



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:29 PM BST

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
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) : trunk27241

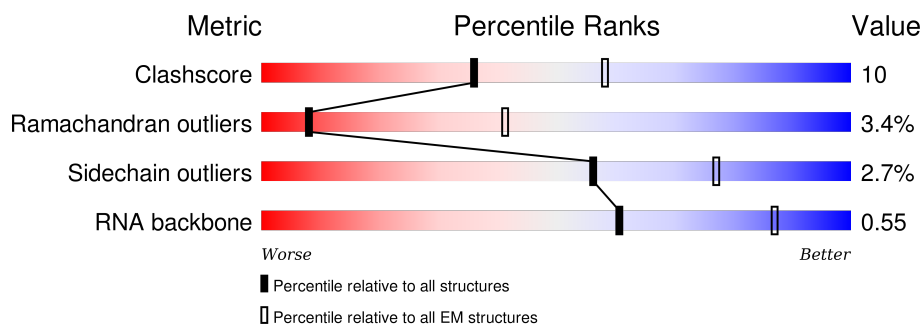
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

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















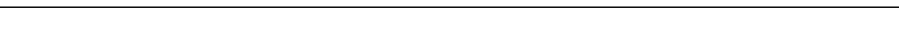

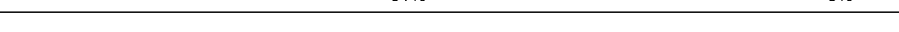

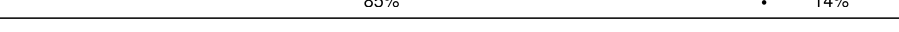








Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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

Mol	Chain	Length	Quality of chain
1	a	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	 53% 37% 9%
26	B	120	 53% 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^{fMet}.

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		
			189	85	31	64	9	0	0

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

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

- 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	S	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	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% 2%



- 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%



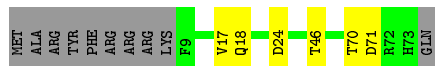
- Molecule 11: 30S ribosomal protein S17

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% .



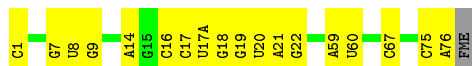
- Molecule 14: 30S ribosomal protein S21

Chain u: 82% 10% 8%



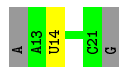
- Molecule 15: P-site fMet-tRNA^{fMet}

Chain v: 76% 23% .



- Molecule 16: mRNA

Chain x: 73% 9% 18%



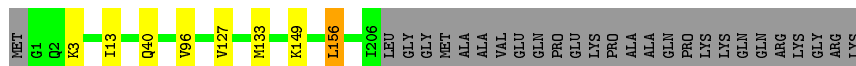
- Molecule 17: Tetracycline resistance protein TetM

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% .



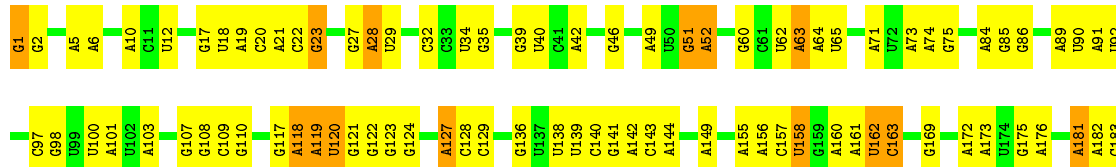
- Molecule 24: 30S ribosomal protein S19

