



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

Mar 2, 2017 – 12:22 pm GMT

PDB ID : 3J9Y  
EMDB ID: : EMD-6311  
Title : Cryo-EM structure of tetracycline resistance protein TetM bound to a translating E.coli ribosome  
Authors : Arenz, S.; Nguyen, F.; Beckmann, R.; Wilson, D.N.  
Deposited on : 2015-03-23  
Resolution : 3.90 Å(reported)  
Based on PDB ID : 5AFI

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.

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MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc29047

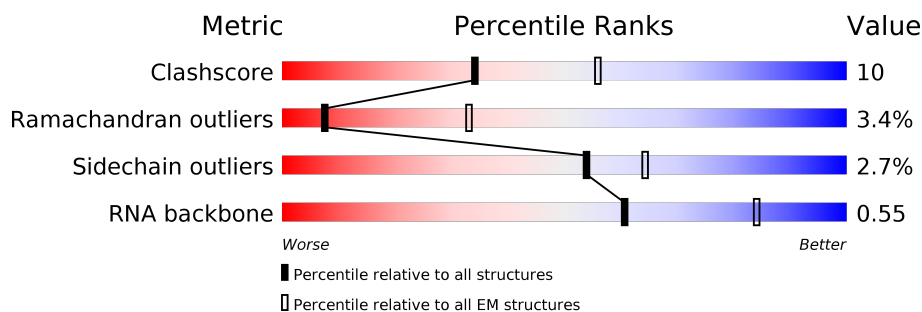
# 1 Overall quality at a glance

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.











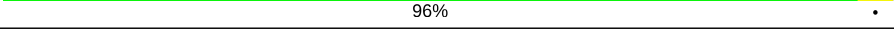







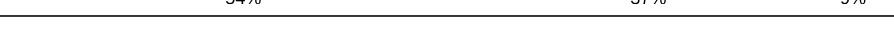

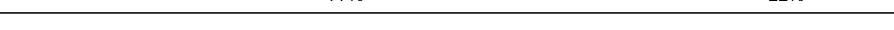
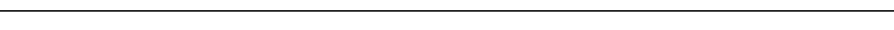
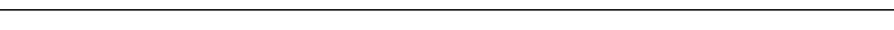
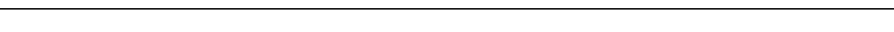
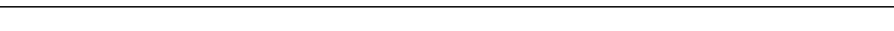
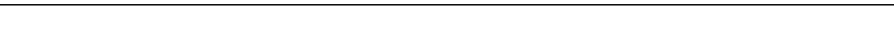

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	a	1539	83% 16%
2	b	240	85% 6% 9%
3	d	206	92% 8%
4	e	167	84% 10% 6%
5	f	135	68% 26%
6	h	130	96%
7	k	129	84% 6% 10%
8	l	124	93% 6%


























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Mol	Chain	Length	Quality of chain
9	o	89	 91% 8% .
10	p	82	 93% 7%
11	q	84	 86% 10% 5%
12	r	75	 79% 8% 13%
13	t	87	 93% 5% .
14	u	71	 82% 10% 8%
15	v	78	 76% 23% .
16	x	11	 73% 9% 18%
17	w	639	 96% .
18	c	233	 85% . 12%
19	g	179	 78% 7% 16%
20	i	130	 88% 10% .
21	j	103	 87% 8% 5%
22	m	118	 91% 6% .
23	n	102	 90% 9% .
24	s	92	 85% . 14%
25	A	2903	 54% 37% 9%
26	B	120	 54% 43% .
27	C	273	 77% 22% ..
28	D	209	 76% 22% .
29	E	201	 75% 23% .
30	F	179	 60% 34% . .
31	G	177	 80% 19% ..
32	H	149	 80% 18% .
33	I	142	 63% 33% . .

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Mol	Chain	Length	Quality of chain
34	J	142	 73%26%.
35	K	123	 68%28%..
36	L	144	 64%33%..
37	M	136	 75%24%.
38	N	127	 67%27%• 6%
39	O	117	 80%18%..
40	P	115	 77%21%..
41	Q	118	 76%23%.
42	R	103	 81%19%
43	S	110	 70%27%.
44	T	100	 70%20%• • 7%
45	U	104	 73%24%..
46	V	94	 76%23%.
47	W	85	 73%15%12%
48	X	78	 78%19%..
49	Y	63	 71%27%.
50	Z	59	 80%19%.
51	0	57	 68%26%• •
52	1	55	 78%13%9%
53	2	46	 70%30%
54	3	65	 72%25%..
55	4	38	 61%39%
56	5	165	 51%26%• 21%
57	6	70	 70%23%• 6%
58	7	69	 99%.

## 2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 148915 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 RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1539	Total	C	N	O	P	0	0
			33029	14738	6052	10700	1539		

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

- 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	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

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

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

- Molecule 6 is a protein called 30S ribosomal protein S8.

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

- Molecule 7 is a protein called 30S ribosomal protein S11.

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

- Molecule 8 is a protein called 30S ribosomal protein S12.

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

- Molecule 9 is a protein called 30S ribosomal protein S15.

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

- Molecule 10 is a protein called 30S ribosomal protein S16.

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

- Molecule 11 is a protein called 30S ribosomal protein S17.

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

- Molecule 12 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	r	65	Total	C	N	O	0	0
			504	317	96	91		

- Molecule 13 is a protein called 30S ribosomal protein S20.

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

- Molecule 14 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	u	65	Total	C	N	O	S	0	0
			495	307	100	87	1		

- Molecule 15 is a RNA chain called P-site fMet-tRNA<sup>fMet</sup>.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	v	77	Total	C	N	O	P	S	0	0
			1644	733	297	536	77	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	77	FME	-	FORMYLATION	GB 147949

- Molecule 16 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	x	9	Total	C	N	O	P	0	0
			189	85	31	64	9		

- Molecule 17 is a protein called Tetracycline resistance protein TetM.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	w	639	Total	C	N	O	0	0
			2590	1308	640	642		

- Molecule 18 is a protein called 30S ribosomal protein S3.

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

- Molecule 19 is a protein called 30S ribosomal protein S7.

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

- Molecule 20 is a protein called 30S ribosomal protein S9.

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

- Molecule 21 is a protein called 30S ribosomal protein S10.

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

- Molecule 22 is a protein called 30S ribosomal protein S13.

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

- Molecule 23 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	INSERTION	UNP P0AG59

- Molecule 24 is a protein called 30S ribosomal protein S19.

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

- Molecule 25 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	2900	Total	C	N	O	P	0	0
			62276	27788	11460	20128	2900		

- Molecule 26 is a RNA chain called 5S ribosomal RNA.



