



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:53 PM BST

PDB ID : 4V5M
EMDB ID: : EMD-1798
Title : tRNA tranlocation on the 70S ribosome: the pre-translocational translocation intermediate TI(PRE)
Authors : Ratje, A.H.; Loerke, J.; Mikolajka, A.; Bruenner, M.; Hildebrand, P.W.; Starosta, A.L.; Doenhoefer, A.; Connell, S.R.; Fucini, P.; Mielke, T.; Whitford, P.C.; Onuchic, J.N.; Yu, Y.; Sanbonmatsu, K.Y.; Hartmann, R.K.; Penczek, P.A.; Wilson, D.N.; Spahn, C.M.T.
Deposited on : 2010-10-01
Resolution : 7.80 Å(reported)
Based on PDB ID : 2WRI,2WRJ

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>

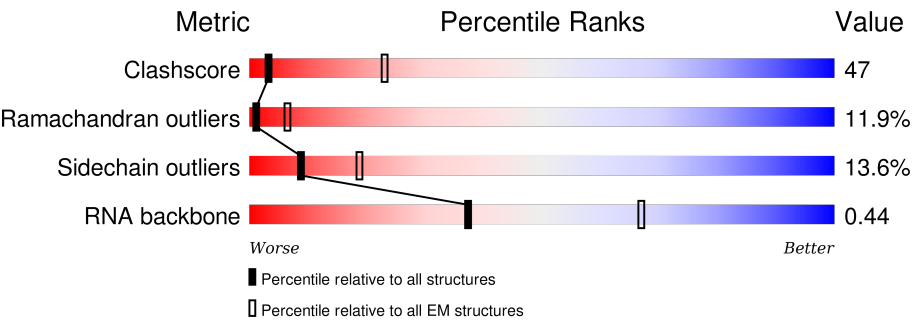
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 7.80 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.



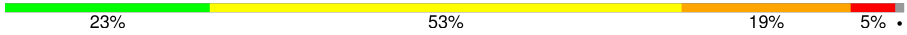


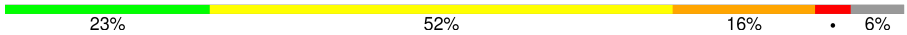

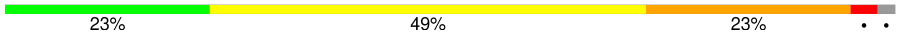

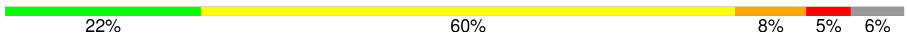
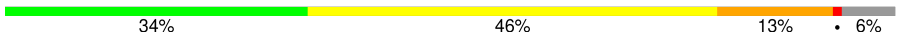
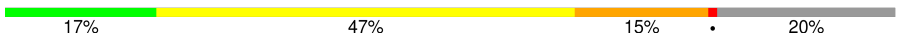
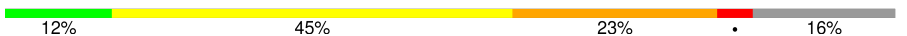
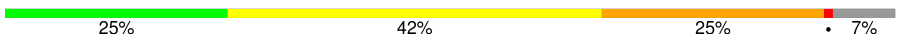
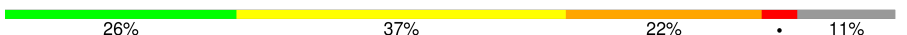


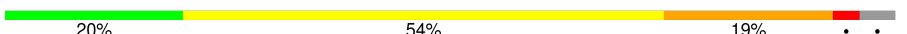



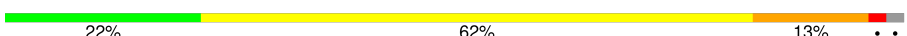

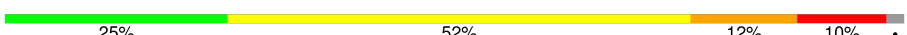



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	AA	1522	<div><div>24%</div><div>57%</div><div>17%</div><div></div></div>
2	AB	256	<div><div>23%</div><div>48%</div><div>16%</div><div>9%</div></div>
3	AC	239	<div><div>22%</div><div>46%</div><div>14%</div><div>14%</div></div>
4	AD	209	<div><div>29%</div><div>49%</div><div>17%</div><div></div></div>
5	AE	162	<div><div>27%</div><div>52%</div><div>13%</div><div>7%</div></div>
6	AF	101	<div><div>24%</div><div>52%</div><div>16%</div><div>8%</div></div>
7	AG	156	<div><div>29%</div><div>53%</div><div>12%</div><div>6%</div></div>
8	AH	138	<div><div>29%</div><div>58%</div><div>10%</div><div></div></div>

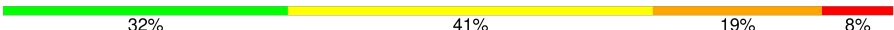
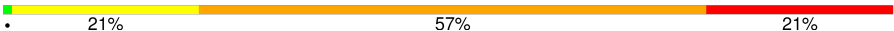


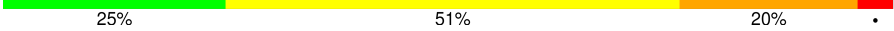
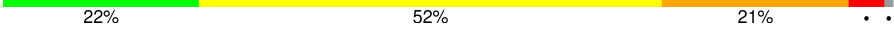
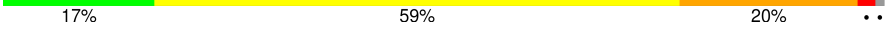


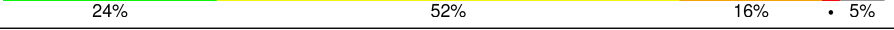
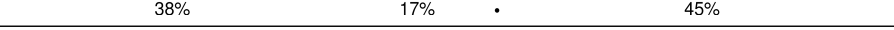


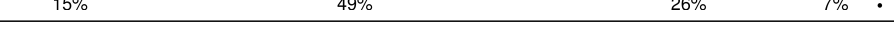
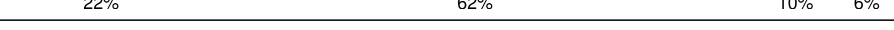
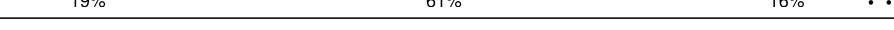


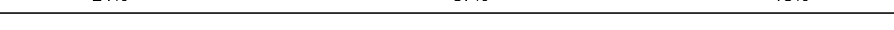


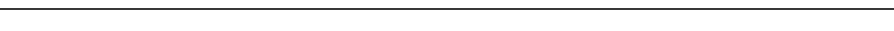


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Mol	Chain	Length	Quality of chain
9	AI	128	
10	AJ	105	
11	AK	129	
12	AL	132	
13	AM	126	
14	AN	61	
15	AO	89	
16	AP	88	
17	AQ	105	
18	AR	88	
19	AS	93	
20	AT	106	
21	AU	27	
22	AV	77	
23	AX	11	
24	AY	691	
25	B0	85	
26	B1	98	
27	B2	72	
28	B3	60	
29	B4	71	
30	B5	60	
31	B6	54	
32	B7	49	
33	B8	65	

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Mol	Chain	Length	Quality of chain
34	B9	37	
35	BA	2915	
36	BB	122	
37	BC	229	
38	BD	276	
39	BE	206	
40	BF	210	
41	BG	182	
42	BH	180	
43	BK	147	
44	BL	121	
45	BN	140	
46	BO	122	
47	BP	150	
48	BQ	141	
49	BR	118	
50	BS	112	
51	BT	146	
52	BU	118	
53	BV	101	
54	BW	113	
55	BX	96	
56	BY	110	
57	BZ	206	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 152777 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 RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1504	Total	C	N	O	P	0	0
			32329	14390	5992	10444	1503		

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	234	Total	C	N	O	S	0	0
			1900	1213	341	341	5		

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0
			1612	1016	314	281	1		

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	150	Total	C	N	O	S	0	0
			1146	724	217	201	4		

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	127	Total	C	N	O	S	0	0
			1010	639	197	174			

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0
			794	499	156	138	1		

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	124	Total	C	N	O	S	0	0
			970	611	195	163	1		

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	124	Total	C	N	O	S	0	0
			987	611	205	169	2		

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14 TYPE Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	83	Total	C	N	O	S	0	0
			700	443	139	117	1		

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	99	Total	C	N	O	S	0	0
			823	528	151	142	2		

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	70	Total	C	N	O		0	0
			574	367	112	95			

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	78	Total	C	N	O	S	0	0
			629	403	114	110	2		

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN THX.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	AU	24	Total	C	N	O	0	0
			208	128	50	30		

- Molecule 22 is a RNA chain called TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 23 is a RNA chain called MRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AX	11	Total	C	N	O	P	0	0
			230	105	41	74	10		

- Molecule 24 is a protein called ELONGATION FACTOR G.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AY	666	Total	C	N	O	S	0	0
			5214	3316	892	988	18		

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B0	84	Total	C	N	O	S	0	0
			662	410	140	111	1		

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B1	93	Total	C	N	O	S	0	0
			731	460	145	125	1		

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B2	71	Total	C	N	O	S	0	0
			598	370	121	106	1		

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B3	59	Total	C	N	O	S	0	0
			467	298	90	78	1		

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B4	57	Total	C	N	O	S	0	0
			450	285	77	83	5		

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B5	59	Total	C	N	O	S	0	0
			459	288	90	76	5		

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B6	50	Total	C	N	O	S	0	0
			433	270	88	71	4		

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B7	48	Total	C	N	O	S	0	0
			418	257	104	55	2		

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B8	63	Total	C	N	O	S	0	0
			507	326	101	78	2		

- Molecule 34 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B9	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 35 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BA	2901	Total	C	N	O	P	0	0
			62474	27806	11681	20087	2900		

- Molecule 36 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BB	119	Total	C	N	O	P	0	0
			2551	1136	471	826	118		

- Molecule 37 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	228	Total	C	N	O	S	0	0
			1742	1101	319	319	3		

- Molecule 38 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BD	275	Total	C	N	O	S	0	0
			2145	1353	428	361	3		

- Molecule 39 is a protein called 50S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BE	204	Total	C	N	O	S	0	0
			1563	988	299	270	6		

- Molecule 40 is a protein called 50S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BF	207	Total	C	N	O	S	0	0
			1623	1035	303	282	3		

- Molecule 41 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BG	181	Total	C	N	O	S	0	0
			1474	942	268	260	4		

- Molecule 42 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BH	166	Total	C	N	O	S	0	0
			1268	803	237	227	1		

- Molecule 43 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BK	139	Total	C	N	O	S	0	0
			1025	653	181	186	5		

- Molecule 44 is a protein called 50S RIBOSOMAL PROTEIN L7/L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	BL	67	Total	C	N	O	0	0
			477	301	81	95		

- Molecule 45 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BN	138	Total	C	N	O	S	0	0
			1104	712	206	182	4		

- Molecule 46 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BO	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

- Molecule 47 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BP	146	Total	C	N	O	S	0	0
			1114	692	227	193	2		

- Molecule 48 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BQ	141	Total	C	N	O	S	0	0
			1122	715	212	188	7		

- Molecule 49 is a protein called 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	BR	117	Total	C	N	O	0	0
			960	599	202	159		

- Molecule 50 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	BS	98	Total	C	N	O	0	0
			770	486	154	130		

- Molecule 51 is a protein called 50S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BT	137	Total	C	N	O	S	0	0
			1141	710	234	196	1		

- Molecule 52 is a protein called 50S RIBOSOMAL PROTEIN L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BU	117	Total	C	N	O	S	0	0
			958	604	202	151	1		

- Molecule 53 is a protein called 50S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BV	101	Total	C	N	O	S	0	0
			779	501	142	135	1		

- Molecule 54 is a protein called 50S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BW	113	Total	C	N	O	S	0	0
			896	563	176	155	2		

- Molecule 55 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	BX	92	Total	C	N	O	0	0
			725	471	131	123		

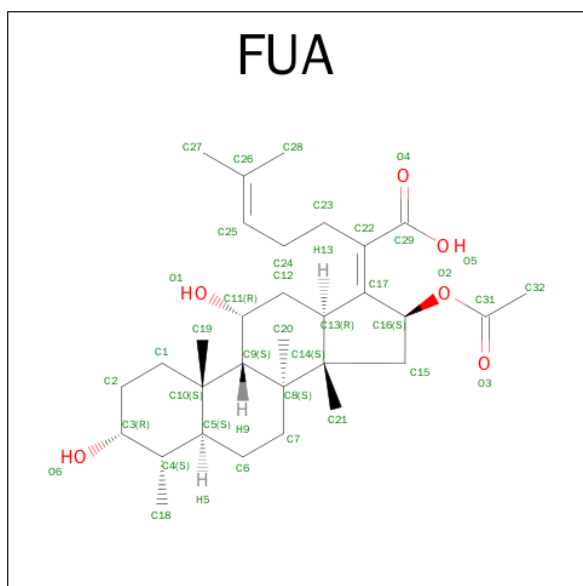
- Molecule 56 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BY	106	Total	C	N	O	S	0	0
			810	520	154	131	5		

- Molecule 57 is a protein called 50S RIBOSOMAL PROTEIN L25.