Chain s:  85% . 14%



- Molecule 25: 23S ribosomal RNA

Chain A:  53% 37% 9%



U1534	G1432	G1331	A1247	G1139	A1067	A981	U	G805	A730	G638	U545	U360	U276	G184
A1535	A1433	G1332	G1248	G1139	G1068	C982	C	C906	C736	U639	U546	G361	G277	G185
C1536	A1434	U1340	U1249	C1140	A1069	A983	C	U807	C737	C640	U547	A454	A278	
G1537	G1435	U1141	G1250	U1141	A1070	A984		U811	C737	U641	U548	C363		G189
U1538		G1341	G1251	A1142	G1071	C985		U812	A739	U642	U549	C364	C281	A190
U1539	G1447	A1342	G1252	A1143	G1072	G989	A896	U813	C740	A643	U550	C365	A282	A191
G1448	G1343	G1343	A1253	A1151	A1073	A990	C997	U814		A644	U551	C366	C283	C192
	C1454	C1345	G1256	C1152	G1075		A900	C815	A743	C645	U552	G367	U284	A196
A1548	U1458	U1352	A1265	C1153	A1076	G993	C901	C816	U744	U646	U553	A460	G285	
A1549			G1266	G1160	A1077	C995		C817	U745	G651	U554	C368	G286	A199
	C1461	G1361	U1267	G1170	A1078	C996	G907	C818	U746	A654	U555	G369	U287	
G1555		C1362	A1268	U1174	C1079	A996	C908	A819	C747	A655	U556	C372	U288	A204
C1558	A1469	G1363	U1269	U1175	A1080	U999	A909	G822	G748	G656	U557	U373	U290	U206
U1559	A1470	C1364	C1270	U1176	U1081		A910		A751	G659	U558	G376	G291	A207
G1560	U1474	A1365	G1271	U1177	A1084	C1005	A911	U827	A752	G659	U559	G377	A294	C208
C1561	G1475	A1366	A1272	C1178	A1085	G1011	U919	U828	U753	A668	U571	G386	U296	A213
U1562	U1476	A1367	U1273	G1179	A1086	U1012	A920	A829	U754	U669	U572	U387	G297	G214
U1563	A1477	G1368	A1274	U1180	G1087	U1013	G923	G830	U755	A670	U573	U390	A300	A216
C1564	G1478	A1378	G1276	U1181	A1088	C1014	G924	U832	A756	G674	U574	A391	G301	A217
C1565	U1379	U1183	G1277	U1182	A1089	U1015	G924	A833	C757		U575	A479	C302	A218
A1566	G1482	U1184	G1278	U1184	A1090		G930	G834	C758		U580	A480	G303	A219
G1567	G1483	G1185	G1279	G1185	U1094	U1019	U931		G759	A677	U581	C394		G220
G1568		G1186		G1186	A1095	A1020	U932	U839	A761	C678	U585	U395	U306	G222
A1569	U1486	A1384	G1283	U1187	A1096	A1021	A933	C840	C765	C679	U589	G396	G307	A221
U1578	U1487	U1385		U1188	A1097	G1022	U934	G841			U590	U404	A310	A227
A1579	A1490	A1386	A1287	U1189	A1098	U1023	C935	U842		G682	U591	U405	A311	C228
A1580	G1491	A1387	G1288	G1190	A1099	G1026	A936	G843	G770	A685	U592	G406		
G1581	G1492	U1391	A1289	U1191	C1102	A1027	G937	A844	G771	U686	U593	G411	U321	G232
C1585	G1493	U1392	G1292	U1192	A1103	A1028	G938	A845	C772	C692	U594	A412	A322	G242
A1586	A1495	C1398	C1293	C1200	U1105	U1033	G940	U847	G773	A693	C595	C413	A324	U243
G1587		C1399	G1298	U1201	G1106		A941	A849	G774	U694	U599	C414		A244
A1590	U1504	U1400	C1298	U1108	G1107	G1038	C946	U850	G776	C695	U600	C415	U328	G245
A1591	A1505	G1401	G1299	C1109	C1107	A1039	A947	C851	G777	U703	C601	C420	G329	G248
C1592	U1506	U1405	G1300	A1205	G1110	A1040	A948	U852	U779	A504	U602	C421	A330	C249
	A1509	U1406	A1302	G1206	A1111	G1041	G949	A861	G780	G506	U603	A422	C331	G250
A1597	G1510	G1410	A1306	G1210	U1112	C1045	G953	G857	A781	A705	A608	A423	A332	A251
C1604	C1511	U1411		G1211	C1114	A1046	G954	G858	A782	A706	A609	G424	A333	G252
C1605	U1513	U1412	G1310	G1212	G1115	G1047	U955	U860	A783	A507	U610	G425	C334	
C1606	G1514	A1413	G1311	A1213		C1052	G956	A862	G785	C786		U427	C335	
C1607	G1515	A1414	G1312	G1218	U1119	A1054	C957	G862	C787	U713	G613	C434	C336	A255
A1610	G1516	G1415	U1312	U1222	C1053	A1054	U958	G869	C788	U714	A614	U434	C337	A256
C1611	G1517	C1416	G1313	U1223	G1055	A1054	A959	U870	A789	A715	U615	C435	A340	G259
C1612	G1518	C1417	C1315	G1223	G1125	G1056	C961	U871	U790	A716	A616	C436	C341	G260
G1613	G1519	G1418	U1316	G1235	A1126	A1057	G962	U872	C791	C717		U438	A345	A265
C1614	A1525	A1419	G1317	G1236	A1127	U1058	G969	C873	A792	A721	A627	A439	A346	G266
C1615	G1526	A1420	U1318	A1237	G1128	G1059	U970	G874	A793	A722	G630	U441	A347	C267
A1616	G1527	C1319	C1319	A1237	A1129	U1060	G971	U875	A794	C723	G631	G442	C353	A270
	A1528	G1422	C1320	G1238	U1130	U1061	A972	G879	C795	U724	A633	A443		
A1626	U1529	A1321	A1321	G1239	G1131	G1062	A973		A800	G725	C634	G446	G356	G271
G1627	G1530	C1428	U1328	U1240	U1132	G1063	G974	U884	A801	G726	C635		C357	A272
	C1531	G1429	A1329	A1133	U1133	U1064	A975	C885	A802	A727	U636		U358	
U1636	C1533	A1431	C1330	C1243	C1135	U1066		A886			A637	U451	G359	C275