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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	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		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	75	Total	C	N	O	S	0	0
			575	356	116	102	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 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 52 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 56 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	5	131	Total	C	N	O	S	0	0
			988	625	175	183	5		


- Molecule 57 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 58 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	7	69	Total	C	N	O	0	0
			276	138	69	69		



Chain e:  84% 10% • 6%



- Molecule 5: 30S ribosomal protein S6

Chain f:  68% • • 26%




- Molecule 6: 30S ribosomal protein S8

Chain h:  96% • •



- Molecule 7: 30S ribosomal protein S11

Chain k:  84% 6% 10%




- Molecule 8: 30S ribosomal protein S12

Chain l:  93% 6% •



- Molecule 9: 30S ribosomal protein S15

Chain o:  91% 8% •




- Molecule 10: 30S ribosomal protein S16

Chain p:  93% 7%



- Molecule 11: 30S ribosomal protein S17

Chain q:  86% 10% 5%



- Molecule 12: 30S ribosomal protein S18

Chain r: 79% 8% 13%



- Molecule 13: 30S ribosomal protein S20

Chain t: 93% 5%



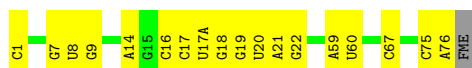
- Molecule 14: 30S ribosomal protein S21

Chain u: 82% 10% 8%



- Molecule 15: P-site fMet-tRNA<sup>fMet</sup>

Chain v: 76% 23%



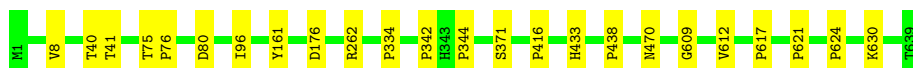
- Molecule 16: mRNA

Chain x: 73% 9% 18%



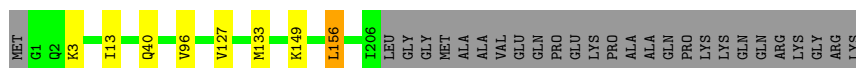
- Molecule 17: Tetracycline resistance protein TetM

Chain w: 96%




- Molecule 18: 30S ribosomal protein S3

Chain c: 85% 12%





- Molecule 19: 30S ribosomal protein S7

Chain g:  78% 7% 16%




- Molecule 20: 30S ribosomal protein S9

Chain i:  88% 10% .



- Molecule 21: 30S ribosomal protein S10

Chain j:  87% 8% 5%



- Molecule 22: 30S ribosomal protein S13

Chain m:  91% 6% .




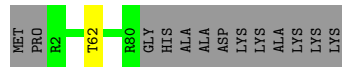
- Molecule 23: 30S ribosomal protein S14

Chain n:  90% 9% .



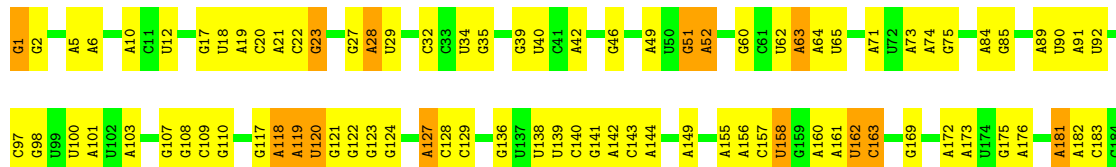
- Molecule 24: 30S ribosomal protein S19

