



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:39 PM BST

PDB ID : 3JA1  
EMDB ID: : EMD-6316  
Title : Activation of GTP Hydrolysis in mRNA-tRNA Translocation by Elongation Factor G  
Authors : Li, W.; Liu, Z.; Koripella, R.K.; Langlois, R.; Sanyal, S.; Frank, J.  
Deposited on : 2015-03-30  
Resolution : 3.60 Å(reported)  
Based on PDB ID : 3J0U

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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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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

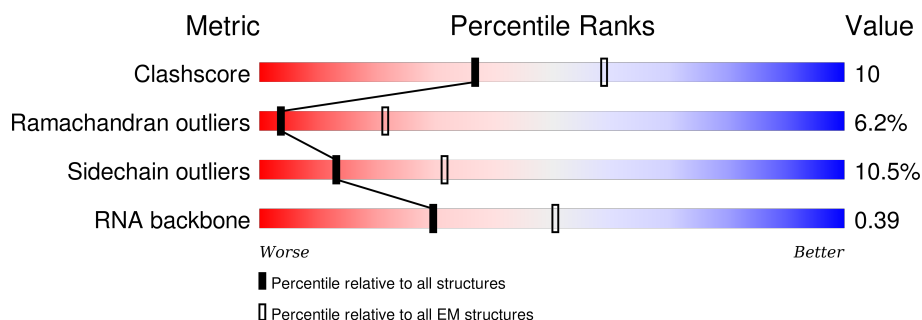
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.60 Å.

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














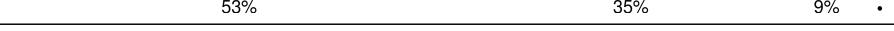







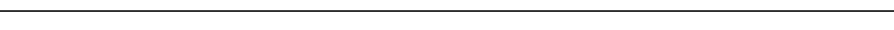

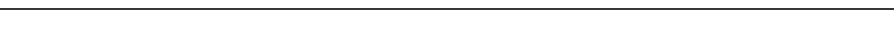
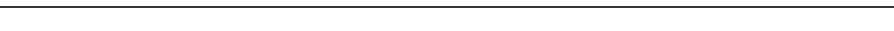


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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

Mol	Chain	Length	Quality of chain
1	SS	91	53% 30% 13% .
2	SA	1542	15% 40% 45%
3	S1	47	. 26% 70%
4	S2	77	14% 40% 45%
5	ST	86	67% 26% 7%
6	SU	70	51% 29% 16% .
7	SG	178	63% 27% 8% .
8	SH	129	60% 29% 9% .











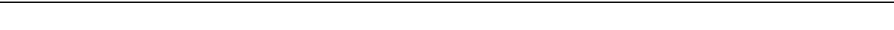

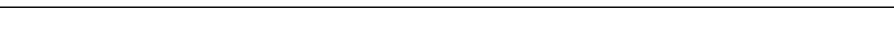
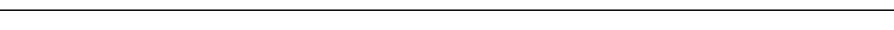











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Mol	Chain	Length	Quality of chain
9	SI	129	
10	SJ	103	
11	SK	128	
12	SL	123	
13	SM	117	
14	SN	100	
15	SO	88	
16	SP	82	
17	SQ	83	
18	SB	240	
19	SC	232	
20	SD	205	
21	SE	166	
22	SF	135	
23	SR	74	
24	S3	702	
25	LB	120	
26	LA	2904	
27	LD	272	
28	LU	110	
29	LV	100	
30	LW	103	
31	LX	94	
32	LY	84	
33	LZ	77	

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Mol	Chain	Length	Quality of chain
34	L0	63	 52% 41% 5% •
35	L1	58	 52% 38% 7% •
36	L2	70	 56% 31% 6% 7%
37	LC	234	 60% 29% 9% •
38	LE	209	 53% 33% 12% •
39	L3	56	 57% 25% 16% •
40	L4	54	 63% 30% • •
41	L5	46	 46% 37% 11% 7%
42	L6	64	 73% 20% 6%
43	L7	38	 63% 26% 5% 5%
44	LF	201	 62% 29% 7% •
45	LG	178	 52% 33% 12% •
46	LH	176	 59% 30% 7% 5%
47	LJ	164	 65% 26% 7% •
48	LN	144	 63% 28% 6% •
49	LK	141	 61% 30% 8% •
50	LL	142	 60% 32% 8% •
51	LI	149	 62% 32% 6% •
52	LO	136	 61% 29% 8% •
53	LP	127	 54% 34% 10% •
54	LM	123	 62% 30% 7% •
55	LQ	117	 59% 28% 9% •
56	LR	114	 53% 32% 13% •
57	LS	117	 54% 29% 14% •
58	LT	103	 64% 22% 13% •

## 2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 156127 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	SS	91	Total	C	N	O	S	0	0
			727	464	139	122	2		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	1542	Total	C	N	O	P	0	0
			33076	14754	6064	10717	1541		

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S1	47	Total	C	N	O	P	0	0
			993	445	167	335	46		

- Molecule 4 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S2	77	Total	C	N	O	P	0	0
			1639	732	297	534	76		

- Molecule 5 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	ST	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 6 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SU	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SG	178	Total	C	N	O	S	0	0
			1400	874	269	253	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SI	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SJ	103	Total	C	N	O	S	0	0
			825	514	158	151	2		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SK	128	Total	C	N	O	S	0	0
			965	595	196	171	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SM	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SO	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SQ	83	Total	C	N	O	S	0	0
			672	425	124	120	3		

- Molecule 18 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SB	240	Total	C	N	O	S	0	0
			1872	1180	332	352	8		

- Molecule 19 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SC	232	Total	C	N	O	S	0	0
			1822	1149	346	323	4		

- Molecule 20 is a protein called 30S ribosomal protein S4.

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

- Molecule 21 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SE	166	Total	C	N	O	S	0	0
			1225	761	232	226	6		

- Molecule 22 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SF	135	Total	C	N	O	S	0	0
			1101	677	198	219	7		

- Molecule 23 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SR	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 24 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S3	702	Total	C	N	O	S	0	0
			5431	3420	938	1048	25		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S3	91	ALA	HIS	ENGINEERED MUTATION	UNP P0A6M8

- Molecule 25 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LB	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LA	2904	Total	C	N	O	P	0	0
			62330	27807	11462	20158	2903		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LA	1618	C	A	CONFLICT	GB 33357927

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Chain	Residue	Modelled	Actual	Comment	Reference
LA	1915	C	U	CONFLICT	GB 33357927
LA	2030	U	A	CONFLICT	GB 33357927
LA	2251	U	G	CONFLICT	GB 33357927

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LD	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 28 is a protein called 50S ribosomal protein L22.

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

- Molecule 29 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LV	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 30 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LW	103	Total	C	N	O	S	0	0
			789	498	148	143			

- Molecule 31 is a protein called 50S ribosomal protein L25.

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

- Molecule 32 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LY	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 33 is a protein called 50S ribosomal protein L28.

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

- Molecule 34 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L0	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 35 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 36 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L2	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 37 is a protein called 50S ribosomal protein L1.

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

- Molecule 38 is a protein called 50S ribosomal protein L3.

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

- Molecule 39 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	L3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 40 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	L4	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 41 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	L5	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 42 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 43 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 44 is a protein called 50S ribosomal protein L4.

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

- Molecule 45 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LG	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 46 is a protein called 50S ribosomal protein L6.

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

- Molecule 47 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LJ	164	Total	C	N	O	S	0	0
			1233	776	220	231	6		

- Molecule 48 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LN	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 49 is a protein called 50S ribosomal protein L11.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L9.

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

- Molecule 52 is a protein called 50S ribosomal protein L16.

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

- Molecule 53 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LP	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 54 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LM	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 55 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LQ	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 56 is a protein called 50S ribosomal protein L19.

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

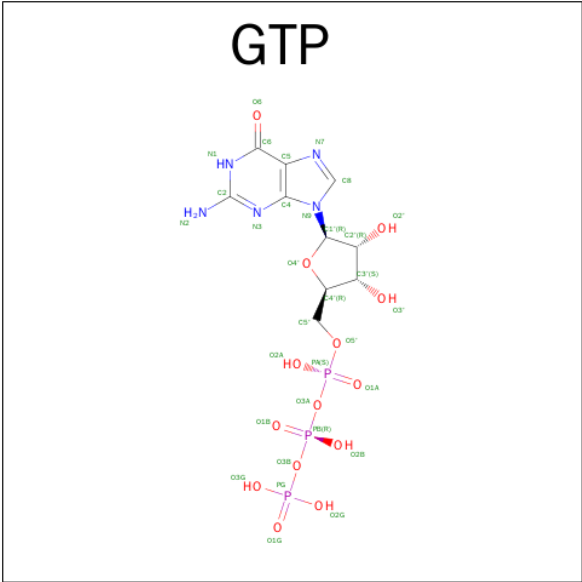
- Molecule 57 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LS	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 58 is a protein called 50S ribosomal protein L21.

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

- Molecule 59 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).

