecule 47: 50S ribosomal protein L27

Chain W: 39% 46% 8% 7%



• Molecule 48: 50S ribosomal protein L28

Chain X: 51% 46% 3%



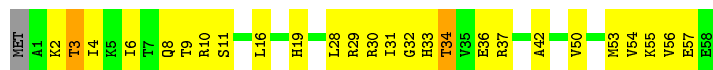
• Molecule 49: 50S ribosomal protein L29

Chain Y: 71% 24% 5%



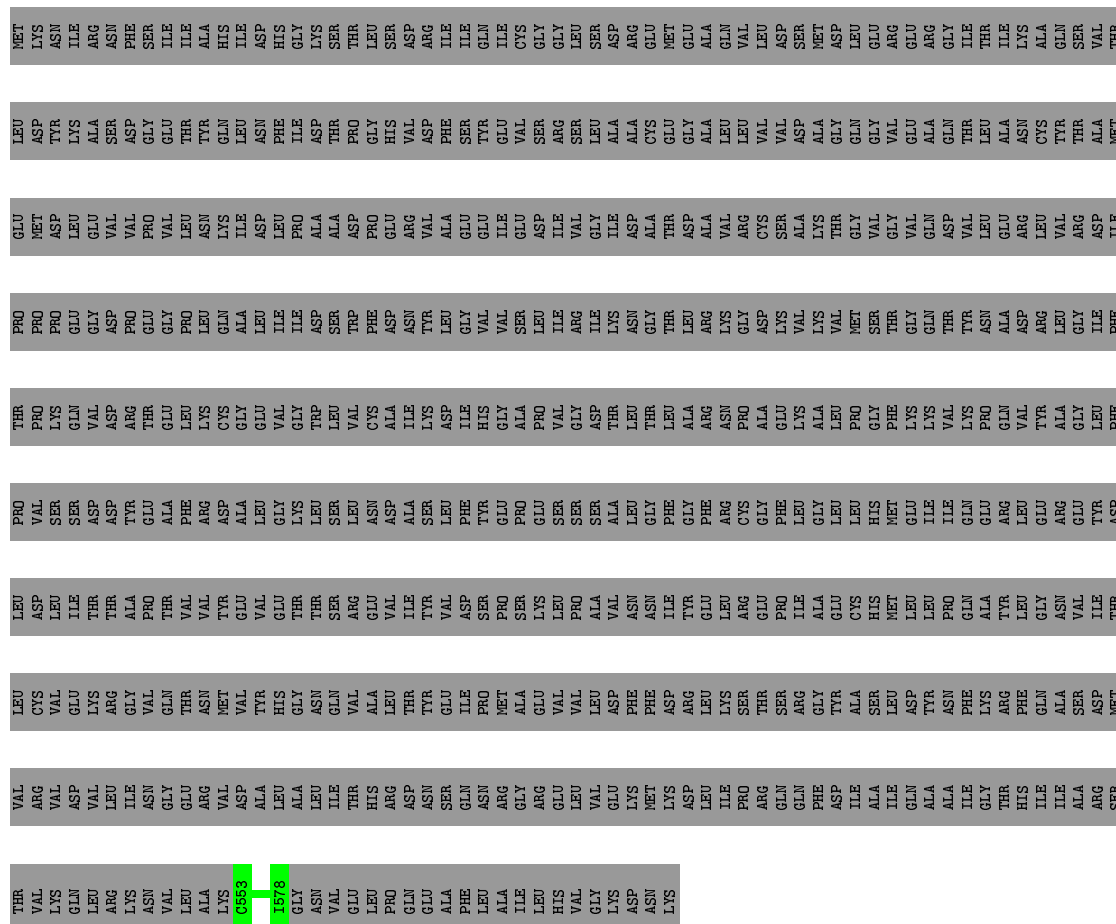
- Molecule 50: 50S ribosomal protein L30