Chain s:  85% . 14%

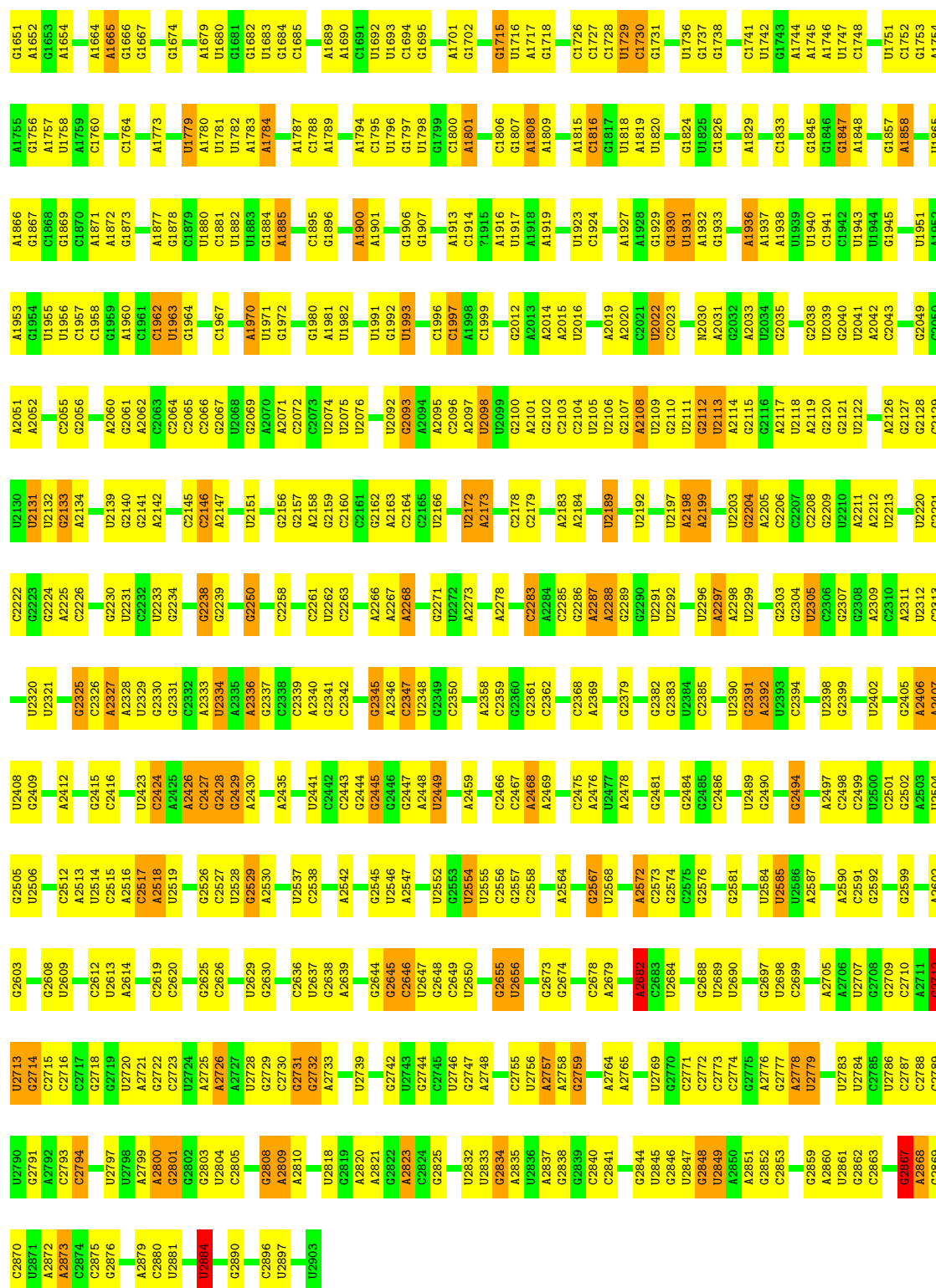


- Molecule 25: 23S ribosomal RNA

Chain A:  54% 37% 9%



G1448	G1452	G1454	G1458	G1461	G1469	G1470	G1474	G1475	G1476	G1486	G1487	G1490	G1491	G1492	G1493	G1494	G1495	G1496	G1497	G1498	G1499	G1500	G1501	G1502	G1503	G1504	G1505	G1506	G1507	G1508	G1509	G1510	G1511	G1512	G1513	G1514	G1515	G1516	G1517	G1518	G1519	G1520	G1521	G1522	G1523	G1524	G1525	G1526	G1527	G1528	G1529	G1530	G1531	G1532	G1533	G1534	G1535	G1536	G1537	G1538	G1539																																																																																																																																																																																																						
G1343	G1344	G1345	G1352	G1361	G1362	G1363	G1364	G1365	G1366	G1378	G1379	G1380	G1381	G1382	G1383	G1384	G1385	G1386	G1387	G1388	G1389	G1390	G1391	G1392	G1393	G1394	G1395	G1396	G1397	G1398	G1399	G1400	G1401	G1402	G1403	G1404	G1405	G1406	G1407	G1408	G1409	G1410	G1411	G1412	G1413	G1414	G1415	G1416	G1417	G1418	G1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	G1427	G1428	G1429	G1430	G1431	G1432	G1433	G1434	G1435	G1436	G1437	G1438	G1439	G1440	G1441	G1442	G1443	G1444	G1445	G1446	G1447																																																																																																																																																																																				
G1252	G1253	G1256	G1265	G1266	G1267	G1268	G1269	G1270	G1271	G1272	G1273	G1274	G1275	G1276	G1277	G1278	G1279	G1280	G1281	G1282	G1283	G1284	G1285	G1286	G1287	G1288	G1289	G1290	G1291	G1292	G1293	G1294	G1295	G1296	G1297	G1298	G1299	G1300	G1301	G1302	G1303	G1304	G1305	G1306	G1307	G1308	G1309	G1310	G1311	G1312	G1313	G1314	G1315	G1316	G1317	G1318	G1319	G1320	G1321	G1322	G1323	G1324	G1325	G1326	G1327	G1328	G1329	G1330	G1331	G1332	G1333	G1334	G1335	G1336	G1337	G1338	G1339	G1340	G1341	G1342																																																																																																																																																																																			
G1142	G1143	G1151	G1152	G1153	G1154	G1155	G1156	G1157	G1158	G1159	G1160	G1161	G1162	G1163	G1164	G1165	G1166	G1167	G1168	G1169	G1170	G1171	G1172	G1173	G1174	G1175	G1176	G1177	G1178	G1179	G1180	G1181	G1182	G1183	G1184	G1185	G1186	G1187	G1188	G1189	G1190	G1191	G1192	G1193	G1194	G1195	G1196	G1197	G1198	G1199	G1200	G1201	G1202	G1203	G1204	G1205	G1206	G1207	G1208	G1209	G1210	G1211	G1212	G1213	G1214	G1215	G1216	G1217	G1218	G1219	G1220	G1221	G1222	G1223	G1224	G1225	G1226	G1227	G1228	G1229	G1230	G1231	G1232	G1233	G1234	G1235	G1236	G1237	G1238	G1239	G1240	G1241	G1242	G1243	G1244	G1245	G1246	G1247	G1248	G1249	G1250	G1251																																																																																																																																																													
G1071	G1072	G1073	G1074	G1075	G1076	G1077	G1078	G1079	G1080	G1081	G1082	G1083	G1084	G1085	G1086	G1087	G1088	G1089	G1090	G1091	G1092	G1093	G1094	G1095	G1096	G1097	G1098	G1099	G1100	G1101	G1102	G1103	G1104	G1105	G1106	G1107	G1108	G1109	G1110	G1111	G1112	G1113	G1114	G1115	G1116	G1117	G1118	G1119	G1120	G1121	G1122	G1123	G1124	G1125	G1126	G1127	G1128	G1129	G1130	G1131	G1132	G1133	G1134	G1135	G1136	G1137	G1138	G1139	G1140	G1141																																																																																																																																																																																													
C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000	C1001	C1002	C1003	C1004	C1005	C1006	C1007	C1008	C1009	C1010	C1011	C1012	C1013	C1014	C1015	C1016	C1017	C1018	C1019	C1020	C1021	C1022	C1023	C1024	C1025	C1026	C1027	C1028	C1029	C1030	C1031	C1032	C1033	C1034	C1035	C1036	C1037	C1038	C1039	C1040	C1041	C1042	C1043	C1044	C1045	C1046	C1047	C1048	C1049	C1050	C1051	C1052	C1053	C1054	C1055	C1056	C1057	C1058	C1059	C1060	C1061	C1062	C1063	C1064	C1065	C1066	C1067	C1068	C1069	C1070																																																																																																																																																																														
U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900	U901	U902	U903	U904	U905	U906	U907	U908	U909	U910	U911	U912	U913	U914	U915	U916	U917	U918	U919	U920	U921	U922	U923	U924	U925	U926	U927	U928	U929	U930	U931	U932	U933	U934	U935	U936	U937	U938	U939	U940	U941	U942	U943	U944	U945	U946	U947	U948	U949	U950	U951	U952	U953	U954	U955	U956	U957	U958	U959	U960	U961	U962	U963	U964	U965	U966	U967	U968	U969	U970	U971	U972	U973	U974	U975	U976	U977	U978	U979	U980	U981	U982	U983	U984	U985	U986	U987	U988	U989	U990	U991	U992	U993	U994	U995	U996	U997	U998	U999	U1000	U1001	U1002	U1003	U1004	U1005	U1006	U1007	U1008	U1009	U1010	U1011	U1012	U1013	U1014	U1015	U1016	U1017	U1018	U1019	U1020	U1021	U1022	U1023	U1024	U1025	U1026	U1027	U1028	U1029	U1030	U1031	U1032	U1033	U1034	U1035	U1036	U1037	U1038	U1039	U1040	U1041	U1042	U1043	U1044	U1045	U1046	U1047	U1048	U1049	U1050	U1051	U1052	U1053	U1054	U1055	U1056	U1057	U1058	U1059	U1060	U1061	U1062	U1063	U1064	U1065	U1066	U1067	U1068	U1069	U1070
U641	U642	U643	U644	U645	U646	U647	U648	U649	U650	U651	U652	U653	U654	U655	U656	U657	U658	U659	U660	U661	U662	U663	U664	U665	U666	U667	U668	U669	U670	U671	U672	U673	U674	U675	U676	U677	U678	U679	U680	U681	U682	U683	U684	U685	U686	U687	U688	U689	U690	U691	U692	U693	U694	U695	U696	U697	U698	U699	U700	U701	U702	U703	U704	U705	U706	U707	U708	U709	U710	U711	U712	U713	U714	U715	U716	U717	U718	U719	U720	U721	U722	U723	U724	U725	U726	U727	U728	U729	U730	U731	U732	U733	U734	U735	U736	U737	U738	U739	U740	U741	U742	U743	U744	U745	U746	U747	U748	U749	U750	U751	U752	U753	U754	U755	U756	U757	U758	U759	U760	U761	U762	U763	U764	U765	U766	U767	U768	U769	U770	U771	U772	U773	U774	U775	U776	U777	U778	U779	U780	U781	U782	U783	U784	U785	U786	U787	U788	U789	U790	U791	U792	U793	U794	U795	U796	U797	U798	U799	U800	U801	U802	U803	U804	U805	U806	U807	U808	U809	U810	U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890										
G548	G549	G550	G551	G552	G553	G554	G555	G556	G557	G558	G559	G560	G561	G562	G563	G564	G565	G566	G567	G568	G569	G570	G571	G572	G573	G574	G575	G576	G577	G578	G579	G580	G581	G582	G583	G584	G585	G586	G587	G588	G589	G590	G591	G592	G593	G594	G595	G596	G597	G598	G599	G600	G601	G602	G603	G604	G605	G606	G607	G608	G609	G610	G611	G612	G613	G614	G615	G616	G617	G618	G619	G620	G621	G622	G623	G624	G625	G626	G627	G628	G629	G630	G631	G632	G633	G634	G635	G636	G637	G638	G639	G640																																																																																																																																																																							
C363	C364	C365	C366	C367	C368	C369	C370	C371	C372	C373	C374	C375	C376	C377	C378	C379	C380	C381	C382	C383	C384	C385	C386	C387	C388	C389	C390	C391	C392	C393	C394	C395	C396	C397	C398	C399	C400	C401	C402	C403	C404	C405	C406	C407	C408	C409	C410	C411	C412	C413	C414	C415	C416	C417	C418	C419	C420	C421	C422	C423	C424	C425	C426	C427	C428	C429	C430	C431	C432	C433	C434	C435	C436	C437	C438	C439	C440	C441	C442	C443	C444	C445	C446	C447	C448	C449	C450	C451	C452	C453	C454	C455																																																																																																																																																																							
G277	G278	G279	G280	G281	G282	G283	G284	G285	G286	G287	G288	G289	G290	G291	G292	G293	G294	G295	G296	G297	G298	G299	G300	G301	G302	G303	G304	G305	G306	G307	G308	G309	G310	G311	G312	G313	G314	G315	G316	G317	G318	G319	G320	G321	G322	G323	G324	G325	G326	G327	G328	G329	G330	G331	G332	G333	G334	G335	G336	G337	G338	G339	G340	G341	G342	G343	G344	G345	G346	G347	G348	G349	G350	G351	G352	G353	G354	G355	G356	G357	G358	G359	G360	G361	G362	G363	G364	G365	G366	G367	G368	G369	G370	G371	G372	G373	G374	G375	G376	G377	G378	G379	G380	G381	G382	G383	G384	G385	G386	G387	G388	G389	G390	G391	G392	G393	G394	G395	G396	G397	G398	G399	G400	G401	G402	G403	G404	G405	G406	G407	G408	G409	G410	G411	G412	G413	G414	G415	G416	G417	G418	G419	G420	G421	G422	G423	G424	G425	G426	G427	G428	G429	G430	G431	G432	G433	G434	G435	G436	G437	G438	G439	G440	G441	G442	G443	G444	G445	G446	G447	G448	G449	G450	G451	G452	G453	G454	G455																																																																																	
G185	G186	G187	G188	G189	G190	G191	G192	G193	G194	G195	G196	G197	G198	G199	G200	G201	G202	G203	G204	G205	G206	G207	G208	G209	G210	G211	G212	G213	G214	G215	G216	G217	G218	G219	G220	G2																																																																																																																																																																																																																															