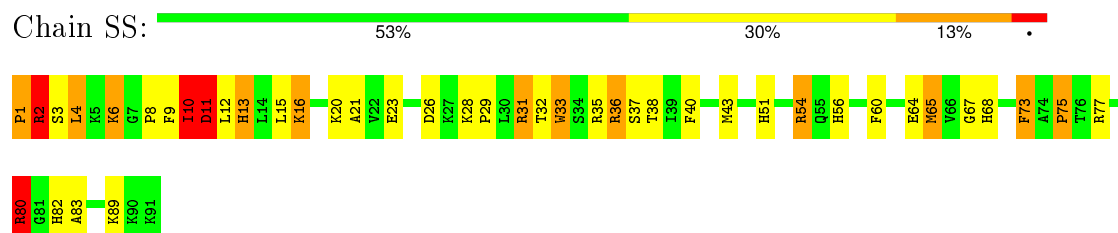


Mol	Chain	Residues	Atoms					AltConf
59	S3	1	Total	C	N	O	P	0
			32	10	5	14	3	

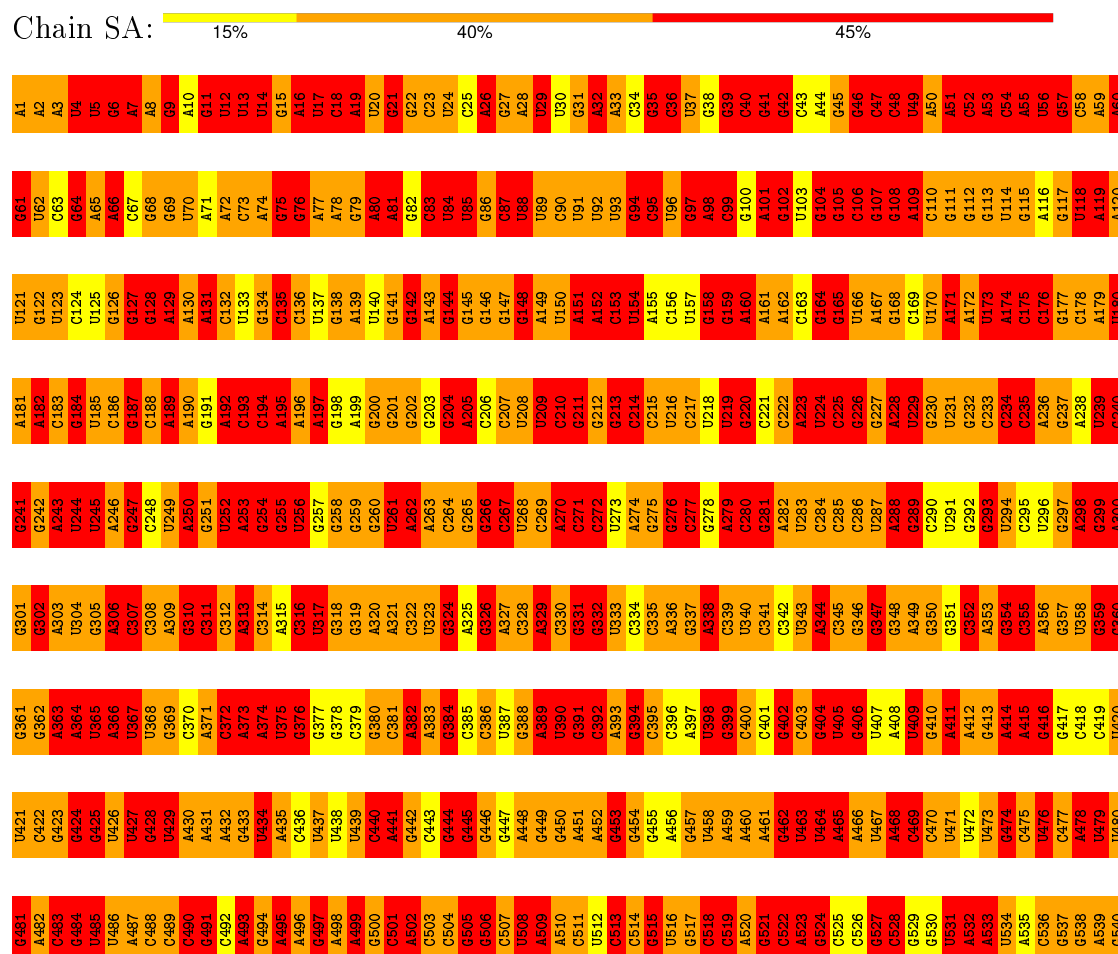
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 30S ribosomal protein S19



- Molecule 2: 16S ribosomal RNA



U1441	U1381	U1321	A1261	A1201	G1141	A1081	A1021	U961	A901	C841	A781	G721	G661	G601	G541
G1442	C1382	C1322	C1262	U1202	G1142	A1082	A1022	C962	G902	U842	A782	G722	U662	A602	G542
C1443	C1383	C1323	U1263	C1203	G1143	U1083	U1023	C963	G903	U843	C783	U723	U663	U603	U543
U1444	C1384	A1324	U1264	A1204	G1144	G1084	G1024	A964	U904	A784	U784	G724	G664	G604	G544
U1445	G1385	C1325	C1265	U1205	A1145	U1085	U1025	U965	U905	A845	G785	G725	U665	U605	C545
A1446	G1386	G1326	G1266	G1206	A1146	U1086	G1026	G966	A906	G846	G786	G726	G666	G606	A546
U1447	G1387	C1327	C1267	G1207	C1147	G1087	C1027	C967	A907	G847	U787	G727	G667	A607	U547
C1448	C1388	C1328	G1268	C1208	U1148	G1088	U1028	A968	A908	C848	U788	A728	G668	A608	G548
C1449	A1389	A1329	U1269	C1209	C1149	G1089	U1029	A969	A909	G849	U789	A729	G669	A609	C549
U1450	U1390	G1330	G1270	C1210	A1150	U1090	U1030	C970	C910	U850	A790	G730	G670	U610	G550
U1451	U1391	G1331	A1271	U1211	A1151	U1091	C1031	G971	U911	G851	G791	G731	G671	C611	U551
G1452	G1392	A1332	G1272	U1212	A1152	A1092	G1032	C972	C912	G852	A792	G732	U672	C612	U552
G1453	U1393	A1333	C1273	A1213	G1153	A1093	G1033	G973	A913	C853	U793	G733	A673	C613	A553
G1454	A1394	G1334	A1274	C1214	G1154	G1094	G1034	A974	A914	U854	A794	G734	G674	C614	A554
G1455	C1395	U1335	A1275	G1215	A1155	U1095	A1035	A975	A915	U855	C795	G735	A675	G615	U555
A1456	A1396	C1336	G1276	A1216	G1156	A1096	A1036	G976	U916	C856	C796	G736	G676	G616	C556
G1457	C1397	G1337	C1277	C1217	A1157	C1097	C1037	A977	G917	C857	C797	G737	U677	G617	A557
G1458	A1398	G1338	G1278	C1218	C1158	C1098	G1038	A978	A918	G858	U798	G738	U678	C618	G558
U1459	C1399	G1339	G1279	A1219	U1159	G1099	G1039	C979	A919	G859	G799	C739	C679	U619	A559
C1460	C1400	A1340	A1280	G1220	G1160	C1100	U1040	C980	U920	A860	G800	U740	C680	C620	A560
G1461	G1401	G1341	C1281	G1221	C1161	A1101	G1041	C981	U921	G861	U801	G741	A681	A621	U561
C1462	C1402	C1342	C1282	G1222	A1162	A1102	A1042	C982	A922	C862	A802	G742	G682	A622	U562
U1463	C1403	G1343	U1283	C1223	C1163	C1103	G1043	A983	A923	U863	G803	A743	G683	C623	A563
U1464	C1404	C1344	C1284	U1224	G1164	G1104	A1044	C984	C924	A864	U804	C744	U684	C624	C564
A1465	G1405	U1345	A1285	A1225	U1165	A1105	G1045	C985	G925	A865	C805	G745	G685	U625	C565
C1466	U1406	A1346	U1286	C1226	G1166	G1106	A1046	U986	G926	C866	C806	A746	U686	G626	G566
G1467	C1407	G1347	A1287	A1227	A1167	C1107	G1047	G987	G927	G867	A807	A747	A687	G627	G567
A1468	A1408	U1348	C1288	C1228	U1168	G1108	G1048	C988	G928	G868	C808	G748	G688	G628	U568
C1469	A1409	A1349	A1289	C1229	A1169	C1109	U1049	C989	G929	U869	G809	A749	C689	A629	C569
U1470	A1410	A1350	G1290	C1230	A1170	A1110	G1050	C990	C930	U870	C810	C750	G690	A630	A570
U1471	C1411	U1351	U1291	G1231	A1171	A1111	C1051	U991	C931	U871	C811	U751	G691	C631	U571
C1412	C1412	C1352	G1292	U1232	C1172	C1112	U1052	U992	C932	A872	G812	G752	U692	U832	A572
A1413	A1413	G1353	C1293	C1233	U1173	C1113	G1053	G993	G933	A873	U813	A753	G693	G633	A573
U1414	G1414	U1354	G1294	C1234	G1174	C1114	C1054	A994	C934	U874	A814	C754	A694	C634	A574
G1415	U1415	U1355	U1295	U1235	G1175	U1115	A1055	C995	A935	U875	A815	G755	A695	A635	G575
G1416	G1416	A1356	C1296	A1236	A1176	U1116	U1056	A996	C936	C876	A816	C756	A696	U636	C576
U1417	G1417	A1357	G1297	C1237	G1177	A1117	G1057	U997	A937	G877	C817	U757	U697	C637	G577
A1418	U1418	U1358	U1298	A1238	G1178	U1118	G1058	C998	A938	A878	C818	C758	G698	U638	C578
G1419	A1419	C1359	A1299	A1239	A1179	C1119	C1059	C999	G939	C879	A819	A759	C699	G639	A579
U1420	U1420	A1360	G1300	U1240	A1180	C1120	U1060	C940	C940	C880	U820	G760	G700	A640	C580
G1421	G1421	G1361	U1301	G1241	G1181	U1121	G1061	C941	G941	G881	G821	U762	A702	U641	G581
G1422	G1422	A1362	C1302	G1242	G1182	U1122	U1062	G942	G942	C882	C822	U762	G703	C642	C582
A1423	A1423	A1363	C1303	C1243	U1183	U1123	C1063	U943	U943	C883	C823	G763	G704	C643	A583
U1424	U1424	U1364	G1304	G1244	G1184	G1124	G1064	C944	C944	U884	G824	C764	A704	U644	G584
U1425	U1425	G1365	G1305	C1245	G1185	U1125	U1065	A945	G945	G885	A825	G765	G705	G645	G585
G1426	G1426	C1366	A1306	A1246	G1186	U1126	C1066	A946	A946	G886	C826	A766	A706	G646	C586
A1428	A1428	U1367	U1307	U1247	G1187	G1127	A1067	G947	G947	G887	U827	A767	U707	C647	G587
G1429	G1429	C1368	U1308	A1248	A1188	C1128	G1068	C948	C948	G888	U828	A768	C708	A648	G588
U1430	A1430	G1369	G1309	C1249	U1189	C1129	C1069	A949	A949	A889	G829	G769	U709	A649	U589
G1431	G1431	G1370	G1310	A1250	G1190	A1130	U1070	U1010	U950	G890	G830	C770	G710	G650	U590
A1431	A1431	G1371	A1311	A1251	A1191	G1131	C1071	C951	G951	U891	A831	G771	G711	C651	U591
G1432	G1432	U1372	G1312	A1252	C1192	C1132	G1072	U952	U952	A892	A832	U772	A712	U652	G592
A1433	A1433	G1373	C1313	G1253	G1193	G1013	U1073	G953	G953	C893	G833	G773	G713	U653	U593
U1434	A1434	A1374	C1314	A1254	U1194	G1134	G1074	A954	G954	G894	U834	G774	G714	G654	U594
U1435	G1435	A1375	U1315	G1255	C1195	U1135	U1075	U955	U955	G895	U835	G775	A715	A655	A595
U1436	U1436	G1376	G1316	A1256	A1196	C1136	U1076	U956	U956	C896	G836	G776	A716	G656	A596
G1437	G1437	A1377	C1317	A1257	A1197	G1137	G1077	U957	U957	C897	U837	A777	U717	U657	G597
U1438	G1438	C1378	A1318	G1258	G1198	G1138	U1078	A958	A958	G898	G838	G778	A718	C658	U598
A1439	A1439	G1379	A1319	C1259	U1199	G1139	G1079	A959	A959	C899	C839	G779	C719	U659	C599
U1440	U1440	U1380	C1320	G1260	C1200	C1140	A1080	G1020	U960	A900	C840	A780	C820	C660	A600





- Molecule 3: mRNA



- Molecule 4: P/E-tRNA



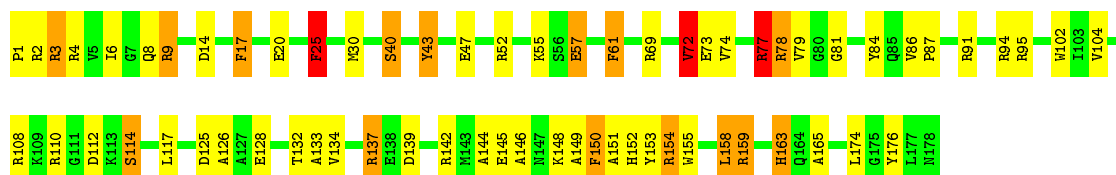
- Molecule 5: 30S ribosomal protein S20



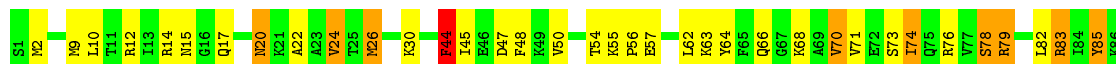
- Molecule 6: 30S ribosomal protein S21



- Molecule 7: 30S ribosomal protein S7



- Molecule 8: 30S ribosomal protein S8





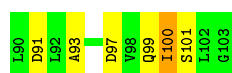
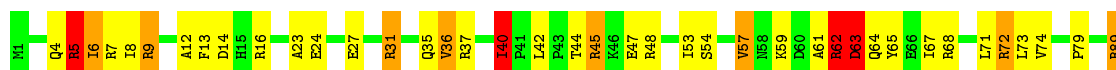
- Molecule 9: 30S ribosomal protein S9