U1637	U1745	U1845	U1940	U2038	U2119	U2208	U2304	U2394	U2494	U2585	U2698	U2777	C2853
U1746	U1746	U1846	U1941	U2039	U2120	U2209	U2305	U2398	U2497	U2586	U2699	U2778	U2859
C1748	U1751	U1847	U1942	U2040	U2121	U2210	C2306	U2399	U2498	U2587	C2705	U2779	U2860
U1648	C1752	U1848	U1943	U2041	U2122	U2211	U2307	U2402	C2501	C2590	U2706	U2783	U2861
G1651	U1753	U1858	U1944	C2043	A2126	U2212	U2308	U2405	C2502	C2591	U2707	U2784	C2862
G1652	C1754	U1859	U1945	U2049	U2127	U2220	U2310	U2406	U2503	C2592	U2708	U2785	C2863
G1653	U1755	U1865	U1951	C2050	U2128	U2221	U2311	U2407	U2504	U2599	C2709	U2786	U2866
G1654	U1756	U1866	U1952	A2052	C2129	U2222	C2312	U2408	U2505	U2602	U2710	C2787	G2867
A1664	U1757	U1867	U1953	U2052	U2130	U2223	U2313	U2409	U2506	U2603	U2711	C2788	U2868
A1665	U1758	U1868	U1954	C2055	U2132	U2224	U2320	U2409	U2507	U2604	U2712	C2789	U2869
A1666	U1759	U1869	U1955	U2056	U2133	U2225	U2321	U2412	U2508	U2605	U2713	U2790	C2870
A1667	C1760	U1871	U1956	U2056	A2134	U2226	U2322	U2413	U2509	U2606	U2714	U2791	U2871
G1674	C1764	U1872	U1957	U2056	U2139	U2227	U2323	U2414	U2510	U2607	U2715	U2792	U2872
U1679	U1773	U1873	U1958	U2060	U2140	U2228	U2324	U2415	U2511	U2608	U2716	U2793	U2873
U1680	U1779	U1874	U1959	A2062	U2141	U2229	U2325	U2416	U2512	U2609	U2717	U2794	U2874
G1681	U1780	U1875	U1960	C2063	U2142	U2230	U2326	U2417	U2513	U2610	U2718	U2795	U2875
G1682	U1781	U1876	U1961	U2064	U2143	U2231	U2327	U2418	U2514	U2611	U2719	U2796	U2876
U1683	U1782	U1877	U1962	U2065	U2144	U2232	U2328	U2419	U2515	U2612	U2720	U2797	U2877
G1684	U1783	U1878	U1963	U2066	U2145	U2233	U2329	U2420	U2516	U2613	U2721	U2798	U2878
C1685	U1784	U1879	U1964	U2067	U2146	U2234	U2330	U2421	U2517	U2614	U2722	U2799	U2879
U1689	U1787	U1880	U1965	U2068	U2147	U2235	U2331	U2422	U2518	U2615	U2723	U2800	U2880
C1690	U1788	U1881	U1966	U2069	U2148	U2236	U2332	U2423	U2519	U2616	U2724	U2801	U2881
C1691	U1789	U1882	U1967	U2070	U2149	U2237	U2333	U2424	U2520	U2617	U2725	U2802	U2882
U1692	U1790	U1883	U1968	U2071	U2150	U2238	U2334	U2425	U2521	U2618	U2726	U2803	U2883
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G1702	U1800	U1886	U1971	U2074	U2153	U2241	U2337	U2428	U2524	U2621	U2729	U2806	U2886
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U1714	U1802	U1888	U1973	U2076	U2155	U2243	U2339	U2430	U2526	U2623	U2731	U2808	U2888
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U1716	U1804	U1890	U1975	U2078	U2157	U2245	U2341	U2432	U2528	U2625	U2733	U2810	U2890
U1717	U1805	U1891	U1976	U2079	U2158	U2246	U2342	U2433	U2529	U2626	U2734	U2811	U2891
U1718	U1806	U1892	U1977	U2080	U2159	U2247	U2343	U2434	U2530	U2627	U2735	U2812	U2892
C1726	U1807	U1893	U1978	U2081	U2160	U2248	U2344	U2435	U2531	U2628	U2736	U2813	U2893
C1727	U1808	U1894	U1979	U2082	U2161	U2249	U2345	U2436	U2532	U2629	U2737	U2814	U2894
U1728	U1809	U1895	U1980	U2083	U2162	U2250	U2346	U2437	U2533	U2630	U2738	U2815	U2895
U1729	U1810	U1896	U1981	U2084	U2163	U2251	U2347	U2438	U2534	U2631	U2739	U2816	U2896
C1730	U1811	U1897	U1982	U2085	U2164	U2252	U2348	U2439	U2535	U2632	U2740	U2817	U2897
G1731	U1812	U1898	U1983	U2086	U2165	U2253	U2349	U2440	U2536	U2633	U2741	U2818	U2898
U1736	U1813	U1899	U1984	U2087	U2166	U2254	U2350	U2441	U2537	U2634	U2742	U2819	U2899
U1737	U1814	U1900	U1985	U2088	U2167	U2255	U2351	U2442	U2538	U2635	U2743	U2820	U2900
G1738	U1815	U1901	U1986	U2089	U2168	U2256	U2352	U2443	U2539	U2636	U2744	U2821	U2901
C1741	U1816	U1902	U1987	U2090	U2169	U2257	U2353	U2444	U2540	U2637	U2745	U2822	U2902
U1742	U1817	U1903	U1988	U2091	U2170	U2258	U2354	U2445	U2541	U2638	U2746	U2823	U2903
G1743	U1818	U1904	U1989	U2092	U2171	U2259	U2355	U2446	U2542	U2639	U2747	U2824	U2904
U1744	U1819	U1905	U1990	U2093	U2172	U2260	U2356	U2447	U2543	U2640	U2748	U2825	U2905
	U1820	U1906	U1991	U2094	U2173	U2261	U2357	U2448	U2544	U2641	U2749	U2826	U2906
	U1821	U1907	U1992	U2095	U2174	U2262	U2358	U2449	U2545	U2642	U2750	U2827	U2907
	U1822	U1908	U1993	U2096	U2175	U2263	U2359	U2450	U2546	U2643	U2751	U2828	U2908
	U1823	U1909	U1994	U2097	U2176	U2264	U2360	U2451	U2547	U2644	U2752	U2829	U2909
	U1824	U1910	U1995	U2098	U2177	U2265	U2361	U2452	U2548	U2645	U2753	U2830	U2910
	U1825	U1911	U1996	U2099	U2178	U2266	U2362	U2453	U2549	U2646	U2754	U2831	U2911
	U1826	U1912	U1997	U2100	U2179	U2267	U2363	U2454	U2550	U2647	U2755	U2832	U2912
	U1827	U1913	U1998	U2101	U2180	U2268	U2364	U2455	U2551	U2648	U2756	U2833	U2913
	U1828	U1914	U1999	U2102	U2181	U2269	U2365	U2456	U2552	U2649	U2757	U2834	U2914
	U1829	U1915	U2000	U2103	U2182	U2270	U2366	U2457	U2553	U2650	U2758	U2835	U2915
	U1830	U1916	U2001	U2104	U2183	U2271	U2367	U2458	U2554	U2651	U2759	U2836	U2916
	U1831	U1917	U2002	U2105	U2184	U2272	U2368	U2459	U2555	U2652	U2760	U2837	U2917
	U1832	U1918	U2003	U2106	U2185	U2273	U2369	U2460	U2556	U2653	U2761	U2838	U2918
	U1833	U1919	U2004	U2107	U2186	U2274	U2370	U2461	U2557	U2654	U2762	U2839	U2919
	U1834	U1920	U2005	U2108	U2187	U2275	U2371	U2462	U2558	U2655	U2763	U2840	U2920
	U1835	U1921	U2006	U2109	U2188	U2276	U2372	U2463	U2559	U2656	U2764	U2841	U2921
	U1836	U1922	U2007	U2110	U2189	U2277	U2373	U2464	U2560	U2657	U2765	U2842	U2922
	U1837	U1923	U2008	U2111	U2190	U2278	U2374	U2465	U2561	U2658	U2766	U2843	U2923
	U1838	U1924	U2009	U2112	U2191	U2279	U2375	U2466	U2562	U2659	U2767	U2844	U2924
	U1839	U1925	U2010	U2113	U2192	U2280	U2376	U2467	U2563	U2660	U2768	U2845	U2925
	U1840	U1926	U2011	U2114	U2193	U2281	U2377	U2468	U2564	U2661	U2769	U2846	U2926
	U1841	U1927	U2012	U2115	U2194	U2282	U2378	U2469	U2565	U2662	U2770	U2847	U2927
	U1842	U1928	U2013	U2116	U2195	U2283	U2379	U2470	U2566	U2663	U2771	U2848	U2928
	U1843	U1929	U2014	U2117	U2196	U2284	U2380	U2471	U2567	U2664	U2772	U2849	U2929
	U1844	U1930	U2015	U2118	U2197	U2285	U2381	U2472	U2568	U2665	U2773	U2850	U2930
	U1845	U1931	U2016	U2119	U2198	U2286	U2382	U2473	U2569	U2666	U2774	U2851	U2931
	U1846	U1932	U2017	U2120	U2199	U2287	U2383	U2474	U2570	U2667	U2775	U2852	U2932
	U1847	U1933	U2018	U2121	U2200	U2288	U2384	U2475	U2571	U2668	U2776	U2853	U2933
	U1848	U1934	U2019	U2122	U2201	U2289	U2385	U2476	U2572	U2669	U2777	U2854	U2934
	U1849	U1935	U2020	U2123	U2202	U2290	U2386	U2477	U2573	U2670	U2778	U2855	U2935
	U1850	U1936	U2021	U2124	U2203	U2291	U2387	U2478	U2574	U2671	U2779	U2856	U2936
	U1851	U1937	U2022	U2125	U2204	U2292	U2388	U2479	U2575	U2672	U2780	U2857	U2937
	U1852	U1938	U2023	U2126	U2205	U2293	U2389	U2480	U2576	U2673	U2781	U2858	U2938
	U1853	U1939	U2024	U2127	U2206	U2294	U2390	U2481	U2577	U2674	U2782	U2859	U2939
	U1854	U1940	U2025	U2128	U2207	U2295	U2391	U2482	U2578	U2675	U2783	U2860	U2940
	U1855	U1941	U2026	U2129	U2208	U2296	U2392	U2483	U2579	U2676	U2784	U2861	U2941
	U1856	U1942	U2027	U2130	U2209	U2297	U2393	U2484	U2580	U2677	U2785	U2862	U2942
	U1857	U1943	U2028	U2131	U2210	U2298	U2394	U2485	U2581	U2678	U2786	U2863	U2943
	U1858	U1944	U2029	U2132	U2211	U2299	U2395	U2486	U2582	U2679	U2787	U2864	U2944
	U1859	U1945	U2030	U2133	U2212	U2300	U2396	U2487	U2583	U2680	U2788	U2865	U2945
	U1860	U1946	U2031	U2134	U2213	U2301	U2397						