G105  
G106  
G107  
A108  
A109  
G110  
U111  
G112  
G113  
C114  
A115  
G116  
G117  
G118  
A119  
A120

• Molecule 27: 50S ribosomal protein L2

Chain C: 77% 22% ..

MET A1 V2 F7 R12 R13 R14 V15 V16 H24 E34 K38 N43 N44 N45 I48 B51 Y61 K70 R73 E78 E81 E86 L92 L104 A105 P106 L109 L129 P130 M131 R132 V143 K149 A154 V161 Q162

A165 G168 T172 L173 R174 L175 R176 E179 M180 R181 G195 N196 M200 L201 R202 V203 L204 G205 I48 K206 W212 R216 R220 G221 T222 H231 E235 F239 V244 T245 P246 Q250 T251 K252 R257 S258 N259 K260 R261 R269 R270 S271 LYS

• Molecule 28: 50S ribosomal protein L3

Chain D: 76% 22% .

M1 L4 R13 T16 V20 V29 E30 A31 N32 R33 V34 Q36 L40 D43 G44 Y45 I48 Q49 V50 T51 T52 G53 A54 K55 H67 V73 G76 R77 W80 E81 A85 E86 G87 E88 F101 V104 T110 K114 F118 T121

T133 H134 G135 P143 Q148 N149 Q150 T151 P152 R169 R179 L188 A196 P205 A209

• Molecule 29: 50S ribosomal protein L4

Chain E: 75% 23% .

M1 E2 L3 D7 T18 F19 V31 R40 Q41 G42 T43 R49 V52 K63 G71 K74 S75 P76 S80 G81 G82 V83 T84 R88 P89 Q90 V96 N97 M100 Y101 R102 G103 A104 L105 K106 R117 V120 V121 E122 K123 A128 P129 K130 T131

L143 L144 D145 V146 L147 T148 L159 A160 A161 R162 N163 K166 V169 R170 D176 P177 V178 A182 K185 L200 A201

• Molecule 30: 50S ribosomal protein L5

Chain F: 60% 34% ..

MET A1 R2 L3 H4 D5 Y6 Y7 K8 D9 V12 M16 N20 V24 V27 P28 R29 V39 G40 E41 L48 N51 B55 L56 T67 R70 V73 I78 P83 T84 G85 G86 K87 V88 T89 I90 R91 G92 M95 V96 E97 E100 R101 L102

A106 I110 F113 L116 S120 M126 Y127 S128 M129 G130 V131 R132 E133 Q134 I136 F137 P138 E139 I140 D141 K144 R147 V148 R149 G150 I153 T156 G165 L168 D173 F174 P175 F176 R177 LYS

• Molecule 31: 50S ribosomal protein L6

Chain G: 80% 19% ..

MET S1 I23 R34 N37 D38 E41 V42 V43 H44 A45 F51 G52 G53 P53 R54 L70 L71 M74 F82 L88 R94 A95 I102 F108 D113 T126 Q127 T128 E129 I130 K133 D136 K137 Q138 V139 P153 E154 P155 K159 G160 V161



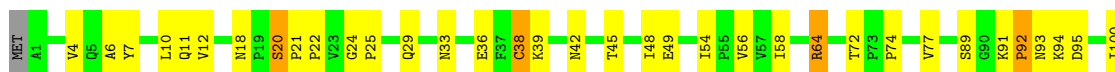
- Molecule 32: 50S ribosomal protein L9

Chain H: 80% 18%



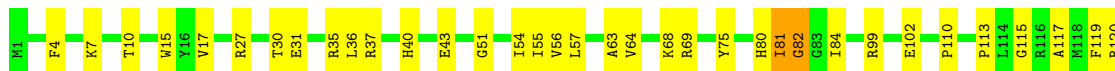
- Molecule 33: 50S ribosomal protein L11

Chain I: 63% 33%



- Molecule 34: 50S ribosomal protein L13

Chain J: 73% 26%



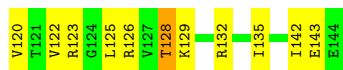
- Molecule 35: 50S ribosomal protein L14

Chain K: 68% 28%

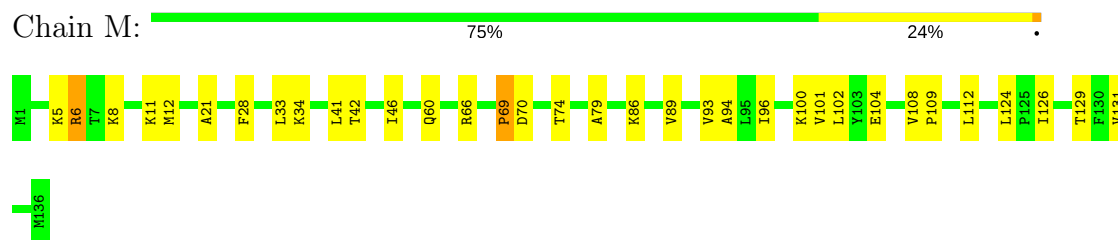


- Molecule 36: 50S ribosomal protein L15

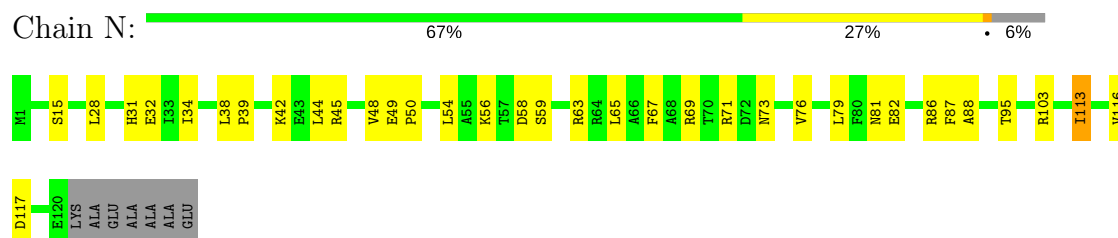
Chain L: 64% 33%



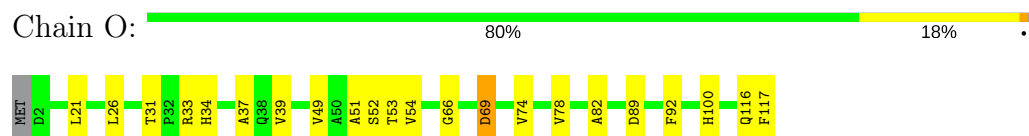
- Molecule 37: 50S ribosomal protein L16