Chain SI: 56% 32% 12%



- Molecule 10: 30S ribosomal protein S10

Chain SJ: 55% 32% 9%



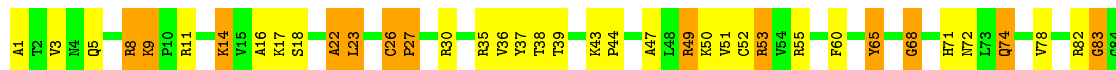
- Molecule 11: 30S ribosomal protein S11

Chain SK: 59% 28% 11%



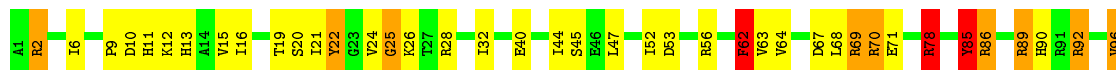
- Molecule 12: 30S ribosomal protein S12

Chain SL: 54% 32% 13%



- Molecule 13: 30S ribosomal protein S13

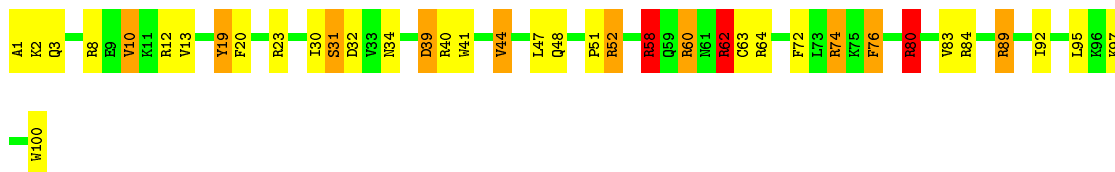
Chain SM: 53% 32% 11%





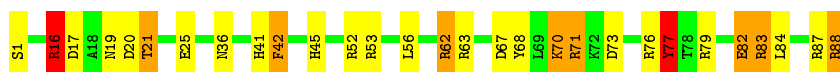
- Molecule 14: 30S ribosomal protein S14

Chain SN: 62% 25% 10% •



- Molecule 15: 30S ribosomal protein S15

Chain SO: 67% 22% 9% •



- Molecule 16: 30S ribosomal protein S16

Chain SP: 61% 28% 7% •



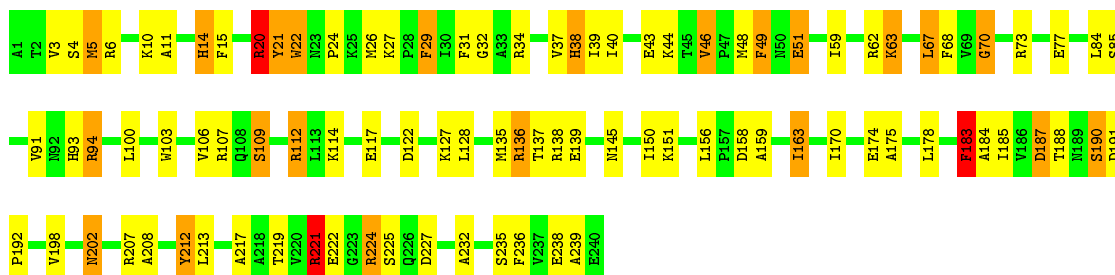
- Molecule 17: 30S ribosomal protein S17

Chain SQ: 66% 25% 7% •



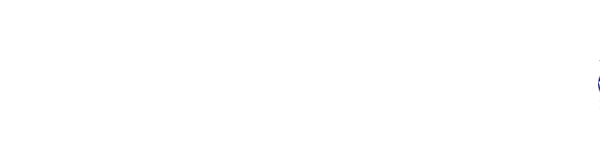
- Molecule 18: 30S ribosomal protein S2

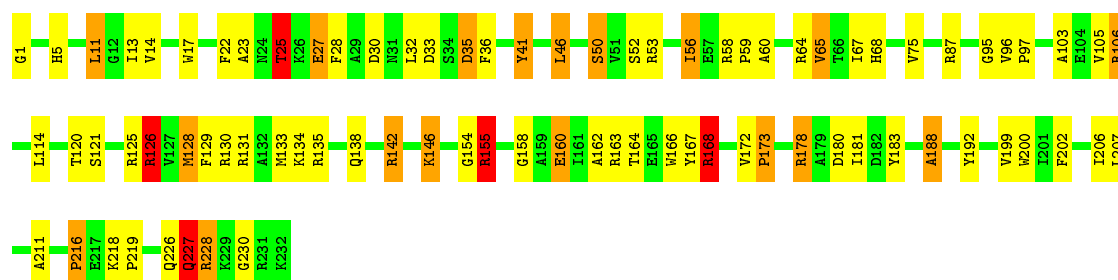
Chain SB: 61% 29% 9% •



- Molecule 19: 30S ribosomal protein S3

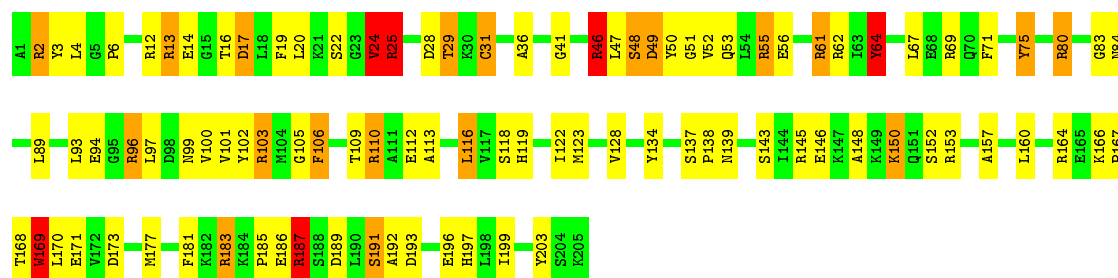
Chain SC: 64% 26% 8% •





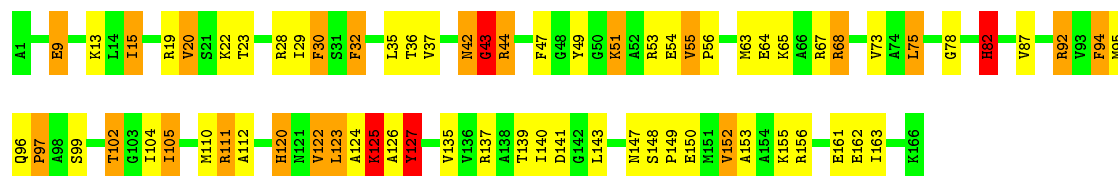
- Molecule 20: 30S ribosomal protein S4

Chain SD: 53% 35% 9% .



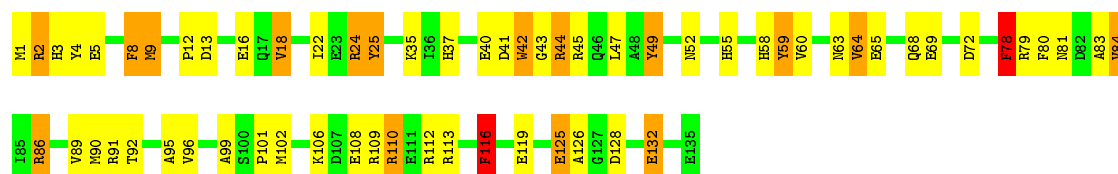
- Molecule 21: 30S ribosomal protein S5

Chain SE: 58% 27% 13% .



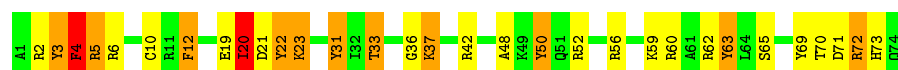
- Molecule 22: 30S ribosomal protein S6

Chain SF: 53% 33% 12% .

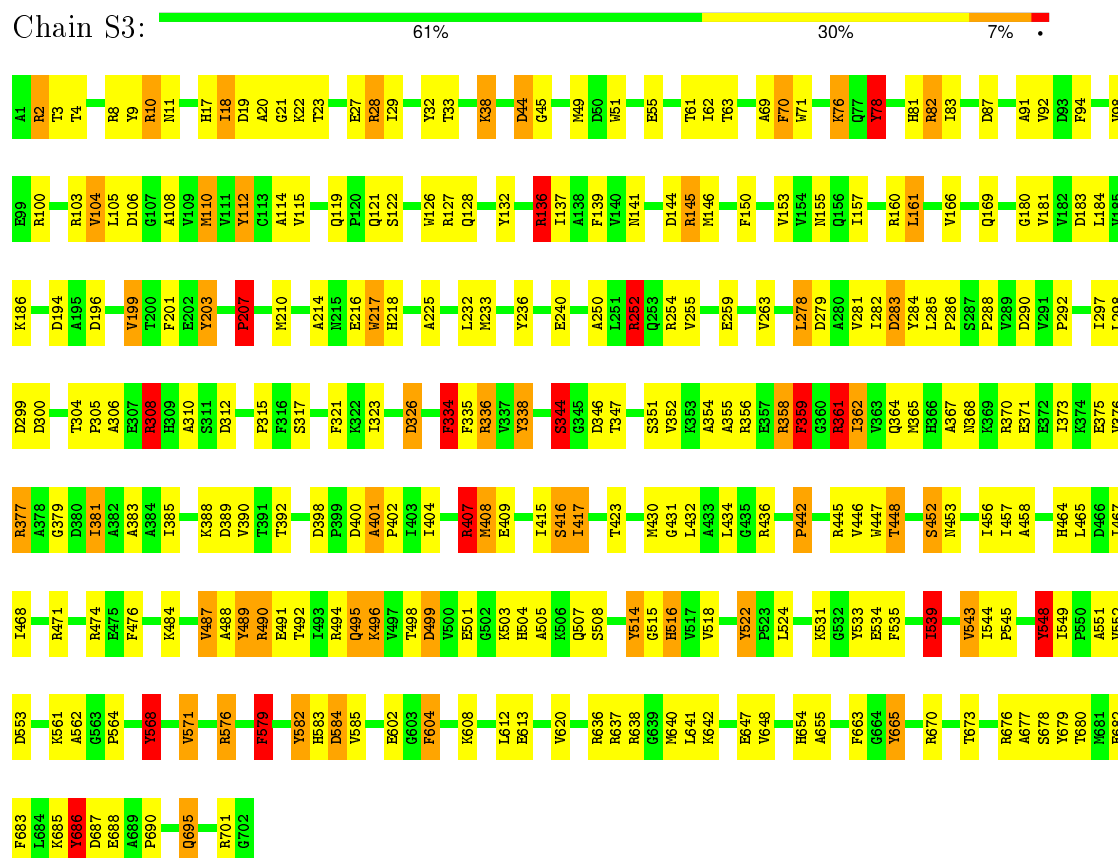


- Molecule 23: 30S ribosomal protein S18

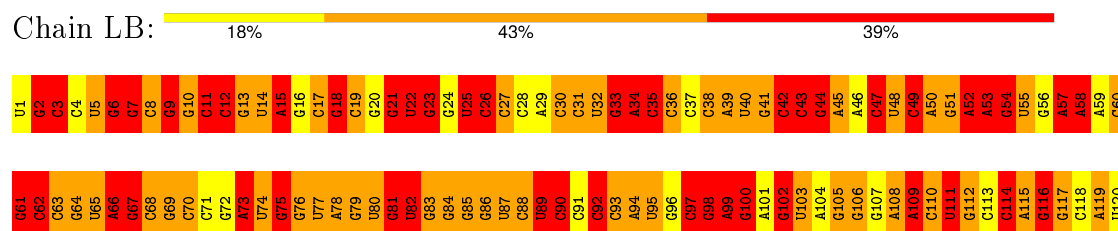
Chain SR: 58% 24% 15% .



