



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:54 PM BST

PDB ID : 4V66
EMDB ID: : EMD-1055
Title : Structure of the E. coli ribosome and the tRNAs in Post-accommodation state
Authors : Devkota, B.; Caulfield, T.R.; Tan, R.-Z.; Harvey, S.C.
Deposited on : 2008-08-03
Resolution : 9.00 Å(reported)
Based on PDB ID : 2I2P, 1EHZ

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 : unknown
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

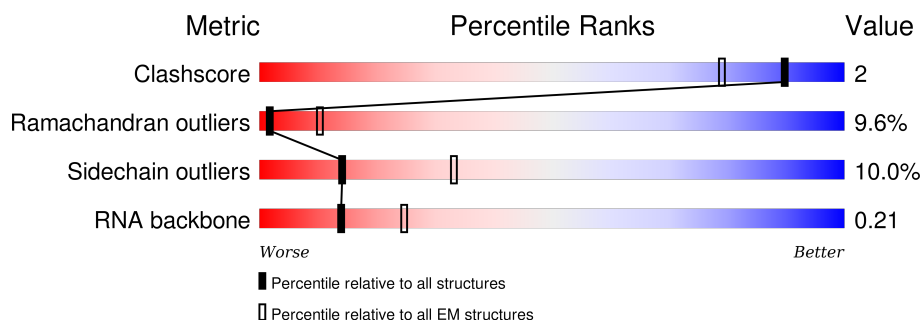
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 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.








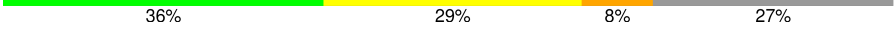



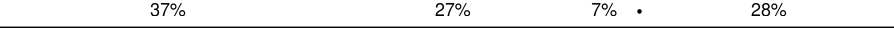

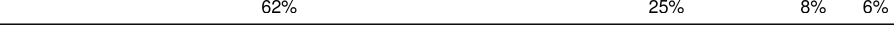







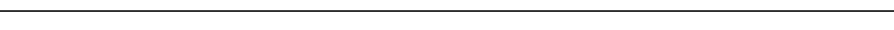

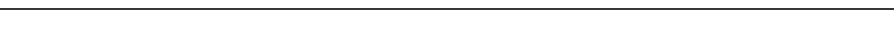
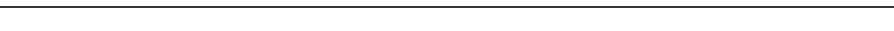


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	76	22% 37% 39% .
1	AE	76	22% 62% 16%
1	AP	76	21% 53% 25% .
2	AM	20	15% 30% 55%
3	A1	1530	15% 47% 38%
4	AB	241	61% 23% 5% 10%
5	AC	129	57% 26% 5% . 9%
6	AD	124	56% 31% 10% . .









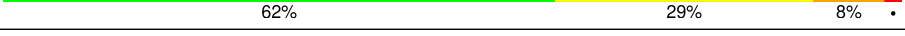
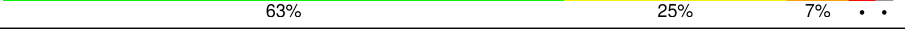
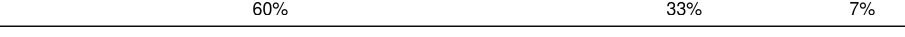

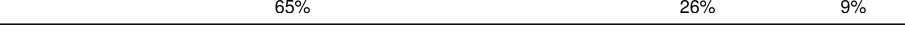
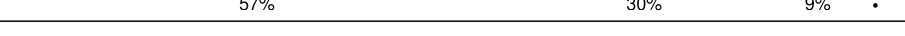
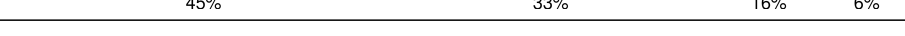


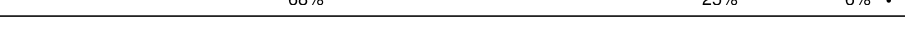
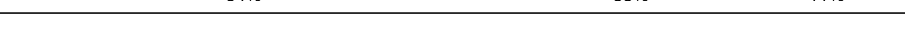

