



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:42 PM BST

PDB ID : 4V6Q
EMDB ID: : EMD-5363
Title : Structural characterization of mRNA-tRNA translocation intermediates (class 5 of the six classes)
Authors : Agirrezabala, X.; Liao, H.; Schreiner, E.; Fu, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on : 2011-12-08
Resolution : 11.50 Å(reported)
Based on PDB ID : 2I2U

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

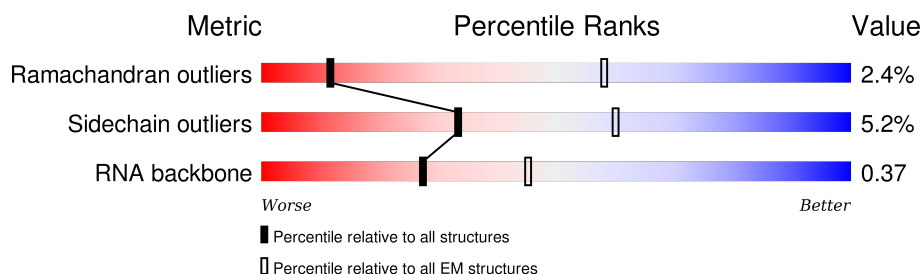
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

1 Overall quality at a glance

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

The reported resolution of this entry is 11.50 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)
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	1542	
2	AB	76	
3	AC	47	
4	AD	77	
5	AE	240	
6	AF	232	
7	AG	205	
8	AH	166	
9	AI	135	














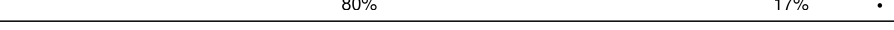







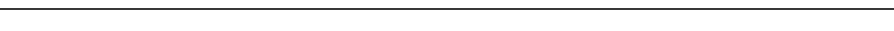


Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
10	AJ	178	
11	AK	129	
12	AL	129	
13	AM	103	
14	AN	128	
15	AO	123	
16	AP	117	
17	AQ	100	
18	AR	88	
19	AS	82	
20	AT	83	
21	AU	74	
22	AV	91	
23	AW	86	
24	AX	70	
25	BA	120	
26	BB	2904	
27	BC	234	
28	BD	272	
29	BE	209	
30	BF	201	
31	BG	178	
32	BH	176	
33	BI	149	
34	BJ	164	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
35	BK	141	 88% 12%
36	BL	142	 73% 23% .
37	BM	123	 76% 18% 6% .
38	BN	144	 76% 20% . .
39	BO	136	 76% 20% .
40	BP	127	 76% 20% .
41	BQ	117	 82% 14% .
42	BR	114	 73% 25% . .
43	BS	117	 75% 21% .
44	BT	103	 73% 21% 6%
45	BU	110	 77% 18% 5%
46	BV	100	 74% 22% .
47	BW	103	 83% 16% .
48	BX	94	 80% 17% .
49	BY	84	 77% 18% 5%
50	BZ	77	 71% 23% 5%
51	B0	63	 78% 17% 5%
52	B1	58	 81% 14% 5%
53	B2	70	 74% 23% .
54	B3	56	 80% 18% .
55	B4	54	 80% 17% .
56	B5	46	 72% 22% 7%
57	B6	64	 80% 17% .
58	B7	38	 76% 18% 5%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 152351 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1542	Total	C	N	O	P	0	0
			33089	14767	6064	10717	1541		

- Molecule 2 is a RNA chain called A site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AB	76	Total	C	N	O	P	S	0	0
			1627	731	287	532	75	2		

- Molecule 3 is a RNA chain called mRNA.

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

- Molecule 4 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AD	77	Total	C	N	O	P	S	0	0
			1641	734	297	533	76	1		

- Molecule 5 is a protein called 30S ribosomal protein S2.

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

- Molecule 6 is a protein called 30S ribosomal protein S3.

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

- Molecule 7 is a protein called 30S ribosomal protein S4.

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

- Molecule 8 is a protein called 30S ribosomal protein S5.

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

- Molecule 9 is a protein called 30S ribosomal protein S6.

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

- Molecule 10 is a protein called 30S ribosomal protein S7.

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

- Molecule 11 is a protein called 30S ribosomal protein S8.

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

- Molecule 12 is a protein called 30S ribosomal protein S9.

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

- Molecule 13 is a protein called 30S ribosomal protein S10.

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

- Molecule 14 is a protein called 30S ribosomal protein S11.

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

- Molecule 15 is a protein called 30S ribosomal protein S12.

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

- Molecule 16 is a protein called 30S ribosomal protein S13.

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

- Molecule 17 is a protein called 30S ribosomal protein S14.

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

- Molecule 18 is a protein called 30S ribosomal protein S15.

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

- Molecule 19 is a protein called 30S ribosomal protein S16.

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

- Molecule 20 is a protein called 30S ribosomal protein S17.

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

- Molecule 21 is a protein called 30S ribosomal protein S18.

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

- Molecule 22 is a protein called 30S ribosomal protein S19.

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

- Molecule 23 is a protein called 30S ribosomal protein S20.

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

- Molecule 24 is a protein called 30S ribosomal protein S21.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BA	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	BB	2904	Total	C	N	O	P	0	0
			62351	27824	11469	20155	2903		

- Molecule 27 is a protein called 50S ribosomal protein L1.

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

- Molecule 28 is a protein called 50S ribosomal protein L2.

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

- Molecule 29 is a protein called 50S ribosomal protein L3.

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

- Molecule 30 is a protein called 50S ribosomal protein L4.

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

- Molecule 31 is a protein called 50S ribosomal protein L5.

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

- Molecule 32 is a protein called 50S ribosomal protein L6.

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

- Molecule 33 is a protein called 50S ribosomal protein L9.

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

- Molecule 34 is a protein called 50S ribosomal protein L10.

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

- Molecule 35 is a protein called 50S ribosomal protein L11.

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

- Molecule 36 is a protein called 50S ribosomal protein L13.

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

- Molecule 37 is a protein called 50S ribosomal protein L14.

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

- Molecule 38 is a protein called 50S ribosomal protein L15.

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

- Molecule 39 is a protein called 50S ribosomal protein L16.

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

- Molecule 40 is a protein called 50S ribosomal protein L17.

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

- Molecule 41 is a protein called 50S ribosomal protein L18.

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

- Molecule 42 is a protein called 50S ribosomal protein L19.

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

- Molecule 43 is a protein called 50S ribosomal protein L20.

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

- Molecule 44 is a protein called 50S ribosomal protein L21.

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

- Molecule 45 is a protein called 50S ribosomal protein L22.

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

- Molecule 46 is a protein called 50S ribosomal protein L23.

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

- Molecule 47 is a protein called 50S ribosomal protein L24.

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

- Molecule 48 is a protein called 50S ribosomal protein L25.

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

- Molecule 49 is a protein called 50S ribosomal protein L27.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B0	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 52 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 53 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B2	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 54 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 55 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	B4	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 56 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	B5	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

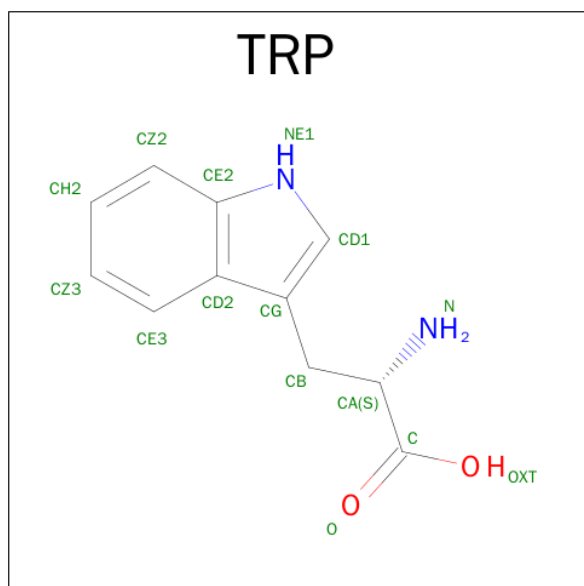
- Molecule 57 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	B6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 58 is a protein called 50S ribosomal protein L36.

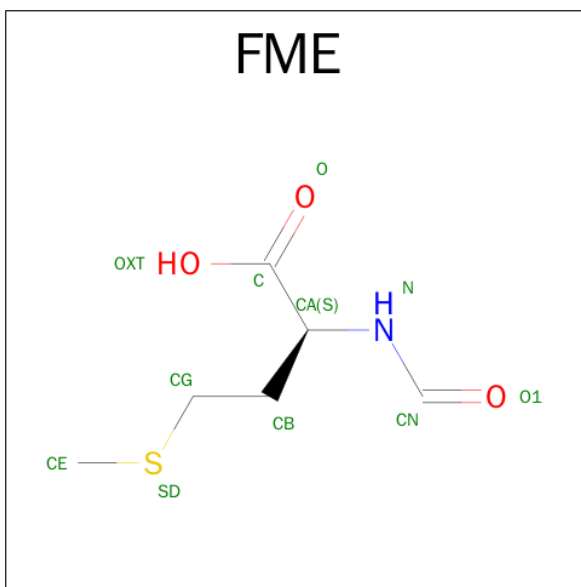
Mol	Chain	Residues	Atoms					AltConf	Trace
58	B7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 59 is TRYPTOPHAN (three-letter code: TRP) (formula: $C_{11}H_{12}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
59	AB	1	Total	C	N	O	0
			14	11	2	1	

- Molecule 60 is N-FORMYLMETHIONINE (three-letter code: FME) (formula: $C_6H_{11}NO_3S$).