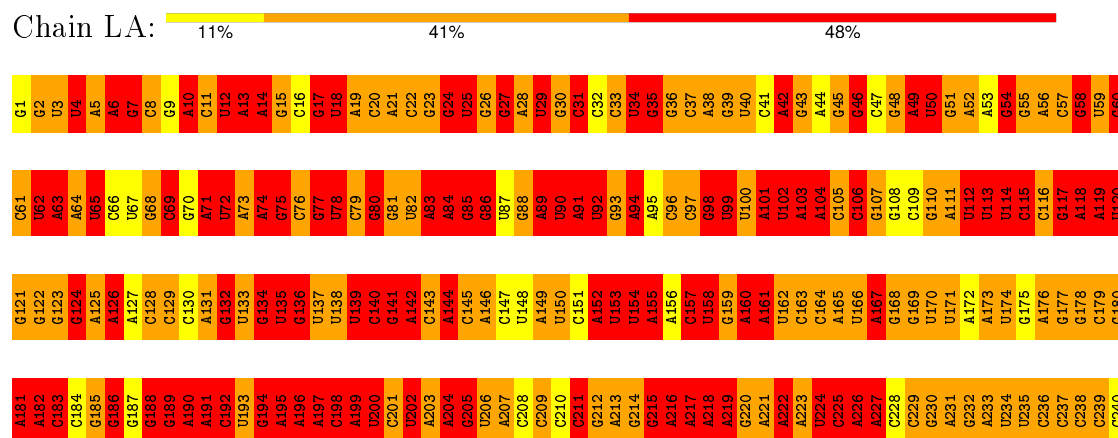
- Molecule 24: Elongation factor G



• Molecule 25: 5S ribosomal RNA



• Molecule 26: 23S ribosomal RNA



U1201	U1441	U1081	A1021	C981	C901	G941	A781	A721	C601	A541	G481	C421	G361	G301	A241
G1202	A1142	U1082	G1022	G962	C902	U942	A782	A722	A602	C542	A482	A422	A362	C302	G242
U1203	A1143	U1083	U1023	U963	G903	G943	A783	C723	A603	G543	A483	A423	G363	G303	U243
A1204	A1144	U1084	G1024	G964	G904	A944	G784	U724	G604	C544	A484	A424	C364	U304	A244
A1205	C1145	A1085	A1025	C965	A905	A945	G785	G725	G605	U545	C485	G425	U365	C305	G245
G1206	C1146	A1086	G1026	G966	U906	G946	G786	G726	U606	U546	C486	G426	C366	U306	G246
C1207	A1147	G1087	A1027	U967	G907	U947	C787	A727	U607	A547	G487	U427	G367	G307	G247
C1208	U1148	A1088	A1028	C968	C908	C948	A788	A728	A608	G548	A488	A428	G368	G308	G248
U1209	C1149	A1089	A1029	G969	A909	A949	A789	G729	A609	G549	G489	A429	U369	A309	C249
G1210	A1150	U1090	G1030	U970	A910	U950	A790	C730	C610	C550	C490	A430	A370	A310	G250
C1211	C1151	G1091	G1031	G971	A911	C951	C791	C731	G612	G552	A492	U432	G372	G312	G252
G1212	C1152	A1092	A1032	A972	C912	U952	A792	G732	G613	U553	G493	C433	U373	G313	C253
A1213	G1153	G1093	U1033	G973	U913	C953	A793	G733	A614	U554	G494	U434	A374	C314	G254
A1214	G1154	U1094	G1034	G974	G914	C954	A794	A734	A615	G555	G495	C435	A375	G315	A255
G1215	A1155	A1095	U1035	A975	C915	G955	C795	A735	U616	A556	G496	C436	G376	C316	A256
G1216	A1156	A1096	G1036	G976	G916	G956	C796	C736	A617	C557	A497	U437	G377	G317	C257
U1217	G1157	U1097	G1037	G977	A917	G957	G797	G737	G618	U558	G498	U438	C378	C318	G258
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U1219	U1159	G1099	A1039	A979	U919	G959	G799	A739	G620	C560	A500	C440	G380	A320	G260
G1220	C1160	C1100	A1040	A980	A920	U960	A800	C740	G621	C561	A501	U441	G381	U321	G261
U1221	C1161	U1101	G1041	A981	C921	U961	A801	U741	G622	U562	A502	G442	A382	C322	G262
U1222	G1162	C1102	G1042	C982	C922	A962	A802	A742	G623	A563	A503	A443	A383	C323	G263
G1223	G1163	A1103	G1043	A983	G923	A963	A803	A743	G624	U564	A504	C444	A384	A324	G264
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A1226	G1166	G1106	A1046	C986	G926	A966	C806	U746	A627	U567	A507	U447	U387	G327	C267
G1227	G1167	G1107	G1047	C987	A927	C967	U807	U747	G628	U568	A508	U448	C388	U328	C268
U1228	C1168	A1108	A1048	A988	G928	G968	G808	G748	G629	U569	A509	A449	G389	G329	C269
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A1230	U1170	G1110	U1050	A990	G930	U970	U810	A750	G631	U571	C511	U451	A391	C331	G271
U1231	G1171	A1111	G1051	C991	U931	U971	C811	A751	A632	A572	G512	U452	U392	A332	A272
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U1234	A1174	G1114	A1054	C994	U934	G974	C814	U754	C635	A575	A515	C455	U395	C335	C275
G1235	A1175	G1115	G1055	C995	U935	G975	C815	U755	G636	U576	C516	C456	G396	C336	G276
U1236	G1176	G1116	G1056	A996	A936	C976	C816	A756	G637	U577	C517	A457	U397	C337	G277
G1237	U1177	C1117	A1057	G997	C937	A977	C817	G757	A638	U578	C518	U458	C398	G338	A278
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U1239	G1179	U1119	G1059	U999	G939	G979	A819	G759	U639	U580	U520	A460	G400	A340	U280
U1240	U1180	G1120	U1060	A1000	G940	G980	A820	G760	C640	C581	U521	C461	A402	A342	A282
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C1243	U1183	G1123	G1063	G1003	A943	G983	C823	G763	A644	G584	C524	U464	G405	A345	G285
A1244	U1184	G1124	C1064	U1004	C944	U984	U824	A764	C645	G585	U525	C465	G406	A346	U286
G1245	G1185	G1125	U1065	C1005	A945	C985	A825	C765	U646	A586	A526	A466	G407	A347	G287
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G1248	U1188	G1128	G1068	A1008	C948	C988	U828	G768	U649	U589	A529	G469	G410	G350	U290
U1249	A1189	A1129	A1069	G949	G949	C889	A829	G769	C650	A590	U530	A470	G411	C351	G291
G1250	G1190	U1130	A1070	C950	G950	C990	G830	G770	G651	U591	C531	A471	A412	A352	U292
C1251	G1191	G1131	C1071	G951	C951	G991	G831	G771	G652	A592	A532	A472	A413	A353	U293
G1252	A1192	U1132	G1072	U1012	G952	A992	U832	C772	U653	U593	C533	G473	C414	A354	A294
A1253	G1193	A1133	A1073	C953	G953	C993	A833	U773	U654	U594	C534	G474	C415	A355	G295
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C1257	G1197	G1137	A1077	C957	G957	C997	C837	G777	U658	U598	A538	A478	U419	G359	A299
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C2161	A2101	U2041	A1981	G1921	G1861	A1801	C1741	G1681	U1621	C1561	G1501	G1441	G1381	A1321	G1261
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A2163	C2103	C2043	G1983	G1923	G1863	A1803	G1743	G1683	G1623	U1563	A1503	U1443	G1383	G1323	G1263
C2164	C2104	C2044	G1984	C1924	U1864	A1804	A1744	G1684	U1624	A1564	A1504	G1444	A1384	G1324	A1264
C2165	U2105	C2045	G1985	C1925	A1865	A1805	A1745	G1685	G1625	U1565	A1505	G1445	G1385	U1325	G1265
U2166	U2106	C1966	C1986	U1926	A1866	A1806	A1746	G1686	A1626	U1566	U1506	G1446	C1386	G1266	
U2167	G2107	C2047	A1987	A1927	G1867	A1807	U1747	G1687	G1627	U1567	C1507	C1447	A1387	U1267	
G2168	A2108	C2048	G1988	A1928	C1868	A1808	U1748	G1688	G1628	U1568	A1508	G1448	A1328	U1268	
A2169	U2109	G2049	G1989	G1929	G1869	A1809	A1749	A1689	U1629	U1569	A1509	G1449	G1389	A1269	
A2170	G2110	C2050	G1990	G1930	A1870	A1810	G1750	A1690	A1630	U1570	G1510	G1450	C1330	C1270	
A2171	U2111	A2051	U1991	U1931	A1871	A1811	U1751	C1691	G1631	U1571	C1451	C1391	G1331	G1271	
U2172	G2112	A2052	G1992	A1932	A1872	A1812	C1752	U1692	A1632	U1572	C1452	G1392	G1332	A1272	
A2173	U2113	G2063	U1993	G1933	G1873	G1813	G1753	U1693	G1633	U1573	U1513	G1393	G1333	U1273	
C2174	A2114	A2054	C1994	C1934	C1874	G1814	A1754	C1694	A1634	C1574	G1454	C1394	G1334	A1274	
C2175	G2115	C2055	U1995	G1935	G1875	A1815	A1755	G1695	A1635	U1575	A1515	G1395	C1335	A1275	
A2176	G2116	C2056	G1996	A1936	A1876	A1816	G1756	G1696	U1636	U1576	A1516	G1396	A1336	A1276	
C2177	A2117	G2057	C1997	U1937	A1877	G1817	U1757	G1697	A1637	U1577	U1517	U1397	G1337	G1277	
C2178	U2118	A2058	A1998	A1938	G1878	U1818	U1758	A1698	G1638	U1578	C1458	C1398	G1338	C1278	
C2179	A2119	A2059	C1999	U1939	C1879	A1819	A1759	G1699	C1639	A1579	U1519	G1399	G1339	G1279	
U2180	G2120	A2060	C2000	U1940	U1880	U1820	C1760	A1700	A1640	U1580	U1520	U1460	U1340	G1280	
U2181	G2121	C2061	C2001	G1941	C1881	A1821	C1761	A1701	A1641	G1581	G1401	G1461	G1341	G1281	
U2182	U2122	U2062	G2002	C1942	U1882	G1822	A1762	G1702	G1642	U1582	U1402	C1462	A1342	U1282	
A2183	G2123	C2063	A2003	U1943	U1883	G1823	G1763	G1703	G1643	U1583	C1403	G1463	G1343	G1283	
A2184	G2124	G2064	G2004	U1944	G1884	G1824	C1764	C1704	C1644	U1584	G1464	G1464	C1404	A1284	
U2185	G2125	C2065	A2005	G1945	A1885	U1825	U1765	A1705	G1645	U1585	A1525	G1465	U1345	A1285	
G2186	A2126	C2066	C2006	U1946	U1886	G1826	G1766	C1706	C1646	U1586	C1526	U1466	G1346	A1286	
U2187	G2127	U2067	U2007	G1947	C1887	U1827	G1767	G1707	U1647	U1587	U1467	U1467	A1347	A1287	
U2188	C2128	C2068	C2008	G1948	G1888	G1828	C1768	G1708	U1648	G1588	A1528	U1468	C1348	G1288	
U2189	C2129	C2069	A2009	G1949	A1889	A1829	U1769	U1709	G1649	U1589	G1469	U1409	C1349	G1289	
G2190	G2130	A2070	G2010	G1950	A1890	C1830	G1770	G1710	A1650	A1590	G1530	A1470	G1350	C1290	
A2191	U2131	U2071	U2011	U1951	G1891	G1831	C1771	A1711	G1651	C1531	U1411	G1471	C1351	G1291	
U2192	G2132	C2072	A1962	U1962	C1892	G1832	A1772	U1712	A1652	C1532	U1412	C1472	G1352	G1292	
G2193	G2133	C2073	C1963	A1963	C1893	G1833	A1773	U1713	G1653	U1593	A1413	G1473	C1353	G1293	
U2194	A2134	U2074	A2014	G1954	C1894	G1834	C1774	G1714	A1654	U1534	C1414	U1474	A1354	U1294	
U2195	A2135	U2075	A2015	U1955	G1895	G1835	U1775	G1715	A1655	U1595	U1415	G1475	G1355	G1295	
C2196	G2136	U2076	U2016	U1956	G1896	C1836	G1776	U1716	C1656	A1596	G1416	U1476	G1356	G1296	
U2197	U2137	A2077	U2017	C1957	G1897	G1837	U1777	A1717	U1657	U1597	G1537	A1477	G1357	C1297	
A2198	G2138	C2078	G2018	C1958	U1898	C1838	U1778	G1718	C1658	A1598	G1538	G1478	G1358	C1298	
A2199	U2139	U2079	A2019	G1959	A1899	G1839	U1779	G1719	G1659	U1599	A1419	G1479	A1359	G1299	
C2200	G2140	A2080	A2020	A1960	A1900	G1840	A1780	U1720	G1660	C1600	G1540	C1480	G1360	G1300	
G2201	A2141	U2081	C2021	C1961	A1901	U1841	U1781	G1721	G1661	C1601	C1541	U1481	G1361	A1301	
U2202	A2142	A2082	U2022	C1962	C1902	G1842	U1782	A1722	U1662	U1602	U1542	G1482	C1362	A1302	
G2203	C2143	G2083	C2023	U1963	G1903	C1843	A1783	G1723	G1663	A1603	G1543	U1483	C1363	G1303	
G2204	G2144	C2084	G2024	G1964	G1904	C1844	A1784	G1724	A1664	C1604	A1544	U1484	G1364	A1304	
G2205	C2145	U2085	C2025	C1965	C1905	G1845	A1785	U1725	A1665	C1605	A1545	U1485	A1365	C1305	
C2206	G2146	U2086	U2026	A1966	G1906	G1846	A1786	C1726	G1666	C1606	G1546	U1486	A1366	C1306	
U2207	A2147	G2087	G2027	C1967	G1907	A1847	A1787	C1727	G1667	C1607	U1547	U1487	A1367	A1307	
G2208	G2148	A2088	U2028	G1968	C1908	A1848	C1788	G1728	A1668	A1608	A1548	C1488	G1368	A1308	
G2209	U2149	C2089	G2029	A1969	C1909	G1849	A1789	U1729	A1669	A1609	A1549	C1489	G1369	G1309	
U2210	C2150	A2090	U2030	U1970	G1910	G1850	C1790	C1730	C1670	A1610	C1550	A1490	C1370	G1310	
A2211	U2151	C2091	A2031	U1971	U1911	U1851	A1791	G1731	U1671	A1611	A1551	G1491	A1431	G1311	
G2212	G2152	U2092	G2032	G1972	A1912	U1852	G1792	C1732	A1672	C1612	A1552	G1492	G1372	G1312	
U2213	C2153	G2093	A2033	C1973	A1913	A1853	C1793	G1733	G1673	A1613	A1553	C1493	A1433	U1313	
C2214	A2154	A2094	U2034	C1974	A1914	A1854	A1794	G1734	G1674	A1614	U1554	A1494	A1434	G1314	
G2215	U2155	A2095	G2035	C1975	C1915	U1855	C1795	A1735	G1675	C1615	G1555	A1495	G1435	G1315	
G2216	G2156	C2096	C2036	U1976	A1916	U1856	U1796	U1736	A1676	A1616	C1556	A1496	G1436	U1316	
G2217	G2157	A2097	A2037	A1977	U1917	G1857	G1797	G1737	A1677	C1617	C1557	U1497	G1437	G1317	
G2218	A2158	U2098	G2038	A1978	A1918	A1858	U1798	A1738	A1678	C1618	C1558	C1498	A1438	U1318	
U2219	G2159	U2099	U2039	A1979	A1919	A1859	G1799	A1739	A1679	U1619	U1559	C1499	A1439	G1319	
U2220	C2160	G2100	G2040	G1980	C1920	G1860	C1800	G1740	U1680	G1620	G1560	G1500	U1440	G1380	