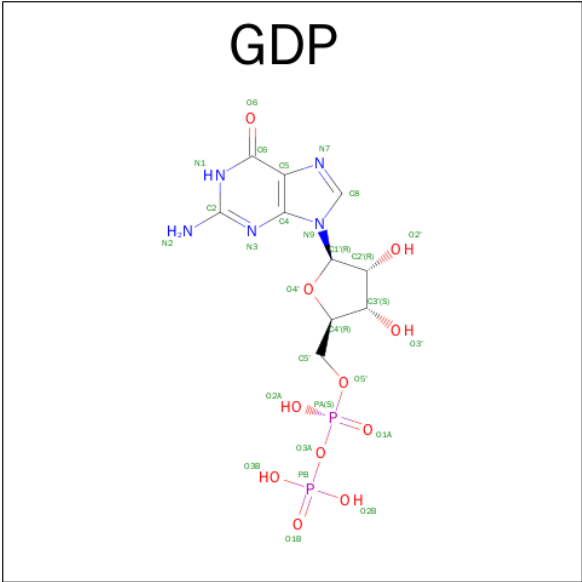
Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	184	Total	C	N	O	S	0	0
			1467	936	261	268	2		

- Molecule 58 is FUSIDIC ACID (three-letter code: FUA) (formula: $C_{31}H_{48}O_6$).



Mol	Chain	Residues	Atoms			AltConf
58	AY	1	Total	C	O	0
			37	31	6	

- Molecule 59 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

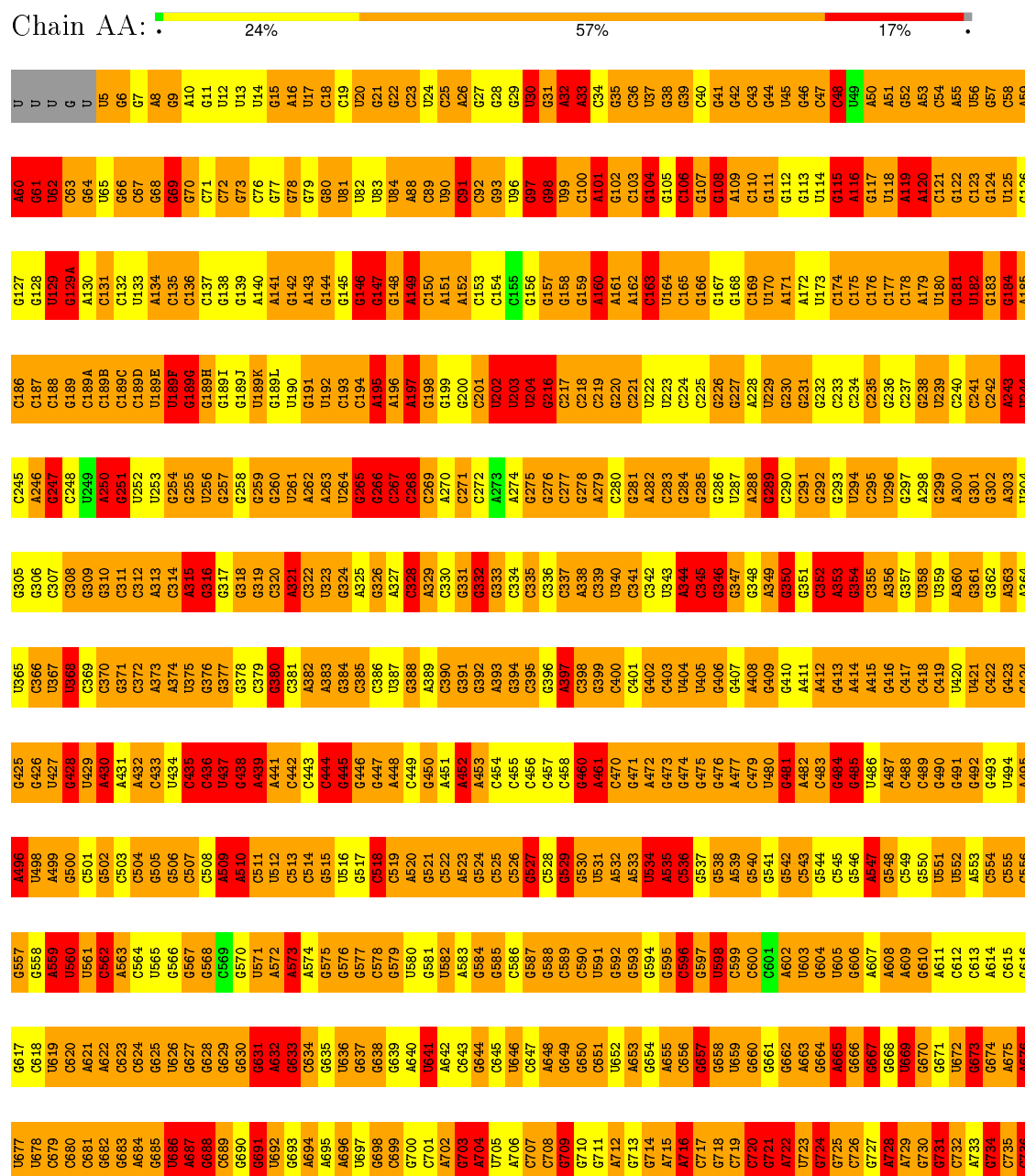


Mol	Chain	Residues	Atoms					AltConf
59	AY	1	Total	C	N	O	P	0
			28	10	5	11	2	

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: 16S rRNA



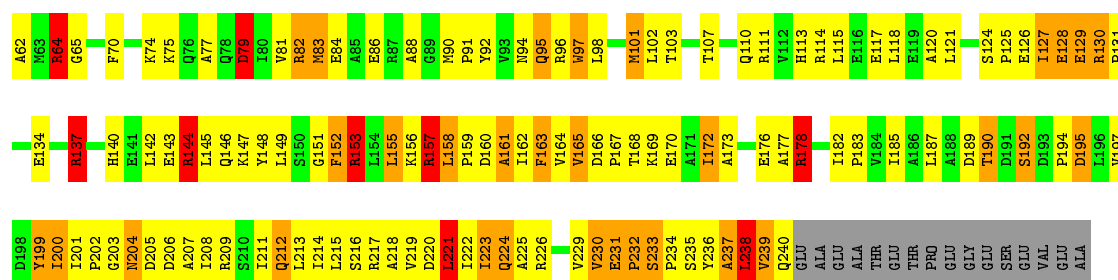
G1523	G1463	A1398	A1339	A1279	U1219	C1458	C1098	C1038	A983	A923	U863	C797	A737
C1524	G1464	C1399	A1340	A1280	G1220	U1159	G1099	C1039	C984	C924	A864	G798	C738
G1525	C1465	C1400	C1341	A1281	G1221	G1160	C1100	U1040	A986	G926	A865	G799	C739
G1526	C1466	G1401	C1342	C1282	G1222	C1161	A1101	A1041	G987	G927	C867	U801	G740
C1527	G1467	C1402	C1343	G1283	C1223	C1163	C1103	G1043	G988	G928	C868	A802	G741
U1528	C1468	C1403	C1344	G1284	G1224	G1164	C1104	A1044	C989	G929	C869	G803	G742
G1529	G1469	G1404	U1345	A1285	A1225	A1226	A1105	C1045	C990	G930	U870	U804	U743
G1530	G1470	U1405	A1346	A1286	C1226	G1166	G1106	A1046	U991	C931	U871	C805	C744
A1531	G1471	U1406	G1347	A1287	A1227	G1167	G1107	G1047	U992	G932	U872	C806	A746
U	U1472	C1407	A1348	A1288	C1228	C1168	C1108	A1048	G993	G933	A873	A807	C747
L11	A1473	A1408	U1349	A1289	G1229	A1169	G1109	U1049	A994	C934	G874	C808	G748
E12	G1474	G1409	A1350	G1290	C1230	A1170	A1110	G1050	C995	A935	C875	G809	C749
A13	G1475	G1410	U1351	G1291	G1231	G1171	A1111	C1051	A996	C936	G876	C810	G750
G14	G1476	C1411	C1352	U1292	U1232	G1172	A1112	U1052	U997	G937	C877	C811	U751
V15	C1477	C1412	G1353	G1293	G1233	G1173	C1113	G1053	A998	A938	C878	C812	G752
H16	C1478	A1413	C1354	G1294	C1234	G1174	C1114	G1054	C999	G939	C879	U813	A753
F17	C1479	U1414	G1355	G1295	U1235	G1175	C1115	A1055	U1000	C940	C880	A814	C754
G18	G1480	G1415	G1356	C1296	A1236	A1176	C1116	U1056	A1001	G941	C881	A815	G755
H19	U1481	G1416	A1357	C1297	C1237	G1177	C1117	G1057	G1001A	G942	C882	A816	C756
E20	G1417	G1417	C1358	C1298	A1238	G1178	C1118	G1058	U1002	U943	C883	C817	U757
R21	A1482	A1418	U1359	A1299	A1239	A1179	C1119	C1059	G1003	G944	U884	G818	G758
K22	C1483	G1419	A1360	G1300	U1240	A1180	C1120	C1060	A1004	G945	U885	A819	G759
R23	U1485	C1420	G1361	U1301	G1241	A1181	G1121	G1061	G1010	U951	U891	G820	G760
W24	G1486	G1421	C1362	U1302	C1242	G1182	U1122	G1062	A1005	U952	C892	G821	G761
N25	G1487	G1422	C1363	C1303	C1243	A1183	U1123	C1063	C1006	G947	C887	C822	G762
P26	G1488	G1423	A1363A	G1304	G1244	G1184	A1123	G1064	C1007	C948	G888	G823	G763
K27	G1489	C1424	U1364	G1305	A1245	G1185	G1124	U1065	C1008	A949	U889	G824	G764
F28	U1490	U1425	G1365	A1306	C1246	G1186	U1125	U1066	G1009	U956	C890	G825	G765
A29	G1491	C1426	C1366	U1307	U1247	G1187	U1126	C1066	G1011	U957	C897	G830	G770
R30	A1492	U1427	C1367	U1308	A1248	A1188	G1127	U1073	G1017	A958	C898	G832	U772
Y31	G1493	G1428	G1368	G1309	G1249	A1189	C1128	C1068	U1012	G953	C893	G826	A766
I32	G1494	C1429	C1369	G1310	A1250	G1190	C1129	C1069	G894	G954	C894	U827	A767
Y33	U1495	U1430	G1370	G1311	A1251	A1191	A1130	U1070	U955	U956	C896	G830	G770
A34	C1496	C1431	G1371	U1312	A1252	G1192	G1131	G1071	A1015	U957	C897	U831	G771
E35	G1497	G1432	U1372	G1313	G1253	G1193	C1132	G1072	A1016	U958	C898	G832	U772
L44	G1504	C1438	G1373	C1314	C1254	U1194	G1133	U1073	G1017	A959	C899	U833	G773
Q45	U1505	C1440	A1374	U1315	G1255	C1195	G1134	C1074	C1018	U960	A900	C834	G774
K46	U1506	G1441	G1375	G1316	A1256	U1196	U1135	C1075	C1019	U961	A901	U835	G775
T47	G1442	G1442	C1382	C1322	C1262	G1202	C1141	G1081	U1025	C966	C907	C840	A780
M48	G1508	G1442A	C1383	A1324	C1263	C1203	G1142	G1082	G1026	C967	A907	U841	A781
E49	A1442B	A1442B	C1384	C1325	G1264	A1204	G1143	U1083	C1027	A968	A908	C848	A782
E50	U1510	G1443	G1385	C1326	G1265	U1205	G1144	G1084	C1028	A969	A909	C849	C783
L51	C1444	C1444	G1386	C1327	G1266	G1206	C1145	U1085	C1029	C970	C910	U850	C784
E52	U1512	U1445	G1387	C1328	C1267	G1207	A1146	U1086	G1030	G971	U911	G851	G785
R53	A1513	U1446	C1388	C1329	A1268	C1208	C1147	G1087	G1030A	C972	C912	G852	G786
T54	C1514	A1447	C1389	A1329	A1269	C1209	U1148	G1088	C1030B	G973	A913	G853	A787
F55	C1515	C1452	U1390	U1330	C1270	C1210	U1149	G1089	C1030C	A974	A914	G854	U788
R56	G1516	G1456	G1391	A1332	G1271	U1211	U1150	U1090	A1030D	A975	A915	G855	U789
F57	G1517	G1457	G1392	A1333	G1272	U1212	A1151	U1091	G1031	G976	G916	C856	A790
L58	A1518	G1458	G1393	G1334	G1273	A1152	C1153	A1092	G1032	A977	G917	C857	G791
E59	C1459	C1458	A1394	G1335	G1274	C1213	G1154	A1093	G1033	C979	A918	G858	A792
D60	G1520	A1460	C1395	C1336	A1275	G1215	G1155	G1094	G1034	C980	A919	A859	U793
L61	U1522	G1461	A1396	C1337	C1277	C1216	G1156	C1095	G1035	U981	U920	G861	C795
			C1397	G1338	U1278	C1218	A1157	C1097	C1037	U982	G922	C862	C796

● Molecule 2: 30S RIBOSOMAL PROTEIN S2

Chain AB:

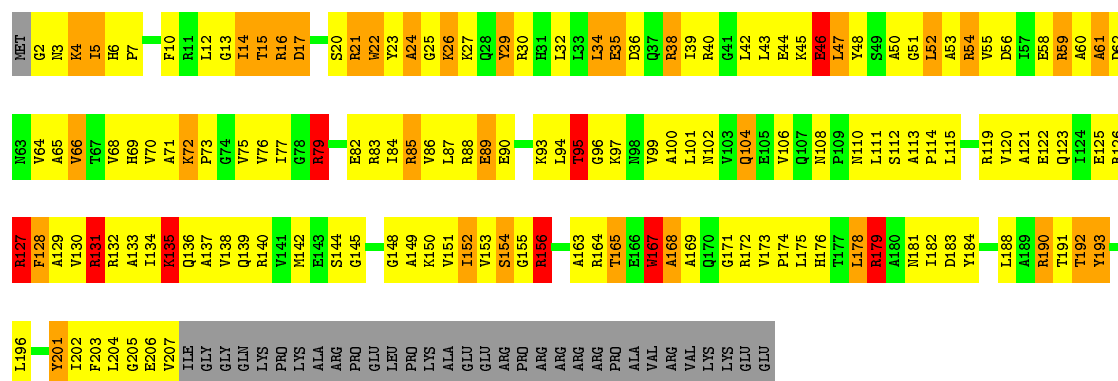


MET	L10	E12	A13	G14	V15	H16	F17	G18	H19	E20	R21	K22	R23	W24	N25	P26	K27	F28	A29	R30	Y31	I32	Y33	A34	E35	R36	I39	H40	I41	I42	D43	L44	Q45	K46	T47	M48	E49	E50	L51	E52	R53	T54	F55	R56	F57	L58	E59	D60	L61
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