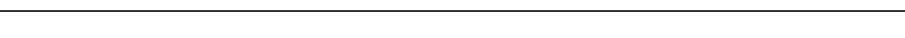

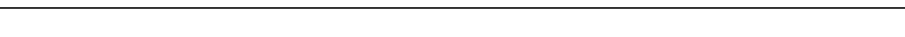
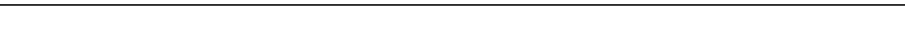
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
7	AF	118	
8	AG	101	
9	AH	89	
10	AI	82	
11	AJ	84	
12	AK	75	
13	AL	92	
14	AN	87	
15	AO	233	
16	AQ	71	
17	AR	206	
18	AS	159	
19	AT	135	
20	AU	179	
21	AV	130	
22	AW	130	
23	AX	103	
24	BA	117	
25	BB	2903	
26	BC	94	
27	BD	123	
28	BE	144	
29	BF	136	
30	BG	127	
31	BH	117	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
32	BI	115	
33	BJ	118	
34	BK	103	
35	BL	110	
36	BM	99	
37	BN	270	
38	BO	103	
39	BP	85	
40	BQ	63	
41	BR	59	
42	BS	70	
43	BT	57	
44	BU	54	
45	BV	46	
46	BW	64	
47	BX	38	
48	BY	209	
49	BZ	213	
50	B1	201	
51	B2	178	
52	B3	177	
53	B4	149	
54	B5	142	
55	B6	140	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 149248 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 A/T, P and E-site tRNAs.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	75	Total	C	N	O	P	0	0
			1600	715	288	523	74		
1	AP	75	Total	C	N	O	P	0	0
			1600	715	288	523	74		
1	AE	76	Total	C	N	O	P	0	0
			1622	725	293	529	75		

- Molecule 2 is a RNA chain called mRNA model.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AM	20	Total	C	N	O	P	0	0
			397	180	40	158	19		

- Molecule 3 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A1	1530	Total	C	N	O	P	0	0
			32828	14642	6024	10633	1529		

- Molecule 4 is a protein called 30S ribosomal protein S2.

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

- Molecule 5 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AC	117	Total	C	N	O	S	0	0
			876	540	174	159	3		

- Molecule 6 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AD	123	Total	C	N	O	S	0	0
			954	590	196	164	4		

- Molecule 7 is a protein called 30S ribosomal protein S13.

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

- Molecule 8 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AG	96	Total	C	N	O	S	0	0
			773	483	160	127	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AH	88	Total	C	N	O	S	0	0
			715	440	146	128	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AI	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
12	AK	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 13 is a protein called 30S ribosomal protein S19.

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

- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

- Molecule 15 is a protein called 30S ribosomal protein S3.

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

- Molecule 16 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 17 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AR	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 18 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 19 is a protein called 30S ribosomal protein S6.

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

- Molecule 20 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AU	150	Total	C	N	O	S	0	0
			1174	730	226	214	4		

- Molecule 21 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AV	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 22 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AW	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

- Molecule 23 is a protein called 30S ribosomal protein S10.

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

- Molecule 24 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BA	117	Total	C	N	O	P	0	0
			2504	1116	459	813	116		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BB	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BC	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 27 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BD	121	Total	C	N	O	S	0	0
			930	582	179	164	5		

- Molecule 28 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BE	144	Total	C	N	O	S	0	0
			1052	654	207	189	2		

- Molecule 29 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BF	136	Total	C	N	O	S	0	0
			1073	686	205	176	6		

- Molecule 30 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BG	127	Total	C	N	O	S	0	0
			1007	621	204	177	5		

- Molecule 31 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BH	117	Total	C	N	O	S	0	0
			899	557	179	162	1		

- Molecule 32 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BI	114	Total	C	N	O	S	0	0
			916	574	179	162	1		

- Molecule 33 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	BJ	117	Total	C	N	O	0	0
			946	604	192	150		

- Molecule 34 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BK	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 35 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BL	110	Total	C	N	O	S	0	0
			856	532	166	155	3		