- Molecule 27: 50S ribosomal protein L2

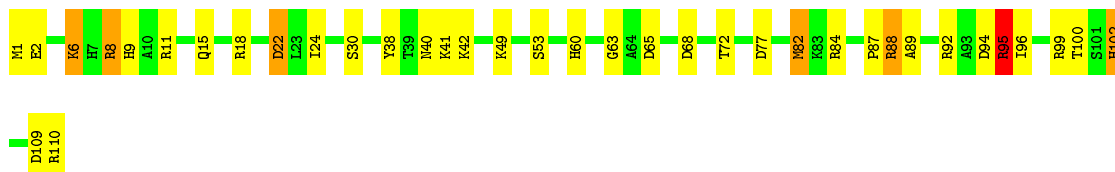
[illegible]





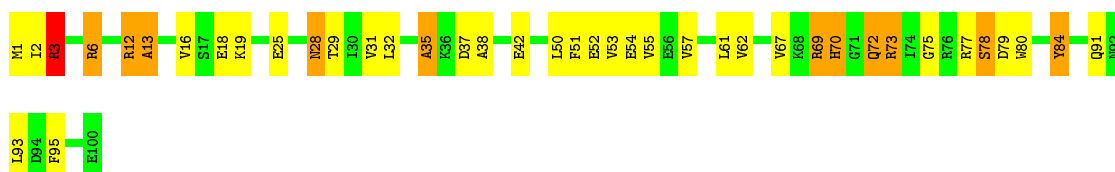
- Molecule 28: 50S ribosomal protein L22

Chain LU: 66% 27% 5% •



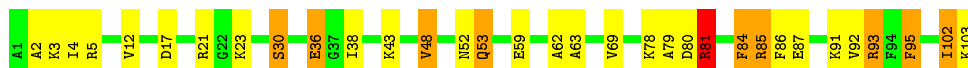
- Molecule 29: 50S ribosomal protein L23

Chain LV: 59% 29% 11% •



- Molecule 30: 50S ribosomal protein L24

Chain LW: 68% 22% 9% •



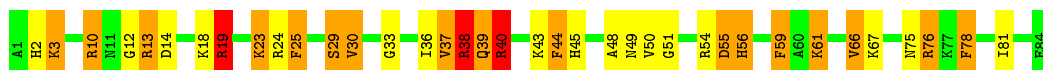
- Molecule 31: 50S ribosomal protein L25

Chain LX: 62% 31% 5% •



- Molecule 32: 50S ribosomal protein L27

Chain LY: 56% 20% 20% •



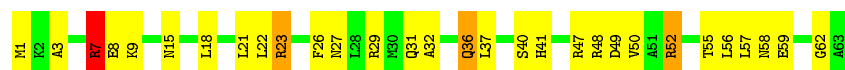
- Molecule 33: 50S ribosomal protein L28

Chain LZ: 58% 31% 6% •



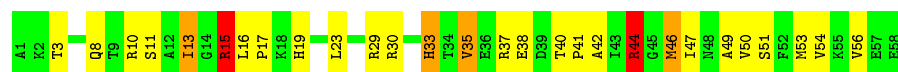
- Molecule 34: 50S ribosomal protein L29

Chain L0: 



- Molecule 35: 50S ribosomal protein L30

Chain L1: 



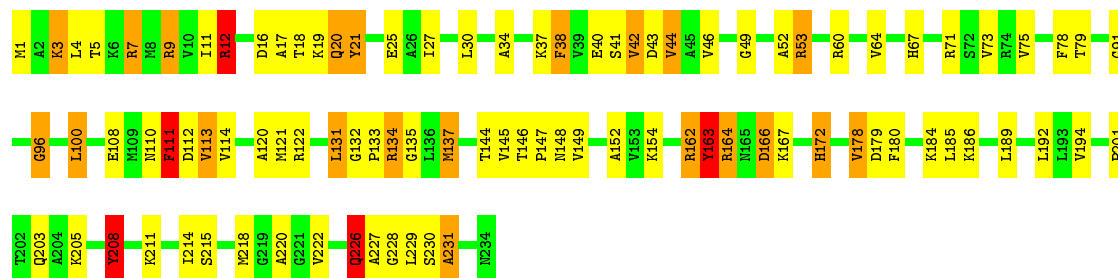
- Molecule 36: 50S ribosomal protein L31

Chain L2: 



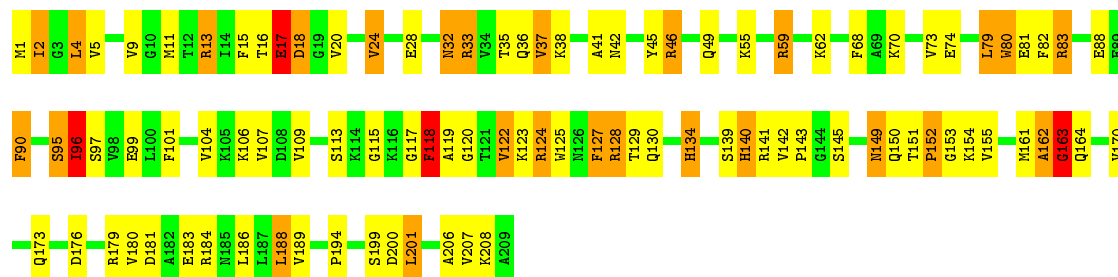
- Molecule 37: 50S ribosomal protein L1

Chain LC: 