A104
G105
G106
G107
A108
A109
G110
U111
G112
G113
G114
A115
G116
G117
C118
A119
A120

• Molecule 27: 50S ribosomal protein L2

Chain C: 77% 22% ..

Met A1 V2 F7 R12 R13 R14 V15 V16 E24 E34 F38 F43 F44 F45 I48 B51 Y61 F70 F73 E78 E81 E86 L92 L104 A105 P106 L109 L129 P130 M131 R132 V143 K149 A154 V161 Q162

A165 G168 T172 L173 R174 R175 R176 E179 M180 R181 G195 N196 M200 L201 R202 V203 L204 G205 I206 W212 R216 F220 G221 T222 E231 E235 F239 V244 T245 P246 Q250 T251 R252 R257 S258 N259 R260 R261 R269 R270 S271 Lys

• Molecule 28: 50S ribosomal protein L3

Chain D: 76% 22% .

M1 L4 R13 T16 V20 V29 E30 R32 R33 R34 T35 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 M149 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 V63 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 M163 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 R8 D9 V12 M16 N20 V24 V27 F28 R29 V39 G40 E41 L48 N51 B55 L56 T67 R70 V73 I78 P83 T84 G85 G86 R87 V88 T89 L90 R91 G92 M95 P96 E97 E100 R101 L102

A106 I110 F113 L116 S120 M126 Y127 S128 M129 G130 V131 R132 E133 Q134 I135 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 R37 D38 E41 V42 V43 H44 A45 F51 G52 G53 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



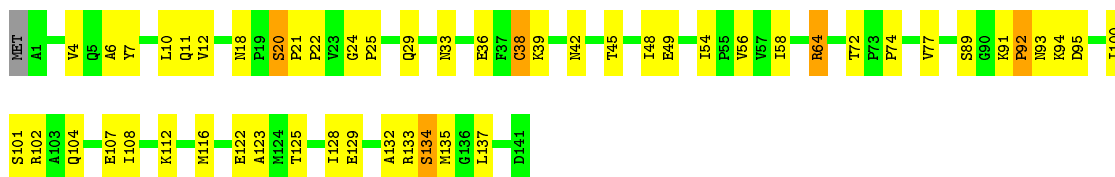
- Molecule 32: 50S ribosomal protein L9

Chain H: 80% 18%



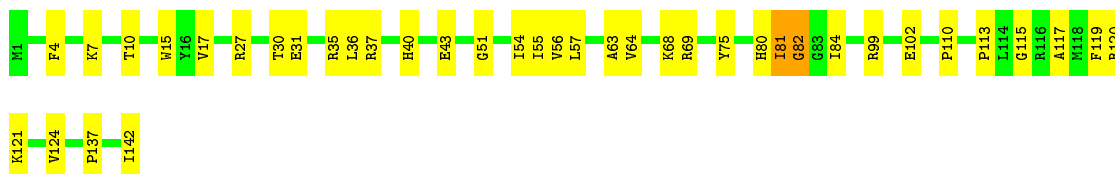
- Molecule 33: 50S ribosomal protein L11