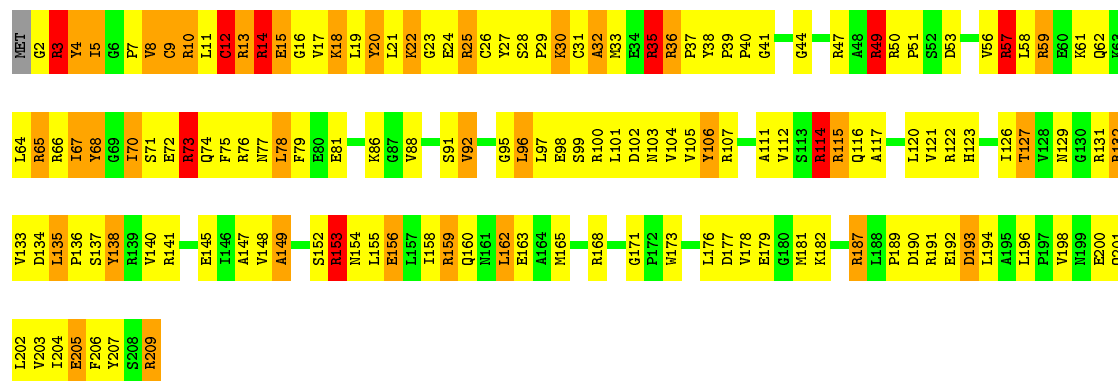
• Molecule 3: 30S RIBOSOMAL PROTEIN S3

Chain AC: 22% 46% 14% 14%



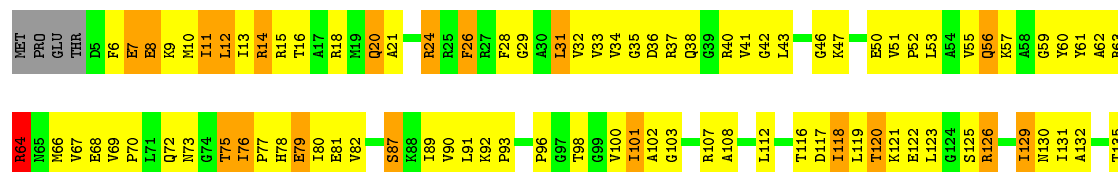
• Molecule 4: 30S RIBOSOMAL PROTEIN S4

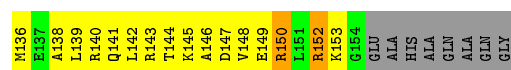
Chain AD: 29% 49% 17% 5%



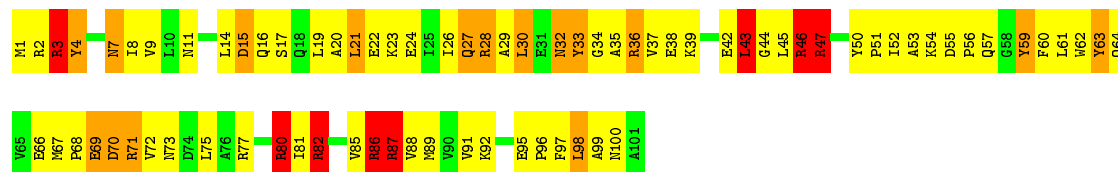
• Molecule 5: 30S RIBOSOMAL PROTEIN S5

Chain AE: 27% 52% 13% 7%

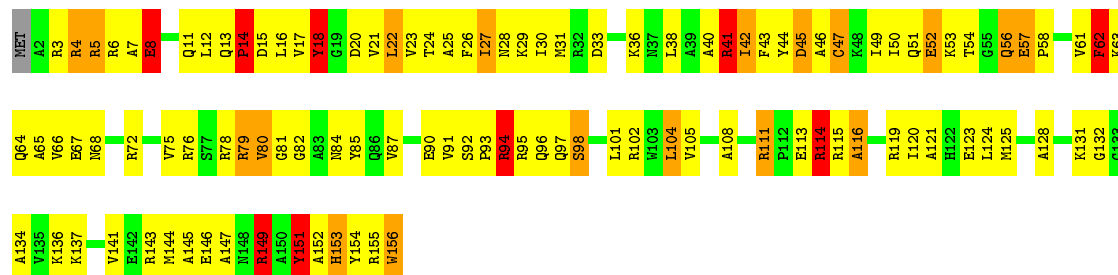




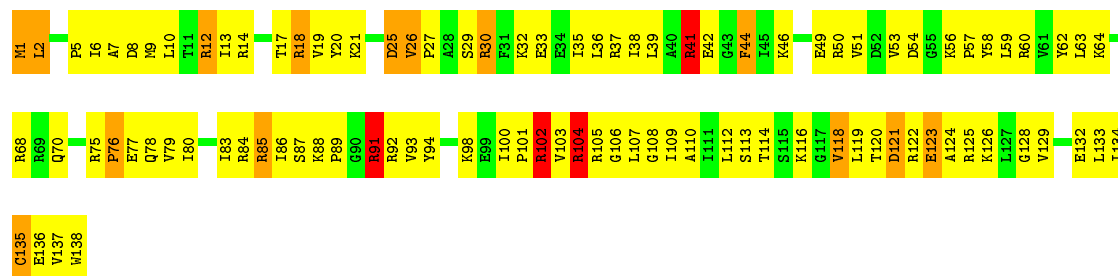
• Molecule 6: 30S RIBOSOMAL PROTEIN S6



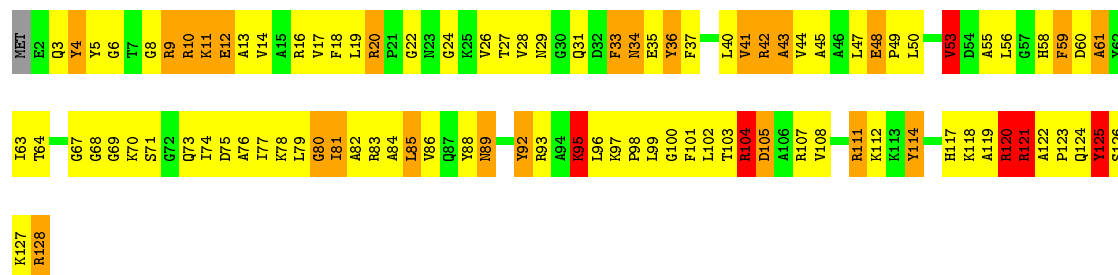
• Molecule 7: 30S RIBOSOMAL PROTEIN S7



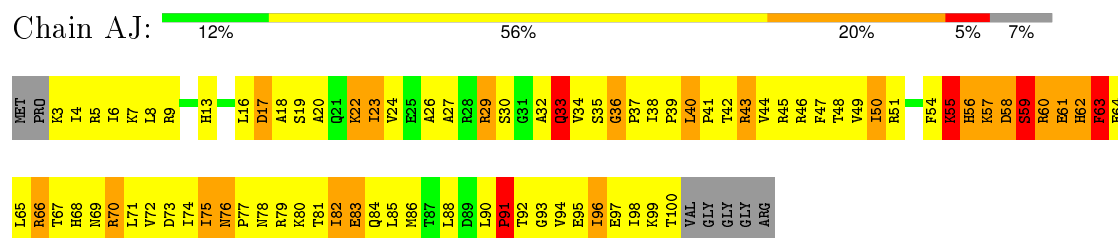
• Molecule 8: 30S RIBOSOMAL PROTEIN S8



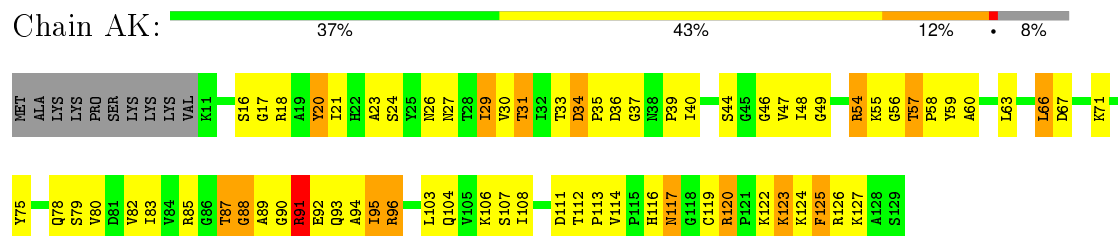
• Molecule 9: 30S RIBOSOMAL PROTEIN S9



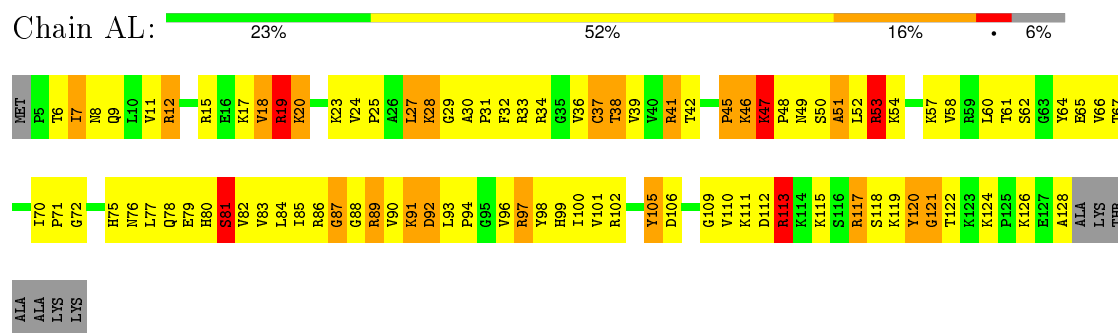
- Molecule 10: 30S RIBOSOMAL PROTEIN S10



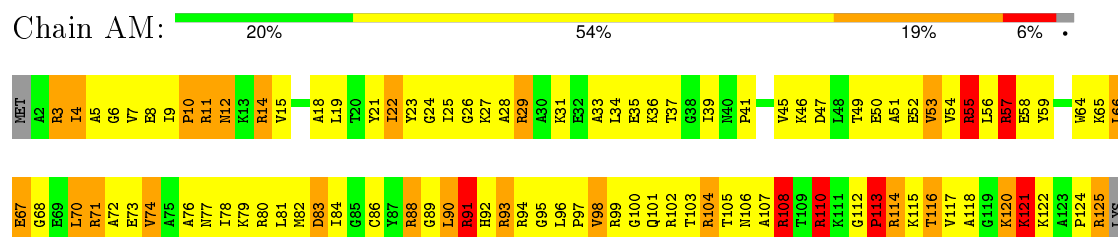
- Molecule 11: 30S RIBOSOMAL PROTEIN S11



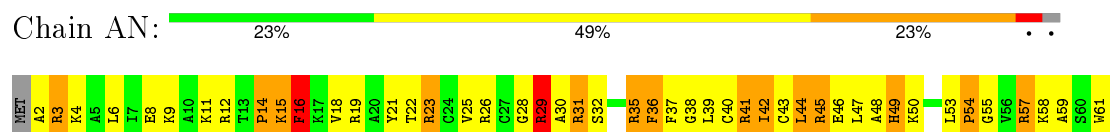
- Molecule 12: 30S RIBOSOMAL PROTEIN S12



- Molecule 13: 30S RIBOSOMAL PROTEIN S13

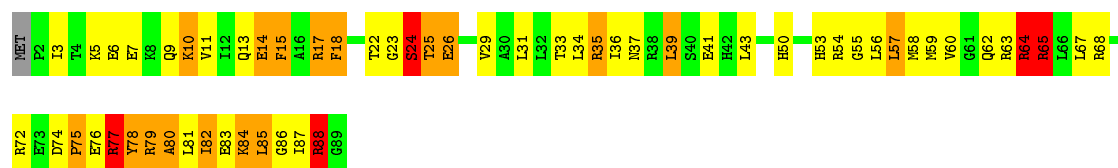


- Molecule 14: 30S RIBOSOMAL PROTEIN S14 TYPE Z



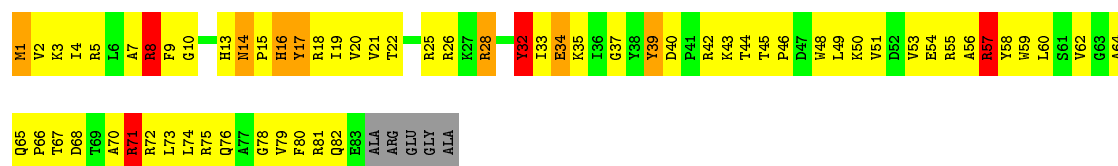
- Molecule 15: 30S RIBOSOMAL PROTEIN S15





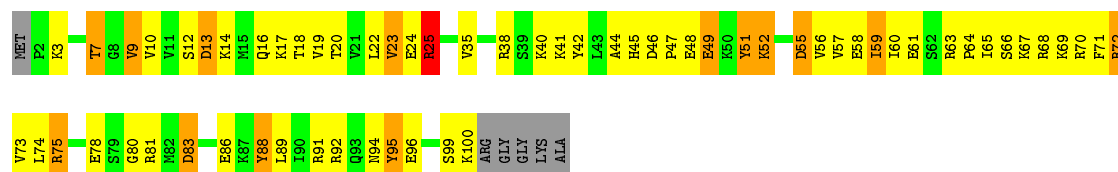
• Molecule 16: 30S RIBOSOMAL PROTEIN S16