- Molecule 38: 50S ribosomal protein L3

Chain LE: 

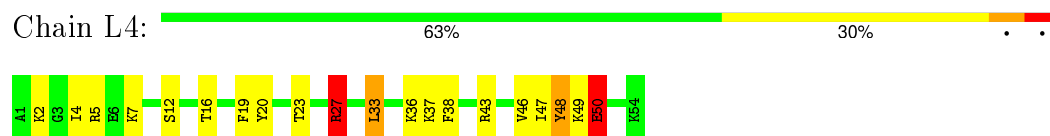


- Molecule 39: 50S ribosomal protein L32

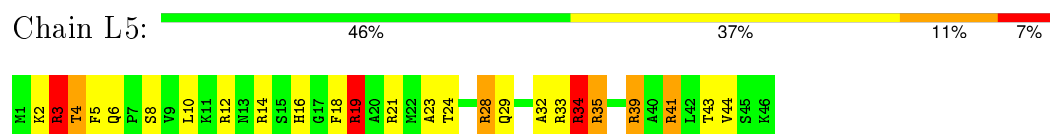
Chain L3: 



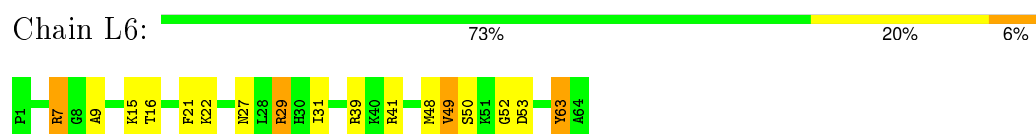
- Molecule 40: 50S ribosomal protein L33



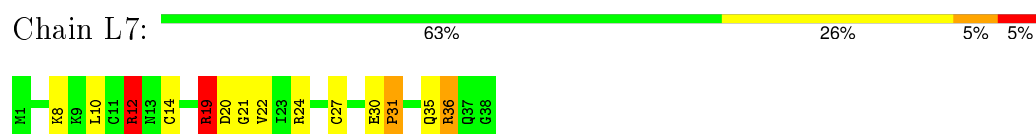
- Molecule 41: 50S ribosomal protein L34



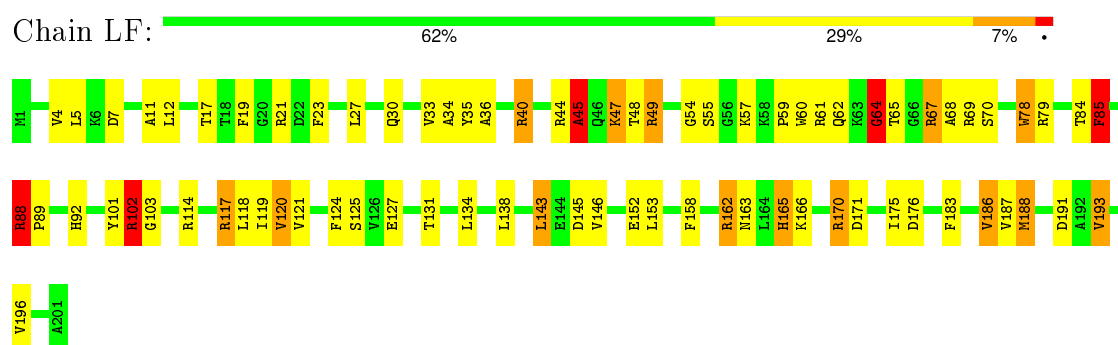
- Molecule 42: 50S ribosomal protein L35



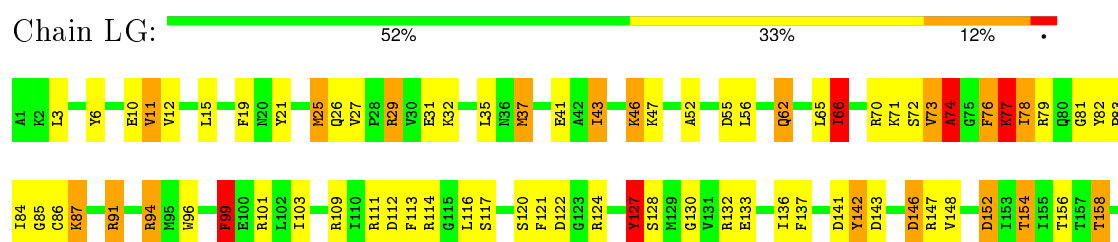
- Molecule 43: 50S ribosomal protein L36



- Molecule 44: 50S ribosomal protein L4



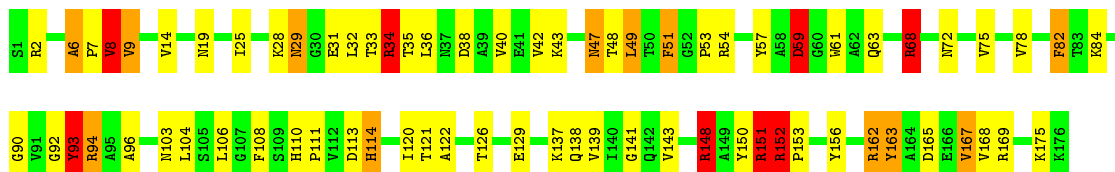
- Molecule 45: 50S ribosomal protein L5





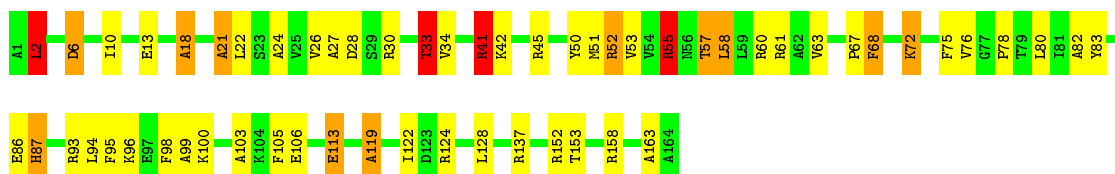
- Molecule 46: 50S ribosomal protein L6

Chain LH: 59% 30% 7% 5%



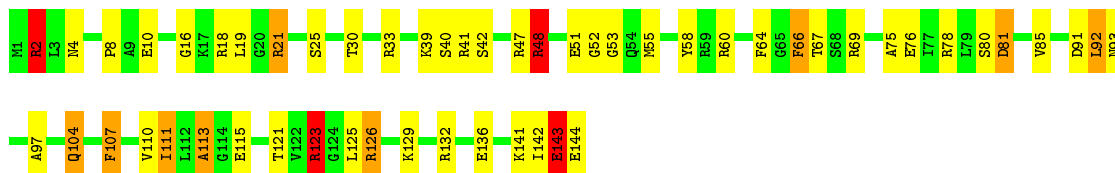
- Molecule 47: 50S ribosomal protein L10

Chain LJ: 65% 26% 7%



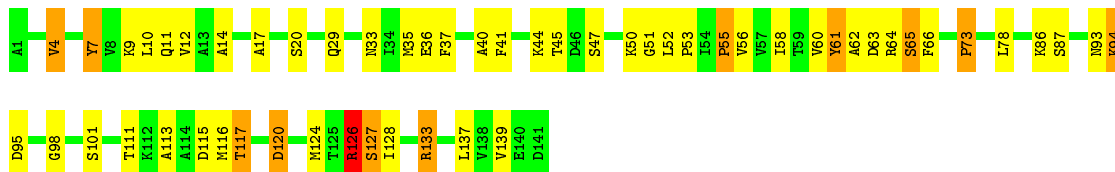
- Molecule 48: 50S ribosomal protein L15

Chain LN: 63% 28% 6%



- Molecule 49: 50S ribosomal protein L11

Chain LK: 61% 30% 8%



- Molecule 50: 50S ribosomal protein L13

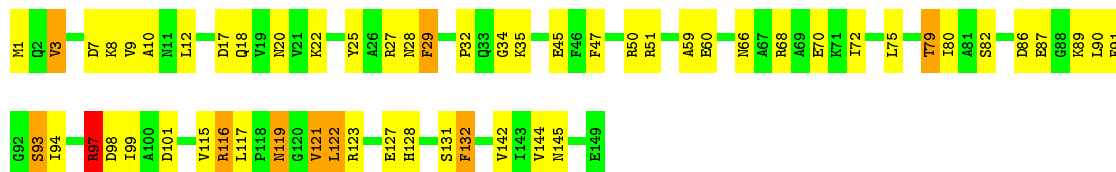
Chain LL: 60% 32% 8%





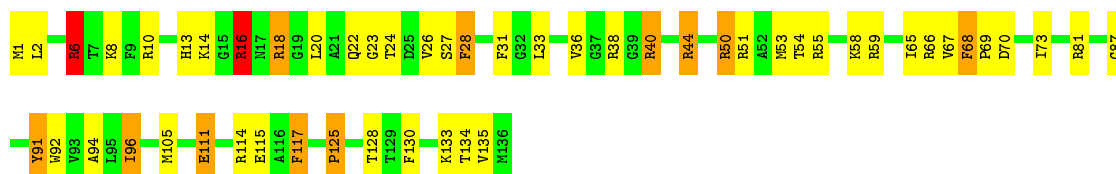
- Molecule 51: 50S ribosomal protein L9

Chain LI: 62% 32% 6% •



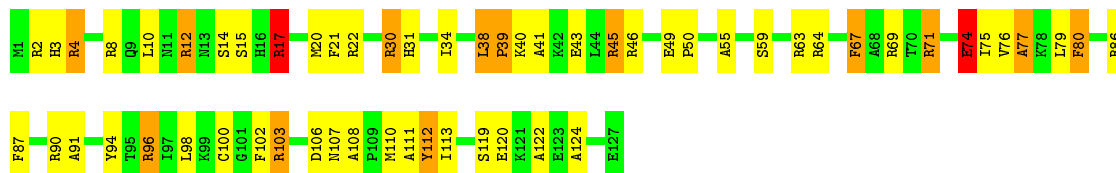
- Molecule 52: 50S ribosomal protein L16

Chain LO: 61% 29% 8% •



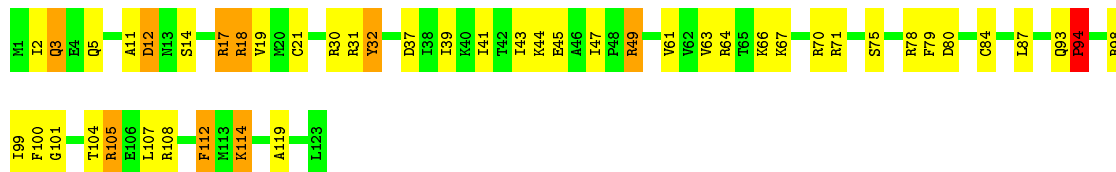
- Molecule 53: 50S ribosomal protein L17

Chain LP: 54% 34% 10% •



- Molecule 54: 50S ribosomal protein L14

Chain LM: 62% 30% 7% •



- Molecule 55: 50S ribosomal protein L18

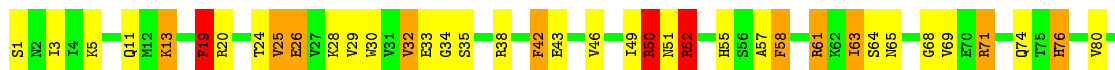
Chain LQ: 59% 28% 9% •





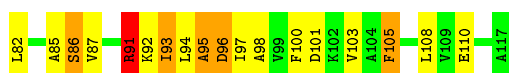
- Molecule 56: 50S ribosomal protein L19