Chain Z: 54% 41%



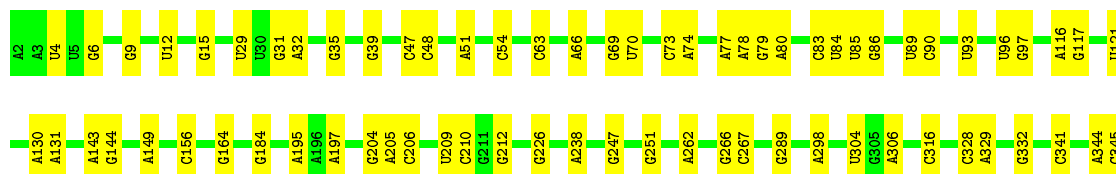
- Molecule 51: Elongation factor 4

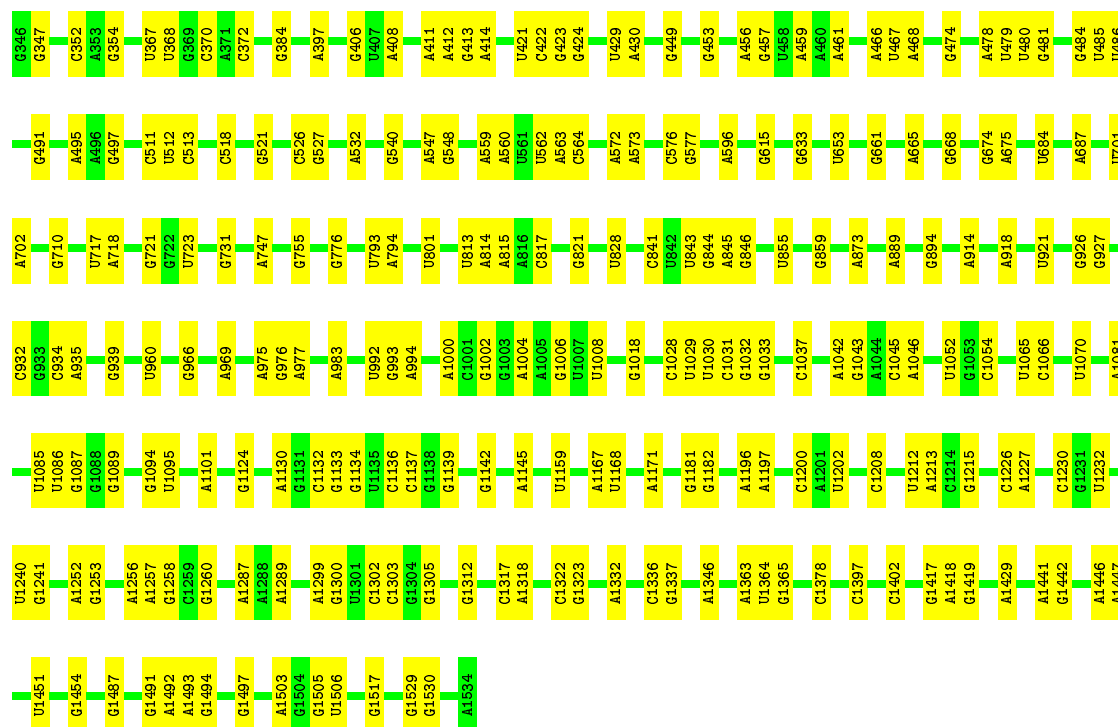
Chain x: 96%



- Molecule 52: 16S ribosomal RNA

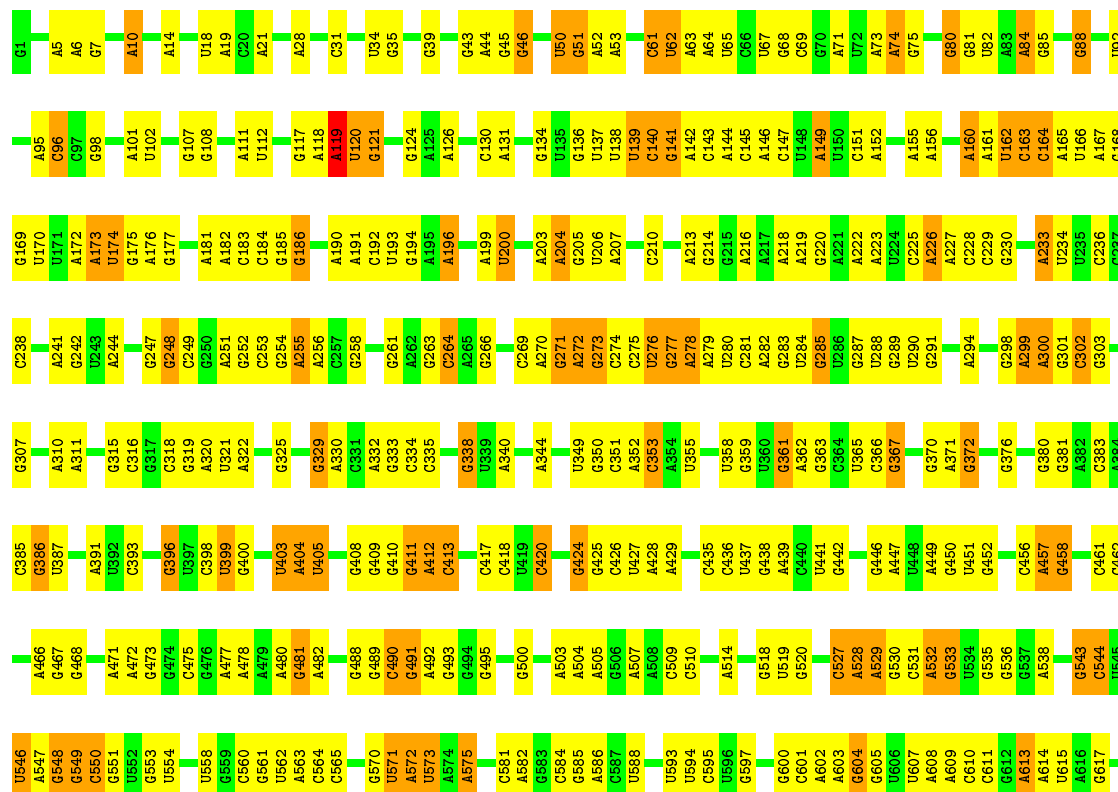
Chain a: 80% 20%





- Molecule 53: 23S ribosomal RNA

Chain A:  43% 46% 11%



G1699	G1617	G1538	G1464	G1388	G1229	A1142	A1073	G1011	G938	A866	C791	A621
G1703	G1618	G1539	G1465	A1392	G1230	A1143	G1074	U1012	G939	G869	A792	A705
C1704	G1620	C1541	U1467	A1393	U1231	A1144	C1075	C1013	G940	G870	G713	C623
A1705	U1621	U1542	U1468	U1394	G1232		A1076	A1014	A941	U870	U714	C624
	G1622	G1543	A1469	A1395		C1150	U1077	U1015	G942	U871	G801	G625
	G1623			U1396	G1236	A1151			A943	U872	A802	A826
		G1546	U1470	U1397	A1237	C1152	C1079	U1018	C944	C874	G717	A627
	A1626	C1547	C1472	A1321	U1238	C1153	A1080	U1019	A945	C875	G805	G628
		A1548	G1473	C1398	G1239	G1154	U1081	A1020	C946	C876	C806	G629
	A1632	U1549	U1474	U1400	U1240	A1155	U1082	A1021	A947	A877	U807	G630
		G1550		U1401	A1241	A1156	U1083	G1022	C948	A878	G808	A631
	U1636		A1477	U1402		G1157	A1084	U1023		G879		
	A1637	U1553	G1478	G1245	A1244	G1160	A1085	G1024	G953	G880	C812	G636
	G1638	U1554	G1479	A1246	G1245		A1086	G1025	G954	G881	U813	A637
	G1639	G1555			G1246		G1087	G1026	U955	G882	C814	G638
			G1482	U1408	A1247	C1164	A1088	A1027	G956	G883	C815	U639
		G1560		U1409	G1248	A1165	A1089	A1028	C957	U884	C816	C640
	G1645			G1410	U1249	G1166	A1090	A1029	U958		C817	
		C1561	U1488		G1250	C1167			A959	A886	G818	
	G1646	C1562		A1413	G1251	G1168	G1093	G1031	A960	U887	A819	U646
	U1647	U1562		C1414	G1252	A1169	U1094	U1032	C961	U888	A820	G647
	U1648	U1563	U1493	U1415	A1253	C1170	A1095	U1033	G962		G738	G648
	G1649		A1494			G1171	A1096	G1034	U963			
	A1650	A1566	A1495	G1416	G1256	C1172	U1097	U1035	C964	G891	C823	G649
	G1651	U1567	A1496	G1417		U1173	A1098			A892	U824	C650
	A1652	G1568	U1497			U1174	G1099	G1036		C893		
	G1653	A1569	A1498	A1419	U1262	A1175	C1100	U1037	G970	U894	U827	G652
	A1654	C1570	C1499	A1420	A1263	U1176	U1101	G1038	U971	U895	U828	U653
	U1655	A1571	G1500	G1346	A1264	U1176		A1039	A972	A896	U744	A654
	C1656		G1501	A1347	A1265	G1177		A1040	A973	C897	G830	A655