Chain AP: 22% 60% 8% 5% 6%



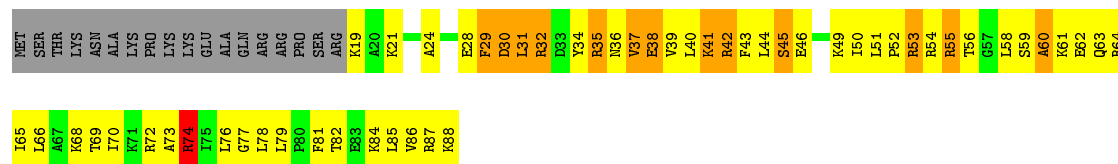
• Molecule 17: 30S RIBOSOMAL PROTEIN S17

Chain AQ: 34% 46% 13% 6%



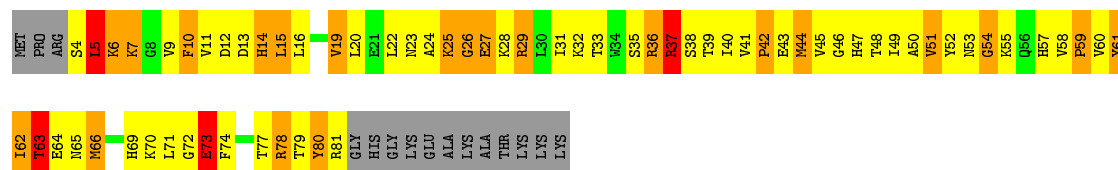
• Molecule 18: 30S RIBOSOMAL PROTEIN S18

Chain AR: 17% 47% 15% 20%



• Molecule 19: 30S RIBOSOMAL PROTEIN S19

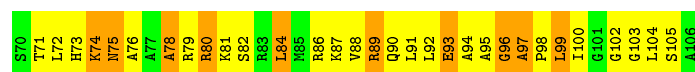
Chain AS: 12% 45% 23% 16%



• Molecule 20: 30S RIBOSOMAL PROTEIN S20

Chain AT: 25% 42% 25% 7%

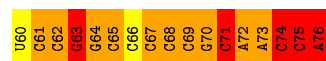




• Molecule 21: 30S RIBOSOMAL PROTEIN THX



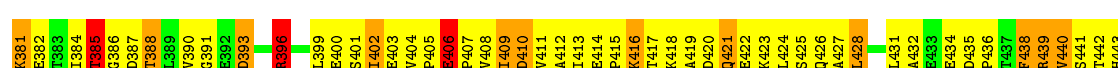
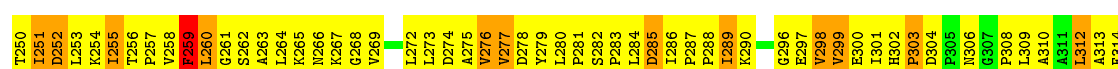
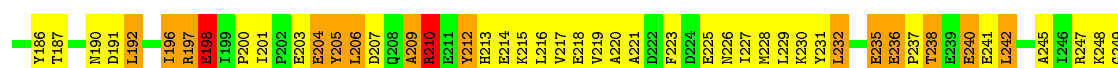
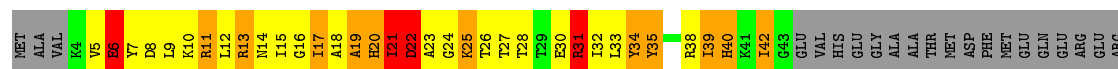
• Molecule 22: TRNA

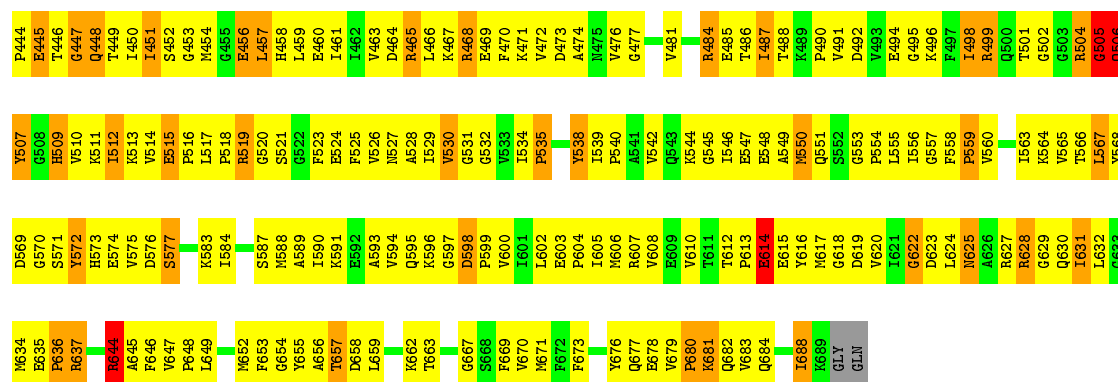


• Molecule 23: MRNA



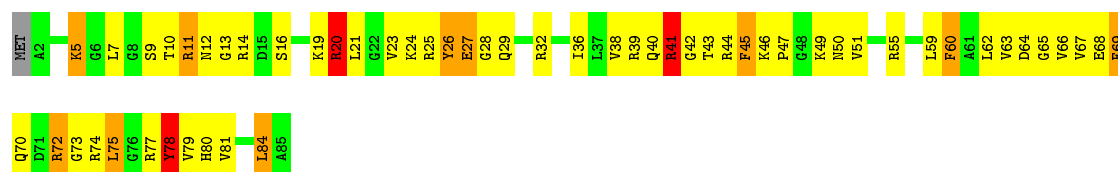
• Molecule 24: ELONGATION FACTOR G





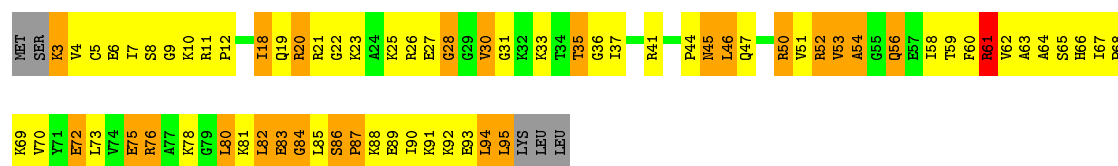
• Molecule 25: 50S RIBOSOMAL PROTEIN L27

Chain B0: 33% 51% 12%



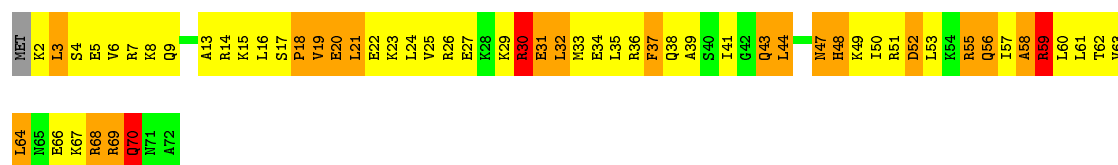
• Molecule 26: 50S RIBOSOMAL PROTEIN L28

Chain B1: 22% 47% 24% 5%



• Molecule 27: 50S RIBOSOMAL PROTEIN L29

Chain B2: 17% 51% 26%



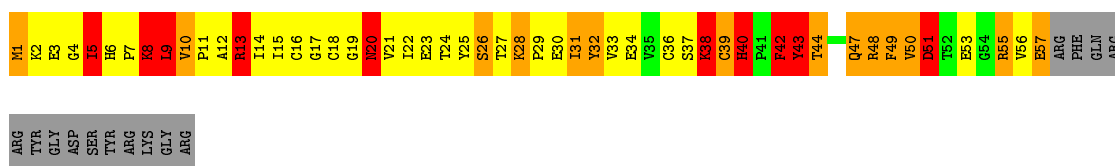
• Molecule 28: 50S RIBOSOMAL PROTEIN L30

Chain B3: 22% 62% 13%



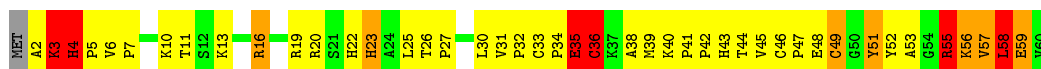
• Molecule 29: 50S RIBOSOMAL PROTEIN L31

Chain B4: 8% 38% 20% 14% 20%



- Molecule 30: 50S RIBOSOMAL PROTEIN L32

Chain B5: 25% 52% 12% 10% •



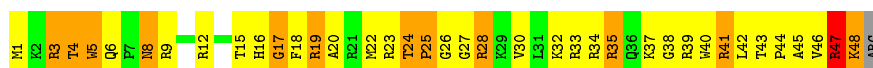
- Molecule 31: 50S RIBOSOMAL PROTEIN L33

Chain B6: 43% 33% 15% 7% •



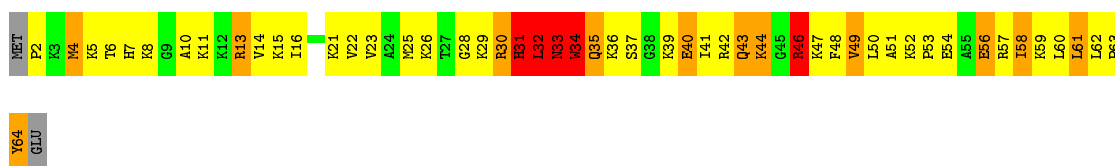
- Molecule 32: 50S RIBOSOMAL PROTEIN L34

Chain B7: 20% 51% 24% • •



- Molecule 33: 50S RIBOSOMAL PROTEIN L35

Chain B8: 18% 52% 18% 8% •



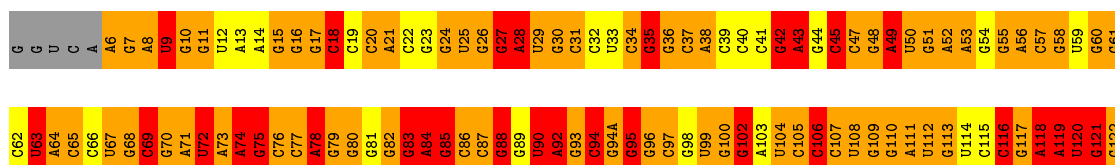
- Molecule 34: 50S RIBOSOMAL PROTEIN L36