Chain I: 63% 33%



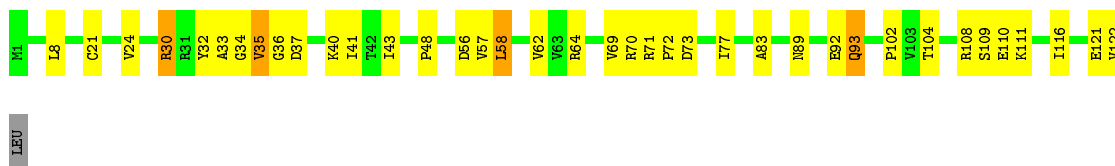
- Molecule 34: 50S ribosomal protein L13

Chain J: 73% 26%



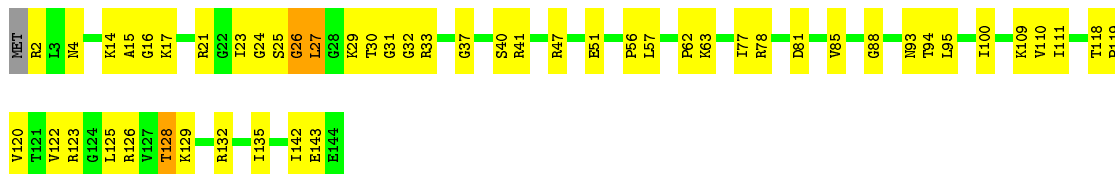
- Molecule 35: 50S ribosomal protein L14

Chain K: 68% 28%

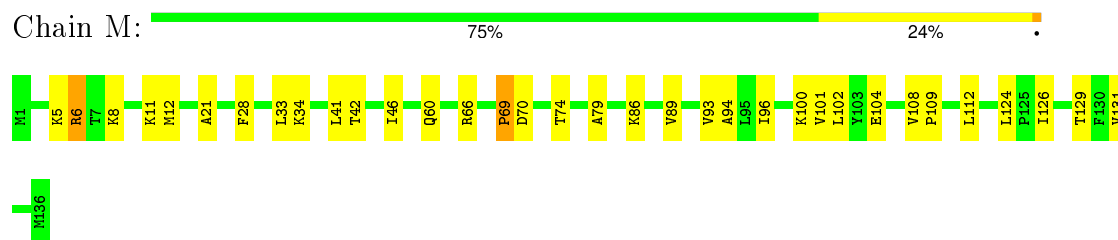


- Molecule 36: 50S ribosomal protein L15

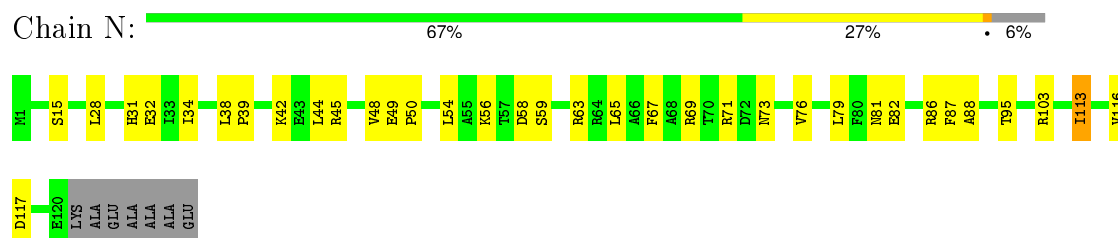
Chain L: 64% 33%



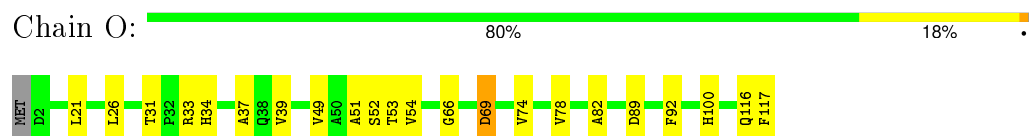
- Molecule 37: 50S ribosomal protein L16



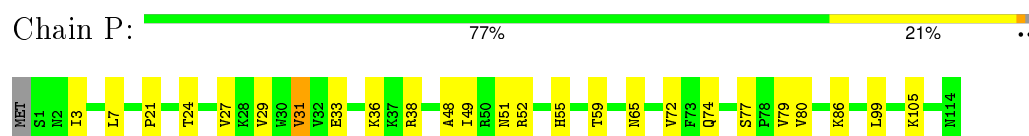
- Molecule 38: 50S ribosomal protein L17



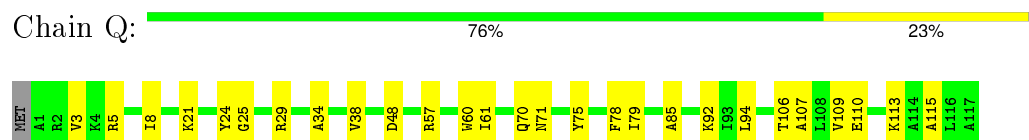
- Molecule 39: 50S ribosomal protein L18



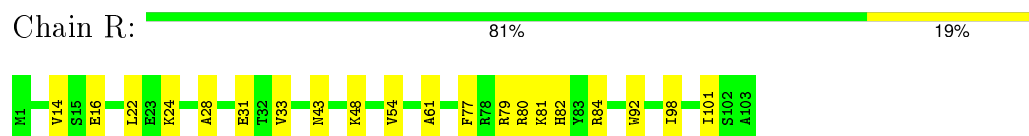
- Molecule 40: 50S ribosomal protein L19



- Molecule 41: 50S ribosomal protein L20



- Molecule 42: 50S ribosomal protein L21



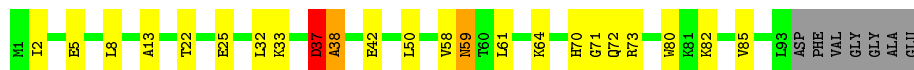
- Molecule 43: 50S ribosomal protein L22