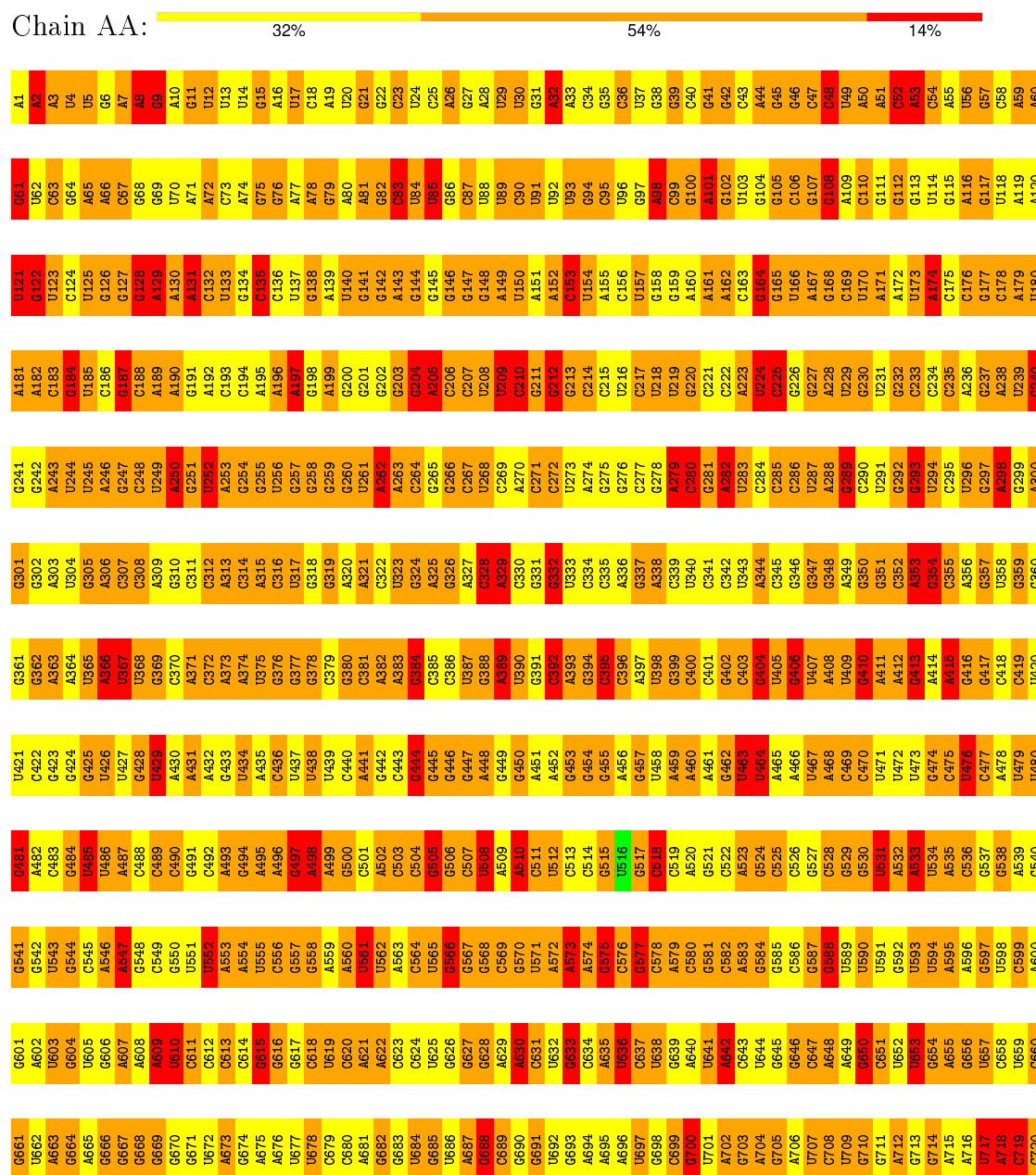


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	BB	1	10	6	1	2	1	0

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 ribosomal RNA



C1501	A1441	U1321	A1261	A1201	C1141	A1081	A1021	U961	A901	C841	A781	G721
A1502	G1442	C1322	C1262	U1202	G1142	A1082	A1022	C962	G902	U842	A782	G722
A1503	C1383	A1323	C1263	C1203	G1143	U1083	U1023	G1083	G903	U843	A783	U723
G1504	U1444	A1324	U1264	A1204	G1084	G1084	G1024	A964	U904	A844	C784	G724
G1505	G1385	C1325	C1265	G1205	A1145	U1085	U1025	U965	U905	A845	G785	G725
U1506	A1445	U1326	G1266	G1206	A1146	U1086	G1026	G966	A906	G846	G786	G726
G1507	G1387	C1327	C1267	G1207	C1147	G1087	C1027	C967	A907	G847	A787	G727
A1508	C1388	C1328	G1268	C1208	U1148	G1088	C1028	U968	A908	G848	U788	A728
C1509	A1329	A1269	C1269	C1209	C1149	G1089	U1029	A969	A909	G849	U789	A729
C1510	U1330	G1270	G1270	C1210	A1150	U1090	U1030	G970	C910	U850	A790	G730
G1511	U1331	A1271	C1271	U1211	A1151	U1091	C1031	G971	U911	G851	G791	G731
U1512	C1332	G1272	C1272	U1212	A1152	A1092	G1032	C972	C912	G852	U792	G732
A1513	A1333	C1273	C1273	A1213	G1153	U1093	G1033	G973	A913	C853	U793	G733
G1514	G1334	A1274	A1274	C1214	G1094	U1094	G1034	A974	A914	U854	A794	G734
G1515	C1335	A1275	A1275	G1215	U1095	U1095	A1035	A975	A915	U855	C795	G735
G1516	U1336	C1336	G1276	A1216	G1156	C1096	A1036	G976	U916	C856	C796	C736
G1517	C1337	G1337	C1277	C1217	A1157	C1097	C1037	A977	G917	C857	U797	C737
C1520	G1458	G1338	G1278	C1218	C1158	C1098	C1038	A978	A918	G858	U798	G738
U1521	A1339	A1339	G1279	A1219	U1159	G1099	G1039	C979	A919	G859	G799	C739
G1522	C1460	A1340	A1280	G1220	C1160	C1100	U1040	C980	U920	A860	G800	U740
G1523	G1461	U1341	C1281	G1221	A1161	A1101	G1041	U981	U921	A861	U801	G741
G1524	C1462	C1342	C1282	G1222	C1162	A1102	A1042	U982	G922	C862	A802	G742
G1525	U1463	G1343	U1283	C1223	A1163	C1103	G1043	A983	A923	U863	G803	A743
G1526	U1464	C1344	C1284	U1224	G1164	G1104	A1044	C984	C924	A864	U804	C744
G1527	A1465	U1345	A1285	A1225	U1165	A1105	C1045	C985	G925	A865	C805	G745
U1528	C1466	A1346	U1286	C1226	G1166	G1106	A1046	U986	G926	C866	C806	A746
G1529	G1467	G1347	A1287	A1227	A1167	C1107	G1047	G987	G927	G867	A807	A747
G1530	A1468	U1348	C1288	C1228	U1168	G1108	A1048	C988	G928	C868	C808	G748
A1531	C1469	A1349	A1289	A1229	A1169	C1109	U1049	U989	G929	G869	A749	A749
U1532	U1470	A1350	G1290	C1230	A1170	A1110	G1050	C990	C930	U870	C810	C750
C1533	U1471	C1351	U1291	G1231	A1171	A1111	C1051	U991	C931	U871	C811	U751
U1534	U1472	C1352	G1292	U1232	C1172	C1112	U1052	C992	C932	A872	G812	G752
C1535	G1473	G1353	C1293	G1233	U1173	C1113	G1053	G993	G933	A873	U813	A753
C1536	U1474	U1354	G1294	U1234	G1174	C1114	A1054	C994	C934	C874	A814	C754
U1537	G1475	G1355	U1295	U1235	G1175	C1115	A1055	C995	A935	U875	A815	G755
C1538	A1476	G1356	C1296	A1236	A1176	U1116	U1056	A996	C936	C876	A816	C756
G1539	U1477	U1357	G1297	C1237	G1177	A1117	G1057	U997	A937	G877	C817	U757
U1540	U1478	U1358	U1298	A1238	G1178	U1118	G1058	C998	A938	A878	G818	C758
A1541	C1479	C1359	A1299	A1239	A1179	C1119	C1059	C999	G939	C879	A819	A759
U1542	U1480	A1360	G1300	U1240	A1180	C1120	U1060	A1000	C940	C880	U820	G760
C1543	G1481	G1361	U1301	G1241	G1181	U1121	G1061	C1001	G941	G881	G821	G761
C1544	G1482	A1362	C1302	G1242	G1182	U1122	U1062	C882	G942	C882	U822	U762
G1545	A1483	A1363	G1303	C1243	U1183	U1123	C1063	G1003	U943	C883	C823	G763
U1546	C1484	U1364	G1304	G1244	G1184	G1124	G1064	A1004	G944	U884	G824	C764
U1547	U1485	G1365	G1305	C1245	G1185	U1125	U1065	A1005	G945	G885	A825	G765
G1548	G1486	C1366	A1306	A1246	G1186	U1126	C1066	C946	A946	G886	C826	A766
U1549	G1487	C1367	U1307	U1247	G1187	G1127	A1067	G947	G947	C887	U827	A767
G1550	G1488	A1368	U1308	A1248	A1188	C1128	G1068	U1008	C948	G888	U828	A768
U1551	G1489	C1369	G1309	C1249	U1189	G1129	C1069	U1009	A949	A889	G829	G769
A1552	U1490	G1370	G1310	A1250	G1190	A1130	U1070	U1010	U950	G890	G830	C770
G1553	A1491	G1371	A1311	A1251	A1191	C1131	C1071	C1011	G951	U891	A831	G771
U1554	G1492	U1372	G1312	A1252	C1192	C1132	G1072	A892	U952	A892	G832	U772
C1555	A1493	G1373	U1313	G1253	G1193	C1133	U1073	G893	G953	C893	G833	G773
U1556	G1494	A1374	C1314	A1254	U1194	G1134	G1074	G894	G954	G894	U834	G774
G1557	U1495	G1375	U1315	G1255	C1195	U1135	U1075	G895	U955	G895	U835	G775
U1558	U1496	U1376	G1316	A1256	G1196	C1136	U1076	C896	U956	G896	G836	G776
G1559	G1497	A1377	C1317	A1257	A1197	C1137	G1077	U897	U957	C897	U837	A777
U1560	U1498	C1378	A1318	C1258	G1198	G1138	U1078	A958	A958	G898	G838	G778
G1561	A1499	G1379	A1319	C1259	G1199	G1139	G1079	C899	A959	C899	C839	C779
C1562	U1500	U1380	C1320	G1260	C1200	C1140	A1080	G1020	U960	A900	C840	A780

• Molecule 2: A site tRNA

Chain AB:  5% 34% 38% 22%

A1	C56
G2	A58
G3	G59
G4	U60
G5	C61
C6	
G7	
U8	
A9	
G10	
U11	
U12	
C13	
A14	
A15	
U16	
U17	
G18	
G19	
U20	
A21	
G22	
A23	
G24	
G25	
A26	
C27	
G28	
G29	
G30	
U31	
C32	
U33	
C34	
C35	
A36	
A37	
A38	
A39	
C40	
C41	
C42	
G43	
C44	
U45	
G46	
U47	
U48	
G49	
G50	
G51	
A52	
C53	
C54	
G55	
A56	
G57	
A58	
G59	
U60	
C61	