Chain B9: 32% 41% 19% 8%



- Molecule 35: 23S RIBOSOMAL RNA

Chain BA: 21% 57% 21%

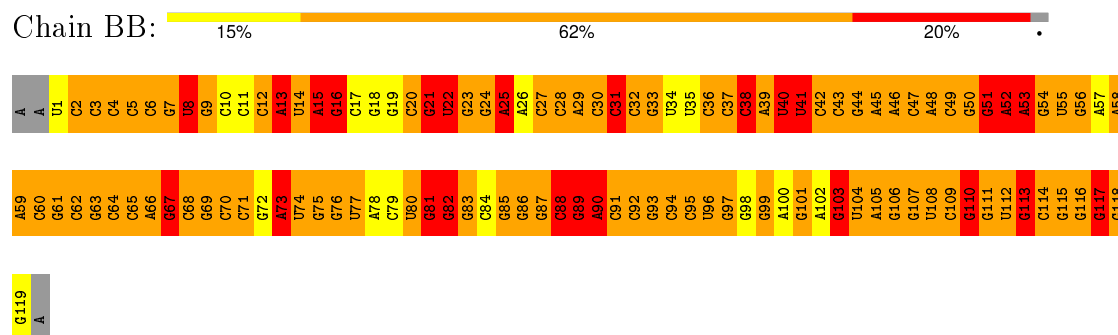


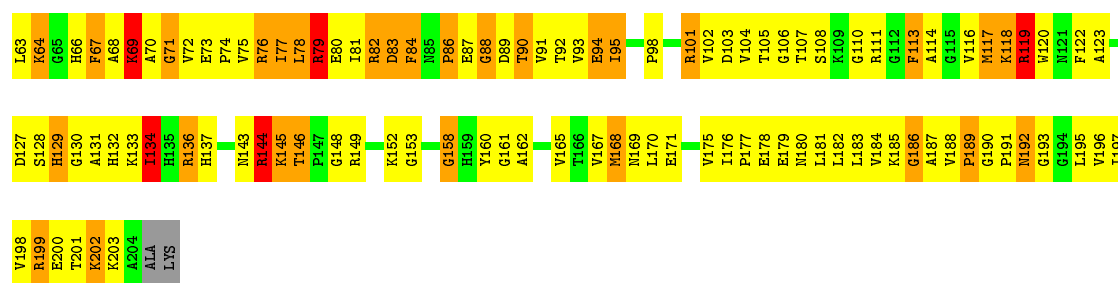
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G1036	C976	G916	G855	C795	A735	A675	A637	G579	C517	C486	U395	G338	A278	C253	U193	G124
G1037	G977	A917	C856	C796	C736	A676	G638	C580	U518	A487	G396	U339	C279	G254	U194	G125
G1038	G978	A918	C857	C797	C737	A677	U639	C581	U519	G488	G397	A340	C280	A255	A195	A126
G1039	G979	G919	U858	C798	G738	G678	C640	G582	G520	U489	G398	G341	G281	A256	A196	A127
G1040	G980	G920	G859	C799	G739	C679	C641	G583	G521	A490	G399	G342	A282	A257	A197	G128
G1041	A981	G921	U860	A800	U740	G680	G642	C584	G522	C461	G400	C343	A283	G258	C198	G129
G1042	C982	U922	A861	G801	G741	G681	A643	G585	G523	C462	A401	G344	U284	G259	A199	G130
G1043	A983	G923	G862	A802	G742	G682	A644	A586	U524	G463	A345	U285	C285	G260	U200	G131
G1044	A984	C924	A863	U803	G743	G683	C645	U525	U525	U464	U403	A346	C286	G261	C201	G132
G1045	C985	C925	G864	A804	G744	G684	A646	U588	A526	G465	A404	A347	C287	A262	U202	C133
G1046	C986	A926	G865	G805	G745	G685	G647	C589	C527	A466	U405	G348	C288	C263	C203	G134
G1047	G987	G927	A866	C806	A746	G686	G648	A590	U528	G467	G406	G349	A289	C264	A204	G135
A1048	A988	G928	C867	U807	U747	C687	G649	C591	A529	G468	G407	U850	G290	A265	G205	G136
G1049	G989	U930	U868	G808	G748	U688	C650	G592	G530	G469	G408	G351	C291	G266	U206	G137
A1050	A990	G931	G869	G809	C749	A689	G651	G593	C531	A470	C409	G352	C292	C267	A207	G139
G1051	C991	G932	A870	U810	A750	G690	C652	U594	A532	A471	G410	G353	U293	C268	C208	G139A
G1052	C992	A933	U871	U811	A751	C691	A653	C595	G533	A472	G411	G354	A294	U269	G209	G140
C1053	G993	G934	A872	C812	A752	C692	A654	C596	U534	G473	A412	G355	G295	A270	C210	A141
A1054	C994	C935	G873	U813	C753	C693	G654A	U597	C535	G474	C414	G356	C296	A271	A211	A142
G1055	C995	G936	G874	C814	C754	U694	C654B	U598	A536	U475	A415	U358	C297	A271A	C212	C142A
G1056	A996	U937	G875	C815	C755	G695	G654C	G599	C537	G476	A416	U359	A298	C271B	A213	G143
A1057	G997	G938	C876	C816	C756	G696	G654D	G600	U538	A477	C416	A359	A299	C271C	G214	C143A
G1058	G998	G939	U877	C817	U757	C697	G654E	G601	C539	A478	G417	G360	A300	G271D	G215	C144
G1059	U999	G940	A878	G818	C758	C698	C654F	G602	C540	A479	G418	G361	G301	U271E	A216	G145
U1060	A1000	A941	G879	A819	G759	A699	C654G	A603	C541	A480	C419	U862	C302	C271F	G217	G146
A1061	A1001	G942	G880	A820	G760	G700	G654H	G604	C542	G481	G420	G363	U303	C271G	A218	U147
G1062	G1002	U943	G881	A821	A761	G701	C654I	C605	C543	A482	U421	A364	A310	C271H	G225	G148
G1063	G1003	G944	G882	U822	U762	G702	G654J	U606	G544	A483	A422	G363B	U306	G271I	G220	A149
C1064	A1004	A945	G883	G823	G763	G703	C654K	U607	C545	C484	A423	G363C	U305	C271J	A221	C150
U1065	G1005	G946	C884	A824	A764	G704	G654L	A608	A547	C485	G424	G363D	G307	U271K	A222	C151
U1066	C1006	G947	C885	C825	G765	A705	G654M	A609	A548	C486	G425	U863E	G308	U271L	G223	G152
A1067	C1007	G948	C886	U826	C766	A706	G654N	G610	G549	C487	G426	A363F	G309	G271M	G224	C153
G1068	G1008	C949	A887	U827	G767	G707	G654P	C611	G551	G488	U427	C364	A311	U271N	A225	G154
A1069	A1009	G950	C888	U828	G768	G708	C654Q	C612	G552	G489	A428	C365	G312	C271O	G226	C154A
G1070	C951	G951	G889	A829	G769	U709	C654R	G613	G553	G491	A429	C366	G313	C271P	A227	U155
G1071	G1011	G952	A890	G830	G770	G710	C654S	U614	U554	A492	G430	G370	C313	G271Q	A228	U156
C1072	U1012	A953	G892	G831	G771	G711	G654S	U614A	U555	G493	U431	A371	A314	G271R	A229	U157
A1073	C1013	G954	C893	G832	C772	G712	C654T	G614B	G556	G494	A432	G372	G315	G271S	U230	U158
G1074	U1014	C955	C894	U833	U773	G713	A654U	A614C	U557	G495	C433	U373	C316	C271T	C231	C172
G1075	G1015	G956	U895	C834	A774	G715	A654V	G615	G558	G496	U434	A374	G317	C271U	A232	G173
C1076	G1016	A957	A896	A835	G775	G716	A655	G616	C559	A497	C435	C375	C318	G271V	G233	G174
A1077	G1017	U958	C897	G836	G776	A716	G656	C618	C560	G498	G436	C376	C319	G271W	C234	G175
U1078	C1018	A959	C898	C837	A777	G717	U657	G619	G561	U499	G437	C377	A320	G271X	U235	G176
C1079	U1019	A960	A899	C838	G778	A718	C658	G620	U562	G500	G438	C378	G321	U271Y	C236	G177
U1080	A1020	C961	A900	U839	U779	C719	C659	A621	G563	A501	G440	G379	A322	C271Z	C237	G178
U1081	C962	A901	A901	C840	G780	C720	G660	G622	C564	A502	U441	U380	G323	G272	C238	G179
U1082	G1022	U963	C902	A841	A781	A721	C661	G623	C565	U503	G442	G381	A324	U272A	U239	G180
U1083	C964	C964	C903	G842	A782	A722	G662	C624	U566	U504	A443	G382	G325	G272B	G240	G181
A1084	G1024	C965	C904	G843	A783	G723	G663	G625	A567	A505	C444	U383	G326	G272C	A241	A181
A1085	G1025	G966	U905	C844	A784	U724	C664	U626	U568	G506	G445	U384	G327	G272D	G242	A182
A1086	U1026	C967	G906	G845	G785	G725	C665	A627	U569	A507	G446	C385	U328	G272E	U243	C183
G1087	A1027	G968	U907	C846	C786	G726	G666	G628	G570	G508	A447	G386	A329	C272F	A244	C184
A1088	C1028	U969	C908	U847	U787	A727	U667	G629	A571	C509	U448	U387	A330	C272G	G245	U185
U1089	A1029	G970	A909	G848	A788	G728	G668	G630	G572	C510	A449	G388	A331	C272H	G246	G186
G1090	G1030	C971	A910	A849	A789	G729	G669	A631	G573	U511	G450	G389	A332	U272I	G247	G187
G1091	G1031	G972	A911	C850	C790	C730	A670	A632	C574	G512	C451	A390	G333	C272J	G248	G188
U1092	A1032	A973	C912	U851	C791	G731	C671	A633	A575	A513	G452	C391	C334	G274	C249	G189
G1093	G974	C974	U913	G852	G792	C732	C672	C634	U576	A514	C453	G392	C335	G275	G250	A190
U1094	G1034	C975	C914	G853	A793	G733	C673	C635	G577	A515	A454	C393	C336	A276	A251	A191

G1959	A1960	C1961	G1962	U1963	G1964	C1965	G1966	C1967	G1968	A1969	G1970	A1971	C1972	A1973	G1974	C1975	G1976	A1977	G1978	A1979	C1980	G1981	C1982	G1983	G1984	G1985	G1986	A1987	C1988	G1989	G1990	U1991	G1992	U1993	C1994	U1995	C1996	G1997	G1998	C1999	G2000	A2001	C2002	G2003	G2004	A2005	C2006	G2007	C2008	G2009	G2010	U2011	G2012	A2013	A2014	A2015	U2016	U2017	G2018																	
G1899	A1900	A1901	C1902	G1903	C1904	C1905	C1906	C1907	G1908	C1909	G1910	U1911	C1912	A1913	C1914	U1915	A1916	U1917	A1918	A1919	C1920	G1921	G1922	U1923	G1924	C1925	G1926	C1927	A1928	C1929	G1930	U1931	G1932	C1933	C1934	G1935	A1936	A1937	A1938	U1939	U1940	C1941	C1942	U1943	U1944	G1945	U1946	C1947	G1948	G1949	U1950	U1951	A1952	A1953	G1954	U1955	U1956	U1957	C1958																	
C1830	G1831	C1832	U1833	U1834	C1835	C1836	C1837	C1838	G1839	C1840	U1841	C1842	C1843	C1844	G1845	G1846	C1847	C1848	G1849	C1850	U1851	C1852	A1853	C1854	C1855	C1856	C1857	C1858	C1859	C1860	C1861	G1862	G1863	U1864	G1865	C1866	A1867	C1868	C1869	C1870	C1871	C1872	C1873	C1874	C1875	C1876	C1877	C1878	C1879	C1880	C1881	C1882	C1883	A1884	G1885	C1886	C1887	C1888	A1889	A1890	G1891	C1892	C1893	C1894	C1895	G1896	G1897	U1898								
G1770	C1771	G1772	A1773	C1774	G1775	C1776	C1777	U1778	C1779	A1780	C1781	C1782	A1783	A1784	C1785	A1786	C1787	C1788	A1789	C1790	U1791	G1792	C1793	U1794	C1795	C1796	C1797	C1798	C1799	C1800	C1801	A1802	C1803	C1804	U1805	C1806	C1807	G1808	A1809	A1810	C1811	A1812	C1813	C1814	A1815	C1816	C1817	C1818	A1819	A1820	A1821	C1822	G1823	G1824	A1825	C1826	G1827	C1828	A1829																	
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A1634	G1635	A1636	A1637	C1638	U1639	C1640	A1641	C1642	C1643	C1644	G1645	C1646	G1647	C1648	C1649	G1650	C1651	A1652	G1653	A1654	A1655	C1656	C1657	C1658	U1659	C1660	C1661	C1662	C1663	C1664	C1665	C1666	C1667	C1668	C1669	U1670	C1671	C1672	C1673	C1674	C1675	C1676	C1677	C1678	U1679	C1680	G1681	C1682	G1683	C1684	C1685	C1686	C1687	C1688	C1689	C1690	C1691	U1692	U1693																	
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A1155	A1156	G1157	C1158	A1098	U1159	G1160	C1161	C1162	G1163	G1164	U1165	C1166	G1167	C1168	G1169	C1170	G1171	C1172	U1173	U1174	C1175	G1176	C1177	C1178	C1179	C1180	C1181	A1182	C1183	C1184	C1185	C1186	C1187	U1188	A1189	C1190	G1191	C1192	G1193	A1194	C1195	C1196	G1197	C1198	U1199	C1200	C1201	C1202	G1203	A1204	U1205	C1206	C1207	C1208	A1209	C1210	C1211	C1212	C1213	G1214	C1215	G1216														
A1095	A1096	U1097	C1098	C1099	G1100	U1101	C1102	C1103	A1104	U1105	C1106	G1107	U1108	C1109	G1110	A1111	C1112	U1113	U1114	C1115	C1116	G1117	C1118	C1119	C1120	C1121	C1122	C1123	C1124	C1125	A1126	C1127	A1128	C1129	G1130	C1131	C1132	U1133	C1135	G1136	C1137	C1138	U1139	C1140	U1141	C1142	A1142A	A1143	G1144	C1145	C1146	C1147	A1148	C1149	C1150	G1151	C1152	C1153	G1154																	