	U1657	C1577		G1424	G1266		C1104	G1041	G974	C898	G831	G656
		U1504		G1425	U1267	U1180	U1105	G1042	A975	A899	U832	
	G1658	A1578			U1352	U1181	G1106	C1043	G978	A900	U833	U657
	A1659	A1579	A1508	C1428	A1353	G1182		C1044	G980	C901	G834	U658
	G1660	U1580	G1429	G1430	G1354	U1183	G1110	C1045	A979	C902	C835	A750
		G1581	A1509	A1431	G1355	U1184	A1111	A1046	A980	C903	G836	
	A1664	C1582	U1510	A1432	G1271	U1185	G1112	G1047	A981	G904	C837	U755
	U1665	G1511	G1432	G1433	A1272	G1186	U1113	A1048	C982	C838	U756	U665
	G1666	U1512	A1433	G1434	U1273	A1186	C1114	C1049	A983	C907	U839	A666
	U1667	U1513	G1514	A1435	A1274	G1190	G1115	C1050	A984	G875	C840	A667
	A1668	A1586	U1514	G1435	A1275		G1116	G1051	C985	A910	G841	A668
		G1587	A1515	G1436		U1199	C1117			A911	U768	
	G1674	G1588		C1437	G1278	U1199	C1118	A1054	G989		U842	G674
	A1675	U1589	G1519	U1438	G1279	C1200	G1118	G1055	A990		G843	A675
	U1676	U1590	U1520	A1439		U1201	U1119	G1056	C915	C916	A844	A676
		A1591	G1521	A1439	G1283		G1120				C845	A677
		C1592	A1522	U1442	A1285	A1205	G1121	A1057	C995		C772	C678
	A1679	U1592	U1523	U1443	A1284	G1206	G1124	U1058	A996	C922	U846	C679
	G1680	A1593	U1524	U1443	A1285	G1207	G1125	G1059	G997	G923	U847	C680
	G1681	U1594	G1524	G1444	A1286		A1126	U1060	C998	G924	G775	
	U1682	C1595	A1525	G1445	A1287		U1127	G1061	U999	A925	U850	
	G1684		U1526	G1446	G1288	G1212	A1127	U1062		G926	C851	U683
		G1601	C1596	G1447			G1128	G1063	A1000	G926		
	U1685	A1592	U1527	C1447		G1215	A1129	G1063	A1001	A927	G855	U686
		U1602	A1528		U1294		G1130	U1064	G1002	A928		
	G1687	A1603	G1529	G1452	G1295		U1130	C1065	G1003		A781	G690
	U1688	C1604	U1530	A1453	G1296	U1219	G1131	U1065	G1004	G931	A782	C691
	A1689	G1605	U1531		G1297		U1132	U1066	U1004	U932	A783	A693
			A1532			G1223	A1133	A1067	C1005	U933	G859	
		U1533	U1457	G1456	G1300	U1224	A1134	G1068	C1006	A932	U860	
		A1608	C1533	U1457	A1383		C1135	U1069	G1007	U934	A861	C692
	G1694	G1695	U1534	U1458	A1301	G1225		A1070	A1008	C935	A788	G700
	A1703	A1610	A1535	G1459	A1302	A1226		G1071	C936		A863	
	G1696	U1536	U1459	A1385	A1302	G1227	G1139	C1072	A1009		G864	G701
	U1697	C1611	U1536	U1460	C1386	G1227		C1073	U937			
	A1698		G1537		C1387	G1228			A1010		U769	