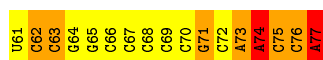
- Molecule 3: mRNA

Chain AC: 19% 49% 32%



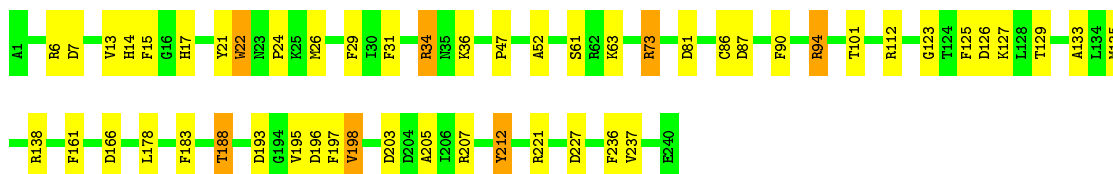
- Molecule 4: P site tRNA

Chain AD: 36% 49% 12%



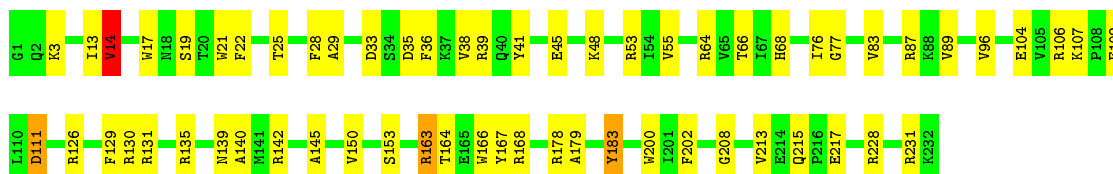
- Molecule 5: 30S ribosomal protein S2

Chain AE: 78% 19%



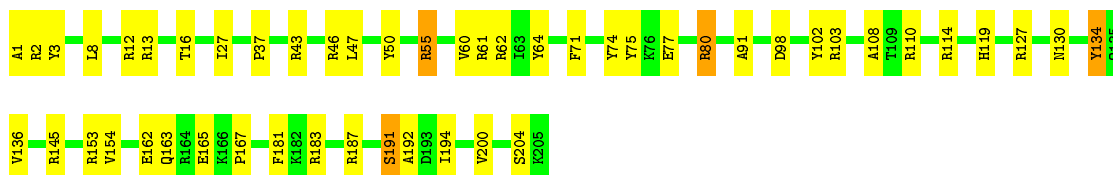
- Molecule 6: 30S ribosomal protein S3

Chain AF: 74% 25%

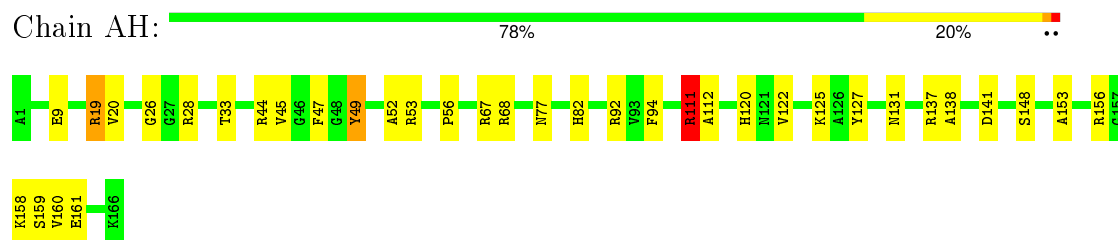


- Molecule 7: 30S ribosomal protein S4

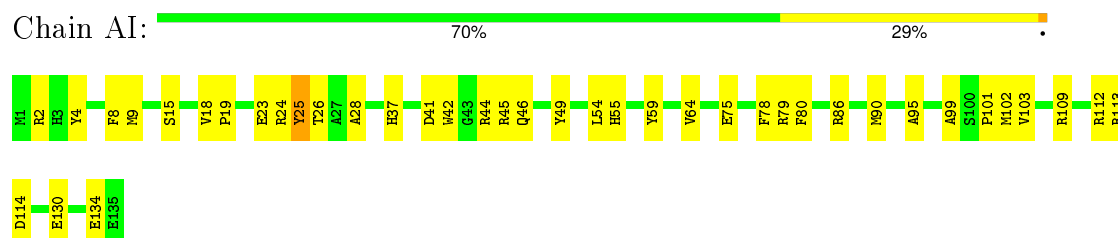
Chain AG: 76% 22%



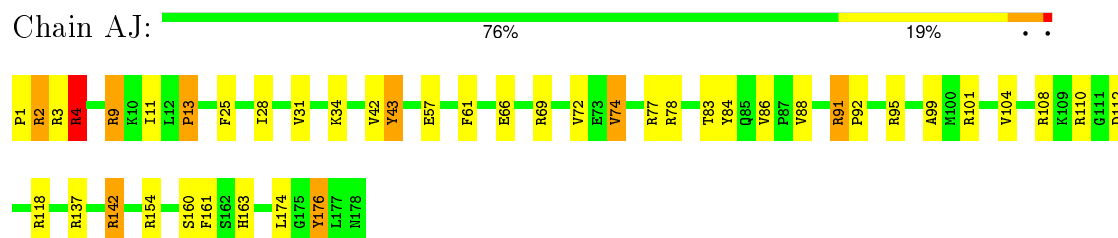
- Molecule 8: 30S ribosomal protein S5



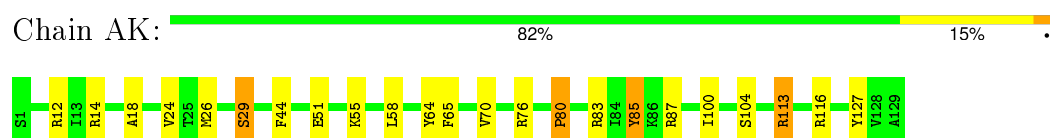
- Molecule 9: 30S ribosomal protein S6



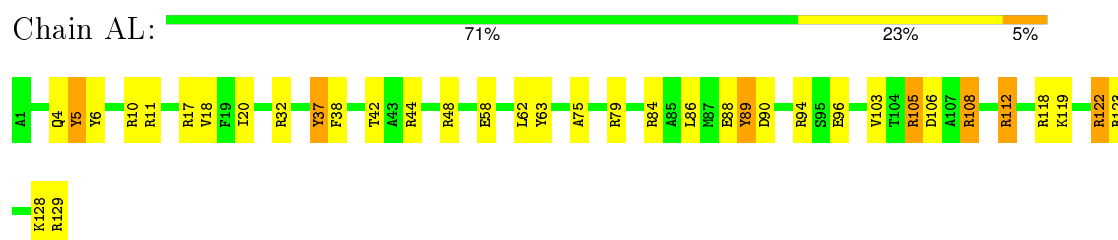
- Molecule 10: 30S ribosomal protein S7



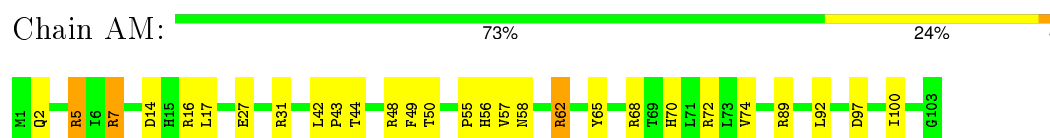
- Molecule 11: 30S ribosomal protein S8



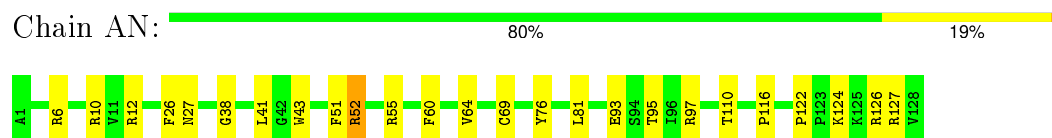
- Molecule 12: 30S ribosomal protein S9



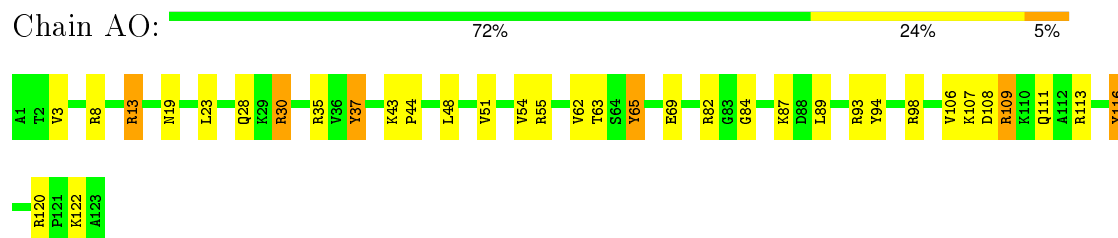
- Molecule 13: 30S ribosomal protein S10



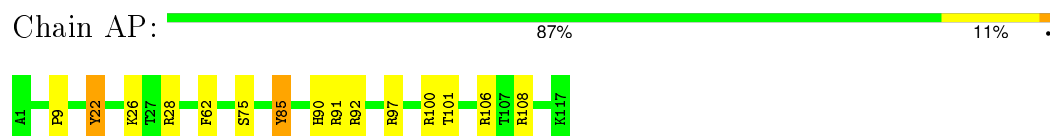
- Molecule 14: 30S ribosomal protein S11



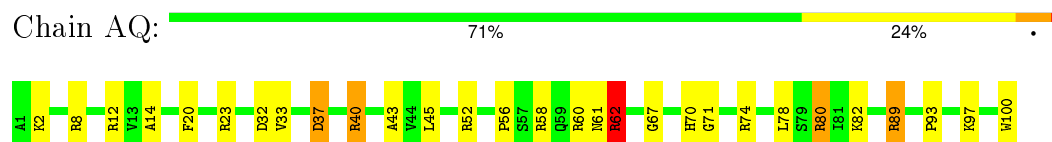
- Molecule 15: 30S ribosomal protein S12



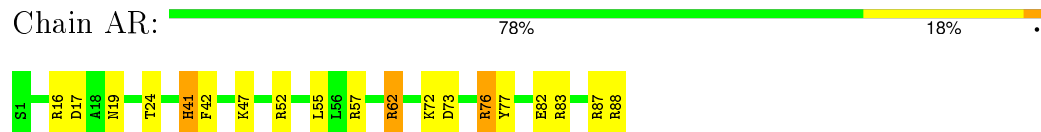
- Molecule 16: 30S ribosomal protein S13



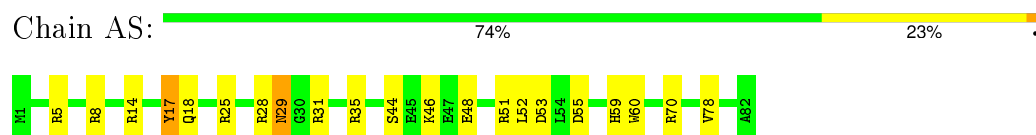
- Molecule 17: 30S ribosomal protein S14



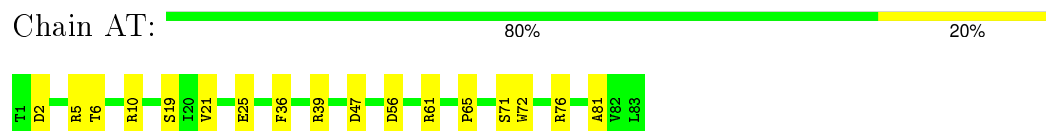
- Molecule 18: 30S ribosomal protein S15



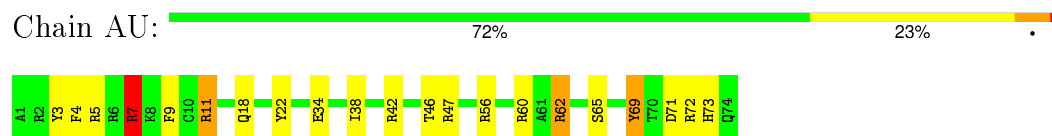
- Molecule 19: 30S ribosomal protein S16



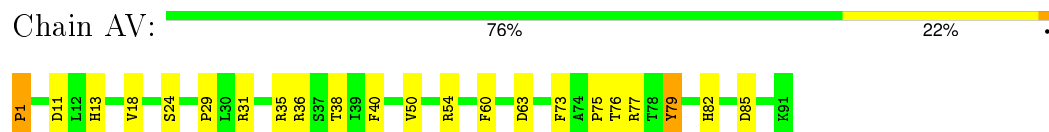
- Molecule 20: 30S ribosomal protein S17



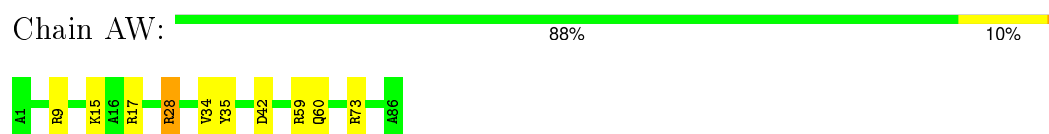
- Molecule 21: 30S ribosomal protein S18



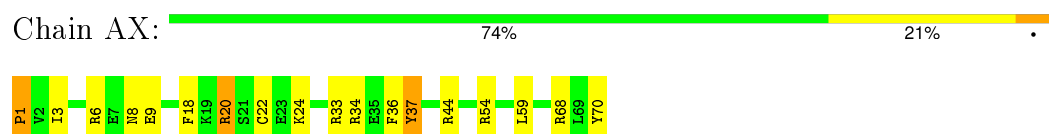
- Molecule 22: 30S ribosomal protein S19



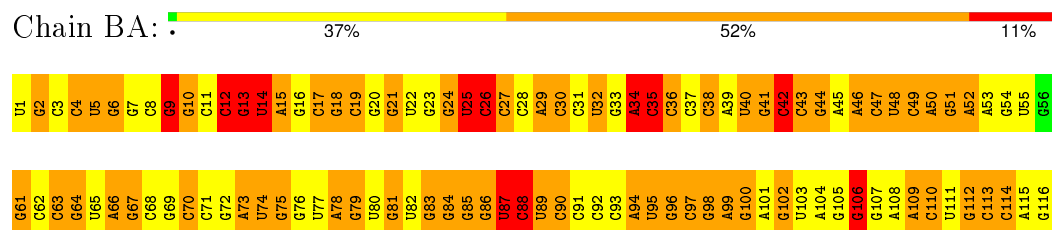
- Molecule 23: 30S ribosomal protein S20



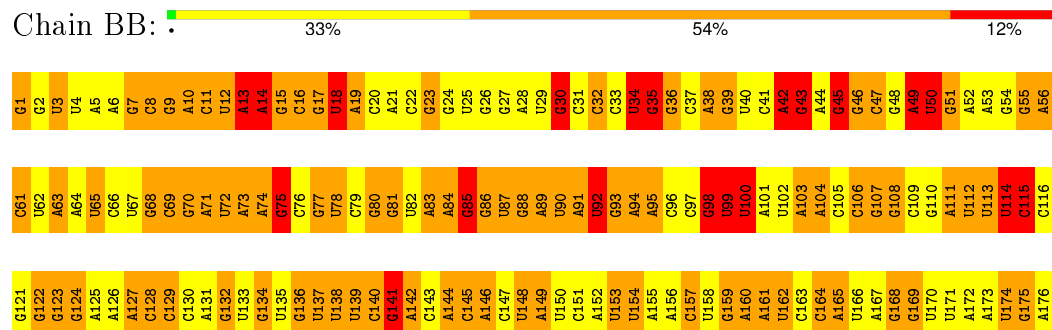
- Molecule 24: 30S ribosomal protein S21