C2871	A2748	G2811	G2329	U2449	G2389	G2329	A2199	C2139	U2079	A2019
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A2873	G2750	A2813	G2631	A2451	G2391	G2271	C2201	G2141	G2081	C2021
G2874	G2751	A2814	A2632	C2452	A2392	U2272	C2202	C2142	A2082	U2022
G2875	G2752	C2815	G2633	A2453	A2393	A2273	U2203	C2143	G2083	G2023
A2876	A2753	G2816	G2634	G2454	C2394	A2274	C2205	U2144	C2084	G2024
G2877	U2754	G2817	G2635	G2455	G2395	G2275	G2206	C2145	C2085	C2025
G2818	C2755	G2818	U2636	A2456	G2396	G2276	G2207	C2146	U2086	C2026
G2819	U2756	G2819	U2637	U2457	G2397	G2277	A2208	C2147	G2087	G2027
C2880	A2757	A2820	G2638	G2458	U2398	A2278	U2218	G2148	U2088	U2028
C2881	A2758	G2821	A2639	A2459	G2399	G2279	G2219	G2149	U2089	G2029
A2882	G2759	G2822	U2640	U2460	U2400	G2280	G2220	U2150	G2090	A2030
A2883	C2760	A2823	G2641	C2461	U2401	G2281	G2221	U2151	U2091	A2031
U2884	G2761	U2702	G2642	U2462	C2402	G2282	G2222	G2152	U2092	G2032
G2885	G2762	C2703	G2643	C2463	C2403	G2283	G2223	G2153	G2093	A2033
G2886	G2763	C2704	G2644	C2464	C2404	G2284	G2224	G2154	G2094	U2034
G2887	A2764	A2705	G2645	U2465	G2405	C2285	A2225	G2155	C2095	G2035
C2888	A2765	G2706	G2646	C2466	U2406	A2286	C2226	G2156	U2096	C2036
C2889	G2766	G2707	U2647	G2467	G2407	A2287	A2227	G2157	G2097	G2037
G2890	C2767	G2708	G2648	U2468	U2408	A2288	G2228	A2158	U2098	G2038
A2892	G2768	G2709	U2649	A2469	A2409	G2289	G2229	A2159	U2099	G2039
G2893	G2769	C2710	U2650	G2470	G2410	G2290	G2230	G2160	G2100	C2040
G2894	G2770	A2711	C2651	C2471	A2411	G2291	C2231	C2161	G2101	U2041
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A2896	C2772	A2712A	G2653	U2473	G2413	G2293	U2233	G2163	C2103	C2043
U2897	C2773	A2713	A2654	C2474	G2414	C2294	G2234	C2164	G2104	C2044
U	G2774	G2714	G2655	C2475	G2415	G2295	G2235	G2165	C2105	C2045
G	A2775	C2715	U2656	A2476	G2416	U2296	G2236	G2166	G2106	G2046
A	A2776	U2716	U2657	C2477	A2417	G2297	G2237	U2167	G2107	U2047
C	G2777	G2717	C2658	A2478	A2418	A2298	G2238	G2168	G2108	G2048
C	A2778	G2718	G2659	G2479	U2419	G2299	G2239	A2169	U2109	G2049
C	U2779	G2719	A2660	C2480	C2420	G2300	C2240	A2170	G2110	C2050
C	G2780	U2720	C2661	G2481	G2421	C2301	A2241	A2171	A2051	A2051
U	A2781	A2721	A2662	G2482	A2422	G2302	G2242	U2172	G2112	G2052
G	G2782	G2722	G2663	C2483	U2423	G2303	U2243	A2173	G2113	G2053
A	G2783	C2723	G2664	G2484	C2424	G2304	U2244	C2174	A2114	A2054
C	G2784	G2724	A2665	G2485	A2425	A2305	U2245	C2175	G2115	C2055
C	C2785	A2725	C2666	G2486	A2426	C2306	G2246	A2176	G2116	G2056
U	U2786	U2726	C2667	G2487	C2427	G2307	A2247	C2177	A2117	A2057
U	C2787	G2727	G2668	A2488	G2428	G2308	C2248	C2178	U2118	A2058
C	G2788	U2728	G2669	G2489	G2429	A2309	U2249	C2179	A2119	A2059
C	G2789	G2729	A2670	G2490	A2430	A2310	G2250	U2180	G2120	A2060
C	A2790	C2730	A2671	U2491	U2431	G2311	G2251	G2181	G2121	G2061
C	G2791	G2731	G2672	U2492	A2432	U2312	G2252	G2182	U2122	A2062
C	G2792	G2732	G2673	U2493	A2433	G2313	G2253	C2183	G2123	C2063
C	G2793	A2733	G2674	G2494	A2434	G2314	G2254	G2184	C2124	C2064
C	C2794	A2734	A2675	U2495	A2435	G2315	G2255	C2185	G2125	C2065
C	G2795	G2735	C2676	C2496	G2436	G2316	G2256	G2186	A2126	C2066
C	U2796	G2736	G2677	A2497	U2437	C2317	U2257	G2187	G2127	G2067
C	G2799	G2737	C2678	C2498	U2438	G2318	G2258	C2188	U2128	U2068
C	A2801	A2738	A2679	C2499	A2439	G2319	G2259	U2189	C2129	G2069
C	A2801A	U2739	C2680	U2500	C2440	A2320	C2260	G2190	U2130	G2070
C	G2802	A2740	C2681	G2501	C2441	G2321	C2261	G2191	A2071	A2071
C	C2803	A2741	U2682	G2502	C2442	A2322	U2262	G2192	U2132	G2072
C	G2804	C2742	C2683	A2503	C2443	G2323	G2263	G2193	C2073	C2073
C	G2805	C2743	U2684	U2504	G2444	C2324	C2264	G2194	A2134	U2074
C	G2807	G2744	G2685	G2505	G2445	G2325	U2265	C2195	A2135	U2075
C	U2808	U2745	G2686	U2506	G2446	C2326	A2266	C2196	C2136	U2076
C	A2809	C2746	U2687	G2507	A2447	U2387	U2267	U2197	A2077	A2077
C	A2810	G2747	U2688	G2508	A2448	A2388	A2268	C2198	C2138	C2078

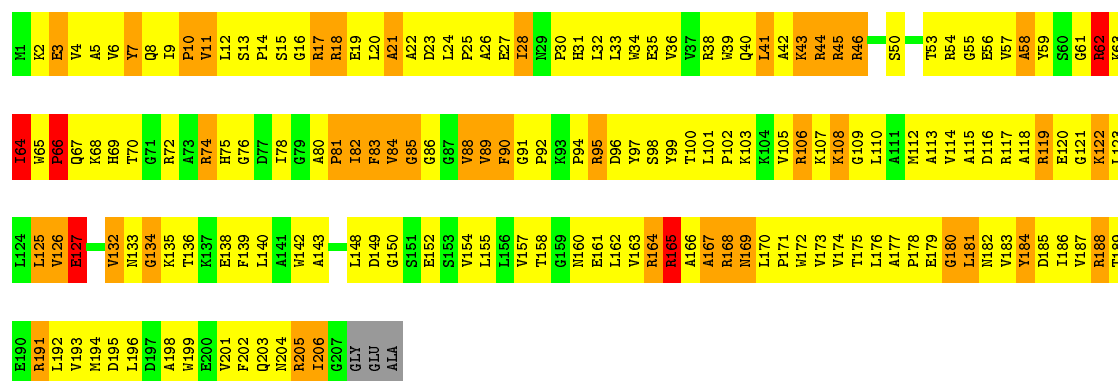
• Molecule 36: 5S RIBOSOMAL RNA

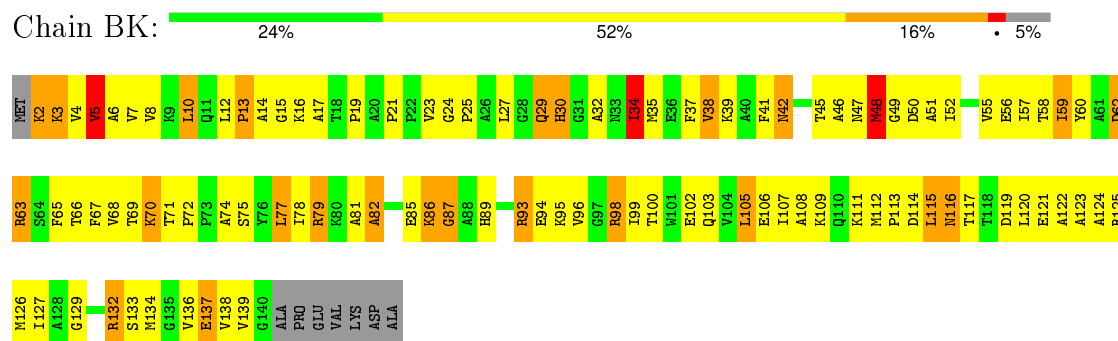




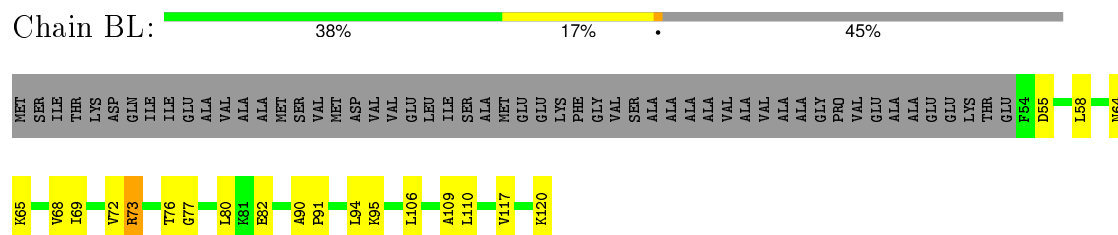
• Molecule 40: 50S RIBOSOMAL PROTEIN L4

Chain BF: 17% 59% 20% ..

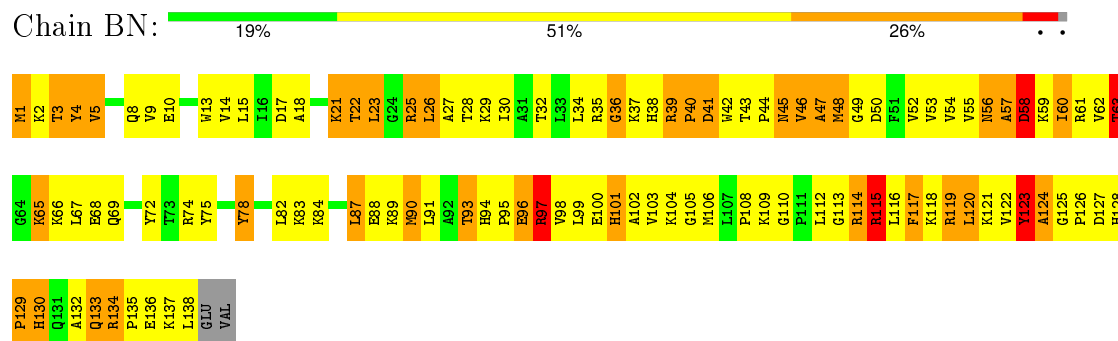




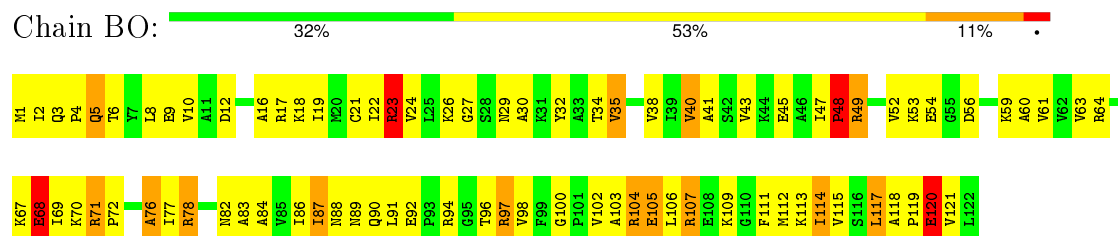
• Molecule 44: 50S RIBOSOMAL PROTEIN L7/L12



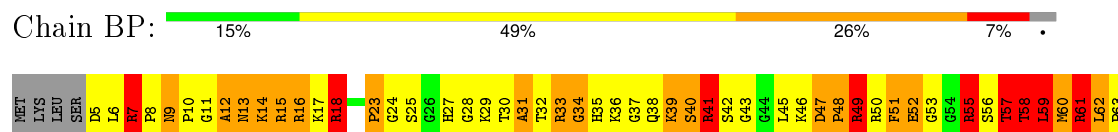
• Molecule 45: 50S RIBOSOMAL PROTEIN L13

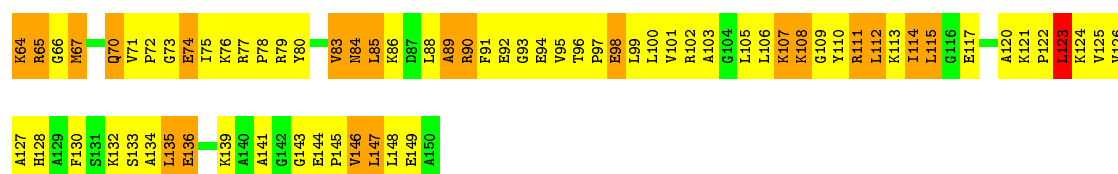


• Molecule 46: 50S RIBOSOMAL PROTEIN L14



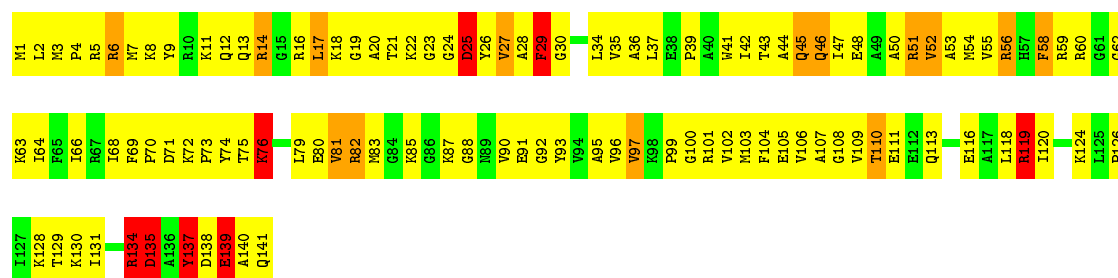
• Molecule 47: 50S RIBOSOMAL PROTEIN L15





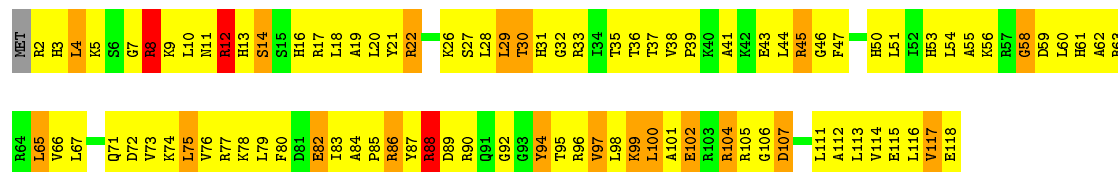
• Molecule 48: 50S RIBOSOMAL PROTEIN L16

Chain BQ: 22% 62% 10% 6%



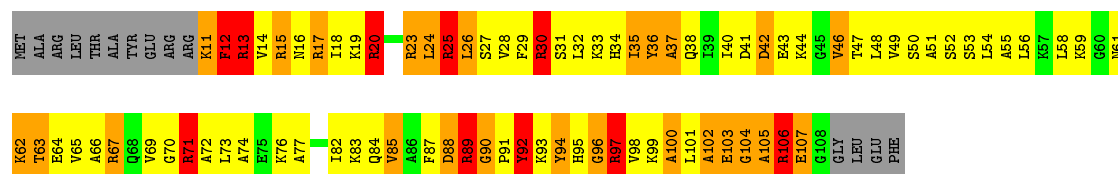
• Molecule 49: 50S RIBOSOMAL PROTEIN L17

Chain BR: 19% 61% 16% ..