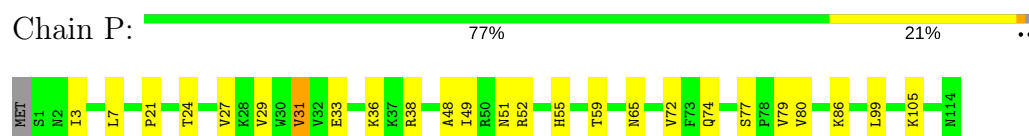
- Molecule 38: 50S ribosomal protein L17



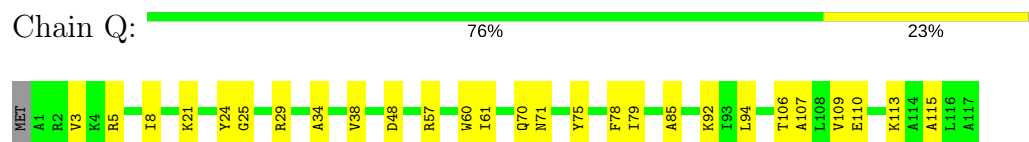
- Molecule 39: 50S ribosomal protein L18



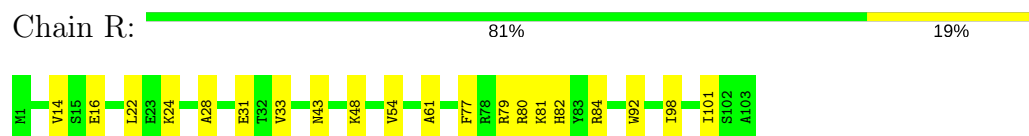
- Molecule 40: 50S ribosomal protein L19



- 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: 70% 20% 7%



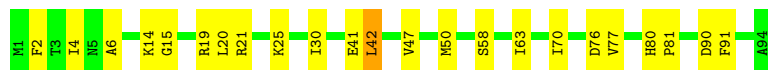
- Molecule 45: 50S ribosomal protein L24

Chain U: 73% 24%



- Molecule 46: 50S ribosomal protein L25

Chain V: 76% 23%



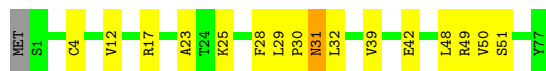
- Molecule 47: 50S ribosomal protein L27

Chain W: 73% 15% 12%



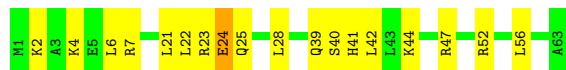
- Molecule 48: 50S ribosomal protein L28

Chain X: 78% 19%



- Molecule 49: 50S ribosomal protein L29

Chain Y: 71% 27%

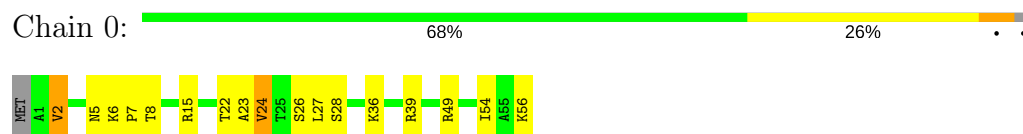


- Molecule 50: 50S ribosomal protein L30

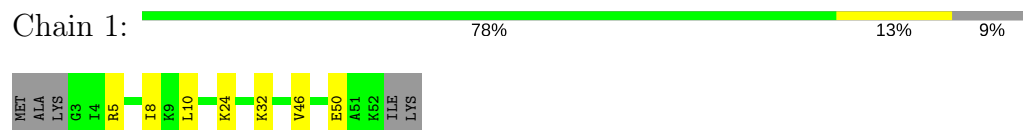
Chain Z: 80% 19%



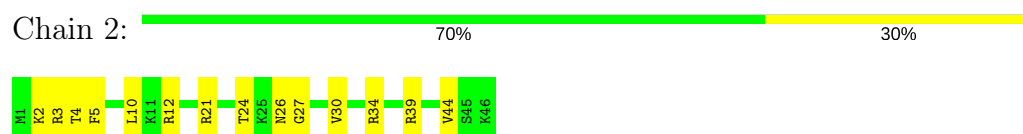
- Molecule 51: 50S ribosomal protein L32



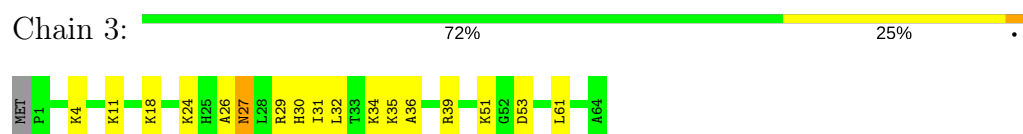
- Molecule 52: 50S ribosomal protein L33



- Molecule 53: 50S ribosomal protein L34



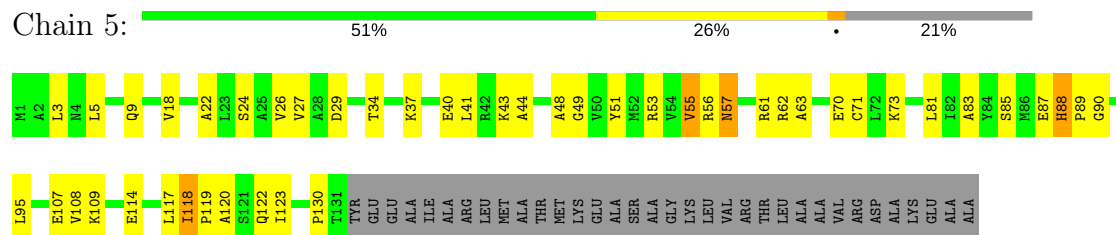
- Molecule 54: 50S ribosomal protein L35



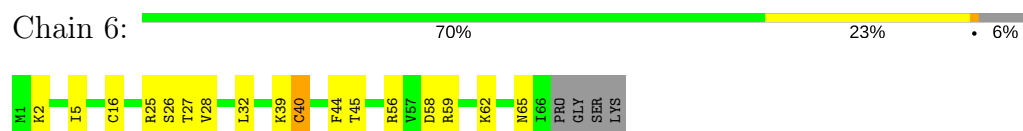
- Molecule 55: 50S ribosomal protein L36



- Molecule 56: 50S ribosomal protein L10



- Molecule 57: 50S ribosomal protein L31





- Molecule 58: 50S ribosomal protein L7/L12

Chain 7:  99% .



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	78186	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Defocus groups	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	28	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	125085	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, 3TD, OMG, 5MC, MA6, H2U, OMC, 2MA, 6MZ, 2MG, OMU, UR3, 4OC, 4SU, 7MG, 1MG, PSU

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	0.39	1/36701 (0.0%)	0.85	12/57246 (0.0%)
10	p	0.33	0/659	0.46	0/884
11	q	0.28	0/657	0.46	0/881
12	r	0.28	0/511	0.43	0/689
13	t	0.38	0/671	0.48	0/888
14	u	0.29	0/500	0.42	0/668
15	v	0.42	1/1747 (0.1%)	0.82	0/2721
16	x	0.58	1/210 (0.5%)	0.78	0/324
17	w	0.17	0/2594	0.35	0/3251
18	c	0.32	0/1651	0.46	0/2225
19	g	0.36	0/1195	0.50	0/1602
2	b	0.30	0/1735	0.44	0/2338
20	i	0.27	0/1034	0.45	0/1375
21	j	0.36	0/796	0.54	0/1077
22	m	0.36	0/892	0.50	0/1193
23	n	0.27	0/811	0.40	0/1081
24	s	0.28	0/652	0.44	0/877
25	A	0.47	1/69174 (0.0%)	0.90	51/107910 (0.0%)
26	B	0.38	1/2876 (0.0%)	0.86	0/4483
27	C	0.31	0/2121	0.47	0/2852
28	D	0.34	0/1586	0.48	0/2134
29	E	0.26	0/1571	0.41	0/2113
3	d	0.28	0/1665	0.44	0/2227
30	F	0.31	0/1434	0.47	0/1926
31	G	0.35	0/1343	0.47	0/1816
32	H	0.23	0/1122	0.40	0/1515
33	I	0.23	0/1046	0.44	0/1410
34	J	0.29	0/1152	0.43	0/1551
35	K	0.28	0/947	0.41	0/1268
36	L	0.26	0/1054	0.45	0/1403
37	M	0.32	0/1093	0.46	0/1460