Chain LR: 53% 32% 13%



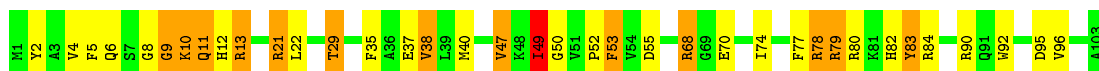
- Molecule 57: 50S ribosomal protein L20

Chain LS: 54% 29% 14%



- Molecule 58: 50S ribosomal protein L21

Chain LT: 64% 22% 13%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	50000	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	CTFFIND3 and CTFIT	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	55000	Depositor
Image detector	DIRECT ELECTRON DE-12 (4k x 3k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP

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	SS	1.56	2/744 (0.3%)	2.24	33/995 (3.3%)
10	SJ	1.65	8/835 (1.0%)	2.13	34/1127 (3.0%)
11	SK	1.67	8/982 (0.8%)	2.23	33/1323 (2.5%)
12	SL	1.66	6/969 (0.6%)	2.28	46/1300 (3.5%)
13	SM	1.61	3/919 (0.3%)	2.36	43/1226 (3.5%)
14	SN	1.59	6/817 (0.7%)	2.23	36/1088 (3.3%)
15	SO	1.56	5/724 (0.7%)	2.20	29/966 (3.0%)
16	SP	1.56	4/659 (0.6%)	2.17	25/884 (2.8%)
17	SQ	1.66	3/681 (0.4%)	2.07	20/913 (2.2%)
18	SB	1.61	10/1904 (0.5%)	2.05	63/2565 (2.5%)
19	SC	1.60	8/1852 (0.4%)	2.10	50/2490 (2.0%)
2	SA	3.39	5085/37035 (13.7%)	3.51	8259/57774 (14.3%)
20	SD	1.65	17/1665 (1.0%)	2.20	62/2227 (2.8%)
21	SE	1.60	8/1239 (0.6%)	2.11	38/1664 (2.3%)
22	SF	1.65	8/1121 (0.7%)	2.34	42/1509 (2.8%)
23	SR	1.71	9/637 (1.4%)	2.26	25/851 (2.9%)
24	S3	1.63	40/5532 (0.7%)	2.11	178/7485 (2.4%)
25	LB	3.37	384/2869 (13.4%)	3.42	601/4474 (13.4%)
26	LA	3.49	10162/69808 (14.6%)	3.51	15513/108905 (14.2%)
27	LD	1.64	14/2131 (0.7%)	2.20	72/2863 (2.5%)
28	LU	1.50	3/864 (0.3%)	2.05	25/1156 (2.2%)
29	LV	1.62	6/794 (0.8%)	2.08	29/1060 (2.7%)
3	S1	3.38	150/1108 (13.5%)	3.59	243/1724 (14.1%)
30	LW	1.58	4/797 (0.5%)	2.12	17/1062 (1.6%)
31	LX	1.61	4/766 (0.5%)	2.09	29/1025 (2.8%)
32	LY	1.71	4/642 (0.6%)	2.27	25/848 (2.9%)
33	LZ	1.74	6/635 (0.9%)	2.24	24/848 (2.8%)
34	L0	1.56	2/510 (0.4%)	2.31	24/677 (3.5%)
35	L1	1.56	2/453 (0.4%)	2.22	19/605 (3.1%)
36	L2	1.57	1/559 (0.2%)	2.11	15/745 (2.0%)
37	LC	1.62	11/1748 (0.6%)	2.15	59/2355 (2.5%)
38	LE	1.66	10/1586 (0.6%)	2.14	61/2134 (2.9%)



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	L3	1.63	2/450 (0.4%)	1.98	9/599 (1.5%)
4	S2	3.42	257/1831 (14.0%)	3.58	423/2853 (14.8%)
40	L4	1.67	4/448 (0.9%)	2.12	11/594 (1.9%)
41	L5	1.66	1/380 (0.3%)	2.65	31/498 (6.2%)
42	L6	1.53	1/513 (0.2%)	2.02	14/676 (2.1%)
43	L7	1.53	0/303	2.12	9/397 (2.3%)
44	LF	1.66	10/1571 (0.6%)	2.07	53/2113 (2.5%)
45	LG	1.60	5/1444 (0.3%)	2.28	64/1937 (3.3%)
46	LH	1.62	8/1343 (0.6%)	2.17	53/1816 (2.9%)
47	LJ	1.60	4/1247 (0.3%)	2.08	46/1679 (2.7%)
48	LN	1.56	5/1062 (0.5%)	2.24	42/1413 (3.0%)
49	LK	1.58	6/1046 (0.6%)	2.07	33/1410 (2.3%)
5	ST	1.63	4/676 (0.6%)	2.23	33/895 (3.7%)
50	LL	1.71	10/1152 (0.9%)	2.19	45/1551 (2.9%)
51	LI	1.58	4/1122 (0.4%)	2.10	30/1515 (2.0%)
52	LO	1.63	9/1093 (0.8%)	2.27	29/1460 (2.0%)
53	LP	1.69	11/1021 (1.1%)	2.21	45/1364 (3.3%)
54	LM	1.59	2/956 (0.2%)	2.32	35/1279 (2.7%)
55	LQ	1.67	6/910 (0.7%)	2.00	28/1219 (2.3%)
56	LR	1.72	8/929 (0.9%)	2.27	32/1242 (2.6%)
57	LS	1.62	6/960 (0.6%)	2.27	39/1278 (3.1%)
58	LT	1.62	2/829 (0.2%)	2.18	32/1107 (2.9%)
6	SU	1.70	5/598 (0.8%)	2.73	30/792 (3.8%)
7	SG	1.68	10/1422 (0.7%)	2.09	48/1908 (2.5%)
8	SH	1.58	5/989 (0.5%)	2.10	33/1326 (2.5%)
9	SI	1.67	6/1048 (0.6%)	2.18	43/1394 (3.1%)
All	All	2.97	16384/168928 (9.7%)	3.17	27062/251183 (10.8%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	SS	0	11
10	SJ	0	9
11	SK	0	7
12	SL	0	10
13	SM	0	8
14	SN	0	11
15	SO	0	7
16	SP	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
17	SQ	0	6
18	SB	0	13
19	SC	0	11
2	SA	0	979
20	SD	0	18
21	SE	0	11
22	SF	0	12
23	SR	0	9
24	S3	0	38
25	LB	0	68
26	LA	5	1948
27	LD	0	24
28	LU	0	8
29	LV	0	5
3	S1	0	36
30	LW	0	8
31	LX	0	5
32	LY	0	8
33	LZ	0	7
34	L0	0	2
35	L1	0	3
36	L2	0	9
37	LC	0	17
38	LE	0	15
39	L3	0	5
4	S2	0	48
40	L4	0	4
41	L5	0	7
42	L6	0	2
43	L7	0	4
44	LF	0	10
45	LG	0	15
46	LH	0	13
47	LJ	0	10
48	LN	0	12
49	LK	0	10
5	ST	0	5
50	LL	0	5
51	LI	0	7
52	LO	0	8
53	LP	0	10
54	LM	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
55	LQ	0	14
56	LR	0	11
57	LS	0	12
58	LT	0	8
6	SU	0	11
7	SG	0	19
8	SH	0	10
9	SI	0	7
All	All	5	3608

The worst 5 of 16384 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	SA	199	A	N7-C5	-23.19	1.25	1.39
26	LA	727	A	N7-C5	-22.32	1.25	1.39
26	LA	1791	A	N9-C4	-20.53	1.25	1.37
2	SA	298	A	N7-C5	-20.39	1.27	1.39
26	LA	743	A	N7-C5	-19.99	1.27	1.39

The worst 5 of 27062 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	SF	44	ARG	NE-CZ-NH1	30.21	135.41	120.30
26	LA	826	U	P-O3'-C3'	28.10	153.42	119.70
26	LA	2451	A	O4'-C1'-N9	27.95	130.56	108.20
26	LA	1005	C	C6-N1-C2	-25.59	110.06	120.30
26	LA	2899	A	N1-C6-N6	23.91	132.94	118.60

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
26	LA	2451	A	C1'
26	LA	2503	A	C2'
26	LA	2504	U	C2',C3'
26	LA	2575	C	C4'

5 of 3608 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	SS	1	PRO	Peptide
1	SS	10	ILE	Peptide
1	SS	2	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	SS	3	SER	Peptide
1	SS	8	PRO	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	SS	727	0	769	10	0
2	SA	33076	0	16190	637	0
3	S1	993	0	496	16	0
4	S2	1639	0	816	32	0
5	ST	670	0	722	2	0
6	SU	590	0	631	6	0
7	SG	1400	0	1449	13	0
8	SH	979	0	1034	5	0
9	SI	1036	0	1084	9	0
10	SJ	825	0	865	9	0
11	SK	965	0	997	13	0
12	SL	955	0	1019	10	0
13	SM	910	0	981	9	0
14	SN	805	0	847	5	0
15	SO	716	0	742	4	0
16	SP	649	0	666	3	0
17	SQ	672	0	716	2	0
18	SB	1872	0	1885	15	0
19	SC	1822	0	1913	13	0
20	SD	1643	0	1710	21	0
21	SE	1225	0	1273	18	0
22	SF	1101	0	1050	11	0
23	SR	626	0	651	6	0
24	S3	5431	0	5403	46	0
25	LB	2566	0	1269	48	0
26	LA	62330	0	30424	1516	0
27	LD	2092	0	2170	21	0
28	LU	857	0	922	5	0
29	LV	787	0	846	5	0
30	LW	789	0	847	9	0
31	LX	753	0	780	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	LY	634	0	655	16	0
33	LZ	625	0	655	2	0
34	L0	509	0	543	5	0
35	L1	449	0	491	3	0
36	L2	549	0	552	5	0
37	LC	1733	0	1824	19	0
38	LE	1565	0	1616	21	0
39	L3	444	0	461	8	0
40	L4	441	0	485	4	0
41	L5	377	0	418	7	0
42	L6	504	0	574	3	0
43	L7	302	0	343	3	0
44	LF	1552	0	1619	18	0
45	LG	1420	0	1460	16	0
46	LH	1323	0	1374	6	0
47	LJ	1233	0	1283	6	0
48	LN	1053	0	1129	7	0
49	LK	1032	0	1088	3	0
50	LL	1129	0	1162	9	0
51	LI	1111	0	1148	6	0
52	LO	1074	0	1157	17	0
53	LP	1008	0	1045	10	0
54	LM	947	0	1023	6	0
55	LQ	900	0	935	9	0
56	LR	917	0	965	5	0
57	LS	947	0	1022	15	0
58	LT	816	0	839	7	0
59	S3	32	0	12	0	0
All	All	156127	0	107045	2623	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 2623 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)
21:SE:123:LEU:HD13	21:SE:124:ALA:H	1.44	0.83
2:SA:1381:U:H1'	7:SG:152:HIS:CE1	2.16	0.80
26:LA:1853:A:H61	26:LA:2087:G:H1'	1.47	0.80
26:LA:1965:C:C2	26:LA:1966:A:H2'	2.18	0.78
2:SA:803:G:C5	2:SA:804:U:C4	2.72	0.78