- Molecule 44: 50S ribosomal protein L23

Chain T: 70% 20% 7%



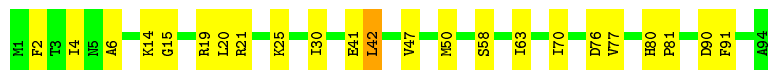
- Molecule 45: 50S ribosomal protein L24

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%



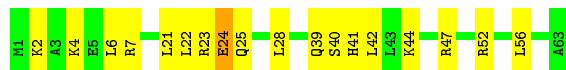
- Molecule 48: 50S ribosomal protein L28

Chain X: 78% 19%



- Molecule 49: 50S ribosomal protein L29

Chain Y: 71% 27%

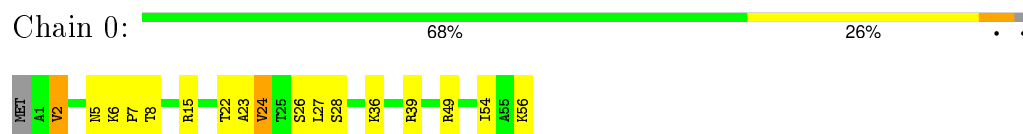


- Molecule 50: 50S ribosomal protein L30

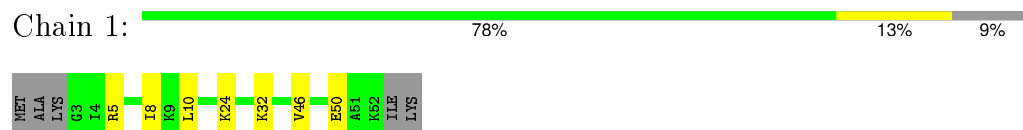
Chain Z: 80% 19%



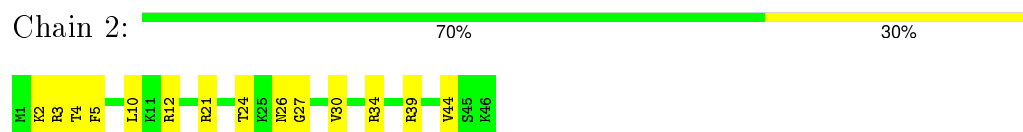
- Molecule 51: 50S ribosomal protein L32



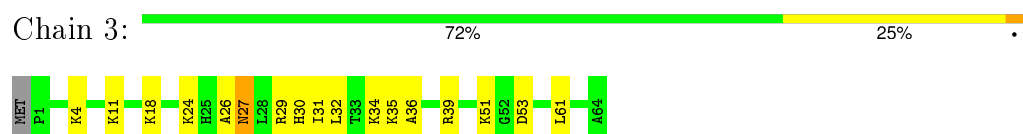
- Molecule 52: 50S ribosomal protein L33



- Molecule 53: 50S ribosomal protein L34



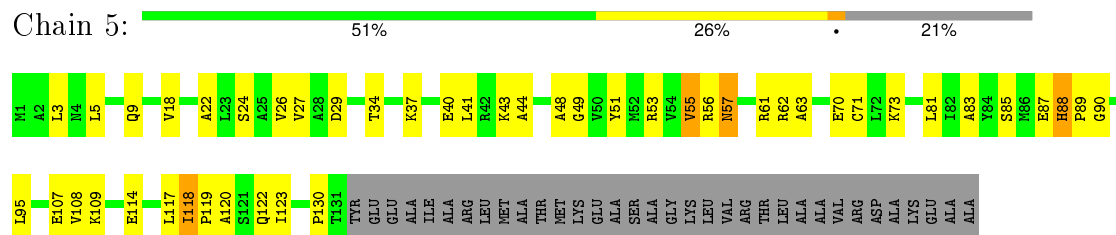
- Molecule 54: 50S ribosomal protein L35



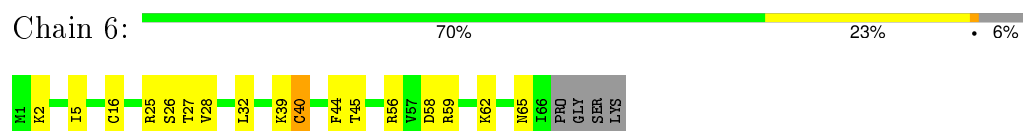
- Molecule 55: 50S ribosomal protein L36



- 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 images	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 ⓘ