- Molecule 25: 5S ribosomal RNA



- Molecule 26: 23S ribosomal RNA




A1142	U1082	G1022	G962	C902	A661	C601	A541	G481	C421	G301	A241	A181
A1143	U1083	U1023	U963	C903	G662	A602	C542	A462	A422	C302	G241	A182
A1144	A1084	G1024	G964	G904	G663	A603	G543	A463	A423	G303	G242	C183
C1145	A1085	G1025	C965	A905	G664	G604	C544	C464	G424	U304	U243	C184
C1146	A1086	G1026	G966	U906	U665	G605	U545	C465	G245	C305	G244	G186
C1147	G1087	U1027	U967	G907	A666	U606	U546	C466	C246	U306	C245	G186
U1148	A1088	A1028	C968	C908	U667	U607	A547	C467	U247	G307	G247	G187
G1149	A1089	A1029	G969	A909	A668	A608	G548	G468	A428	G308	G248	G188
C1150	C1030	U1030	U970	A910	G669	A609	G549	G469	A429	A309	C249	G189
A1151	G1091	G1031	A911	C911	A670	C610	C550	C490	A430	A310	A250	A190
C1152	C1092	A1032	G972	C912	C671	C611	G551	G491	U431	A311	A251	A191
C1153	G1093	U1033	G973	U913	C672	G612	U552	A492	A432	G312	G252	C192
G1154	U1094	G1034	G974	G914	G673	A613	G553	G493	C433	G313	C253	U193
A1155	A1095	U1035	A975	C915	G674	A614	U554	G494	U434	C314	G254	G194
A1156	A1096	G1036	G976	G916	A675	U615	G555	G495	C435	G315	A255	A195
G1157	U1097	G1037	G977	A917	A676	A616	A556	G496	C436	C316	A256	A196
C1158	G1098	G1038	G978	A918	A677	G617	C557	A497	U437	G317	C257	A197
U1159	G1099	A1039	G979	U919	C678	G618	U558	G498	U438	C318	G258	C198
G1160	C1100	A1040	A980	A920	C679	G619	G559	U499	A439	G319	G259	A199
C1161	U1101	G1041	A881	C921	C680	G620	C560	G500	C440	A320	G260	U200
G1162	C1102	C922	C982	C922	A681	A621	G561	A501	U441	U321	C261	C201
G1163	A1103	C1043	A983	G923	A682	G622	U562	A502	A442	A322	A262	U202
C1164	C1104	G924	A984	G924	U683	C623	A563	A503	A443	C323	G263	A203
A1165	U1105	C1045	C985	A925	G684	C624	C564	A504	C444	A324	C264	C204
G1166	G1106	A1046	C986	G926	A685	G625	C565	A505	C445	C325	A265	G205
C1167	G1107	G1047	C987	A927	U686	A626	U566	G506	G446	G326	G266	U206
G1168	U1108	A1048	A988	A928	U687	A627	U567	A507	A447	G327	C267	A207
A1169	C1109	G1049	G989	U929	U688	G628	U568	A508	U448	U328	C268	C208
C1170	G1110	U1050	A990	G930	A689	G629	U569	C509	A449	G329	C269	C209
G1171	A1111	G1051	U981	U931	G690	G630	U570	C510	A450	U330	A270	C210
C1172	G1112	C1052	C992	U932	C691	A631	U571	U511	U451	C331	G271	C211
U1173	U1113	C1053	G993	A933	C692	A632	A572	A512	G452	U332	A272	G212
U1174	A1114	A1054	C994	U934	A693	A633	U573	A513	A453	G333	G273	A213
A1175	G1115	G1055	C995	G935	U694	C634	A574	A514	C454	C334	C274	G214
U1176	U1116	A1056	A996	A936	G695	C635	A575	A515	C455	U335	C275	G215
G1177	C1117	A1057	G997	C937	U696	G636	U576	C516	C456	C336	U276	A216
C1178	G1118	U1058	C998	G938	G697	A637	G577	G517	A457	C337	G277	A217
G1179	U1119	G1059	U999	G939	C698	C638	G578	G518	G458	C338	A278	A218
U1180	G1120	U1060	A1000	G940	A699	U639	G579	U519	U459	U339	A279	A219
U1181	C1121	U1061	A1001	A941	G700	C640	U580	G520	G460	A340	U280	G220
G1182	G1122	G1062	G1002	G942	G701	U641	C581	U521	C461	C341	C281	A221
U1183	C1123	G1063	G1003	A943	U702	U642	A582	A522	C462	A342	A282	A222
U1184	G1124	C1064	U1004	C944	U703	A643	G583	C523	G463	C343	G283	A223
G1185	U1125	U1065	A945	A945	G704	A644	C584	G524	U464	A344	U284	U224
G1186	A1126	U1066	C946	C946	A705	C645	G585	U525	G465	A345	G285	C225
U1187	G1127	A1067	C1007	A947	U706	U646	A586	A526	A466	A346	U286	A226
U1188	G1128	G1068	C948	G948	G707	G647	C587	C527	G467	A347	G287	A227
A1189	A1129	A1069	A1009	G949	U708	G648	U588	A528	G468	A348	U288	C228
G1190	U1130	A1070	A1010	G950	U709	G649	U589	A529	G469	U349	G289	C229
G1191	G1131	G1071	G1011	C951	U710	C650	A590	G530	A470	G350	U290	G230
G1192	U1132	C1072	U1012	G952	G711	G651	U591	C531	A471	C351	G291	A231
G1193	A1133	A1073	C1013	G953	G712	U652	A592	A532	A472	A352	U292	G232
A1194	A1134	G1074	U894	G954	G713	U653	U593	G533	C473	C353	U293	A233
G1195	C1135	C1075	U1015	U955	U714	A654	U594	U534	G474	A354	A294	U234
C1196	G1136	G1076	G956	A956	A715	A655	C595	G535	C475	U355	G295	U235
G1197	G1137	A1077	C957	C957	U716	G656	U596	G536	G476	U356	U296	C236
U1198	G1138	U1078	U958	U958	G717	U657	G597	G537	A477	C357	G297	C237
G1199	G1139	C1079	A959	A959	G718	U658	U598	A538	A478	U358	G298	C238
C1200	C1140	A1080	U960	A960	C719	G659	U599	A539	A479	G359	A299	C239
U1201	U1141	U1081	A1021	C961	U720	C660	G600	C540	A480	U360	A300	C240

G2102	A2042	U1982	G1922	A1802	U1742	G1682	G1622	U1562	A1502	U1442	G1382	A1322	A1262	G1202
C2103	C2043	G1983	U1923	A1803	G1743	U1683	G1623	U1563	A1503	U1443	A1383	C1323	U1263	U1203
C2104	C2044	G1984	C1924	A1804	A1744	G1684	G1624	C1564	A1504	G1444	A1384	G1324	A1264	A1204
U2105	C2045	G1985	C1925	A1805	A1745	G1685	C1625	C1565	A1505	G1445	A1385	U1325	A1265	A1205
U2106	G2046	G1986	U1926	A1806	U1746	G1686	A1626	A1566	U1506	G1446	G1386	U1326	G1266	G1206
G2107	C2047	A1987	G1927	A1807	U1747	G1687	G1627	G1567	U1507	G1447	A1387	A1327	U1267	C1207
A2108	G2048	G1988	A1928	A1808	C1748	U1688	G1628	G1568	A1508	G1448	G1388	A1328	A1268	G1208
U2109	G2049	G1989	G1929	A1809	A1749	U1689	G1629	A1569	A1509	G1449	G1389	U1329	A1269	U1209
G2110	C2050	G1990	G1930	A1810	G1750	A1690	A1630	A1570	G1510	G1450	C1330	C1270	G1210	G1210
U2111	A2051	U1991	U1931	G1811	U1751	G1691	A1631	A1571	A1391	C1451	A1391	G1331	G1271	C1211
G2112	A2052	G1992	A1932	U1812	C1752	U1692	A1632	A1572	C1512	G1452	A1272	G1332	A1272	G1212
U2113	G2053	U1993	G1933	G1813	A1753	U1693	G1633	G1573	A1393	A1453	G1333	G1333	G1273	A1213
A2114	A2054	C1994	C1934	G1814	G1754	G1694	A1634	C1574	G1514	C1454	A1274	G1334	A1274	A1214
G2115	C2055	U1995	G1935	A1815	A1755	G1695	A1635	C1575	A1515	G1455	A1275	C1335	A1275	G1215
G2116	G2056	G1996	A1936	G1816	G1756	G1696	U1636	G1576	U1396	G1456	U1396	A1336	A1276	G1216
A2117	C2057	A1997	U1937	G1817	A1757	G1697	A1637	U1577	U1397	U1457	G1277	G1337	G1277	U1217
U2118	A2058	G1998	A1938	U1818	U1758	A1698	G1638	U1578	C1398	G1458	C1398	G1338	C1278	G1218
A2119	A2059	G1999	U1939	A1819	A1759	G1699	G1639	A1579	G1459	G1459	G1399	G1339	G1279	U1219
G2120	A2060	C2000	U1940	U1820	C1760	A1700	A1640	A1580	U1520	U1460	U1400	U1340	G1280	G1220
G2121	G2061	C2001	C1941	A1821	C1761	A1701	A1641	G1581	G1521	C1461	G1401	G1341	G1281	C1221
U2122	A2062	G2002	C1942	U1822	A1762	G1702	A1642	A1582	A1402	C1462	U1402	A1342	U1282	U1222
G2123	C2063	A2003	U1943	G1823	G1763	G1703	G1643	A1583	U1523	G1463	A1403	G1343	G1283	G1223
G2124	C2064	G2004	U1944	G1824	C1764	C1704	A1644	U1584	G1524	G1464	C1404	U1344	A1284	U1224
G2125	C2065	A2005	G1945	U1825	U1765	A1705	G1645	A1585	A1525	G1465	U1405	C1345	A1285	G1225
A2126	C2066	C2006	U1946	G1826	G1766	C1706	G1646	A1586	C1526	U1466	U1406	G1346	A1286	G1226
G2127	G2067	U2007	C1947	U1827	G1767	G1707	U1647	G1587	G1527	U1467	G1407	A1347	A1287	G1227
G2128	U2068	C2008	G1948	G1828	C1768	C1708	U1648	G1588	A1528	U1468	G1408	C1348	G1288	G1228
C2129	C2069	A2009	G1949	A1829	U1769	U1709	G1649	U1589	U1529	U1469	U1409	G1349	C1229	C1229
U2130	A2070	G2010	U1950	G1830	G1770	G1710	A1650	A1590	G1530	A1470	C1350	G1350	C1290	A1230
U2131	A2071	U2011	U1951	G1831	C1771	A1711	A1651	A1591	C1531	G1471	U1411	C1351	C1291	U1231
U2132	C2072	G2012	A1952	C1832	A1772	U1712	A1652	C1592	A1532	C1472	U1412	U1352	G1292	G1232
G2133	C2073	A2013	A1953	C1833	A1773	A1713	G1653	A1593	C1533	G1473	A1413	A1353	C1293	C1233
A2134	C2074	U2014	G1954	U1834	C1774	U1714	A1654	U1594	U1534	U1474	C1414	A1354	U1294	U1234
A2135	U2075	A2015	U1955	G1835	U1775	G1715	A1655	C1595	A1535	G1475	U1415	G1355	C1295	G1235
G2136	U2076	U2016	G1956	G1836	G1776	A1716	G1656	A1596	G1536	G1476	G1416	G1356	G1296	G1236
U2137	A2077	U2017	G1957	C1837	U1777	A1717	U1657	A1597	G1537	A1477	C1417	C1357	G1297	A1237
G2138	C2078	G2018	C1958	G1838	U1778	G1718	G1658	A1598	G1538	G1478	G1418	G1358	G1298	G1238
U2139	U2079	A2019	G1959	G1839	U1779	G1719	G1659	U1599	U1539	G1479	A1419	A1359	G1299	G1239
G2140	A2080	A2020	A1960	G1840	A1780	U1720	G1660	C1600	G1540	C1480	A1420	G1360	G1300	U1240
G2141	U2081	C2021	C1961	U1841	U1781	G1721	G1661	G1601	U1541	U1481	G1421	G1361	A1301	A1241
A2142	A2082	U2022	C1962	G1842	U1782	A1722	U1662	U1602	U1542	G1482	G1422	C1362	A1302	U1242
C2143	G2083	G1903	C1843	C1843	A1783	G1723	G1663	A1603	G1543	G1483	G1423	C1363	C1303	C1243
G2144	C2084	G1904	G1844	C1844	A1784	G1724	A1664	C1604	A1544	U1484	G1424	G1364	A1304	A1244
C2145	U2085	C1905	G1845	G1845	A1785	U1725	A1665	C1605	A1545	U1485	G1425	A1365	C1305	G1245
C2146	U2086	U2026	G1906	G1846	A1786	C1726	G1666	C1606	G1546	U1486	G1426	A1366	C1306	A1246
A2147	G2087	C1907	G1907	A1847	A1787	C1727	G1667	C1607	C1547	U1487	A1427	A1367	A1307	A1247
G2148	A2088	U2028	G1968	A1848	C1788	G1728	A1668	A1608	A1548	C1488	G1428	G1368	A1308	G1248
U2149	C2089	G2029	G1909	G1849	A1789	U1729	A1669	A1609	A1549	C1489	G1429	G1369	A1309	U1249
C2150	A2090	U1970	G1910	G1850	C1790	G1730	C1670	A1610	G1550	A1490	G1430	C1370	G1310	G1250
U2151	C2091	U1971	U1911	U1851	A1791	G1731	U1671	C1611	A1551	G1491	A1431	G1371	G1311	C1251
G2152	U2092	G2032	G1972	U1852	G1792	C1732	A1672	C1612	A1552	G1492	G1432	U1372	U1312	G1252
C2153	G2093	A2033	G1973	A1853	C1793	G1733	G1673	G1613	A1553	G1493	A1433	A1373	U1313	A1253
A2154	A2094	U2034	C1974	A1854	A1794	G1734	G1674	A1614	U1554	A1494	A1434	G1374	C1314	A1254
U2155	A2095	G2035	G1975	U1855	C1795	A1735	C1675	C1615	G1555	A1495	G1435	U1375	G1315	U1255
G2156	C2096	U2036	U1976	G1856	U1796	U1736	A1676	A1616	C1556	A1496	G1436	G1376	U1316	G1256
G2157	A2097	U2037	G1977	G1857	G1797	G1737	A1677	C1617	C1557	U1497	C1437	G1377	G1317	C1257
A2158	U2098	G2038	A1978	A1858	U1798	G1738	A1678	U1618	C1558	C1498	U1438	A1378	U1318	U1258
G2159	U2099	U2039	A1979	U1859	G1799	A1739	A1679	G1619	U1559	C1499	A1439	U1379	G1319	G1259
C2160	G2100	G2040	G1980	G1860	C1800	G1740	A1680	G1620	U1560	U1440	G1320	G1380	A1260	C1260
C2161	A2101	U2041	A1981	G1861	A1801	C1741	G1681	U1621	C1561	G1501	G1441	G1381	A1321	G1261