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	SS	89/91 (98%)	71 (80%)	13 (15%)	5 (6%)	2	26
5	ST	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
6	SU	68/70 (97%)	46 (68%)	14 (21%)	8 (12%)	0	8
7	SG	176/178 (99%)	154 (88%)	14 (8%)	8 (4%)	3	31
8	SH	127/129 (98%)	103 (81%)	16 (13%)	8 (6%)	2	23
9	SI	127/129 (98%)	99 (78%)	22 (17%)	6 (5%)	3	30
10	SJ	101/103 (98%)	83 (82%)	11 (11%)	7 (7%)	1	20
11	SK	126/128 (98%)	102 (81%)	18 (14%)	6 (5%)	3	30
12	SL	121/123 (98%)	95 (78%)	14 (12%)	12 (10%)	1	12
13	SM	115/117 (98%)	97 (84%)	11 (10%)	7 (6%)	2	24
14	SN	98/100 (98%)	81 (83%)	12 (12%)	5 (5%)	2	28
15	SO	86/88 (98%)	76 (88%)	7 (8%)	3 (4%)	4	40
16	SP	80/82 (98%)	72 (90%)	4 (5%)	4 (5%)	3	29
17	SQ	81/83 (98%)	67 (83%)	9 (11%)	5 (6%)	2	24
18	SB	238/240 (99%)	212 (89%)	14 (6%)	12 (5%)	3	29
19	SC	230/232 (99%)	196 (85%)	18 (8%)	16 (7%)	1	20
20	SD	203/205 (99%)	166 (82%)	26 (13%)	11 (5%)	2	27
21	SE	164/166 (99%)	127 (77%)	24 (15%)	13 (8%)	1	16
22	SF	133/135 (98%)	114 (86%)	11 (8%)	8 (6%)	2	24
23	SR	72/74 (97%)	57 (79%)	10 (14%)	5 (7%)	1	20
24	S3	700/702 (100%)	611 (87%)	61 (9%)	28 (4%)	4	35
27	LD	270/272 (99%)	215 (80%)	42 (16%)	13 (5%)	3	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	LU	108/110 (98%)	95 (88%)	11 (10%)	2 (2%)	10	53
29	LV	98/100 (98%)	75 (76%)	13 (13%)	10 (10%)	1	11
30	LW	101/103 (98%)	84 (83%)	12 (12%)	5 (5%)	3	29
31	LX	92/94 (98%)	83 (90%)	5 (5%)	4 (4%)	3	33
32	LY	82/84 (98%)	57 (70%)	15 (18%)	10 (12%)	0	8
33	LZ	75/77 (97%)	63 (84%)	10 (13%)	2 (3%)	6	46
34	L0	61/63 (97%)	51 (84%)	8 (13%)	2 (3%)	5	41
35	L1	56/58 (97%)	45 (80%)	7 (12%)	4 (7%)	1	19
36	L2	68/70 (97%)	44 (65%)	15 (22%)	9 (13%)	0	6
37	LC	232/234 (99%)	192 (83%)	29 (12%)	11 (5%)	3	30
38	LE	207/209 (99%)	151 (73%)	34 (16%)	22 (11%)	0	10
39	L3	54/56 (96%)	40 (74%)	7 (13%)	7 (13%)	0	7
40	L4	52/54 (96%)	45 (86%)	5 (10%)	2 (4%)	4	37
41	L5	44/46 (96%)	34 (77%)	7 (16%)	3 (7%)	1	21
42	L6	62/64 (97%)	53 (86%)	8 (13%)	1 (2%)	12	56
43	L7	36/38 (95%)	26 (72%)	5 (14%)	5 (14%)	0	6
44	LF	199/201 (99%)	163 (82%)	21 (11%)	15 (8%)	1	17
45	LG	176/178 (99%)	133 (76%)	26 (15%)	17 (10%)	1	12
46	LH	174/176 (99%)	127 (73%)	29 (17%)	18 (10%)	1	11
47	LJ	162/164 (99%)	143 (88%)	11 (7%)	8 (5%)	3	29
48	LN	142/144 (99%)	116 (82%)	22 (16%)	4 (3%)	6	45
49	LK	139/141 (99%)	114 (82%)	17 (12%)	8 (6%)	2	25
50	LL	140/142 (99%)	116 (83%)	14 (10%)	10 (7%)	1	19
51	LI	147/149 (99%)	121 (82%)	16 (11%)	10 (7%)	1	21
52	LO	134/136 (98%)	111 (83%)	14 (10%)	9 (7%)	1	21
53	LP	125/127 (98%)	109 (87%)	10 (8%)	6 (5%)	3	30
54	LM	121/123 (98%)	91 (75%)	18 (15%)	12 (10%)	1	12
55	LQ	115/117 (98%)	108 (94%)	5 (4%)	2 (2%)	11	55
56	LR	112/114 (98%)	79 (70%)	17 (15%)	16 (14%)	0	5
57	LS	115/117 (98%)	104 (90%)	5 (4%)	6 (5%)	2	27
58	LT	101/103 (98%)	87 (86%)	11 (11%)	3 (3%)	5	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	7019/7125 (98%)	5781 (82%)	805 (12%)	433 (6%)	4	24

5 of 433 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	SS	11	ASP
1	SS	37	SER
1	SS	75	PRO
6	SU	10	PRO
6	SU	18	PHE

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	SS	78/78 (100%)	65 (83%)	13 (17%)	3	19
5	ST	65/65 (100%)	60 (92%)	5 (8%)	16	56
6	SU	60/60 (100%)	54 (90%)	6 (10%)	9	43
7	SG	146/146 (100%)	134 (92%)	12 (8%)	14	53
8	SH	104/104 (100%)	90 (86%)	14 (14%)	5	29
9	SI	106/106 (100%)	91 (86%)	15 (14%)	4	27
10	SJ	90/90 (100%)	80 (89%)	10 (11%)	8	38
11	SK	98/98 (100%)	90 (92%)	8 (8%)	14	53
12	SL	103/103 (100%)	97 (94%)	6 (6%)	25	66
13	SM	95/95 (100%)	81 (85%)	14 (15%)	4	25
14	SN	83/83 (100%)	78 (94%)	5 (6%)	24	65
15	SO	76/76 (100%)	69 (91%)	7 (9%)	11	48
16	SP	65/65 (100%)	58 (89%)	7 (11%)	8	40
17	SQ	77/77 (100%)	75 (97%)	2 (3%)	54	83
18	SB	198/198 (100%)	183 (92%)	15 (8%)	16	56
19	SC	189/189 (100%)	170 (90%)	19 (10%)	9	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	SD	172/172 (100%)	152 (88%)	20 (12%)	7	36
21	SE	125/125 (100%)	111 (89%)	14 (11%)	7	38
22	SF	116/116 (100%)	103 (89%)	13 (11%)	7	38
23	SR	64/64 (100%)	58 (91%)	6 (9%)	11	47
24	S3	575/575 (100%)	514 (89%)	61 (11%)	8	40
27	LD	217/217 (100%)	188 (87%)	29 (13%)	5	29
28	LU	93/93 (100%)	82 (88%)	11 (12%)	6	34
29	LV	84/84 (100%)	77 (92%)	7 (8%)	14	52
30	LW	84/84 (100%)	80 (95%)	4 (5%)	31	72
31	LX	78/78 (100%)	70 (90%)	8 (10%)	9	42
32	LY	62/62 (100%)	54 (87%)	8 (13%)	5	31
33	LZ	67/67 (100%)	55 (82%)	12 (18%)	2	15
34	L0	55/55 (100%)	49 (89%)	6 (11%)	8	39
35	L1	48/48 (100%)	39 (81%)	9 (19%)	2	13
36	L2	62/62 (100%)	52 (84%)	10 (16%)	3	21
37	LC	181/181 (100%)	164 (91%)	17 (9%)	11	47
38	LE	164/164 (100%)	143 (87%)	21 (13%)	5	31
39	L3	47/47 (100%)	43 (92%)	4 (8%)	13	52
40	L4	48/48 (100%)	44 (92%)	4 (8%)	14	52
41	L5	38/38 (100%)	35 (92%)	3 (8%)	15	54
42	L6	51/51 (100%)	48 (94%)	3 (6%)	24	66
43	L7	34/34 (100%)	32 (94%)	2 (6%)	24	66
44	LF	165/165 (100%)	153 (93%)	12 (7%)	17	58
45	LG	149/149 (100%)	133 (89%)	16 (11%)	8	40
46	LH	137/137 (100%)	119 (87%)	18 (13%)	5	30
47	LJ	122/122 (100%)	109 (89%)	13 (11%)	8	40
48	LN	103/103 (100%)	87 (84%)	16 (16%)	3	23
49	LK	109/109 (100%)	93 (85%)	16 (15%)	4	25
50	LL	116/116 (100%)	108 (93%)	8 (7%)	19	60
51	LI	114/114 (100%)	99 (87%)	15 (13%)	5	30
52	LO	109/109 (100%)	96 (88%)	13 (12%)	6	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	LP	103/103 (100%)	95 (92%)	8 (8%)	16	55
54	LM	104/104 (100%)	99 (95%)	5 (5%)	31	72
55	LQ	87/87 (100%)	80 (92%)	7 (8%)	15	54
56	LR	99/99 (100%)	87 (88%)	12 (12%)	6	33
57	LS	89/89 (100%)	78 (88%)	11 (12%)	6	32
58	LT	84/84 (100%)	78 (93%)	6 (7%)	18	59
All	All	5788/5788 (100%)	5182 (90%)	606 (10%)	13	41

5 of 606 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	LD	42	ARG
33	LZ	7	THR
53	LP	75	ILE
27	LD	116	GLN
28	LU	72	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
31	LX	87	GLN
36	L2	20	ASN
53	LP	107	ASN
31	LX	88	HIS
33	LZ	19	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	SA	1541/1542 (99%)	362 (23%)	122 (7%)
25	LB	119/120 (99%)	21 (17%)	9 (7%)
26	LA	2903/2904 (99%)	645 (22%)	221 (7%)
3	S1	46/47 (97%)	36 (78%)	12 (26%)
4	S2	77/77 (100%)	20 (25%)	10 (12%)
All	All	4686/4690 (99%)	1084 (23%)	374 (7%)

5 of 1084 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	SA	3	A
2	SA	4	U
2	SA	5	U
2	SA	8	A
2	SA	9	G

5 of 374 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	LA	140	C
26	LA	669	G
26	LA	2547	A
26	LA	231	A
26	LA	455	C

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is 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
59	GTP	S3	801	-	26,34,34	1.83	7 (26%)	29,54,54	2.56	8 (27%)

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
59	GTP	S3	801	-	-	0/18/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	S3	801	GTP	C8-N7	-4.38	1.26	1.34
59	S3	801	GTP	PG-O2G	-2.40	1.46	1.54
59	S3	801	GTP	C2-N2	-2.19	1.29	1.34
59	S3	801	GTP	PA-O2A	-2.09	1.46	1.55
59	S3	801	GTP	C6-C5	2.09	1.45	1.41

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	S3	801	GTP	C5-C6-N1	-8.14	112.88	123.52
59	S3	801	GTP	C6-C5-C4	-5.33	114.77	120.86
59	S3	801	GTP	O5'-PA-O1A	-3.14	96.38	109.21
59	S3	801	GTP	O4'-C4'-C3'	-2.74	99.61	105.16
59	S3	801	GTP	N3-C2-N1	-2.34	124.37	127.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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.