5.3.1 Protein backbone ⓘ

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	33
3	d	203/206 (98%)	172 (85%)	21 (10%)	10 (5%)	3	32
4	e	155/167 (93%)	130 (84%)	16 (10%)	9 (6%)	2	28
5	f	98/135 (73%)	81 (83%)	11 (11%)	6 (6%)	2	27
6	h	127/130 (98%)	110 (87%)	14 (11%)	3 (2%)	7	49
7	k	114/129 (88%)	92 (81%)	16 (14%)	6 (5%)	2	30
8	l	121/124 (98%)	96 (79%)	20 (16%)	5 (4%)	3	36
9	o	86/89 (97%)	71 (83%)	10 (12%)	5 (6%)	2	28
10	p	80/82 (98%)	67 (84%)	11 (14%)	2 (2%)	7	48
11	q	78/84 (93%)	65 (83%)	8 (10%)	5 (6%)	2	26
12	r	63/75 (84%)	53 (84%)	5 (8%)	5 (8%)	1	19
13	t	83/87 (95%)	77 (93%)	4 (5%)	2 (2%)	7	49
14	u	63/71 (89%)	44 (70%)	14 (22%)	5 (8%)	1	19
17	w	637/639 (100%)	562 (88%)	51 (8%)	24 (4%)	4	38
18	c	204/233 (88%)	184 (90%)	18 (9%)	2 (1%)	19	64
19	g	149/179 (83%)	124 (83%)	15 (10%)	10 (7%)	1	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	i	125/130 (96%)	98 (78%)	19 (15%)	8 (6%)	2	26
21	j	96/103 (93%)	74 (77%)	16 (17%)	6 (6%)	2	26
22	m	112/118 (95%)	99 (88%)	8 (7%)	5 (4%)	3	33
23	n	99/102 (97%)	82 (83%)	12 (12%)	5 (5%)	2	31
24	s	77/92 (84%)	66 (86%)	11 (14%)	0	100	100
27	C	269/273 (98%)	242 (90%)	22 (8%)	5 (2%)	10	53
28	D	207/209 (99%)	185 (89%)	20 (10%)	2 (1%)	19	64
29	E	199/201 (99%)	172 (86%)	20 (10%)	7 (4%)	4	41
30	F	175/179 (98%)	149 (85%)	20 (11%)	6 (3%)	5	42
31	G	174/177 (98%)	148 (85%)	21 (12%)	5 (3%)	6	45
32	H	147/149 (99%)	128 (87%)	15 (10%)	4 (3%)	6	46
33	I	139/142 (98%)	110 (79%)	20 (14%)	9 (6%)	1	26
34	J	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	14	58
35	K	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	7	48
36	L	141/144 (98%)	110 (78%)	20 (14%)	11 (8%)	1	20
37	M	134/136 (98%)	117 (87%)	14 (10%)	3 (2%)	8	50
38	N	118/127 (93%)	103 (87%)	12 (10%)	3 (2%)	7	48
39	O	114/117 (97%)	102 (90%)	11 (10%)	1 (1%)	21	65
40	P	112/115 (97%)	93 (83%)	18 (16%)	1 (1%)	21	65
41	Q	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
42	R	101/103 (98%)	81 (80%)	18 (18%)	2 (2%)	9	52
43	S	108/110 (98%)	90 (83%)	12 (11%)	6 (6%)	2	29
44	T	91/100 (91%)	77 (85%)	11 (12%)	3 (3%)	5	42
45	U	100/104 (96%)	81 (81%)	16 (16%)	3 (3%)	5	44
46	V	92/94 (98%)	78 (85%)	12 (13%)	2 (2%)	8	50
47	W	73/85 (86%)	66 (90%)	6 (8%)	1 (1%)	14	58
48	X	75/78 (96%)	69 (92%)	5 (7%)	1 (1%)	15	59
49	Y	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	12	56
50	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
51	0	54/57 (95%)	49 (91%)	4 (7%)	1 (2%)	10	53
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%)	12	56
55	4	36/38 (95%)	28 (78%)	8 (22%)	0	100	100
56	5	129/165 (78%)	100 (78%)	22 (17%)	7 (5%)	2	30
57	6	64/70 (91%)	53 (83%)	10 (16%)	1 (2%)	12	56
58	7	67/69 (97%)	58 (87%)	8 (12%)	1 (2%)	13	57
All	All	6551/6928 (95%)	5610 (86%)	716 (11%)	225 (3%)	8	42

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%)	51	79
3	d	172/173 (99%)	166 (96%)	6 (4%)	43	76
4	e	114/126 (90%)	105 (92%)	9 (8%)	15	54
5	f	87/116 (75%)	83 (95%)	4 (5%)	33	70
6	h	104/105 (99%)	103 (99%)	1 (1%)	82	91
7	k	89/99 (90%)	87 (98%)	2 (2%)	60	84
8	l	103/104 (99%)	100 (97%)	3 (3%)	50	79
9	o	76/77 (99%)	74 (97%)	2 (3%)	54	81
10	p	65/65 (100%)	61 (94%)	4 (6%)	23	62
11	q	74/78 (95%)	71 (96%)	3 (4%)	37	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	r	48/65 (74%)	47 (98%)	1 (2%)	61	85
13	t	65/66 (98%)	63 (97%)	2 (3%)	47	78
14	u	44/61 (72%)	42 (96%)	2 (4%)	34	71
17	w	6/576 (1%)	6 (100%)	0	100	100
18	c	170/190 (90%)	163 (96%)	7 (4%)	37	73
19	g	124/147 (84%)	122 (98%)	2 (2%)	70	88
20	i	105/107 (98%)	100 (95%)	5 (5%)	31	69
21	j	86/90 (96%)	84 (98%)	2 (2%)	58	83
22	m	92/96 (96%)	90 (98%)	2 (2%)	60	84
23	n	79/84 (94%)	75 (95%)	4 (5%)	29	68
24	s	70/79 (89%)	69 (99%)	1 (1%)	74	89
27	C	216/218 (99%)	208 (96%)	8 (4%)	41	75
28	D	164/164 (100%)	161 (98%)	3 (2%)	66	87
29	E	165/165 (100%)	160 (97%)	5 (3%)	48	78
30	F	148/150 (99%)	141 (95%)	7 (5%)	32	70
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%)	51	79
34	J	116/116 (100%)	114 (98%)	2 (2%)	68	88
35	K	103/104 (99%)	98 (95%)	5 (5%)	31	69
36	L	102/103 (99%)	100 (98%)	2 (2%)	63	86
37	M	109/109 (100%)	108 (99%)	1 (1%)	84	92
38	N	100/103 (97%)	98 (98%)	2 (2%)	63	86
39	O	86/87 (99%)	84 (98%)	2 (2%)	58	83
40	P	99/100 (99%)	96 (97%)	3 (3%)	48	78
41	Q	89/90 (99%)	87 (98%)	2 (2%)	60	84
42	R	84/84 (100%)	83 (99%)	1 (1%)	78	90
43	S	93/93 (100%)	90 (97%)	3 (3%)	46	78
44	T	80/84 (95%)	77 (96%)	3 (4%)	40	74
45	U	83/85 (98%)	82 (99%)	1 (1%)	78	90
46	V	78/78 (100%)	77 (99%)	1 (1%)	76	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	W	57/63 (90%)	56 (98%)	1 (2%)	66	87
48	X	67/68 (98%)	67 (100%)	0	100	100
49	Y	55/55 (100%)	54 (98%)	1 (2%)	66	87
50	Z	48/49 (98%)	48 (100%)	0	100	100
51	0	47/48 (98%)	45 (96%)	2 (4%)	35	72
52	1	45/49 (92%)	44 (98%)	1 (2%)	60	84
53	2	38/38 (100%)	38 (100%)	0	100	100
54	3	51/52 (98%)	50 (98%)	1 (2%)	63	86
55	4	34/34 (100%)	34 (100%)	0	100	100
56	5	100/123 (81%)	97 (97%)	3 (3%)	48	78
57	6	59/62 (95%)	58 (98%)	1 (2%)	68	88
All	All	4829/5638 (86%)	4698 (97%)	131 (3%)	56	80