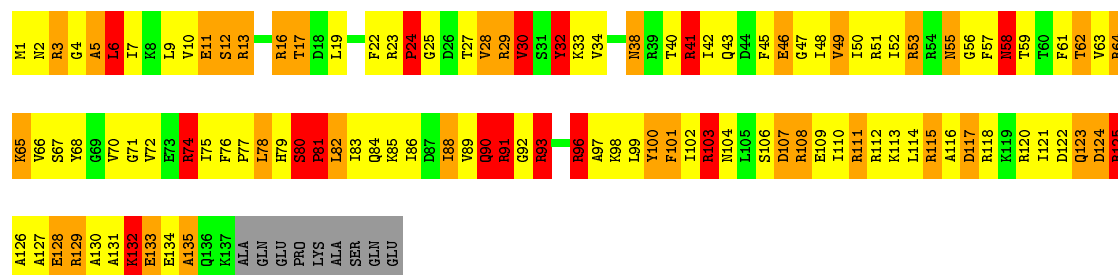
• Molecule 50: 50S RIBOSOMAL PROTEIN L18

Chain BS: 13% 44% 22% 9% 13%

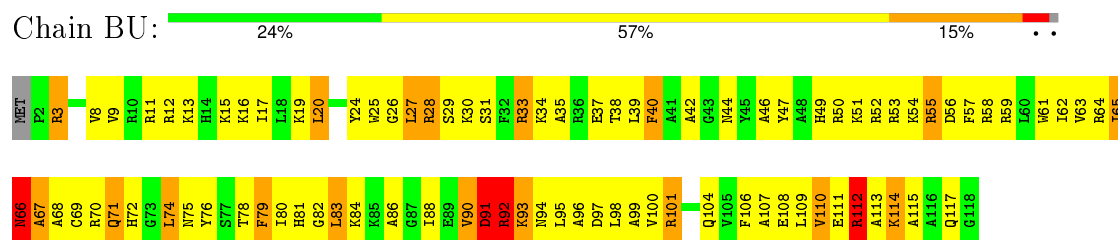


• Molecule 51: 50S RIBOSOMAL PROTEIN L19

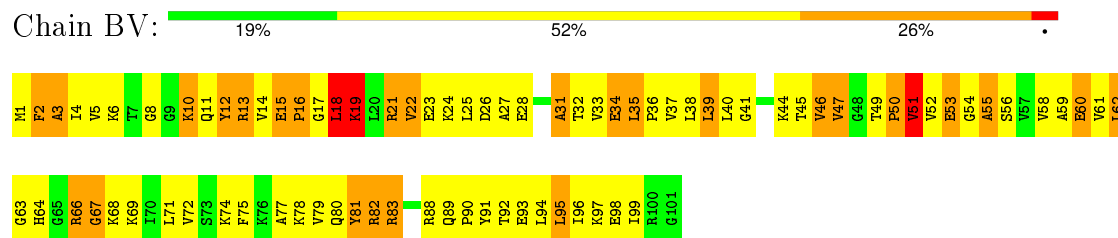
Chain BT: 16% 44% 23% 11% 6%



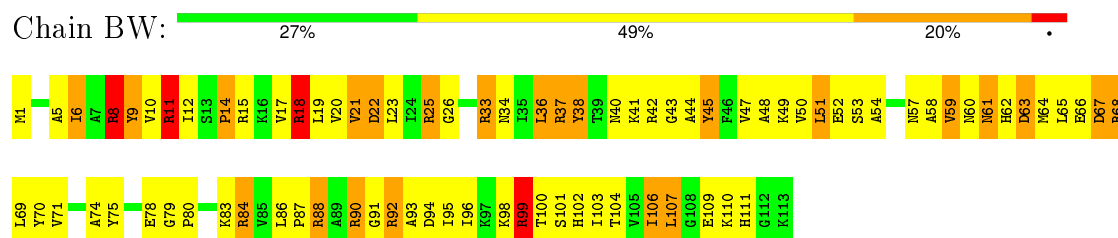
- Molecule 52: 50S RIBOSOMAL PROTEIN L20



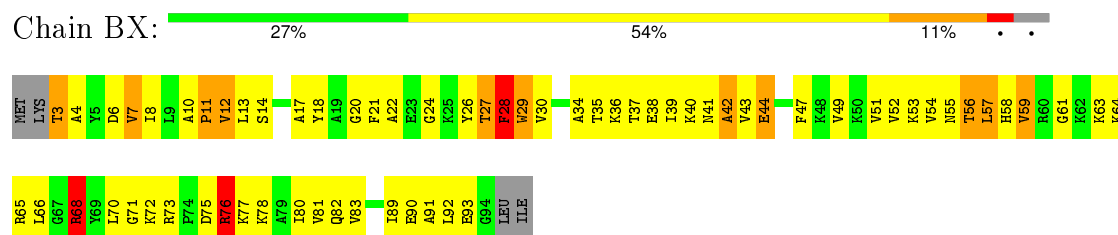
- Molecule 53: 50S RIBOSOMAL PROTEIN L21



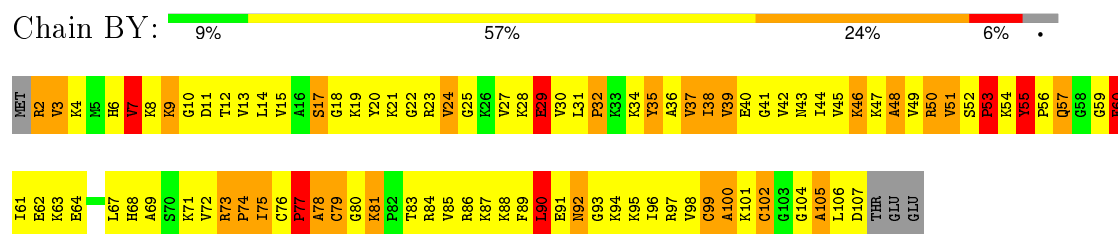
- Molecule 54: 50S RIBOSOMAL PROTEIN L22



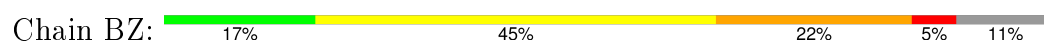
- Molecule 55: 50S RIBOSOMAL PROTEIN L23



- Molecule 56: 50S RIBOSOMAL PROTEIN L24



- Molecule 57: 50S RIBOSOMAL PROTEIN L25





4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	DEFOCUS GROUPS	Depositor
Microscope	OTHER	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO163 FILM	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	AA	2.74	2653/36190 (7.3%)	2.42	3123/56486 (5.5%)
10	AJ	1.35	0/807	1.50	6/1085 (0.6%)
11	AK	1.40	1/900 (0.1%)	1.48	9/1213 (0.7%)
12	AL	1.45	0/986	1.56	9/1320 (0.7%)
13	AM	1.39	1/998 (0.1%)	1.64	17/1336 (1.3%)
14	AN	1.49	2/501 (0.4%)	1.71	9/664 (1.4%)
15	AO	1.35	0/745	1.59	13/992 (1.3%)
16	AP	1.34	1/716 (0.1%)	1.62	11/963 (1.1%)
17	AQ	1.45	2/836 (0.2%)	1.57	11/1117 (1.0%)
18	AR	1.40	0/579	1.59	7/768 (0.9%)
19	AS	1.28	0/642	1.48	5/865 (0.6%)
2	AB	1.43	2/1935 (0.1%)	1.55	20/2609 (0.8%)
20	AT	1.31	0/765	1.52	12/1007 (1.2%)
21	AU	1.33	0/212	1.76	6/277 (2.2%)
22	AV	2.74	134/1832 (7.3%)	2.54	182/2855 (6.4%)
23	AX	2.60	15/257 (5.8%)	2.50	24/398 (6.0%)
24	AY	1.31	7/5312 (0.1%)	1.51	49/7193 (0.7%)
25	B0	1.27	0/671	1.52	11/892 (1.2%)
26	B1	1.37	2/738 (0.3%)	1.59	6/981 (0.6%)
27	B2	1.25	0/600	1.51	4/793 (0.5%)
28	B3	1.35	0/472	1.46	4/634 (0.6%)
29	B4	1.32	0/460	1.78	10/621 (1.6%)
3	AC	1.49	3/1636 (0.2%)	1.59	25/2205 (1.1%)
30	B5	1.35	1/473 (0.2%)	1.48	3/639 (0.5%)
31	B6	1.49	3/440 (0.7%)	1.68	7/586 (1.2%)
32	B7	1.38	0/426	1.66	9/561 (1.6%)
33	B8	1.33	1/515 (0.2%)	1.56	6/679 (0.9%)
34	B9	1.37	0/310	1.59	6/407 (1.5%)
35	BA	2.69	4866/69972 (7.0%)	2.42	6058/109237 (5.5%)
36	BB	2.71	196/2853 (6.9%)	2.45	289/4451 (6.5%)
37	BC	1.35	0/1774	1.44	16/2391 (0.7%)
38	BD	1.38	3/2195 (0.1%)	1.59	25/2955 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	BE	1.37	1/1596 (0.1%)	1.58	19/2153 (0.9%)
4	AD	1.40	1/1733 (0.1%)	1.59	25/2318 (1.1%)
40	BF	1.40	2/1658 (0.1%)	1.63	27/2244 (1.2%)
41	BG	1.35	1/1499 (0.1%)	1.93	24/2016 (1.2%)
42	BH	1.35	4/1292 (0.3%)	1.51	12/1744 (0.7%)
43	BK	1.29	2/1044 (0.2%)	1.38	4/1416 (0.3%)
44	BL	1.10	0/478	1.50	2/640 (0.3%)
45	BN	1.33	2/1131 (0.2%)	1.57	13/1525 (0.9%)
46	BO	1.43	1/943 (0.1%)	1.50	11/1269 (0.9%)
47	BP	1.34	0/1131	1.64	13/1504 (0.9%)
48	BQ	1.38	2/1143 (0.2%)	1.52	11/1527 (0.7%)
49	BR	1.28	0/974	1.52	12/1302 (0.9%)
5	AE	1.48	1/1162 (0.1%)	1.54	9/1564 (0.6%)
50	BS	1.31	1/778 (0.1%)	1.74	23/1036 (2.2%)
51	BT	1.37	1/1155 (0.1%)	1.78	25/1542 (1.6%)
52	BU	1.38	0/975	1.51	8/1297 (0.6%)
53	BV	1.34	2/790 (0.3%)	1.49	7/1057 (0.7%)
54	BW	1.31	1/907 (0.1%)	1.59	14/1216 (1.2%)
55	BX	1.39	0/739	1.46	5/993 (0.5%)
56	BY	1.24	1/823 (0.1%)	1.55	9/1098 (0.8%)
57	BZ	1.34	0/1499	1.53	18/2035 (0.9%)
6	AF	1.39	3/856 (0.4%)	1.69	15/1154 (1.3%)
7	AG	1.39	1/1276 (0.1%)	1.51	15/1709 (0.9%)
8	AH	1.48	2/1136 (0.2%)	1.67	20/1527 (1.3%)
9	AI	1.47	2/1029 (0.2%)	2.08	19/1379 (1.4%)
All	All	2.36	7924/165495 (4.8%)	2.21	10352/246445 (4.2%)

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	AA	0	107
10	AJ	0	2
11	AK	0	2
12	AL	0	3
13	AM	0	3
14	AN	0	2
15	AO	0	3
16	AP	0	6
17	AQ	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
18	AR	0	3
19	AS	0	3
2	AB	0	5
20	AT	0	2
21	AU	0	3
22	AV	0	5
23	AX	0	1
24	AY	0	13
25	B0	0	1
26	B1	0	3
27	B2	0	6
28	B3	0	2
29	B4	0	3
3	AC	0	3
30	B5	0	2
31	B6	0	3
32	B7	0	1
33	B8	0	2
34	B9	0	2
35	BA	1	152
36	BB	0	6
37	BC	0	6
38	BD	0	2
39	BE	0	3
4	AD	0	3
40	BF	0	3
41	BG	0	5
42	BH	0	8
43	BK	0	3
45	BN	0	3
46	BO	0	3
47	BP	0	5
48	BQ	0	3
49	BR	0	2
5	AE	0	4
50	BS	0	6
51	BT	0	6
52	BU	0	4
53	BV	0	2
54	BW	0	4
55	BX	0	2
56	BY	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
57	BZ	0	4
6	AF	0	6
7	AG	0	6
8	AH	0	4
9	AI	0	5
All	All	1	457

The worst 5 of 7924 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	473	G	N7-C5	-17.52	1.28	1.39
1	AA	710	G	C8-N7	-15.43	1.21	1.30
1	AA	809	G	C8-N7	-15.17	1.21	1.30
1	AA	188	C	N1-C6	-15.00	1.28	1.37
1	AA	1311	G	C8-N7	-14.67	1.22	1.30

The worst 5 of 10352 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	BG	112	PRO	O-C-N	-40.65	57.66	122.70
9	AI	53	VAL	O-C-N	-36.52	64.27	122.70
9	AI	104	ARG	O-C-N	-30.37	74.11	122.70
41	BG	112	PRO	CA-C-N	21.56	164.63	117.20
26	B1	20	ARG	NE-CZ-NH2	-18.37	111.11	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
35	BA	1992	G	C3'

5 of 457 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	106	C	Sidechain
1	AA	108	G	Sidechain
1	AA	30	U	Sidechain
1	AA	5	U	Sidechain
1	AA	69	G	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32329	0	16041	1544	0
2	AB	1900	0	1951	244	0
3	AC	1612	0	1677	208	0
4	AD	1703	0	1767	205	0
5	AE	1146	0	1207	140	0
6	AF	843	0	857	95	0
7	AG	1257	0	1296	119	0
8	AH	1116	0	1177	110	0
9	AI	1010	0	1037	142	0
10	AJ	794	0	840	185	0
11	AK	885	0	904	92	0
12	AL	970	0	1057	144	0
13	AM	987	0	1059	139	0
14	AN	492	0	533	78	0
15	AO	734	0	771	74	0
16	AP	700	0	720	83	0
17	AQ	823	0	891	68	0
18	AR	574	0	644	77	0
19	AS	629	0	652	116	0
20	AT	763	0	861	112	0
21	AU	208	0	221	28	0
22	AV	1640	0	831	100	0
23	AX	230	0	114	17	0
24	AY	5214	0	5288	791	0
25	B0	662	0	688	91	0
26	B1	731	0	808	116	0
27	B2	598	0	653	94	0
28	B3	467	0	523	53	0
29	B4	450	0	449	93	0
30	B5	459	0	480	98	0
31	B6	433	0	461	148	0
32	B7	418	0	467	58	0
33	B8	507	0	576	103	0
34	B9	307	0	338	35	0
35	BA	62474	0	31032	3281	0
36	BB	2551	0	1281	164	0
37	BC	1742	0	1798	171	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	BD	2145	0	2234	305	0
39	BE	1563	0	1629	246	0
40	BF	1623	0	1677	283	0
41	BG	1474	0	1535	287	0
42	BH	1268	0	1337	232	0
43	BK	1025	0	1066	177	0
44	BL	477	0	509	14	0
45	BN	1104	0	1180	202	0
46	BO	933	0	996	124	0
47	BP	1114	0	1187	295	0
48	BQ	1122	0	1179	166	0
49	BR	960	0	1021	158	0
50	BS	770	0	832	168	0
51	BT	1141	0	1202	228	0
52	BU	958	0	1015	170	0
53	BV	779	0	852	148	0
54	BW	896	0	953	103	0
55	BX	725	0	778	93	0
56	BY	810	0	901	186	0
57	BZ	1467	0	1492	230	0
58	AY	37	0	47	12	0
59	AY	28	0	12	7	0
All	All	152777	0	105584	12189	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 47.