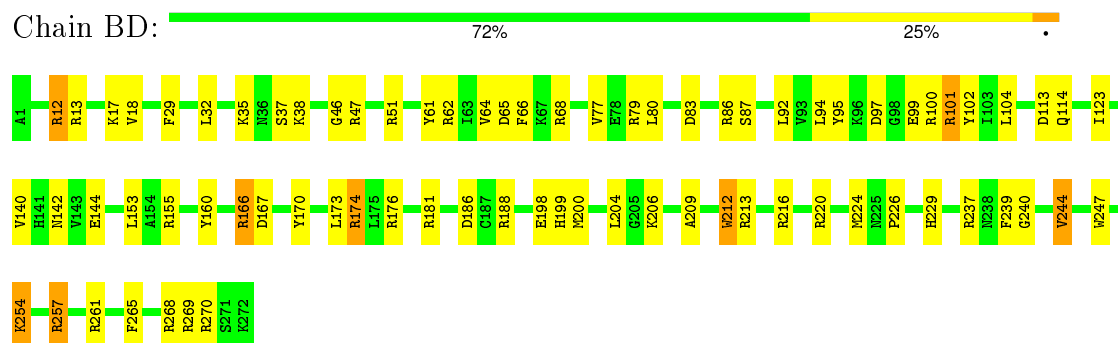
A2882	G2822	G2702	G2642	G2582	U2522	C2462	U2402	C2342	C2282	G2222	A2162
A2883	A2823	C2703	G2643	G2583	G2523	C2463	C2403	U2343	C2283	G2223	A2163
G2884	G2824	A2704	G2644	U2584	G2524	G2464	U2404	C2344	A2284	G2224	C2164
G2885	G2825	A2705	G2645	U2585	G2525	C2465	C2405	C2345	C2285	A2225	C2165
A2886	A2826	A2706	C2646	U2586	G2526	C2466	A2406	A2346	C2286	C2226	U2166
G2887	G2827	C2707	U2647	A2587	C2527	C2467	C2407	C2347	A2287	A2227	U2167
G2888	G2828	G2708	G2648	U2588	G2528	A2468	U2408	U2348	A2288	G2228	G2168
G2889	A2829	G2709	C2649	A2589	G2529	A2469	G2409	G2349	G2229	U2229	A2169
G2890	C2830	C2710	U2650	A2590	A2530	G2470	G2410	C2350	G2230	A2170	A2170
U2891	G2831	C2711	C2651	C2591	A2531	A2471	A2411	A2351	U2291	U2231	A2171
G2892	U2832	C2712	C2652	G2592	G2532	A2472	A2412	A2352	U2292	C2232	A2172
A2893	C2833	G2713	U2653	U2593	U2533	U2473	G2413	G2353	G2293	G2233	C2173
G2894	G2834	G2714	A2654	C2594	A2534	U2474	G2414	C2354	G2294	G2234	A2174
A2895	A2835	C2715	G2655	G2595	G2535	C2475	G2415	G2355	C2295	G2235	C2175
C2896	U2836	C2716	U2656	U2596	G2536	A2476	A2416	U2356	U2296	U2236	A2176
U2897	A2837	C2717	A2657	G2597	U2537	U2477	C2417	G2357	A2297	G2237	A2177
U2898	G2838	G2718	C2658	U2598	C2538	U2478	A2418	A2358	A2298	C2238	C2178
A2899	G2839	G2719	G2659	A2599	C2539	U2479	U2419	C2359	U2299	G2239	C2179
A2900	C2840	U2720	A2660	A2600	C2540	C2480	C2420	G2360	C2300	U2240	U2180
C2901	C2841	A2721	G2661	C2601	A2541	G2481	G2421	G2361	C2301	A2241	U2181
C2902	G2842	G2722	A2662	A2602	A2542	G2482	G2422	G2362	A2302	G2242	U2182
U2903	G2843	C2723	G2663	G2603	G2543	C2483	U2423	G2363	G2303	A2243	A2183
U2904	G2844	U2724	G2664	U2604	G2544	G2484	C2424	G2364	G2304	U2244	A2184
	U2845	A2725	A2665	U2605	G2545	G2485	A2425	G2365	U2305	U2245	U2185
	G2846	A2726	C2666	U2606	U2546	G2486	A2426	G2366	C2306	G2246	G2186
	U2847	A2727	C2667	G2607	A2547	G2487	C2427	G2367	C2307	A2247	U2187
	G2848	U2728	G2668	G2608	U2548	G2488	G2428	C2368	G2308	G2248	U2188
	U2849	G2729	G2669	U2609	G2549	U2489	G2429	A2369	U2309	U2249	U2189
	A2850	C2730	A2670	C2610	G2550	G2490	A2430	G2370	C2310	G2250	A2190
	A2851	G2731	G2671	C2611	C2551	U2491	U2431	U2371	A2311	G2251	A2191
	G2852	G2732	U2672	C2612	U2552	U2492	A2432	U2372	U2312	G2252	U2192
	C2853	A2733	G2673	U2613	G2553	U2493	A2433	G2373	C2313	G2253	G2193
	G2854	A2734	G2674	A2614	U2554	G2494	A2434	C2374	A2314	G2254	U2194
	C2855	G2735	A2675	U2615	U2555	G2495	A2435	G2375	C2315	G2255	U2195
	A2856	A2736	C2676	C2616	G2556	C2496	G2436	A2376	G2316	G2256	C2196
	G2857	G2737	G2677	U2617	G2557	A2497	G2437	A2377	A2317	U2257	U2197
	U2797	A2738	G2678	G2618	C2558	C2498	U2438	A2378	G2318	C2258	A2198
	A2798	U2739	C2679	C2619	C2559	C2499	A2439	G2379	G2319	U2259	A2199
	A2800	A2740	U2680	C2620	A2560	U2500	C2440	G2380	C2320	G2260	G2200
	G2801	A2741	C2681	G2621	U2561	C2501	U2441	A2381	U2321	G2261	G2201
	G2802	G2742	A2682	U2622	U2562	G2502	G2442	G2382	A2322	U2262	U2202
	G2803	U2743	C2683	G2623	U2563	A2503	C2443	G2383	G2323	C2263	U2203
	U2804	G2744	U2684	G2624	A2564	G2504	G2444	U2384	U2324	C2264	G2204
	C2805	C2745	G2685	G2625	A2565	G2505	G2445	C2385	G2325	U2265	A2205
	C2806	U2746	G2686	C2626	A2566	U2506	G2446	A2386	C2326	A2266	G2206
	U2807	G2747	U2687	G2627	G2567	C2507	G2447	U2387	A2327	A2267	G2207
	G2808	A2748	G2688	C2628	U2568	U2508	A2448	A2388	A2328	A2268	C2208
	A2809	A2749	U2689	U2629	G2569	G2509	U2449	U2389	U2329	G2269	G2209
	G2810	U2750	U2690	G2630	G2570	C2510	A2450	U2390	G2330	A2270	U2210
	G2811	G2751	C2691	G2631	U2571	U2511	A2451	G2391	G2331	G2271	A2211
	G2812	C2752	G2692	A2632	A2572	C2512	C2452	A2392	C2332	U2272	A2212
	A2813	A2753	G2693	G2633	C2573	A2513	A2453	U2393	A2333	A2273	U2213
	A2814	U2754	G2694	G2634	U2574	U2514	G2454	C2394	A2334	A2274	C2214
	C2815	C2755	U2695	A2635	C2575	G2515	G2455	C2395	A2335	C2275	C2215
	G2816	U2756	U2696	C2636	G2576	A2516	C2456	G2396	A2336	G2276	G2216
	U2817	A2757	G2697	U2637	A2577	C2517	U2457	G2397	G2337	G2277	G2217
	U2818	A2758	U2698	G2638	G2578	A2518	G2458	U2398	C2338	A2278	G2218
	G2819	G2759	C2699	A2639	U2579	U2519	A2459	G2399	A2339	G2279	U2219
	A2820	C2760	A2700	U2640	U2580	G2520	U2460	A2340	A2340	G2280	U2220
	A2821	A2761	U2701	G2641	C2581	C2521	A2461	U2401	G2341	A2281	G2221

• Molecule 27: 50S ribosomal protein L1

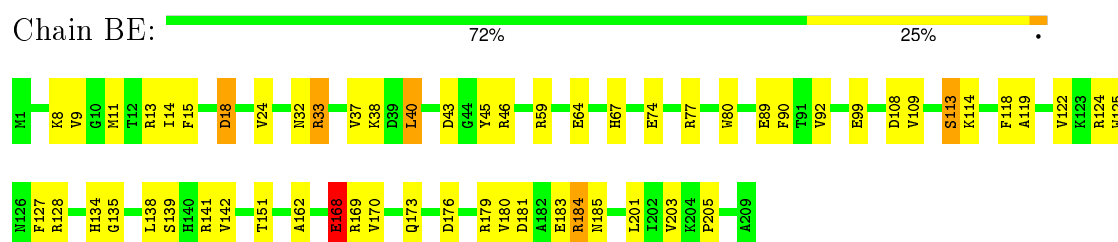
Chain BC:  85% 13%

K1	G206
K6	S213
R7	
H8	
R9	T217
R12	Q226
D16	N234
Y21	
E25	
V39	
E40	
S41	
L48	
R53	
K54	
S55	
D56	
Q57	
R60	
R71	
S73	
V73	
V75	
F78	
E93	
P118	
M121	
L127	
R134	
V145	
T146	
P147	
G159	
R162	
Y163	
R164	
D181	
Q203	

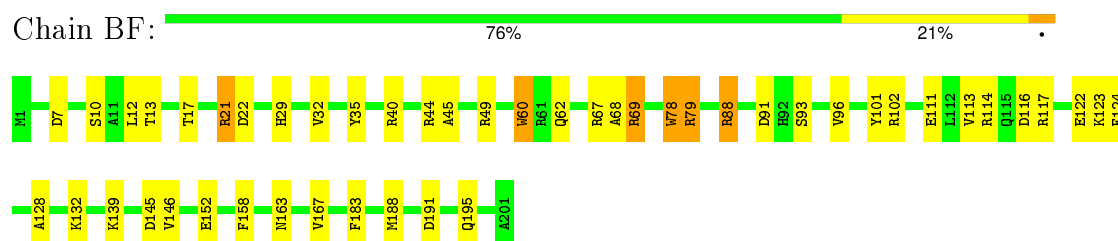
- Molecule 28: 50S ribosomal protein L2



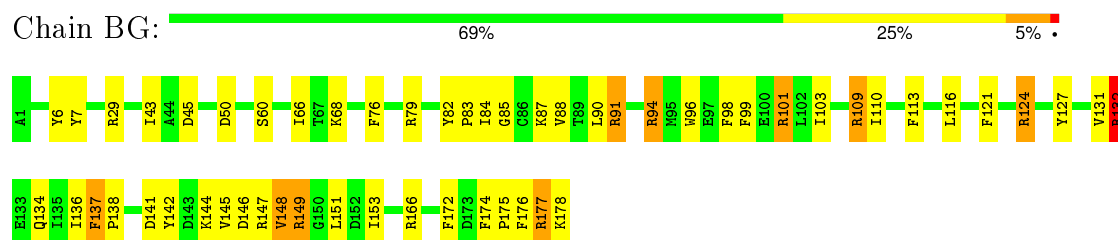
- Molecule 29: 50S ribosomal protein L3



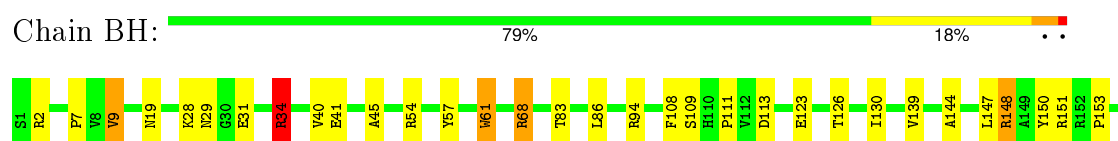
- Molecule 30: 50S ribosomal protein L4

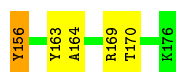


- Molecule 31: 50S ribosomal protein L5



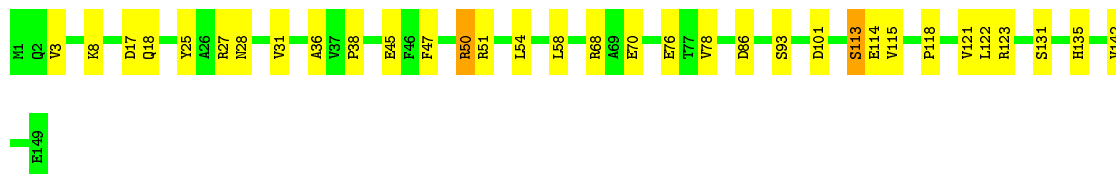
- Molecule 32: 50S ribosomal protein L6





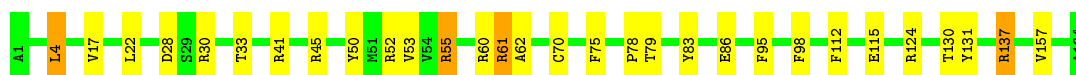
- Molecule 33: 50S ribosomal protein L9

Chain BI: 78% 21% .