U2897	U2898	A2899	A2900	C2901	C2902	U2903	U	C2806	G2729	U2728	C2559	C2475	U2398	A2327	U2259	A2170	A2108	G2035	U1955	U1865
U2898	A2899	A2900	C2901	C2902	U2903	U		A2809	G2730	U2729	C2560	A2476	G2399	G2330	C2260	A2171	U2109	C2036	U1956	A1866
C2901	C2902	U2903	U					G2812	G2731	U2730	U2561	U2477	U2401	G2331	U2261	A2172	U2110	G2040	A1960	G1869
C2902	U2903	U						A2813	G2732	U2731	U2562	U2478	U2402	G2332	U2262	A2173	U2111	U2041	G1965	A1870
U2903	U							G2814	G2733	U2732	U2563	U2479	U2403	G2333	C2263	C2174	U2112	A2042	A1966	A1871
U								G2815	U2734	U2733	U2564	U2480	U2404	G2334	C2264	C2175	U2113	C2043	A1967	A1872
								G2816	U2735	U2734	U2565	U2481	U2405	G2335	U2265	C2176	U2114		G1968	G1875
								G2817	U2736	U2735	U2566	U2482	U2406	G2336	A2266	C2177	U2115	G2048	G1969	A1876
								G2818	U2737	U2736	U2567	U2483	U2407	G2337	U2267	C2178	U2116	G2049	A1969	A1877
								G2819	U2738	U2737	U2568	U2484	U2408	G2338	U2268	C2179	U2117	C2050	A1970	A1878
								A2820	U2739	U2738	U2569	U2485	U2409	G2339	U2269	U2180	U2118	G2051	A1971	G1879
								G2821	U2740	U2739	U2570	U2486	U2410	G2340	U2270	U2181	U2119	A2051	G1972	U1880
								G2822	U2741	U2740	U2571	U2487	U2411	G2341	U2271	U2182	U2120	A2052		C1881
								G2823	U2742	U2741	U2572	U2488	U2412	G2342	U2272	U2183	U2121		A1977	A1882
								G2824	U2743	U2742	U2573	U2489	U2413	G2343	U2273	U2184	U2122	C2055	A1978	U1883
								A2825	U2744	U2743	U2574	U2490	U2414	G2344	U2274	U2185	U2123	G2056	U1979	U1884
								G2826	U2745	U2744	U2575	U2491	U2415	G2345	U2275	U2186	U2124	A2059	G1980	G1885
								G2827	U2746	U2745	U2576	U2492	U2416	G2346	U2276	U2187	U2125	A2060	A1981	A1886
								G2828	U2747	U2746	U2577	U2493	U2417	G2347	U2277	U2188	U2126	G2061	U1982	A1889
								G2829	U2748	U2747	U2578	U2494	U2418	G2348	U2278	U2189	U2127	G2062	A1983	A1890
								G2830	U2749	U2748	U2579	U2495	U2419	G2349	U2279	U2190	U2128	G2063	A1984	G1891
								G2831	U2750	U2749	U2580	U2496	U2420	G2350	U2280	U2191	U2129	G2064	A1985	
								G2832	U2751	U2750	U2581	U2497	U2421	G2351	U2281	U2192	U2130	G2065	U1991	G1896
								G2833	U2752	U2751	U2582	U2498	U2422	G2352	U2282	U2193	U2131	C2066	G1992	G1897
								G2834	U2753	U2752	U2583	U2499	U2423	G2353	U2283	U2194	U2132	G2067	U1993	U1898
								G2835	U2754	U2753	U2584	U2500	U2424	G2354	U2284	U2195	U2133	G2068	U1994	A1899
								G2836	U2755	U2754	U2585	U2501	U2425	G2355	U2285	U2196	U2134	G2069	U1995	A1900
								G2837	U2756	U2755	U2586	U2502	U2426	G2356	U2286	U2197	U2135	A2070	U1996	A1901
								G2838	U2757	U2756	U2587	U2503	U2427	G2357	U2287	U2198	U2136	C2071	C1902	G1903
								G2839	U2758	U2757	U2588	U2504	U2428	G2358	U2288	U2199	U2137	C2072	C1903	
								G2840	U2759	U2758	U2589	U2505	U2429	G2359	U2289	U2200	U2138	U2075	U1999	G1906
								G2841	U2760	U2759	U2590	U2506	U2430	G2360	U2290	U2201	U2139	U2076	C2000	G1907
								G2842	U2761	U2760	U2591	U2507	U2431	G2361	U2291	U2202	C2143	U2077	C2001	A1913
								G2843	U2762	U2761	U2592	U2508	U2432	G2362	U2292	U2203	C2144	A2082	G2002	A1914
								G2844	U2763	U2762	U2593	U2509	U2433	G2363	U2293	U2204	C2145	G2083	G2003	
								G2845	U2764	U2763	U2594	U2510	U2434	G2364	U2294	U2205	C2146	G2084	G2004	U1917