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
38	N	0.28	0/973	0.44	0/1301
39	O	0.33	0/902	0.44	0/1209
4	e	0.32	0/1154	0.46	0/1554
40	P	0.28	0/929	0.43	0/1242
41	Q	0.34	0/960	0.43	0/1278
42	R	0.34	0/829	0.52	0/1107
43	S	0.28	0/864	0.47	0/1156
44	T	0.29	0/744	0.45	0/994
45	U	0.35	0/787	0.44	0/1051
46	V	0.31	0/766	0.45	0/1025
47	W	0.33	0/582	0.47	0/769
48	X	0.28	0/635	0.40	0/848
49	Y	0.33	0/510	0.46	0/677
5	f	0.35	0/835	0.48	0/1128
50	Z	0.25	0/453	0.41	0/605
51	0	0.26	0/450	0.41	0/599
52	1	0.26	0/416	0.41	0/554
53	2	0.29	0/380	0.44	0/498
54	3	0.27	0/513	0.43	0/676
55	4	0.28	0/303	0.41	0/397
56	5	0.25	0/1001	0.45	0/1350
57	6	0.33	0/531	0.54	0/709
58	7	0.33	0/275	0.73	0/342
6	h	0.27	0/989	0.45	0/1326
7	k	0.28	0/885	0.48	0/1195
8	l	0.29	0/969	0.47	0/1300
9	o	0.32	0/722	0.44	0/964
All	All	0.40	5/160557 (0.0%)	0.79	63/239242 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	B	1	U	OP3-P	-10.61	1.48	1.61
15	v	1	C	OP3-P	-10.59	1.48	1.61
25	A	1	G	OP3-P	-10.57	1.48	1.61
1	a	2	A	OP3-P	-10.49	1.48	1.61
16	x	14	U	C1'-N1	5.54	1.57	1.48

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	974	G	N1-C6-O6	9.38	125.53	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	1936	A	N1-C6-N6	9.08	124.05	118.60
25	A	1936	A	C2-N3-C4	-7.41	106.90	110.60
25	A	783	A	N7-C8-N9	7.26	117.43	113.80
1	a	1297	G	P-O3'-C3'	7.22	128.36	119.70

There are no chirality outliers.

There are no planarity outliers.

## 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	33029	0	16642	0	0
2	b	1704	0	1732	0	0
3	d	1643	0	1710	0	0
4	e	1141	0	1169	0	0
5	f	817	0	808	0	0
6	h	979	0	1034	0	0
7	k	869	0	878	0	0
8	l	955	0	1019	0	0
9	o	714	0	737	0	0
10	p	649	0	666	0	0
11	q	648	0	691	0	0
12	r	504	0	502	0	0
13	t	665	0	714	0	0
14	u	495	0	486	0	0
15	v	1644	0	840	0	0
16	x	189	0	96	0	0
17	w	2590	0	731	0	0
18	c	1624	0	1699	0	0
19	g	1181	0	1240	0	0
20	i	1022	0	1070	0	0
21	j	786	0	828	0	0
22	m	883	0	944	0	0
23	n	799	0	841	0	0
24	s	637	0	665	0	0
25	A	62276	0	31346	868	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	B	2572	0	1302	27	0
27	C	2082	0	2157	39	0
28	D	1565	0	1616	34	0
29	E	1552	0	1619	30	0
30	F	1410	0	1447	46	0
31	G	1323	0	1374	22	0
32	H	1111	0	1148	18	0
33	I	1032	0	1088	34	0
34	J	1129	0	1162	30	0
35	K	938	0	1012	24	0
36	L	1045	0	1117	35	0
37	M	1074	0	1157	20	0
38	N	960	0	1000	25	0
39	O	892	0	923	13	0
40	P	917	0	965	23	0
41	Q	947	0	1022	21	0
42	R	816	0	839	13	0
43	S	857	0	922	22	0
44	T	738	0	807	17	0
45	U	779	0	834	16	0
46	V	753	0	780	14	0
47	W	575	0	592	9	0
48	X	625	0	655	12	0
49	Y	509	0	543	10	0
50	Z	449	0	491	7	0
51	0	444	0	461	14	0
52	1	409	0	440	4	0
53	2	377	0	418	18	0
54	3	504	0	574	17	0
55	4	302	0	343	12	0
56	5	988	0	1025	33	0
57	6	522	0	524	13	0
58	7	276	0	79	0	0
All	All	148915	0	99524	1374	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 10.

The worst 5 of 1374 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)
25:A:1422:G:OP1	35:K:48:PRO:HG3	96.78	1.14
25:A:1055:G:H1	25:A:1104:C:H42	1.11	0.96
48:X:17:ARG:HE	48:X:23:ALA:HB2	1.29	0.94
25:A:704:G:H2'	25:A:726:G:H22	1.30	0.93
25:A:335:C:H4'	25:A:1434:A:O4'	117.09	0.90