- Molecule 36 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BM	99	Total	C	N	O	S	0	0
			777	491	145	139	2		

- Molecule 37 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BN	267	Total	C	N	O	S	0	0
			2053	1271	416	359	7		

- Molecule 38 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	BO	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 39 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BP	84	Total	C	N	O	S	0	0
			633	391	129	112	1		

- Molecule 40 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BQ	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 41 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BR	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 42 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BS	70	Total	C	N	O	S	0	0
			548	339	104	99	6		

- Molecule 43 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BT	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

- Molecule 44 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BU	54	Total	C	N	O	S	0	0
			440	284	81	75			

- Molecule 45 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BV	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 46 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BW	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 47 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BX	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 48 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BY	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 49 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BZ	213	Total	C	N	O	S	0	0
			1687	1078	300	308	1		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BZ	1	MET	-	INSERTION	UNP P35024
BZ	?	-	MET	DELETION	UNP P35024
BZ	70	SER	PHE	CONFLICT	UNP P35024
BZ	82	LYS	ASN	CONFLICT	UNP P35024
BZ	?	-	MET	DELETION	UNP P35024
BZ	?	-	MET	DELETION	UNP P35024
BZ	?	-	MET	DELETION	UNP P35024

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B1	201	Total	C	N	O	S	0	0
			1551	974	283	289	5		

- Molecule 51 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B2	178	Total	C	N	O	S	0	0
			1419	905	251	257	6		

- Molecule 52 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B3	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 53 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B4	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 54 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B5	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

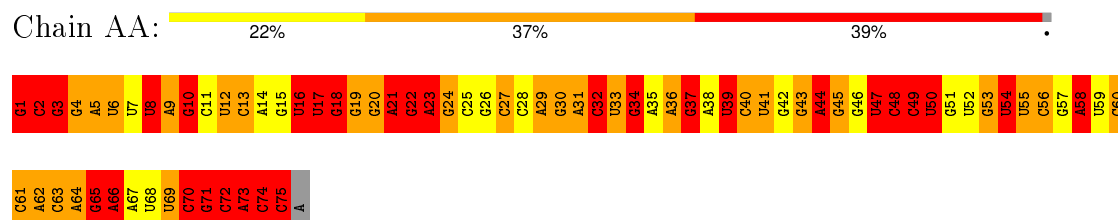
- Molecule 55 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B6	140	Total	C	N	O	S	0	0
			1112	704	210	194	4		

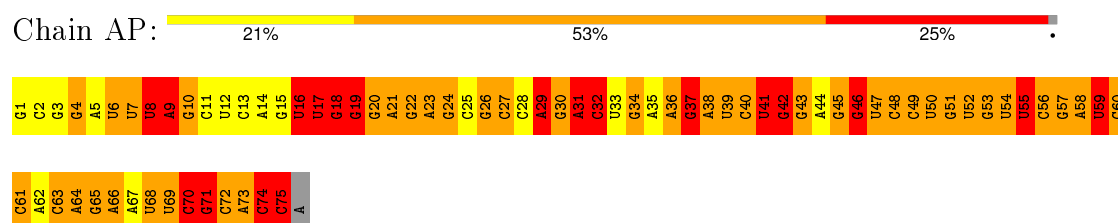
3 Residue-property plots

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.