- Molecule 34: 50S ribosomal protein L10

Chain BJ: 82% 16% .



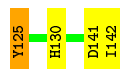
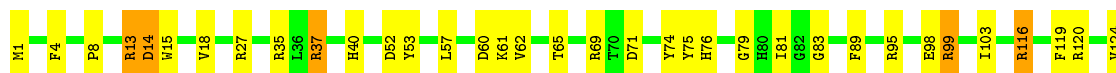
- Molecule 35: 50S ribosomal protein L11

Chain BK: 88% 12% .



- Molecule 36: 50S ribosomal protein L13

Chain BL: 73% 23% .



- Molecule 37: 50S ribosomal protein L14

Chain BM: 76% 18% 6% .




- Molecule 38: 50S ribosomal protein L15

Chain BN: 76% 20% . .




E144


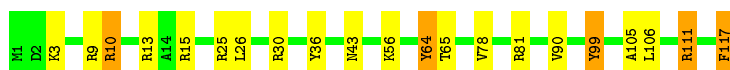
- Molecule 39: 50S ribosomal protein L16

Chain BO:  76% 20%

- Molecule 40: 50S ribosomal protein L17

Chain BP:  76% 20%


- Molecule 41: 50S ribosomal protein L18

Chain BQ:  82% 14%

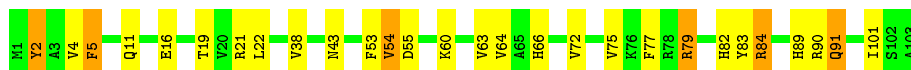
- Molecule 42: 50S ribosomal protein L19

Chain BR:  73% 25%


- Molecule 43: 50S ribosomal protein L20

Chain BS:  75% 21%

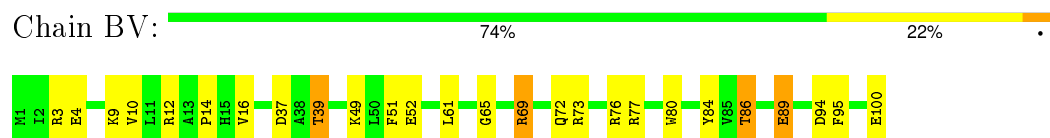
- Molecule 44: 50S ribosomal protein L21

Chain BT:  73% 21% 6%

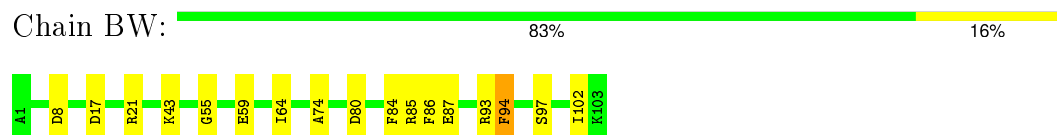
- Molecule 45: 50S ribosomal protein L22

Chain BU:  77% 18% 5%

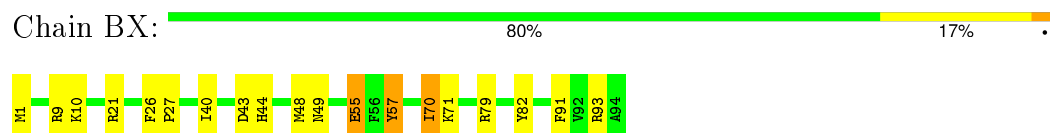
- Molecule 46: 50S ribosomal protein L23



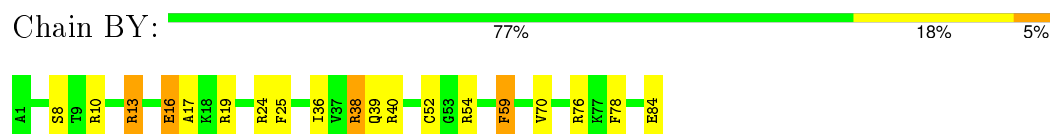
- Molecule 47: 50S ribosomal protein L24



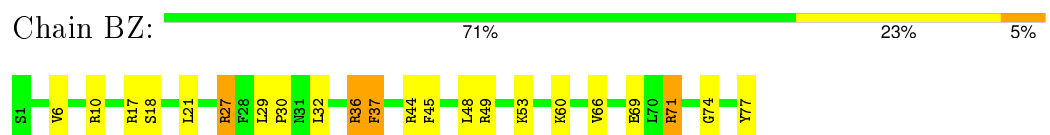
- Molecule 48: 50S ribosomal protein L25



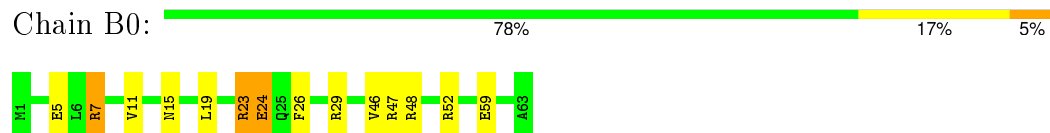
- Molecule 49: 50S ribosomal protein L27



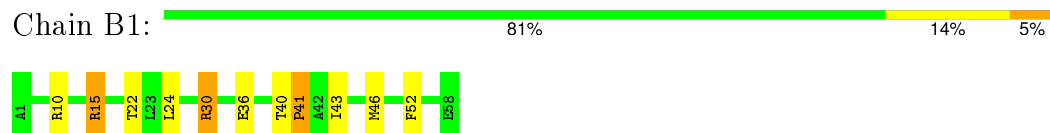
- Molecule 50: 50S ribosomal protein L28




- Molecule 51: 50S ribosomal protein L29



- Molecule 52: 50S ribosomal protein L30




- Molecule 53: 50S ribosomal protein L31

Chain B2:  74% 23% .




- Molecule 54: 50S ribosomal protein L32

Chain B3:  80% 18% .



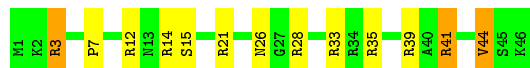
- Molecule 55: 50S ribosomal protein L33

Chain B4:  80% 17% .




- Molecule 56: 50S ribosomal protein L34

Chain B5:  72% 22% 7% .




- Molecule 57: 50S ribosomal protein L35

Chain B6:  80% 17% .



- Molecule 58: 50S ribosomal protein L36

Chain B7:  76% 18% 5% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	40000	Depositor
Resolution determination method	FSC at 0.5 cut-off	Depositor
CTF correction method	Volumes were CTF-corrected in defocus groups	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	TVIPS TemCam-F415 (CCD)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 2$	RMSZ	# $ Z > 2$
1	AA	3.07	3887/36769 (10.6%)	3.55	8401/57354 (14.6%)
10	AJ	1.54	9/1422 (0.6%)	1.97	38/1908 (2.0%)
11	AK	1.50	3/989 (0.3%)	1.90	19/1326 (1.4%)
12	AL	1.58	6/1048 (0.6%)	2.12	34/1394 (2.4%)
13	AM	1.49	3/835 (0.4%)	2.05	23/1127 (2.0%)
14	AN	1.52	4/982 (0.4%)	1.95	24/1323 (1.8%)
15	AO	1.56	7/969 (0.7%)	2.02	29/1300 (2.2%)
16	AP	1.50	1/919 (0.1%)	1.82	17/1226 (1.4%)
17	AQ	1.53	3/817 (0.4%)	1.97	28/1088 (2.6%)
18	AR	1.49	0/724	1.90	16/966 (1.7%)
19	AS	1.57	5/659 (0.8%)	1.97	17/884 (1.9%)
2	AB	3.08	186/1600 (11.6%)	3.55	373/2492 (15.0%)
20	AT	1.52	3/681 (0.4%)	1.93	13/913 (1.4%)
21	AU	1.49	2/637 (0.3%)	2.13	17/851 (2.0%)
22	AV	1.46	2/744 (0.3%)	2.10	18/995 (1.8%)
23	AW	1.47	1/676 (0.1%)	1.92	14/895 (1.6%)
24	AX	1.61	3/598 (0.5%)	2.14	16/792 (2.0%)
25	BA	3.11	315/2869 (11.0%)	3.52	638/4474 (14.3%)
26	BB	3.08	7296/69257 (10.5%)	3.51	15472/108040 (14.3%)
27	BC	1.41	4/1748 (0.2%)	1.90	27/2355 (1.1%)
28	BD	1.59	15/2131 (0.7%)	2.01	74/2863 (2.6%)
29	BE	1.50	7/1586 (0.4%)	1.92	42/2134 (2.0%)
3	AC	3.05	112/1108 (10.1%)	3.41	210/1724 (12.2%)
30	BF	1.47	2/1571 (0.1%)	2.10	41/2113 (1.9%)
31	BG	1.54	6/1444 (0.4%)	2.14	52/1937 (2.7%)
32	BH	1.49	5/1343 (0.4%)	1.94	26/1816 (1.4%)
33	BI	1.46	2/1122 (0.2%)	1.88	25/1515 (1.7%)
34	BJ	1.52	5/1247 (0.4%)	1.92	29/1679 (1.7%)
35	BK	1.50	2/1046 (0.2%)	1.73	13/1410 (0.9%)
36	BL	1.52	7/1152 (0.6%)	2.06	33/1551 (2.1%)
37	BM	1.43	3/956 (0.3%)	1.98	28/1279 (2.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
38	BN	1.60	7/1062 (0.7%)	1.94	30/1413 (2.1%)
39	BO	1.54	7/1093 (0.6%)	2.13	38/1460 (2.6%)
4	AD	2.99	170/1721 (9.9%)	3.48	380/2683 (14.2%)
40	BP	1.50	3/1021 (0.3%)	2.07	33/1364 (2.4%)
41	BQ	1.52	4/910 (0.4%)	1.97	21/1219 (1.7%)
42	BR	1.55	5/929 (0.5%)	2.02	27/1242 (2.2%)
43	BS	1.52	4/960 (0.4%)	2.00	27/1278 (2.1%)
44	BT	1.50	4/829 (0.5%)	1.93	22/1107 (2.0%)
45	BU	1.44	2/864 (0.2%)	1.98	24/1156 (2.1%)
46	BV	1.49	0/794	1.92	23/1060 (2.2%)
47	BW	1.45	2/797 (0.3%)	1.79	10/1062 (0.9%)
48	BX	1.47	5/766 (0.7%)	1.99	18/1025 (1.8%)
49	BY	1.47	1/642 (0.2%)	2.11	19/848 (2.2%)
5	AE	1.48	5/1904 (0.3%)	1.91	50/2565 (1.9%)
50	BZ	1.47	2/635 (0.3%)	2.07	22/848 (2.6%)
51	B0	1.50	1/510 (0.2%)	2.11	15/677 (2.2%)
52	B1	1.54	6/453 (1.3%)	1.89	7/605 (1.2%)
53	B2	1.45	1/559 (0.2%)	2.22	15/745 (2.0%)
54	B3	1.51	3/450 (0.7%)	1.94	7/599 (1.2%)
55	B4	1.48	2/448 (0.4%)	2.10	7/594 (1.2%)
56	B5	1.48	0/380	2.06	15/498 (3.0%)
57	B6	1.56	7/513 (1.4%)	1.97	12/676 (1.8%)
58	B7	1.49	1/303 (0.3%)	1.91	6/397 (1.5%)
6	AF	1.48	11/1852 (0.6%)	2.01	58/2490 (2.3%)
7	AG	1.54	5/1665 (0.3%)	2.05	55/2227 (2.5%)
8	AH	1.53	5/1239 (0.4%)	1.91	30/1664 (1.8%)
9	AI	1.54	5/1121 (0.4%)	2.02	30/1509 (2.0%)
All	All	2.69	12174/164069 (7.4%)	3.17	26808/244735 (11.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	907
10	AJ	0	5
11	AK	0	2
12	AL	0	6
13	AM	0	1
14	AN	0	1
15	AO	0	7