								G2846	U2765	U2764	U2595	U2511	U2435	G2365	U2295	U2206	C2147	C2085	A2005	U1918
								G2847	U2766	U2765	U2596	U2512	U2436	G2366	U2296	U2207	G2148	U2086	U2007	U1919
								G2848	U2767	U2766	U2597	U2513	U2437	G2367	U2297	U2208	C2149	U2087	G2008	C1920
								G2849	U2768	U2767	U2598	U2514	U2438	G2368	U2298	U2209	C2150	A2088	A2009	
								G2850	U2769	U2768	U2599	U2515	U2439	G2369	U2299	U2210	C2151	C2089	G2010	A1927
								G2851	U2770	U2769	U2600	U2516	U2440	G2370	U2300	U2211	C2152	A2090	U2011	A1928
								G2852	U2771	U2770	U2601	U2517	U2441	G2371	U2301	U2212	C2153	C2091	G2012	A1929
								G2853	U2772	U2771	U2602	U2518	U2442	G2372	U2302	U2213	C2154	U2092	A2013	G1933
								G2854	U2773	U2772	U2603	U2519	U2443	G2373	U2303	U2214	C2155	U2093	G2022	G1934
								G2855	U2774	U2773	U2604	U2520	U2444	G2374	U2304	U2215	C2156	A2094	G2023	G1935
								G2856	U2775	U2774	U2605	U2521	U2445	G2375	U2305	U2216	C2157	C2095	G2024	A1936
								G2857	U2776	U2775	U2606	U2522	U2446	G2376	U2306	U2217	C2158	A2095	G2025	A1937
								G2858	U2777	U2776	U2607	U2523	U2447	G2377	U2307	U2218	C2159	C2096	G2026	G1938
								G2859	U2778	U2777	U2608	U2524	U2448	G2378	U2308	U2219	C2160	A2097	G2027	U1939
								G2860	U2779	U2778	U2609	U2525	U2449	G2379	U2309	U2220	C2161	A2101	U2028	U1940
								G2861	U2780	U2779	U2610	U2526	U2450	G2380	U2310	U2221	C2162	A2102	G2029	G1947
								G2862	U2781	U2780	U2611	U2527	U2451	G2381	U2311	U2222	C2163	G2102	A2030	G1948
								G2863	U2782	U2781	U2612	U2528	U2452	G2382	U2312	U2223	C2164	C2103	A2031	G1949
								G2864	U2783	U2782	U2613	U2529	U2453	G2383	U2313	U2224	C2165	C2104	U2105	U2032
								G2865	U2784	U2783	U2614	U2530	U2454	G2384	U2314	U2225	C2166	U2106	A2033	U2034
								G2866	U2785	U2784	U2615	U2531	U2455	G2385	U2315	U2226	C2167	G2107		
								G2867	U2786	U2785	U2616	U2532	U2456	G2386	U2316	U2227	C2168			
								G2868	U2787	U2786	U2617	U2533	U2457	G2387	U2317	U2228	C2169			
								G2869	U2788	U2787	U2618	U2534	U2458	G2388	U2318	U2229	C2170			
								G2870	U2789	U2788	U2619	U2535	U2459	G2389	U2319	U2230	C2171			
								G2871	U2790	U2789	U2620	U2536	U2460	G2390	U2320	U2231	C2172			
								G2872	U2791	U2790	U2621	U2537	U2461	G2391	U2321	U2232	C2173			
								G2873	U2792	U2791	U2622	U2538	U2462	G2392	U2322	U2233	C2174			
								G2874	U2793	U2792	U2623	U2539	U2463	G2393	U2323	U2234	C2175			
								G2875	U2794	U2793	U2624	U2540	U2464	G2394	U2324	U2235	C2176			
								G2876	U2795	U2794	U2625	U2541	U2465	G2395	U2325	U2236	C2177			
								G2877	U2796	U2795	U2626	U2542	U2466	G2396	U2326	U2237	C2178			
								G2878	U2797	U2796	U2627	U2543	U2467	G2397	U2327	U2238	C2179			
								G2879	U2798	U2797	U2628	U2544	U2468	G2398	U2328	U2239	C2180			
								G2880	U2799	U2798	U2629	U2545	U2469	G2399	U2329	U2240	C2181			
								G2881	U2800	U2799	U2630	U2546	U2470	G2400	U2330	U2241	C2182			
								G2882	U2801	U2800	U2631	U2547	U2471	G2401	U2331	U2242	C2183			
								G2883	U2802	U2801	U2632	U2548	U2472	G2402	U2332	U2243	C2184			
								G2884	U2803	U2802	U2633	U2549	U2473	G2403	U2333	U2244	C2185			
								G2885	U2804	U2803	U2634	U2550	U2474	G2404	U2334	U2245	C2186			
								G2886	U2805	U2804	U2635	U2551	U2475	G2405	U2335	U2246	C2187			
								G2												