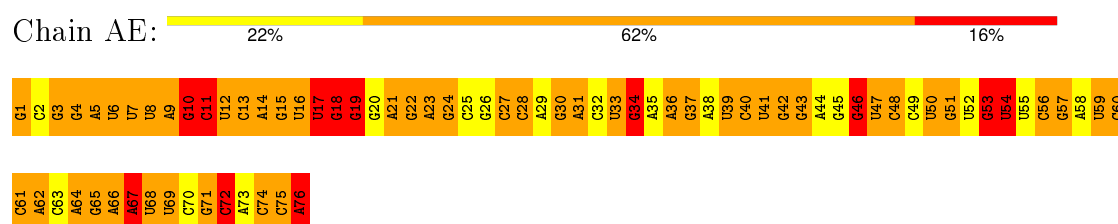
- Molecule 1: A/T, P and E-site tRNAs



- Molecule 1: A/T, P and E-site tRNAs



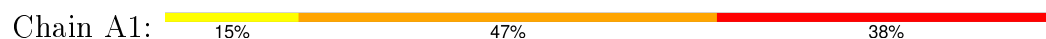
- Molecule 1: A/T, P and E-site tRNAs



- Molecule 2: mRNA model



- Molecule 3: 16S rRNA





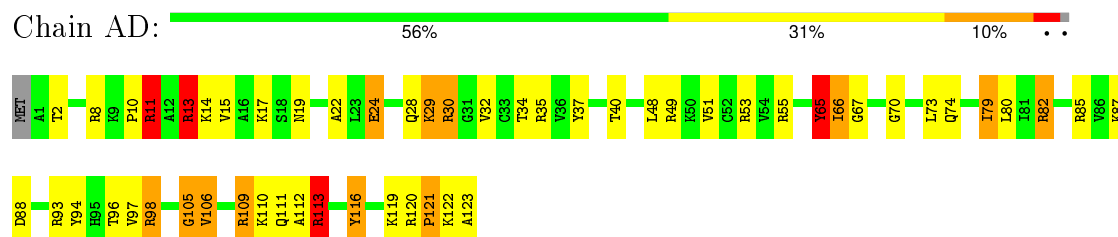

U1025	G1026	U1085	A1145	U1205	G1265	C1325	G1385	U1445	G1505
G1027	C1028	U1087	C1147	G1206	G1266	U1326	G1386	A1446	U1506
C1028	U1029	G1088	C1148	C1207	G1267	U1327	G1387	A1447	U1507
U1030	U1090	C1029	C1149	C1208	G1268	C1328	G1388	A1448	A1508
C1031	U1091	U1030	A1150	C1209	G1269	C1329	G1389	A1449	C1509
G1032	U1092	U1091	A1151	C1210	G1270	U1330	U1390	U1450	C1510
G1033	U1093	U1092	A1152	U1211	A1271	G1331	U1391	U1451	G1511
G1034	U1094	U1093	A1153	U1212	G1272	A1332	G1392	C1452	U1512
A1035	U1095	U1094	G1154	C1213	C1273	A1333	G1393	G1453	A1513
A1036	G1096	U1095	G1155	C1214	A1274	G1334	A1394	G1454	G1514
C1037	G1097	U1096	A1156	G1215	A1275	U1335	G1395	G1455	G1515
C1038	C1098	U1097	A1157	A1216	G1276	G1336	A1396	A1456	G1516
G1039	U1099	C1098	C1158	C1217	G1277	G1337	G1397	G1457	G1517
U1040	U1100	U1099	U1159	C1218	G1278	G1338	A1398	G1458	A1518
U1041	A1101	U1100	C1160	A1219	G1279	A1339	G1399	G1459	A1519
A1042	A1102	U1107	C1161	C1220	A1280	U1340	C1400	C1460	C1520
G1043	A1103	C1107	C1162	G1221	C1281	U1341	G1401	G1461	C1521
A1044	G1103	A1108	A1163	G1222	C1282	C1342	C1402	C1462	U1522
C1045	G1104	U1109	G1164	C1223	U1283	G1343	C1403	U1463	G1523
U1046	A1105	A1110	U1165	U1224	C1284	C1344	C1404	A1464	C1524
G1047	C1106	A1111	G1166	A1225	A1285	U1345	G1405	A1465	G1525
U1048	U1107	U1115	A1167	C1226	U1286	A1346	U1406	C1466	G1526
U1049	G1108	U1116	C1168	A1227	A1287	G1347	C1407	C1467	U1527
G1050	U1109	U1117	A1169	C1228	A1288	U1348	A1408	A1468	U1528
C1051	A1110	U1118	A1170	A1229	A1289	U1349	C1409	C1469	G1529
C1052	C1112	U1119	A1171	C1230	G1290	A1350	A1410	U1470	G1530
G1053	C1113	C1120	C1172	G1231	U1291	U1351	C1411	U1471	A1531