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
16	AP	0	1
17	AQ	0	3
18	AR	0	5
19	AS	0	2
2	AB	0	36
21	AU	0	5
22	AV	0	3
23	AW	0	1
24	AX	0	3
25	BA	0	66
26	BB	0	1683
27	BC	0	3
28	BD	0	10
29	BE	0	5
3	AC	0	31
30	BF	0	3
31	BG	0	9
32	BH	0	4
33	BI	0	2
34	BJ	0	5
35	BK	0	1
36	BL	0	9
37	BM	0	7
38	BN	0	5
39	BO	0	2
4	AD	0	44
40	BP	0	3
41	BQ	0	4
42	BR	0	2
43	BS	0	2
44	BT	0	2
45	BU	0	4
46	BV	0	2
47	BW	0	2
48	BX	0	1
49	BY	0	7
5	AE	0	5
50	BZ	0	2
52	B1	0	1
53	B2	0	4
54	B3	0	2
55	B4	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
56	B5	0	1
57	B6	0	1
58	B7	0	1
6	AF	0	2
7	AG	0	7
8	AH	0	6
9	AI	0	5
All	All	0	2945

The worst 5 of 12174 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	BB	2297	A	N3-C4	17.57	1.45	1.34
26	BB	764	A	N3-C4	15.94	1.44	1.34
26	BB	453	A	N3-C4	15.86	1.44	1.34
1	AA	914	A	N3-C4	15.76	1.44	1.34
26	BB	1972	G	C8-N7	15.68	1.40	1.30

The worst 5 of 26808 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	28	A	O4'-C1'-N9	21.28	125.23	108.20
53	B2	63	ARG	NE-CZ-NH1	21.04	130.82	120.30
26	BB	2041	U	O4'-C1'-N1	20.83	124.87	108.20
1	AA	1323	G	N9-C4-C5	20.57	113.63	105.40
1	AA	1142	G	C8-N9-C4	-20.50	98.20	106.40

There are no chirality outliers.

5 of 2945 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	11	G	Sidechain
1	AA	2	A	Sidechain
1	AA	4	U	Sidechain
1	AA	8	A	Sidechain
1	AA	9	G	Sidechain

5.2 Too-close contacts [i](#)

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	33089	0	16596	0	0
2	AB	1627	0	840	0	0
3	AC	993	0	501	0	0
4	AD	1641	0	839	0	0
5	AE	1872	0	1885	0	0
6	AF	1822	0	1913	0	0
7	AG	1643	0	1710	0	0
8	AH	1225	0	1273	0	0
9	AI	1101	0	1050	0	0
10	AJ	1400	0	1449	0	0
11	AK	979	0	1034	0	0
12	AL	1036	0	1084	0	0
13	AM	825	0	865	0	0
14	AN	965	0	997	0	0
15	AO	955	0	1019	0	0
16	AP	910	0	981	0	0
17	AQ	805	0	847	0	0
18	AR	716	0	742	0	0
19	AS	649	0	666	0	0
20	AT	672	0	716	0	0
21	AU	626	0	651	0	0
22	AV	727	0	769	0	0
23	AW	670	0	722	0	0
24	AX	590	0	631	0	0
25	BA	2566	0	1295	0	0
26	BB	62351	0	31202	0	0
27	BC	1733	0	1824	0	0
28	BD	2092	0	2170	0	0
29	BE	1565	0	1616	0	0
30	BF	1552	0	1619	0	0
31	BG	1420	0	1460	0	0
32	BH	1323	0	1374	0	0
33	BI	1111	0	1148	0	0
34	BJ	1233	0	1283	0	0
35	BK	1032	0	1088	0	0
36	BL	1129	0	1162	0	0
37	BM	947	0	1023	0	0
38	BN	1053	0	1129	0	0
39	BO	1074	0	1157	0	0
40	BP	1008	0	1045	0	0
41	BQ	900	0	935	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	BR	917	0	965	0	0
43	BS	947	0	1022	0	0
44	BT	816	0	839	0	0
45	BU	857	0	922	0	0
46	BV	787	0	846	0	0
47	BW	789	0	847	0	0
48	BX	753	0	780	0	0
49	BY	634	0	656	0	0
50	BZ	625	0	655	0	0
51	B0	509	0	543	0	0
52	B1	449	0	491	0	0
53	B2	549	0	552	0	0
54	B3	444	0	461	0	0
55	B4	441	0	485	0	0
56	B5	377	0	418	0	0
57	B6	504	0	574	0	0
58	B7	302	0	343	0	0
59	AB	14	0	9	0	0
60	BB	10	0	10	0	0
All	All	152351	0	103728	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	
5	AE	238/240 (99%)	217 (91%)	14 (6%)	7 (3%)	6	43
6	AF	230/232 (99%)	217 (94%)	8 (4%)	5 (2%)	8	49

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	AG	203/205 (99%)	187 (92%)	13 (6%)	3 (2%)	13	57
8	AH	164/166 (99%)	148 (90%)	14 (8%)	2 (1%)	16	61
9	AI	133/135 (98%)	122 (92%)	10 (8%)	1 (1%)	24	69
10	AJ	176/178 (99%)	165 (94%)	9 (5%)	2 (1%)	17	63
11	AK	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
12	AL	127/129 (98%)	112 (88%)	12 (9%)	3 (2%)	7	47
13	AM	101/103 (98%)	90 (89%)	6 (6%)	5 (5%)	3	31
14	AN	126/128 (98%)	111 (88%)	14 (11%)	1 (1%)	24	69
15	AO	121/123 (98%)	106 (88%)	14 (12%)	1 (1%)	24	69
16	AP	115/117 (98%)	109 (95%)	5 (4%)	1 (1%)	21	67
17	AQ	98/100 (98%)	84 (86%)	7 (7%)	7 (7%)	1	22
18	AR	86/88 (98%)	81 (94%)	4 (5%)	1 (1%)	16	61
19	AS	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
20	AT	81/83 (98%)	72 (89%)	8 (10%)	1 (1%)	16	61
21	AU	72/74 (97%)	61 (85%)	7 (10%)	4 (6%)	2	28
22	AV	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	17	63
23	AW	84/86 (98%)	78 (93%)	6 (7%)	0	100	100
24	AX	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	3	33
27	BC	232/234 (99%)	216 (93%)	11 (5%)	5 (2%)	8	49
28	BD	270/272 (99%)	235 (87%)	25 (9%)	10 (4%)	4	38
29	BE	207/209 (99%)	174 (84%)	26 (13%)	7 (3%)	5	40
30	BF	199/201 (99%)	174 (87%)	15 (8%)	10 (5%)	3	31
31	BG	176/178 (99%)	151 (86%)	16 (9%)	9 (5%)	2	30
32	BH	174/176 (99%)	157 (90%)	12 (7%)	5 (3%)	6	43
33	BI	147/149 (99%)	130 (88%)	12 (8%)	5 (3%)	5	40
34	BJ	162/164 (99%)	157 (97%)	4 (2%)	1 (1%)	30	74
35	BK	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
36	BL	140/142 (99%)	120 (86%)	16 (11%)	4 (3%)	6	43
37	BM	121/123 (98%)	109 (90%)	8 (7%)	4 (3%)	5	40
38	BN	142/144 (99%)	124 (87%)	14 (10%)	4 (3%)	6	44
39	BO	134/136 (98%)	123 (92%)	10 (8%)	1 (1%)	26	71

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	BP	125/127 (98%)	116 (93%)	8 (6%)	1 (1%)	24	69
41	BQ	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
42	BR	112/114 (98%)	98 (88%)	11 (10%)	3 (3%)	6	45
43	BS	115/117 (98%)	108 (94%)	4 (4%)	3 (3%)	7	45
44	BT	101/103 (98%)	90 (89%)	7 (7%)	4 (4%)	4	35
45	BU	108/110 (98%)	98 (91%)	6 (6%)	4 (4%)	4	38
46	BV	98/100 (98%)	76 (78%)	19 (19%)	3 (3%)	5	42
47	BW	101/103 (98%)	88 (87%)	10 (10%)	3 (3%)	5	42
48	BX	92/94 (98%)	87 (95%)	4 (4%)	1 (1%)	17	63
49	BY	82/84 (98%)	64 (78%)	16 (20%)	2 (2%)	7	47
50	BZ	75/77 (97%)	68 (91%)	4 (5%)	3 (4%)	4	35
51	B0	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	12	56
52	B1	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
53	B2	68/70 (97%)	65 (96%)	2 (3%)	1 (2%)	13	57
54	B3	54/56 (96%)	48 (89%)	4 (7%)	2 (4%)	4	38
55	B4	52/54 (96%)	49 (94%)	1 (2%)	2 (4%)	4	37
56	B5	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	3	33
57	B6	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	12	56
58	B7	36/38 (95%)	30 (83%)	3 (8%)	3 (8%)	1	18
All	All	6319/6423 (98%)	5706 (90%)	460 (7%)	153 (2%)	12	47

5 of 153 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	AF	163	ARG
8	AH	77	ASN
13	AM	57	VAL
14	AN	52	ARG
17	AQ	2	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	AE	198/198 (100%)	189 (96%)	9 (4%)	34	69
6	AF	189/189 (100%)	178 (94%)	11 (6%)	25	61
7	AG	172/172 (100%)	166 (96%)	6 (4%)	43	74
8	AH	125/125 (100%)	116 (93%)	9 (7%)	18	55
9	AI	116/116 (100%)	111 (96%)	5 (4%)	35	70
10	AJ	146/146 (100%)	133 (91%)	13 (9%)	12	44
11	AK	104/104 (100%)	97 (93%)	7 (7%)	20	57
12	AL	106/106 (100%)	99 (93%)	7 (7%)	21	57
13	AM	90/90 (100%)	86 (96%)	4 (4%)	35	69
14	AN	98/98 (100%)	95 (97%)	3 (3%)	47	77
15	AO	103/103 (100%)	98 (95%)	5 (5%)	31	67
16	AP	95/95 (100%)	94 (99%)	1 (1%)	80	91
17	AQ	83/83 (100%)	80 (96%)	3 (4%)	42	74
18	AR	76/76 (100%)	72 (95%)	4 (5%)	28	64
19	AS	65/65 (100%)	61 (94%)	4 (6%)	23	60
20	AT	77/77 (100%)	74 (96%)	3 (4%)	39	72
21	AU	64/64 (100%)	61 (95%)	3 (5%)	32	68
22	AV	78/78 (100%)	74 (95%)	4 (5%)	29	66
23	AW	65/65 (100%)	64 (98%)	1 (2%)	72	88
24	AX	60/60 (100%)	57 (95%)	3 (5%)	30	66
27	BC	181/181 (100%)	171 (94%)	10 (6%)	27	63
28	BD	217/217 (100%)	207 (95%)	10 (5%)	33	68
29	BE	164/164 (100%)	150 (92%)	14 (8%)	13	48
30	BF	165/165 (100%)	157 (95%)	8 (5%)	31	67
31	BG	149/149 (100%)	137 (92%)	12 (8%)	15	50
32	BH	137/137 (100%)	124 (90%)	13 (10%)	11	41
33	BI	114/114 (100%)	110 (96%)	4 (4%)	43	74
34	BJ	122/122 (100%)	118 (97%)	4 (3%)	45	76
35	BK	109/109 (100%)	107 (98%)	2 (2%)	66	87
36	BL	116/116 (100%)	109 (94%)	7 (6%)	24	60

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	BM	104/104 (100%)	100 (96%)	4 (4%)	40	73
38	BN	103/103 (100%)	100 (97%)	3 (3%)	50	78
39	BO	109/109 (100%)	103 (94%)	6 (6%)	27	63
40	BP	103/103 (100%)	99 (96%)	4 (4%)	39	72
41	BQ	87/87 (100%)	82 (94%)	5 (6%)	25	62
42	BR	99/99 (100%)	94 (95%)	5 (5%)	29	66
43	BS	89/89 (100%)	84 (94%)	5 (6%)	26	62
44	BT	84/84 (100%)	77 (92%)	7 (8%)	14	49
45	BU	93/93 (100%)	89 (96%)	4 (4%)	35	70
46	BV	84/84 (100%)	77 (92%)	7 (8%)	14	49
47	BW	84/84 (100%)	80 (95%)	4 (5%)	31	67
48	BX	78/78 (100%)	73 (94%)	5 (6%)	22	58
49	BY	62/62 (100%)	58 (94%)	4 (6%)	21	58
50	BZ	67/67 (100%)	63 (94%)	4 (6%)	24	60
51	B0	55/55 (100%)	50 (91%)	5 (9%)	12	43
52	B1	48/48 (100%)	46 (96%)	2 (4%)	36	70
53	B2	62/62 (100%)	59 (95%)	3 (5%)	31	67
54	B3	47/47 (100%)	47 (100%)	0	100	100
55	B4	48/48 (100%)	45 (94%)	3 (6%)	22	59
56	B5	38/38 (100%)	35 (92%)	3 (8%)	15	51
57	B6	51/51 (100%)	50 (98%)	1 (2%)	63	85
58	B7	34/34 (100%)	34 (100%)	0	100	100
All	All	5213/5213 (100%)	4940 (95%)	273 (5%)	33	65