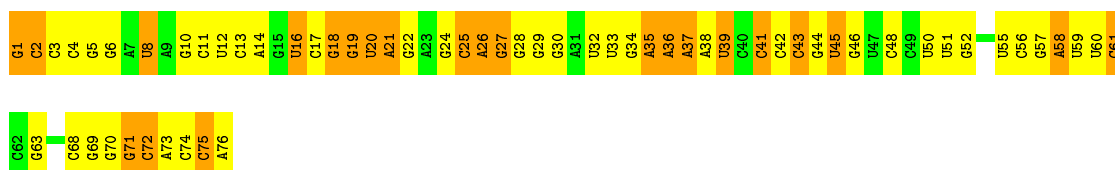
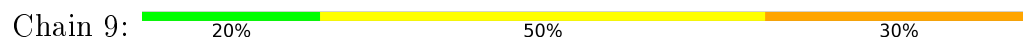
- Molecule 55: tRNA



- Molecule 56: tRNA



- Molecule 56: tRNA



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	18772	Depositor
Resolution determination method	Not provided	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)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	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	b	0.30	0/1735	0.55	0/2338
10	k	0.35	0/893	0.52	0/1205
11	l	0.35	0/969	0.54	0/1300
12	m	0.32	0/892	0.56	0/1193
13	n	0.33	0/785	0.52	0/1043
14	o	0.35	0/722	0.51	0/964
15	p	0.34	0/659	0.48	0/884
16	q	0.33	0/657	0.55	0/881
17	r	0.36	0/462	0.48	0/621
18	s	0.30	0/652	0.50	0/877
19	t	0.36	0/671	0.51	0/888
2	c	0.34	0/1651	0.50	0/2225
20	u	0.34	0/430	0.56	0/570
21	0	0.36	0/450	0.52	0/599
22	1	0.36	0/416	0.58	0/554
23	2	0.36	0/380	0.52	0/498
24	3	0.38	0/513	0.56	0/676
25	4	0.32	0/303	0.54	0/397
26	5	0.27	0/1748	0.60	0/2355
27	C	0.39	0/2115	0.58	1/2844 (0.0%)
28	D	0.37	0/1586	0.57	0/2134
29	E	0.34	0/1571	0.54	0/2113
3	d	0.32	0/1665	0.52	0/2227
30	F	0.32	0/1434	0.53	0/1926
31	G	0.31	0/1343	0.53	0/1816
32	H	0.30	0/1122	0.59	0/1515
33	I	0.26	0/1046	0.54	0/1410
34	J	0.39	0/1152	0.56	0/1551
35	K	0.40	0/947	0.57	0/1268
36	L	0.33	0/1054	0.56	0/1403
37	M	0.36	0/1093	0.57	0/1460
38	N	0.38	0/973	0.55	0/1301
39	O	0.31	0/902	0.51	1/1209 (0.1%)
4	e	0.35	0/1118	0.54	0/1504

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  > 2	RMSZ	# Z  > 2
40	P	0.37	0/929	0.56	0/1242
41	Q	0.43	0/960	0.51	0/1278
42	R	0.35	0/829	0.53	0/1107
43	S	0.37	0/864	0.55	0/1156
44	T	0.36	0/744	0.61	0/994
45	U	0.33	0/787	0.57	0/1051
46	V	0.33	0/766	0.50	0/1025
47	W	0.35	0/603	0.64	0/797
48	X	0.37	0/635	0.56	0/848
49	Y	0.32	0/510	0.51	0/677
5	f	0.33	0/851	0.56	0/1150
50	Z	0.32	0/453	0.57	0/605
51	x	0.31	0/214	0.54	0/275
52	a	0.52	0/36834	0.77	0/57462
53	A	0.58	0/69799	0.81	6/108892 (0.0%)
54	B	0.46	0/2828	0.77	0/4410
55	7	0.48	0/213	0.91	0/329
56	8	0.51	1/1813 (0.1%)	0.79	0/2823
56	9	0.39	1/1813 (0.1%)	0.83	3/2823 (0.1%)
6	g	0.32	0/1195	0.50	0/1602
7	h	0.36	0/989	0.53	0/1326
8	i	0.32	0/1034	0.52	0/1375
9	j	0.31	0/796	0.57	0/1077
All	All	0.50	2/160568 (0.0%)	0.74	11/240073 (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
20	u	0	1
31	G	0	1
35	K	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	9	1	G	OP3-P	-10.74	1.48	1.61
56	8	1	G	OP3-P	-10.71	1.48	1.61

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	9	39	U	C2-N1-C1'	7.25	126.40	117.70
56	9	39	U	N1-C2-O2	7.22	127.85	122.80
56	9	39	U	N3-C2-O2	-6.07	117.95	122.20
53	A	1415	U	C2-N1-C1'	6.02	124.92	117.70
39	O	106	LEU	CA-CB-CG	5.67	128.34	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
31	G	83	THR	Peptide
35	K	71	ARG	Peptide
20	u	39	GLU	Peptide