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%)	91 (3%)
26	B	119/120 (99%)	17 (14%)	4 (3%)
All	All	4632/4651 (99%)	830 (17%)	95 (2%)

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

5 of 95 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	A	1111	A
25	A	1275	A
25	A	2798	U
25	A	1130	U
25	A	1142	A

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

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	17,25,26	1.11	1 (5%)	15,36,39	2.55	2 (13%)
25	2MG	A	1835	25	18,26,27	0.91	2 (11%)	21,38,41	2.08	6 (28%)
25	PSU	A	1911	25	15,21,22	1.45	1 (6%)	16,30,33	2.11	4 (25%)
25	3TD	A	1915	25	15,22,23	1.29	3 (20%)	17,32,35	1.57	3 (17%)
25	PSU	A	1917	25	15,21,22	1.42	1 (6%)	16,30,33	2.30	4 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	5MU	A	1939	25	13,22,23	0.72	1 (7%)	16,32,35	2.33	2 (12%)
25	5MC	A	1962	25	14,22,23	1.33	1 (7%)	17,32,35	0.99	1 (5%)
25	6MZ	A	2030	25	17,25,26	1.03	1 (5%)	15,36,39	2.87	3 (20%)
25	7MG	A	2069	25	20,26,27	1.17	2 (10%)	23,39,42	3.18	6 (26%)
25	OMG	A	2251	25,15	18,26,27	0.94	2 (11%)	21,38,41	2.09	4 (19%)
25	2MG	A	2445	25	18,26,27	0.88	2 (11%)	21,38,41	2.34	7 (33%)
25	H2U	A	2449	25	17,21,22	0.96	2 (11%)	23,30,33	2.05	5 (21%)
25	PSU	A	2457	25	15,21,22	1.80	1 (6%)	16,30,33	2.20	4 (25%)
25	OMC	A	2498	25	15,22,23	0.78	1 (6%)	20,31,34	1.44	1 (5%)
25	2MA	A	2503	25	17,25,26	1.58	3 (17%)	18,37,40	2.71	1 (5%)
25	PSU	A	2504	25	15,21,22	1.52	1 (6%)	16,30,33	2.41	4 (25%)
25	OMU	A	2552	25	14,22,23	0.69	0	19,31,34	1.49	1 (5%)
25	PSU	A	2580	25	15,21,22	1.68	2 (13%)	16,30,33	2.20	3 (18%)
25	PSU	A	2604	25	15,21,22	1.60	2 (13%)	16,30,33	2.47	4 (25%)
25	PSU	A	2605	25	15,21,22	1.26	2 (13%)	16,30,33	2.38	4 (25%)
25	1MG	A	745	25	17,26,27	1.50	3 (17%)	19,39,42	0.84	0
25	PSU	A	746	25	15,21,22	1.38	1 (6%)	16,30,33	2.11	3 (18%)
25	5MC	A	747	25	14,22,23	1.36	1 (7%)	17,32,35	1.36	3 (17%)
25	PSU	A	955	25	15,21,22	1.62	4 (26%)	16,30,33	2.27	4 (25%)
1	2MG	a	1207	1	18,26,27	1.19	2 (11%)	21,38,41	2.22	6 (28%)
1	4OC	a	1402	1	15,23,24	1.74	4 (26%)	21,32,35	2.79	10 (47%)
1	5MC	a	1407	1	14,22,23	1.27	1 (7%)	17,32,35	1.00	1 (5%)
1	UR3	a	1498	1	13,22,23	0.68	0	18,32,35	0.75	0
1	2MG	a	1516	1	18,26,27	1.22	2 (11%)	21,38,41	2.28	6 (28%)
1	MA6	a	1518	1	18,26,27	1.11	1 (5%)	15,38,41	2.45	2 (13%)
1	MA6	a	1519	1	18,26,27	0.91	1 (5%)	15,38,41	2.68	4 (26%)
1	PSU	a	516	1	15,21,22	1.48	3 (20%)	16,30,33	2.08	3 (18%)
1	7MG	a	527	1	20,26,27	1.25	2 (10%)	23,39,42	3.12	6 (26%)
1	2MG	a	966	1	18,26,27	1.14	2 (11%)	21,38,41	2.21	6 (28%)
1	5MC	a	967	1	14,22,23	1.20	1 (7%)	17,32,35	1.08	1 (5%)
15	H2U	v	20	15	17,21,22	0.95	2 (11%)	23,30,33	1.93	4 (17%)
15	5MU	v	54	15	13,22,23	0.57	0	16,32,35	2.40	2 (12%)
15	PSU	v	55	15	15,21,22	1.14	1 (6%)	16,30,33	2.25	4 (25%)
15	4SU	v	8	15	12,21,22	0.69	0	15,30,33	1.07	1 (6%)

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 62 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	2457	PSU	C5-C1'	-6.04	1.47	1.52
25	A	2580	PSU	C5-C1'	-5.38	1.47	1.52
25	A	2604	PSU	C5-C1'	-5.12	1.47	1.52
25	A	955	PSU	C5-C1'	-4.93	1.47	1.52
25	A	2504	PSU	C5-C1'	-4.84	1.48	1.52

The worst 5 of 135 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	1519	MA6	N3-C2-N1	-8.21	122.42	128.87
1	a	527	7MG	C5-C4-N3	-7.87	118.72	126.74
25	A	2069	7MG	C5-C4-N3	-7.73	118.86	126.74
1	a	1518	MA6	N3-C2-N1	-7.36	123.09	128.87
25	A	1939	5MU	C5-C4-N3	-6.92	119.54	125.35

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.