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	
2	b	216/240 (90%)	183 (85%)	23 (11%)	10 (5%)	3	30
3	d	203/206 (98%)	172 (85%)	21 (10%)	10 (5%)	2	29
4	e	155/167 (93%)	130 (84%)	16 (10%)	9 (6%)	2	26
5	f	98/135 (73%)	81 (83%)	11 (11%)	6 (6%)	2	25
6	h	127/130 (98%)	110 (87%)	14 (11%)	3 (2%)	7	45
7	k	114/129 (88%)	92 (81%)	16 (14%)	6 (5%)	2	28
8	l	121/124 (98%)	96 (79%)	20 (16%)	5 (4%)	3	33
9	o	86/89 (97%)	71 (83%)	10 (12%)	5 (6%)	2	26
10	p	80/82 (98%)	67 (84%)	11 (14%)	2 (2%)	6	44
11	q	78/84 (93%)	65 (83%)	8 (10%)	5 (6%)	1	24
12	r	63/75 (84%)	53 (84%)	5 (8%)	5 (8%)	1	18
13	t	83/87 (95%)	77 (93%)	4 (5%)	2 (2%)	7	45
14	u	63/71 (89%)	44 (70%)	14 (22%)	5 (8%)	1	18
17	w	637/639 (100%)	562 (88%)	51 (8%)	24 (4%)	4	35
18	c	204/233 (88%)	184 (90%)	18 (9%)	2 (1%)	18	61
19	g	149/179 (83%)	124 (83%)	15 (10%)	10 (7%)	1	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	i	125/130 (96%)	98 (78%)	19 (15%)	8 (6%)	1	24
21	j	96/103 (93%)	74 (77%)	16 (17%)	6 (6%)	1	24
22	m	112/118 (95%)	99 (88%)	8 (7%)	5 (4%)	3	31
23	n	99/102 (97%)	82 (83%)	12 (12%)	5 (5%)	2	28
24	s	77/92 (84%)	66 (86%)	11 (14%)	0	100	100
27	C	269/273 (98%)	242 (90%)	22 (8%)	5 (2%)	9	50
28	D	207/209 (99%)	185 (89%)	20 (10%)	2 (1%)	18	61
29	E	199/201 (99%)	172 (86%)	20 (10%)	7 (4%)	4	38
30	F	175/179 (98%)	149 (85%)	20 (11%)	6 (3%)	4	39
31	G	174/177 (98%)	148 (85%)	21 (12%)	5 (3%)	5	42
32	H	147/149 (99%)	128 (87%)	15 (10%)	4 (3%)	6	43
33	I	139/142 (98%)	110 (79%)	20 (14%)	9 (6%)	1	24
34	J	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	13	55
35	K	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	6	44
36	L	141/144 (98%)	110 (78%)	20 (14%)	11 (8%)	1	18
37	M	134/136 (98%)	117 (87%)	14 (10%)	3 (2%)	8	47
38	N	118/127 (93%)	103 (87%)	12 (10%)	3 (2%)	6	44
39	O	114/117 (97%)	102 (90%)	11 (10%)	1 (1%)	20	63
40	P	112/115 (97%)	93 (83%)	18 (16%)	1 (1%)	20	63
41	Q	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
42	R	101/103 (98%)	81 (80%)	18 (18%)	2 (2%)	9	49
43	S	108/110 (98%)	90 (83%)	12 (11%)	6 (6%)	2	27
44	T	91/100 (91%)	77 (85%)	11 (12%)	3 (3%)	4	39
45	U	100/104 (96%)	81 (81%)	16 (16%)	3 (3%)	5	41
46	V	92/94 (98%)	78 (85%)	12 (13%)	2 (2%)	8	47
47	W	73/85 (86%)	66 (90%)	6 (8%)	1 (1%)	13	55
48	X	75/78 (96%)	69 (92%)	5 (7%)	1 (1%)	14	57
49	Y	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	11	53
50	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
51	0	54/57 (95%)	49 (91%)	4 (7%)	1 (2%)	9	50
52	1	48/55 (87%)	43 (90%)	5 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	3	62/65 (95%)	54 (87%)	7 (11%)	1 (2%)	11	53
55	4	36/38 (95%)	28 (78%)	8 (22%)	0	100	100
56	5	129/165 (78%)	100 (78%)	22 (17%)	7 (5%)	2	28
57	6	64/70 (91%)	53 (83%)	10 (16%)	1 (2%)	11	53
58	7	67/69 (97%)	58 (87%)	8 (12%)	1 (2%)	12	54
All	All	6551/6928 (95%)	5610 (86%)	716 (11%)	225 (3%)	7	39

5 of 225 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	e	122	VAL
5	f	63	ASN
10	p	8	ARG
11	q	79	GLU
12	r	17	VAL

### 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	
2	b	180/198 (91%)	175 (97%)	5 (3%)	49	76
3	d	172/173 (99%)	166 (96%)	6 (4%)	41	72
4	e	114/126 (90%)	105 (92%)	9 (8%)	14	50
5	f	87/116 (75%)	83 (95%)	4 (5%)	31	66
6	h	104/105 (99%)	103 (99%)	1 (1%)	80	90
7	k	89/99 (90%)	87 (98%)	2 (2%)	57	81
8	l	103/104 (99%)	100 (97%)	3 (3%)	48	75
9	o	76/77 (99%)	74 (97%)	2 (3%)	51	78
10	p	65/65 (100%)	61 (94%)	4 (6%)	21	58
11	q	74/78 (95%)	71 (96%)	3 (4%)	35	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	r	48/65 (74%)	47 (98%)	1 (2%)	59	82
13	t	65/66 (98%)	63 (97%)	2 (3%)	45	74
14	u	44/61 (72%)	42 (96%)	2 (4%)	32	67
17	w	6/576 (1%)	6 (100%)	0	100	100
18	c	170/190 (90%)	163 (96%)	7 (4%)	35	69
19	g	124/147 (84%)	122 (98%)	2 (2%)	68	86
20	i	105/107 (98%)	100 (95%)	5 (5%)	30	65
21	j	86/90 (96%)	84 (98%)	2 (2%)	56	80
22	m	92/96 (96%)	90 (98%)	2 (2%)	57	81
23	n	79/84 (94%)	75 (95%)	4 (5%)	28	63
24	s	70/79 (89%)	69 (99%)	1 (1%)	71	87
27	C	216/218 (99%)	208 (96%)	8 (4%)	39	71
28	D	164/164 (100%)	161 (98%)	3 (2%)	64	85
29	E	165/165 (100%)	160 (97%)	5 (3%)	46	75
30	F	148/150 (99%)	141 (95%)	7 (5%)	30	65
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%)	106 (97%)	3 (3%)	49	76
34	J	116/116 (100%)	114 (98%)	2 (2%)	66	86
35	K	103/104 (99%)	98 (95%)	5 (5%)	29	64
36	L	102/103 (99%)	100 (98%)	2 (2%)	60	83
37	M	109/109 (100%)	108 (99%)	1 (1%)	82	92
38	N	100/103 (97%)	98 (98%)	2 (2%)	60	83
39	O	86/87 (99%)	84 (98%)	2 (2%)	56	80
40	P	99/100 (99%)	96 (97%)	3 (3%)	46	75
41	Q	89/90 (99%)	87 (98%)	2 (2%)	57	81
42	R	84/84 (100%)	83 (99%)	1 (1%)	75	89
43	S	93/93 (100%)	90 (97%)	3 (3%)	44	74
44	T	80/84 (95%)	77 (96%)	3 (4%)	38	70
45	U	83/85 (98%)	82 (99%)	1 (1%)	75	89
46	V	78/78 (100%)	77 (99%)	1 (1%)	73	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	W	57/63 (90%)	56 (98%)	1 (2%)	64	85
48	X	67/68 (98%)	67 (100%)	0	100	100
49	Y	55/55 (100%)	54 (98%)	1 (2%)	64	85
50	Z	48/49 (98%)	48 (100%)	0	100	100
51	0	47/48 (98%)	45 (96%)	2 (4%)	33	68
52	1	45/49 (92%)	44 (98%)	1 (2%)	57	81
53	2	38/38 (100%)	38 (100%)	0	100	100
54	3	51/52 (98%)	50 (98%)	1 (2%)	60	83
55	4	34/34 (100%)	34 (100%)	0	100	100
56	5	100/123 (81%)	97 (97%)	3 (3%)	46	75
57	6	59/62 (95%)	58 (98%)	1 (2%)	66	86
All	All	4829/5638 (86%)	4698 (97%)	131 (3%)	54	77

5 of 131 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	j	64	GLN
27	C	212	TRP
47	W	67	VAL
22	m	99	GLN
24	s	62	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
21	j	70	HIS
24	s	51	HIS
45	U	65	GLN
22	m	90	HIS
24	s	56	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1535/1539 (99%)	254 (16%)	0
15	v	76/78 (97%)	17 (22%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	x	8/11 (72%)	0	0
25	A	2894/2903 (99%)	542 (18%)	0
26	B	119/120 (99%)	17 (14%)	0
All	All	4632/4651 (99%)	830 (17%)	0

5 of 830 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	9	G
1	a	14	U
1	a	22	G
1	a	30	U
1	a	32	A

There are no RNA pucker outliers to report.