## 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	b	1704	0	1732	0	0
2	c	1624	0	1696	0	0
3	d	1643	0	1707	0	0
4	e	1105	0	1148	0	0
5	f	832	0	824	0	0
6	g	1181	0	1238	0	0
7	h	979	0	1031	0	0
8	i	1022	0	1070	0	0
9	j	786	0	828	0	0
10	k	877	0	887	0	0
11	l	955	0	1016	0	0
12	m	883	0	941	0	0
13	n	774	0	824	0	0
14	o	714	0	734	0	0
15	p	649	0	666	0	0
16	q	648	0	691	0	0
17	r	455	0	478	0	0
18	s	637	0	665	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	t	665	0	714	0	0
20	u	425	0	449	0	0
21	0	444	0	461	12	0
22	1	409	0	440	19	0
23	2	377	0	418	6	0
24	3	504	0	574	14	0
25	4	302	0	340	16	0
26	5	1733	0	1824	98	0
27	C	2076	0	2152	68	0
28	D	1565	0	1616	51	0
29	E	1552	0	1619	49	0
30	F	1410	0	1447	51	0
31	G	1323	0	1374	48	0
32	H	1111	0	1148	49	0
33	I	1032	0	1088	50	0
34	J	1129	0	1162	45	0
35	K	938	0	1012	37	0
36	L	1045	0	1117	25	0
37	M	1074	0	1157	31	0
38	N	960	0	1000	25	0
39	O	892	0	923	28	0
40	P	917	0	965	23	0
41	Q	947	0	1022	36	0
42	R	816	0	839	21	0
43	S	857	0	922	23	0
44	T	738	0	807	27	0
45	U	779	0	834	31	0
46	V	753	0	780	21	0
47	W	596	0	610	51	0
48	X	625	0	655	32	0
49	Y	509	0	543	10	0
50	Z	449	0	491	20	0
51	x	214	0	244	0	0
52	a	32895	0	16553	0	0
53	A	62320	0	31343	1212	0
54	B	2529	0	1281	51	0
55	7	191	0	97	3	0
56	8	1623	0	821	46	0
56	9	1623	0	821	94	0
All	All	147815	0	99839	2145	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 14.

The worst 5 of 2145 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:A:271:G:C5	53:A:367:G:C2	1.87	1.62
53:A:271:G:C8	53:A:367:G:N2	1.70	1.54
53:A:271:G:N7	53:A:367:G:C2	1.77	1.45
53:A:271:G:N7	53:A:367:G:N1	1.67	1.40
53:A:272:A:C2	53:A:273:G:C5	2.10	1.39

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	b	216/241 (90%)	181 (84%)	23 (11%)	12 (6%)	2	28
2	c	204/233 (88%)	190 (93%)	7 (3%)	7 (3%)	5	43
3	d	203/206 (98%)	179 (88%)	15 (7%)	9 (4%)	3	35
4	e	148/167 (89%)	128 (86%)	15 (10%)	5 (3%)	5	43
5	f	100/135 (74%)	79 (79%)	13 (13%)	8 (8%)	1	18
6	g	149/179 (83%)	125 (84%)	18 (12%)	6 (4%)	4	38
7	h	127/130 (98%)	115 (91%)	11 (9%)	1 (1%)	24	70
8	i	125/130 (96%)	109 (87%)	12 (10%)	4 (3%)	5	44
9	j	96/103 (93%)	78 (81%)	13 (14%)	5 (5%)	2	30
10	k	115/129 (89%)	104 (90%)	8 (7%)	3 (3%)	7	48
11	l	121/124 (98%)	105 (87%)	14 (12%)	2 (2%)	11	57
12	m	112/118 (95%)	103 (92%)	5 (4%)	4 (4%)	4	41
13	n	92/101 (91%)	77 (84%)	8 (9%)	7 (8%)	1	19
14	o	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	16	63

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	p	80/82 (98%)	70 (88%)	8 (10%)	2 (2%)	7	49
16	q	78/84 (93%)	65 (83%)	8 (10%)	5 (6%)	2	25
17	r	53/75 (71%)	51 (96%)	1 (2%)	1 (2%)	10	55
18	s	77/92 (84%)	68 (88%)	6 (8%)	3 (4%)	4	38
19	t	83/87 (95%)	80 (96%)	1 (1%)	2 (2%)	7	51
20	u	49/71 (69%)	36 (74%)	10 (20%)	3 (6%)	2	26
21	0	54/57 (95%)	49 (91%)	2 (4%)	3 (6%)	2	28
22	1	48/55 (87%)	43 (90%)	3 (6%)	2 (4%)	3	36
23	2	44/46 (96%)	39 (89%)	3 (7%)	2 (4%)	3	34
24	3	62/64 (97%)	54 (87%)	7 (11%)	1 (2%)	12	58
25	4	36/38 (95%)	29 (81%)	2 (6%)	5 (14%)	0	6
26	5	232/234 (99%)	198 (85%)	32 (14%)	2 (1%)	21	68
27	C	268/273 (98%)	233 (87%)	20 (8%)	15 (6%)	2	28
28	D	207/209 (99%)	168 (81%)	28 (14%)	11 (5%)	2	29
29	E	199/201 (99%)	170 (85%)	18 (9%)	11 (6%)	2	29
30	F	175/179 (98%)	153 (87%)	13 (7%)	9 (5%)	2	31
31	G	174/177 (98%)	142 (82%)	24 (14%)	8 (5%)	3	33
32	H	147/149 (99%)	114 (78%)	22 (15%)	11 (8%)	1	20
33	I	139/142 (98%)	121 (87%)	13 (9%)	5 (4%)	4	41
34	J	140/142 (99%)	120 (86%)	13 (9%)	7 (5%)	3	31
35	K	120/123 (98%)	96 (80%)	17 (14%)	7 (6%)	2	27
36	L	141/144 (98%)	115 (82%)	14 (10%)	12 (8%)	1	16
37	M	134/136 (98%)	114 (85%)	13 (10%)	7 (5%)	2	30
38	N	118/127 (93%)	105 (89%)	10 (8%)	3 (2%)	7	49
39	O	114/117 (97%)	105 (92%)	7 (6%)	2 (2%)	11	56
40	P	112/115 (97%)	98 (88%)	8 (7%)	6 (5%)	2	29
41	Q	115/118 (98%)	109 (95%)	5 (4%)	1 (1%)	21	68
42	R	101/103 (98%)	86 (85%)	11 (11%)	4 (4%)	4	38
43	S	108/110 (98%)	93 (86%)	9 (8%)	6 (6%)	2	28
44	T	91/100 (91%)	65 (71%)	17 (19%)	9 (10%)	1	13
45	U	100/104 (96%)	79 (79%)	13 (13%)	8 (8%)	1	18