5 of 273 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	BD	239	PHE
31	BG	131	VAL
50	BZ	32	LEU
29	BE	38	LYS
29	BE	205	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1538/1542 (99%)	309 (20%)	98 (6%)
2	AB	74/76 (97%)	28 (37%)	8 (10%)
25	BA	119/120 (99%)	16 (13%)	11 (9%)
26	BB	2898/2904 (99%)	534 (18%)	181 (6%)
3	AC	46/47 (97%)	21 (45%)	7 (15%)
4	AD	76/77 (98%)	13 (17%)	3 (3%)
All	All	4751/4766 (99%)	921 (19%)	308 (6%)

5 of 921 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	A
1	AA	3	A
1	AA	5	U
1	AA	7	A
1	AA	8	A

5 of 308 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	BB	219	A
26	BB	680	C
26	BB	2571	U
26	BB	242	G
26	BB	479	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MG	AA	1207	1	18,26,27	1.83	5 (27%)	21,38,41	2.98	8 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	4OC	AA	1402	1	15,23,24	1.67	4 (26%)	21,32,35	2.34	4 (19%)
1	5MC	AA	1407	1	14,22,23	1.76	3 (21%)	17,32,35	1.90	3 (17%)
1	UR3	AA	1498	1	13,22,23	2.12	4 (30%)	18,32,35	2.14	6 (33%)
1	2MG	AA	1516	1	18,26,27	1.77	3 (16%)	21,38,41	3.04	8 (38%)
1	MA6	AA	1518	1	18,26,27	1.58	5 (27%)	15,38,41	1.78	4 (26%)
1	MA6	AA	1519	1	18,26,27	1.93	5 (27%)	15,38,41	1.90	4 (26%)
1	PSU	AA	516	1	15,21,22	1.75	4 (26%)	16,30,33	4.16	6 (37%)
1	7MG	AA	527	1	20,26,27	2.42	7 (35%)	23,39,42	2.03	2 (8%)
1	2MG	AA	966	1	18,26,27	2.09	5 (27%)	21,38,41	2.50	7 (33%)
1	5MC	AA	967	1	14,22,23	1.55	3 (21%)	17,32,35	2.27	5 (29%)
2	H2U	AB	16	2	17,21,22	2.05	5 (29%)	23,30,33	1.86	5 (21%)
2	H2U	AB	17	2	17,21,22	1.54	3 (17%)	23,30,33	1.61	7 (30%)
2	H2U	AB	20	2	17,21,22	1.53	3 (17%)	23,30,33	2.41	6 (26%)
2	OMC	AB	32	2	15,22,23	1.33	3 (20%)	20,31,34	1.86	6 (30%)
2	MIA	AB	37	2	22,31,32	3.20	5 (22%)	26,44,47	1.93	7 (26%)
2	7MG	AB	46	2	20,26,27	2.61	8 (40%)	23,39,42	2.51	7 (30%)
2	5MU	AB	54	2	13,22,23	1.44	2 (15%)	16,32,35	5.59	5 (31%)
2	PSU	AB	55	2	15,21,22	1.97	4 (26%)	16,30,33	4.17	6 (37%)
2	4SU	AB	8	2	12,21,22	1.59	4 (33%)	15,30,33	2.01	4 (26%)
4	H2U	AD	21	4	17,21,22	1.49	3 (17%)	23,30,33	1.82	6 (26%)
4	OMC	AD	33	4	15,22,23	1.42	2 (13%)	20,31,34	2.09	5 (25%)
4	5MU	AD	55	4	13,22,23	1.76	2 (15%)	16,32,35	5.31	3 (18%)
4	PSU	AD	56	4	15,21,22	2.11	4 (26%)	16,30,33	3.95	4 (25%)
4	4SU	AD	8	4	12,21,22	2.00	3 (25%)	15,30,33	2.43	4 (26%)
26	6MZ	BB	1618	26	17,25,26	1.79	3 (17%)	15,36,39	1.68	5 (33%)
26	2MG	BB	1835	26	18,26,27	1.52	3 (16%)	21,38,41	3.08	6 (28%)
26	PSU	BB	1911	26	15,21,22	2.27	5 (33%)	16,30,33	3.57	4 (25%)
26	3TD	BB	1915	26	15,22,23	2.46	4 (26%)	17,32,35	2.01	4 (23%)
26	PSU	BB	1917	26	15,21,22	2.04	3 (20%)	16,30,33	4.21	4 (25%)
26	5MU	BB	1939	26	13,22,23	1.34	2 (15%)	16,32,35	4.79	6 (37%)
26	5MC	BB	1962	26	14,22,23	2.09	2 (14%)	17,32,35	1.98	4 (23%)
26	6MZ	BB	2030	26	17,25,26	1.23	2 (11%)	15,36,39	2.40	6 (40%)
26	7MG	BB	2069	26	20,26,27	2.41	7 (35%)	23,39,42	2.86	6 (26%)
26	OMG	BB	2251	26	18,26,27	1.67	4 (22%)	21,38,41	3.51	10 (47%)
26	2MG	BB	2445	26	18,26,27	1.67	2 (11%)	21,38,41	3.27	11 (52%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	H2U	BB	2449	26	17,21,22	1.50	3 (17%)	23,30,33	0.92	2 (8%)
26	PSU	BB	2457	26	15,21,22	2.13	4 (26%)	16,30,33	3.78	4 (25%)
26	OMC	BB	2498	26	15,22,23	1.54	2 (13%)	20,31,34	2.12	4 (20%)
26	2MA	BB	2503	26	17,25,26	2.12	5 (29%)	18,37,40	2.85	6 (33%)
26	PSU	BB	2504	26	15,21,22	1.81	3 (20%)	16,30,33	4.63	7 (43%)
26	OMU	BB	2552	26	14,22,23	1.29	2 (14%)	19,31,34	3.52	5 (26%)
26	CH	BB	2575	26	14,21,22	1.42	3 (21%)	18,30,33	1.60	3 (16%)
26	PSU	BB	2580	26	15,21,22	1.83	5 (33%)	16,30,33	3.92	6 (37%)
26	PSU	BB	2605	26	15,21,22	2.58	5 (33%)	16,30,33	3.59	5 (31%)
26	1MG	BB	745	26	17,26,27	1.63	4 (23%)	19,39,42	2.53	6 (31%)
26	PSU	BB	746	26	15,21,22	2.33	4 (26%)	16,30,33	3.83	5 (31%)
26	5MU	BB	747	26	13,22,23	1.99	4 (30%)	16,32,35	4.25	6 (37%)
26	PSU	BB	955	26	15,21,22	2.47	5 (33%)	16,30,33	4.35	6 (37%)

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
1	2MG	AA	1207	1	-	0/5/27/28	0/3/3/3
1	4OC	AA	1402	1	-	0/7/29/30	0/2/2/2
1	5MC	AA	1407	1	-	0/3/25/26	0/2/2/2
1	UR3	AA	1498	1	-	0/3/25/26	0/2/2/2
1	2MG	AA	1516	1	-	0/5/27/28	0/3/3/3
1	MA6	AA	1518	1	-	0/7/29/30	0/3/3/3
1	MA6	AA	1519	1	-	0/7/29/30	0/3/3/3
1	PSU	AA	516	1	-	0/7/25/26	0/2/2/2
1	7MG	AA	527	1	-	0/7/37/38	0/3/3/3
1	2MG	AA	966	1	-	0/5/27/28	0/3/3/3
1	5MC	AA	967	1	-	0/3/25/26	0/2/2/2
2	H2U	AB	16	2	-	0/7/38/39	0/2/2/2
2	H2U	AB	17	2	-	0/7/38/39	0/2/2/2
2	H2U	AB	20	2	-	0/7/38/39	0/2/2/2
2	OMC	AB	32	2	-	0/5/27/28	0/2/2/2
2	MIA	AB	37	2	-	0/11/33/34	0/3/3/3
2	7MG	AB	46	2	-	0/7/37/38	0/3/3/3
2	5MU	AB	54	2	-	0/3/25/26	0/2/2/2
2	PSU	AB	55	2	-	0/7/25/26	0/2/2/2
2	4SU	AB	8	2	-	0/3/25/26	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	H2U	AD	21	4	-	0/7/38/39	0/2/2/2
4	OMC	AD	33	4	-	0/5/27/28	0/2/2/2
4	5MU	AD	55	4	-	0/3/25/26	0/2/2/2
4	PSU	AD	56	4	-	0/7/25/26	0/2/2/2
4	4SU	AD	8	4	-	0/3/25/26	0/2/2/2
26	6MZ	BB	1618	26	-	0/5/27/28	0/3/3/3
26	2MG	BB	1835	26	-	0/5/27/28	0/3/3/3
26	PSU	BB	1911	26	-	0/7/25/26	0/2/2/2
26	3TD	BB	1915	26	-	0/7/25/26	0/2/2/2
26	PSU	BB	1917	26	-	0/7/25/26	0/2/2/2
26	5MU	BB	1939	26	-	0/3/25/26	0/2/2/2
26	5MC	BB	1962	26	-	0/3/25/26	0/2/2/2
26	6MZ	BB	2030	26	-	0/5/27/28	0/3/3/3
26	7MG	BB	2069	26	-	0/7/37/38	0/3/3/3
26	OMG	BB	2251	26	-	0/5/27/28	0/3/3/3
26	2MG	BB	2445	26	-	0/5/27/28	0/3/3/3
26	H2U	BB	2449	26	-	0/7/38/39	0/2/2/2
26	PSU	BB	2457	26	-	0/7/25/26	0/2/2/2
26	OMC	BB	2498	26	-	0/5/27/28	0/2/2/2
26	2MA	BB	2503	26	-	0/3/25/26	0/3/3/3
26	PSU	BB	2504	26	-	0/7/25/26	0/2/2/2
26	OMU	BB	2552	26	-	0/5/27/28	0/2/2/2
26	CH	BB	2575	26	-	0/3/25/26	0/2/2/2
26	PSU	BB	2580	26	-	0/7/25/26	0/2/2/2
26	PSU	BB	2605	26	-	0/7/25/26	0/2/2/2
26	1MG	BB	745	26	-	0/3/25/26	0/3/3/3
26	PSU	BB	746	26	-	0/7/25/26	0/2/2/2
26	5MU	BB	747	26	-	0/3/25/26	0/2/2/2
26	PSU	BB	955	26	-	0/7/25/26	0/2/2/2

The worst 5 of 185 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	BB	2069	7MG	C8-N9	-6.93	1.35	1.45
2	AB	46	7MG	C8-N9	-6.57	1.35	1.45
26	BB	955	PSU	O4'-C1'	-5.40	1.36	1.44
2	AB	16	H2U	C4-N3	-5.35	1.29	1.37
1	AA	527	7MG	C8-N9	-5.04	1.38	1.45

The worst 5 of 263 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	54	5MU	C5-C4-N3	-17.18	110.93	125.35
4	AD	55	5MU	C5-C4-N3	-14.85	112.88	125.35
26	BB	1939	5MU	C5-C4-N3	-12.22	115.09	125.35
26	BB	747	5MU	C5-C4-N3	-11.51	115.68	125.35
26	BB	2069	7MG	C5-C6-N1	-9.68	108.97	123.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	$\# Z > 2$
59	TRP	AB	101	60,2	14,15,16	2.03	4 (28%)	8,20,22	1.94	3 (37%)
60	FME	BB	3001	59	8,9,10	0.94	0	5,9,11	0.95	0

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	TRP	AB	101	60,2	-	0/5/6/8	0/2/2/2
60	FME	BB	3001	59	-	1/6/9/11	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AB	101	TRP	OXT-C	-4.52	1.22	1.42
59	AB	101	TRP	CZ2-CE2	-2.09	1.38	1.41
59	AB	101	TRP	C-CA	3.40	1.57	1.52
59	AB	101	TRP	CZ3-CE3	3.51	1.44	1.36

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AB	101	TRP	CH2-CZ2-CE2	-2.06	116.84	120.07
59	AB	101	TRP	CZ2-CE2-CD2	2.28	125.20	121.12
59	AB	101	TRP	OXT-C-CA	3.56	121.20	111.77

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	BB	3001	FME	O1-CN-N-CA

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.