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

39 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
25	6MZ	A	1618	25	18,25,26	1.13	1 (5%)	16,36,39	2.88	4 (25%)
25	2MG	A	1835	25	19,26,27	0.99	2 (10%)	20,38,41	2.11	7 (35%)
25	PSU	A	1911	25	16,21,22	1.49	1 (6%)	20,30,33	3.40	6 (30%)
25	3TD	A	1915	25	16,22,23	1.34	3 (18%)	19,32,35	1.68	5 (26%)
25	PSU	A	1917	25	16,21,22	1.45	1 (6%)	20,30,33	3.60	6 (30%)
25	5MU	A	1939	25	14,22,23	0.80	1 (7%)	16,32,35	2.15	3 (18%)
25	5MC	A	1962	25	15,22,23	1.42	1 (6%)	17,32,35	1.07	1 (5%)
25	6MZ	A	2030	25	18,25,26	1.06	1 (5%)	16,36,39	3.18	4 (25%)
25	7MG	A	2069	25	20,26,27	1.32	2 (10%)	22,39,42	2.80	5 (22%)
25	OMG	A	2251	25,15	18,26,27	1.01	2 (11%)	22,38,41	2.05	6 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
25	2MG	A	2445	25	19,26,27	1.06	4 (21%)	20,38,41	2.30	8 (40%)
25	H2U	A	2449	25	17,21,22	0.99	2 (11%)	21,30,33	2.08	3 (14%)
25	PSU	A	2457	25	16,21,22	1.81	2 (12%)	20,30,33	3.51	6 (30%)
25	OMC	A	2498	25	15,22,23	0.87	1 (6%)	19,31,34	0.83	0
25	2MA	A	2503	25	18,25,26	1.56	3 (16%)	17,37,40	1.77	2 (11%)
25	PSU	A	2504	25	16,21,22	1.57	1 (6%)	20,30,33	3.72	6 (30%)
25	OMU	A	2552	25	14,22,23	0.85	0	18,31,34	1.78	1 (5%)
25	PSU	A	2580	25	16,21,22	1.73	5 (31%)	20,30,33	3.60	6 (30%)
25	PSU	A	2604	25	16,21,22	1.63	2 (12%)	20,30,33	3.60	6 (30%)
25	PSU	A	2605	25	16,21,22	1.32	2 (12%)	20,30,33	3.54	6 (30%)
25	1MG	A	745	25	18,26,27	1.52	3 (16%)	18,39,42	1.70	2 (11%)
25	PSU	A	746	25	16,21,22	1.41	2 (12%)	20,30,33	3.52	6 (30%)
25	5MC	A	747	25	15,22,23	1.43	1 (6%)	17,32,35	1.38	3 (17%)
25	PSU	A	955	25	16,21,22	1.67	4 (25%)	20,30,33	3.44	6 (30%)
1	2MG	a	1207	1	19,26,27	1.36	3 (15%)	20,38,41	2.24	7 (35%)
1	4OC	a	1402	1	16,23,24	1.66	3 (18%)	19,32,35	2.71	8 (42%)
1	5MC	a	1407	1	15,22,23	1.36	1 (6%)	17,32,35	1.14	2 (11%)
1	UR3	a	1498	1	14,22,23	0.77	0	16,32,35	0.79	0
1	2MG	a	1516	1	19,26,27	1.31	2 (10%)	20,38,41	2.28	8 (40%)
1	MA6	a	1518	1	16,26,27	1.12	1 (6%)	18,38,41	2.59	6 (33%)
1	MA6	a	1519	1	16,26,27	0.93	1 (6%)	18,38,41	2.66	7 (38%)
1	PSU	a	516	1	16,21,22	1.52	3 (18%)	20,30,33	3.32	7 (35%)
1	7MG	a	527	1	20,26,27	1.40	2 (10%)	22,39,42	2.72	5 (22%)
1	2MG	a	966	1	19,26,27	1.22	2 (10%)	20,38,41	2.25	7 (35%)
1	5MC	a	967	1	15,22,23	1.29	1 (6%)	17,32,35	1.15	1 (5%)
15	H2U	v	20	15	17,21,22	0.99	2 (11%)	21,30,33	1.92	3 (14%)
15	5MU	v	54	15	14,22,23	0.73	0	16,32,35	2.16	3 (18%)
15	PSU	v	55	15	16,21,22	1.20	1 (6%)	20,30,33	3.56	8 (40%)
15	4SU	v	8	15	14,21,22	1.30	1 (7%)	15,30,33	1.38	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	6MZ	A	1618	25	-	0/5/27/28	0/3/3/3
25	2MG	A	1835	25	-	0/5/27/28	0/3/3/3
25	PSU	A	1911	25	-	0/7/25/26	0/2/2/2
25	3TD	A	1915	25	-	0/7/25/26	0/2/2/2
25	PSU	A	1917	25	-	0/7/25/26	0/2/2/2
25	5MU	A	1939	25	-	0/3/25/26	0/2/2/2
25	5MC	A	1962	25	-	0/3/25/26	0/2/2/2
25	6MZ	A	2030	25	-	0/5/27/28	0/3/3/3
25	7MG	A	2069	25	-	0/7/37/38	0/3/3/3
25	OMG	A	2251	25,15	-	0/5/27/28	0/3/3/3
25	2MG	A	2445	25	-	0/5/27/28	0/3/3/3
25	H2U	A	2449	25	-	0/7/38/39	0/2/2/2
25	PSU	A	2457	25	-	0/7/25/26	0/2/2/2
25	OMC	A	2498	25	-	0/5/27/28	0/2/2/2
25	2MA	A	2503	25	-	0/3/25/26	0/3/3/3
25	PSU	A	2504	25	-	0/7/25/26	0/2/2/2
25	OMU	A	2552	25	-	0/5/27/28	0/2/2/2
25	PSU	A	2580	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2604	25	-	0/7/25/26	0/2/2/2
25	PSU	A	2605	25	-	0/7/25/26	0/2/2/2
25	1MG	A	745	25	-	0/3/25/26	0/3/3/3
25	PSU	A	746	25	-	0/7/25/26	0/2/2/2
25	5MC	A	747	25	-	0/3/25/26	0/2/2/2
25	PSU	A	955	25	-	0/7/25/26	0/2/2/2
1	2MG	a	1207	1	-	0/5/27/28	0/3/3/3
1	4OC	a	1402	1	-	0/7/29/30	0/2/2/2
1	5MC	a	1407	1	-	0/3/25/26	0/2/2/2
1	UR3	a	1498	1	-	0/3/25/26	0/2/2/2
1	2MG	a	1516	1	-	0/5/27/28	0/3/3/3
1	MA6	a	1518	1	-	0/7/29/30	0/3/3/3
1	MA6	a	1519	1	-	0/7/29/30	0/3/3/3
1	PSU	a	516	1	-	0/7/25/26	0/2/2/2
1	7MG	a	527	1	-	0/7/37/38	0/3/3/3
1	2MG	a	966	1	-	0/5/27/28	0/3/3/3
1	5MC	a	967	1	-	0/3/25/26	0/2/2/2
15	H2U	v	20	15	-	0/7/38/39	0/2/2/2
15	5MU	v	54	15	-	0/3/25/26	0/2/2/2
15	PSU	v	55	15	-	0/7/25/26	0/2/2/2
15	4SU	v	8	15	-	0/3/25/26	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	2457	PSU	C5-C1'	-6.07	1.47	1.52
25	A	2580	PSU	C5-C1'	-5.42	1.47	1.52
25	A	2604	PSU	C5-C1'	-5.15	1.47	1.52
25	A	955	PSU	C5-C1'	-4.96	1.47	1.52
25	A	2504	PSU	C5-C1'	-4.87	1.48	1.52

The worst 5 of 182 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	2580	PSU	C5-C4-N3	-10.15	117.10	125.43
25	A	746	PSU	N1-C2-N3	-9.55	121.53	128.40
15	v	55	PSU	N1-C2-N3	-9.46	121.60	128.40
25	A	2504	PSU	N1-C2-N3	-9.33	121.69	128.40
25	A	2605	PSU	N1-C2-N3	-9.32	121.70	128.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	A	1917	PSU	1	0
25	A	1962	5MC	1	0
25	A	2030	6MZ	2	0
25	A	2445	2MG	1	0
25	A	2449	H2U	1	0
25	A	2552	OMU	1	0
25	A	745	1MG	1	0
25	A	747	5MC	1	0
25	A	955	PSU	1	0

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

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.