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	V	92/94 (98%)	84 (91%)	6 (6%)	2 (2%)	8	52
47	W	77/85 (91%)	55 (71%)	13 (17%)	9 (12%)	0	8
48	X	75/78 (96%)	65 (87%)	7 (9%)	3 (4%)	4	38
49	Y	61/63 (97%)	51 (84%)	7 (12%)	3 (5%)	3	32
50	Z	56/59 (95%)	48 (86%)	6 (11%)	2 (4%)	4	41
51	x	24/599 (4%)	23 (96%)	1 (4%)	0	100	100
All	All	5878/6817 (86%)	5045 (86%)	567 (10%)	266 (4%)	6	34

5 of 266 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	72	LYS
1	b	163	ILE
3	d	151	LYS
5	f	63	ASN
5	f	93	LYS

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	180/199 (90%)	180 (100%)	0	100	100
2	c	170/190 (90%)	170 (100%)	0	100	100
3	d	172/173 (99%)	172 (100%)	0	100	100
4	e	113/126 (90%)	113 (100%)	0	100	100
5	f	89/116 (77%)	89 (100%)	0	100	100
6	g	124/147 (84%)	124 (100%)	0	100	100
7	h	104/105 (99%)	104 (100%)	0	100	100
8	i	105/107 (98%)	105 (100%)	0	100	100
9	j	86/90 (96%)	86 (100%)	0	100	100
10	k	90/99 (91%)	90 (100%)	0	100	100

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	l	103/104 (99%)	103 (100%)	0	100	100
12	m	92/96 (96%)	92 (100%)	0	100	100
13	n	79/84 (94%)	79 (100%)	0	100	100
14	o	76/77 (99%)	76 (100%)	0	100	100
15	p	65/65 (100%)	65 (100%)	0	100	100
16	q	74/78 (95%)	74 (100%)	0	100	100
17	r	48/65 (74%)	48 (100%)	0	100	100
18	s	70/79 (89%)	70 (100%)	0	100	100
19	t	65/66 (98%)	65 (100%)	0	100	100
20	u	44/61 (72%)	44 (100%)	0	100	100
21	0	47/48 (98%)	47 (100%)	0	100	100
22	1	45/49 (92%)	45 (100%)	0	100	100
23	2	38/38 (100%)	38 (100%)	0	100	100
24	3	51/51 (100%)	51 (100%)	0	100	100
25	4	34/34 (100%)	34 (100%)	0	100	100
26	5	181/181 (100%)	181 (100%)	0	100	100
27	C	215/218 (99%)	215 (100%)	0	100	100
28	D	164/164 (100%)	164 (100%)	0	100	100
29	E	165/165 (100%)	165 (100%)	0	100	100
30	F	148/150 (99%)	148 (100%)	0	100	100
31	G	137/138 (99%)	137 (100%)	0	100	100
32	H	114/114 (100%)	114 (100%)	0	100	100
33	I	109/110 (99%)	109 (100%)	0	100	100
34	J	116/116 (100%)	116 (100%)	0	100	100
35	K	103/104 (99%)	103 (100%)	0	100	100
36	L	102/103 (99%)	102 (100%)	0	100	100
37	M	109/109 (100%)	109 (100%)	0	100	100
38	N	100/103 (97%)	100 (100%)	0	100	100
39	O	86/87 (99%)	86 (100%)	0	100	100
40	P	99/100 (99%)	99 (100%)	0	100	100
41	Q	89/90 (99%)	89 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	R	84/84 (100%)	84 (100%)	0	100	100
43	S	93/93 (100%)	93 (100%)	0	100	100
44	T	80/84 (95%)	80 (100%)	0	100	100
45	U	83/85 (98%)	83 (100%)	0	100	100
46	V	78/78 (100%)	78 (100%)	0	100	100
47	W	59/63 (94%)	59 (100%)	0	100	100
48	X	67/68 (98%)	67 (100%)	0	100	100
49	Y	55/55 (100%)	55 (100%)	0	100	100
50	Z	48/49 (98%)	48 (100%)	0	100	100
51	x	23/511 (4%)	23 (100%)	0	100	100
All	All	4871/5569 (88%)	4871 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
26	5	234	ASN
28	D	49	GLN
44	T	70	HIS
27	C	52	HIS
27	C	199	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	a	1532/1533 (99%)	301 (19%)	0
53	A	2902/2904 (99%)	597 (20%)	16 (0%)
54	B	117/120 (97%)	21 (17%)	0
55	7	8/15 (53%)	4 (50%)	0
56	8	75/76 (98%)	8 (10%)	2 (2%)
56	9	75/76 (98%)	33 (44%)	1 (1%)
All	All	4709/4724 (99%)	964 (20%)	19 (0%)

5 of 964 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	a	4	U
52	a	6	G
52	a	9	G
52	a	12	U
52	a	15	G

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	A	1020	A
53	A	1331	G
53	A	2474	U
53	A	880	G
56	8	20	U

#### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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.