The worst 5 of 12189 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)
1:AA:509:A:H5'	1:AA:510:A:OP2	1.26	1.30
24:AY:496:LYS:HE2	24:AY:498:ILE:CD1	1.66	1.25
53:BV:15:GLU:HB3	53:BV:16:PRO:HD2	1.23	1.20
41:BG:63:ILE:HA	41:BG:143:GLU:HG3	1.22	1.19
35:BA:996:A:H4'	52:BU:92:ARG:HE	1.01	1.18

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	AB	232/256 (91%)	146 (63%)	55 (24%)	31 (13%)	0	7
3	AC	204/239 (85%)	129 (63%)	58 (28%)	17 (8%)	1	18
4	AD	206/209 (99%)	133 (65%)	52 (25%)	21 (10%)	1	13
5	AE	148/162 (91%)	116 (78%)	27 (18%)	5 (3%)	5	40
6	AF	99/101 (98%)	78 (79%)	15 (15%)	6 (6%)	2	26
7	AG	153/156 (98%)	107 (70%)	34 (22%)	12 (8%)	1	20
8	AH	136/138 (99%)	106 (78%)	23 (17%)	7 (5%)	2	30
9	AI	125/128 (98%)	84 (67%)	26 (21%)	15 (12%)	0	8
10	AJ	96/105 (91%)	64 (67%)	19 (20%)	13 (14%)	0	7
11	AK	117/129 (91%)	93 (80%)	18 (15%)	6 (5%)	2	30
12	AL	122/132 (92%)	81 (66%)	26 (21%)	15 (12%)	0	8
13	AM	122/126 (97%)	77 (63%)	25 (20%)	20 (16%)	0	5
14	AN	58/61 (95%)	48 (83%)	6 (10%)	4 (7%)	1	23
15	AO	86/89 (97%)	53 (62%)	25 (29%)	8 (9%)	1	16
16	AP	81/88 (92%)	58 (72%)	19 (24%)	4 (5%)	3	31
17	AQ	97/105 (92%)	76 (78%)	16 (16%)	5 (5%)	2	30
18	AR	68/88 (77%)	51 (75%)	11 (16%)	6 (9%)	1	17
19	AS	76/93 (82%)	39 (51%)	20 (26%)	17 (22%)	0	2
20	AT	97/106 (92%)	52 (54%)	30 (31%)	15 (16%)	0	5
21	AU	22/27 (82%)	14 (64%)	6 (27%)	2 (9%)	1	17
24	AY	662/691 (96%)	442 (67%)	135 (20%)	85 (13%)	0	8
25	B0	82/85 (96%)	64 (78%)	16 (20%)	2 (2%)	7	47
26	B1	91/98 (93%)	60 (66%)	20 (22%)	11 (12%)	0	8
27	B2	69/72 (96%)	34 (49%)	22 (32%)	13 (19%)	0	3
28	B3	57/60 (95%)	41 (72%)	12 (21%)	4 (7%)	1	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	B4	55/71 (78%)	25 (46%)	16 (29%)	14 (26%)	0	1
30	B5	57/60 (95%)	40 (70%)	6 (10%)	11 (19%)	0	3
31	B6	48/54 (89%)	22 (46%)	10 (21%)	16 (33%)	0	0
32	B7	46/49 (94%)	35 (76%)	9 (20%)	2 (4%)	3	34
33	B8	61/65 (94%)	35 (57%)	17 (28%)	9 (15%)	0	5
34	B9	35/37 (95%)	23 (66%)	8 (23%)	4 (11%)	0	10
37	BC	226/229 (99%)	173 (76%)	42 (19%)	11 (5%)	3	31
38	BD	273/276 (99%)	185 (68%)	55 (20%)	33 (12%)	0	8
39	BE	202/206 (98%)	121 (60%)	49 (24%)	32 (16%)	0	5
40	BF	205/210 (98%)	134 (65%)	44 (22%)	27 (13%)	0	7
41	BG	179/182 (98%)	113 (63%)	44 (25%)	22 (12%)	0	8
42	BH	164/180 (91%)	89 (54%)	37 (23%)	38 (23%)	0	2
43	BK	137/147 (93%)	89 (65%)	36 (26%)	12 (9%)	1	17
44	BL	65/121 (54%)	56 (86%)	9 (14%)	0	100	100
45	BN	136/140 (97%)	89 (65%)	31 (23%)	16 (12%)	0	9
46	BO	120/122 (98%)	94 (78%)	17 (14%)	9 (8%)	1	21
47	BP	144/150 (96%)	75 (52%)	44 (31%)	25 (17%)	0	4
48	BQ	139/141 (99%)	104 (75%)	28 (20%)	7 (5%)	3	31
49	BR	115/118 (98%)	79 (69%)	24 (21%)	12 (10%)	1	12
50	BS	96/112 (86%)	43 (45%)	34 (35%)	19 (20%)	0	3
51	BT	135/146 (92%)	76 (56%)	34 (25%)	25 (18%)	0	3
52	BU	115/118 (98%)	70 (61%)	33 (29%)	12 (10%)	1	12
53	BV	99/101 (98%)	67 (68%)	15 (15%)	17 (17%)	0	4
54	BW	111/113 (98%)	80 (72%)	18 (16%)	13 (12%)	0	9
55	BX	90/96 (94%)	62 (69%)	23 (26%)	5 (6%)	2	28
56	BY	104/110 (94%)	45 (43%)	35 (34%)	24 (23%)	0	2
57	BZ	182/206 (88%)	108 (59%)	41 (22%)	33 (18%)	0	4
All	All	6645/7104 (94%)	4378 (66%)	1475 (22%)	792 (12%)	1	9

5 of 792 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	13	ALA

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Mol	Chain	Res	Type
2	AB	20	GLU
2	AB	95	GLN
2	AB	190	THR
2	AB	195	ASP

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	AB	202/220 (92%)	178 (88%)	24 (12%)	6	31
3	AC	160/188 (85%)	133 (83%)	27 (17%)	2	18
4	AD	180/181 (99%)	158 (88%)	22 (12%)	6	31
5	AE	115/123 (94%)	101 (88%)	14 (12%)	6	31
6	AF	90/90 (100%)	80 (89%)	10 (11%)	8	34
7	AG	126/127 (99%)	113 (90%)	13 (10%)	9	37
8	AH	119/119 (100%)	106 (89%)	13 (11%)	8	35
9	AI	98/99 (99%)	88 (90%)	10 (10%)	9	37
10	AJ	88/92 (96%)	75 (85%)	13 (15%)	4	24
11	AK	90/99 (91%)	82 (91%)	8 (9%)	12	44
12	AL	104/109 (95%)	93 (89%)	11 (11%)	8	36
13	AM	99/101 (98%)	86 (87%)	13 (13%)	5	28
14	AN	49/50 (98%)	42 (86%)	7 (14%)	4	25
15	AO	79/80 (99%)	70 (89%)	9 (11%)	7	33
16	AP	72/74 (97%)	69 (96%)	3 (4%)	36	70
17	AQ	94/97 (97%)	86 (92%)	8 (8%)	13	48
18	AR	61/77 (79%)	58 (95%)	3 (5%)	31	67
19	AS	69/80 (86%)	59 (86%)	10 (14%)	4	24
20	AT	76/82 (93%)	66 (87%)	10 (13%)	5	28
21	AU	19/22 (86%)	19 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	AY	563/582 (97%)	481 (85%)	82 (15%)	4	24
25	B0	66/67 (98%)	56 (85%)	10 (15%)	3	22
26	B1	78/83 (94%)	64 (82%)	14 (18%)	2	15
27	B2	66/67 (98%)	58 (88%)	8 (12%)	6	31
28	B3	51/52 (98%)	47 (92%)	4 (8%)	16	51
29	B4	51/63 (81%)	36 (71%)	15 (29%)	0	3
30	B5	51/52 (98%)	45 (88%)	6 (12%)	6	32
31	B6	49/52 (94%)	37 (76%)	12 (24%)	1	6
32	B7	41/42 (98%)	34 (83%)	7 (17%)	2	17
33	B8	53/55 (96%)	46 (87%)	7 (13%)	5	28
34	B9	34/34 (100%)	28 (82%)	6 (18%)	2	16
37	BC	180/181 (99%)	162 (90%)	18 (10%)	9	38
38	BD	217/218 (100%)	178 (82%)	39 (18%)	2	15
39	BE	165/166 (99%)	141 (86%)	24 (14%)	4	24
40	BF	165/166 (99%)	154 (93%)	11 (7%)	20	57
41	BG	155/156 (99%)	129 (83%)	26 (17%)	2	19
42	BH	136/148 (92%)	118 (87%)	18 (13%)	5	28
43	BK	104/111 (94%)	88 (85%)	16 (15%)	3	22
44	BL	46/85 (54%)	41 (89%)	5 (11%)	8	35
45	BN	117/119 (98%)	95 (81%)	22 (19%)	2	13
46	BO	100/100 (100%)	92 (92%)	8 (8%)	15	50
47	BP	112/116 (97%)	86 (77%)	26 (23%)	1	7
48	BQ	111/111 (100%)	94 (85%)	17 (15%)	3	22
49	BR	100/101 (99%)	89 (89%)	11 (11%)	8	34
50	BS	77/88 (88%)	66 (86%)	11 (14%)	4	25
51	BT	120/127 (94%)	95 (79%)	25 (21%)	1	10
52	BU	92/94 (98%)	82 (89%)	10 (11%)	8	35
53	BV	82/82 (100%)	70 (85%)	12 (15%)	4	24
54	BW	91/92 (99%)	78 (86%)	13 (14%)	4	25
55	BX	74/78 (95%)	63 (85%)	11 (15%)	4	23
56	BY	87/91 (96%)	75 (86%)	12 (14%)	4	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	BZ	162/179 (90%)	134 (83%)	28 (17%)	2	17
All	All	5586/5868 (95%)	4824 (86%)	762 (14%)	9	27

5 of 762 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	B3	38	GLU
38	BD	61	LEU
54	BW	67	ASP
29	B4	32	TYR
33	B8	31	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 177 such sidechains are listed below:

Mol	Chain	Res	Type
26	B1	45	ASN
34	B9	29	ASN
53	BV	11	GLN
27	B2	9	GLN
30	B5	43	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1503/1522 (98%)	277 (18%)	47 (3%)
22	AV	76/77 (98%)	17 (22%)	0
23	AX	10/11 (90%)	5 (50%)	0
35	BA	2900/2915 (99%)	633 (21%)	77 (2%)
36	BB	118/122 (96%)	27 (22%)	2 (1%)
All	All	4607/4647 (99%)	959 (20%)	126 (2%)

5 of 959 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	9	G
1	AA	31	G
1	AA	32	A
1	AA	33	A
1	AA	39	G

5 of 126 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BA	331	A
35	BA	961	C
35	BA	2762	G
35	BA	363(F)	A
35	BA	614(C)	A

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](#)

2 ligands 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
58	FUA	AY	701	-	37,40,40	2.16	8 (21%)	51,64,64	1.88	12 (23%)
59	GDP	AY	702	-	24,30,30	1.57	4 (16%)	26,47,47	2.06	8 (30%)

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
58	FUA	AY	701	-	-	0/10/92/92	0/4/4/4
59	GDP	AY	702	-	-	0/12/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	AY	701	FUA	C23-C22	-7.71	1.37	1.51
58	AY	701	FUA	C23-C24	-3.98	1.39	1.53
58	AY	701	FUA	C15-C14	-3.78	1.46	1.54
58	AY	701	FUA	C19-C10	-3.61	1.47	1.54
58	AY	701	FUA	C24-C25	-3.21	1.38	1.50

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	AY	701	FUA	C8-C9-C10	-6.40	109.63	116.47
59	AY	702	GDP	C4'-O4'-C1'	-4.90	104.45	109.64
59	AY	702	GDP	N3-C2-N1	-4.66	121.22	127.56
59	AY	702	GDP	C5-C6-N1	-4.08	118.19	123.52
58	AY	701	FUA	C6-C5-C10	-4.00	106.16	111.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	AY	701	FUA	12	0
59	AY	702	GDP	7	0

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.