A1055	U1115	U1121	G1173	C1232	C1292	C1352	C1412	U1472	U1532
U1056	U1116	U1122	G1174	U1233	C1293	G1353	A1413	G1473	C1533
G1057	U1117	U1123	G1175	U1234	C1294	U1354	U1414	U1474	A1534
C1058	U1118	U1124	C1176	U1235	U1295	G1355	G1415	G1475	
C1059	U1119	U1125	A1177	A1236	C1296	G1356	G1416	A1476	
U1060	U1120	U1126	A1178	C1237	G1297	U1357	G1417	U1477	
G1061	U1121	G1127	A1180	A1238	U1298	U1358	U1418	U1478	
U1062	U1122	U1128	A1181	U1239	A1299	C1359	G1419	C1479	
C1063	U1123	U1129	G1182	U1240	G1300	A1360	U1420	A1480	
G1064	U1124	U1130	C1183	G1241	U1301	G1361	G1421	U1481	
U1065	U1125	G1133	G1185	G1242	C1302	A1362	G1422	G1482	
C1066	U1126	U1134	G1186	C1243	C1303	A1363	G1423	A1483	
A1067	G1127	U1135	A1187	U1244	G1304	U1364	U1424	C1484	
G1068	C1128	U1136	U1188	A1245	G1305	G1365	U1425	U1485	
C1069	U1129	A1196	U1189	G1246	A1306	C1366	G1426	G1486	
U1070	A1130	U1197	G1190	U1247	U1307	C1367	C1427	G1487	
C1071	G1131	G1137	A1191	A1248	U1308	A1368	A1428	G1488	
G1072	C1132	U1138	C1192	C1249	G1309	C1369	A1429	G1489	
U1073	G1133	U1139	G1193	A1250	G1310	G1370	A1430	U1490	
G1074	U1134	G1140	U1194	A1251	A1311	G1371	A1431	G1491	
U1075	U1135	C1141	C1195	A1252	A1312	U1372	G1432	A1492	
U1076	U1136	G1142	G1196	G1253	U1313	G1373	A1433	A1493	
G1077	C1137	U1143	A1197	A1254	C1314	A1374	A1434	G1494	
U1078	G1138	G1144	U1198	G1255	U1315	A1375	G1435	U1495	
G1079	U1139	C1145	G1199	A1256	G1316	U1376	U1436	A1496	
A1080	C1140	A1201	C1200	C1257	C1317	A1377	A1437	G1497	
A1081	C1141	G1260	A1202	G1258	A1318	G1378	G1438	U1498	
U1082	G1142	A1261	U1202	U1199	A1319	G1379	A1439	A1499	
U1083	G1143	A1262	C1262	C1259	A1320	U1380	U1440	A1500	
G1084	G1144	C1263	C1263	U1264	U1321	U1381	A1441	C1501	
					G1322	C1382	G1442	A1502	
					C1323	C1383	C1443	A1503	
					A1324	C1384	U1444	G1504	

• Molecule 4: 30S ribosomal protein S2

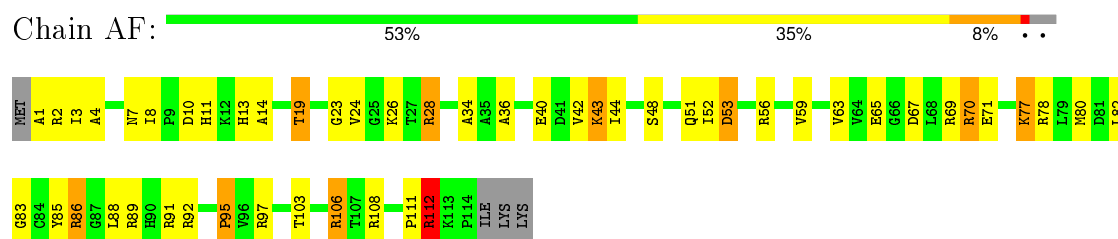
Chain AB:  61% 23% 5% 10%

R224	R225	GLN	ASP	LEU	ALA	SER	GLN	ALA	GLU	GLU	SER	PHE	VAL	GLU	ALA	GLU
T105	R106	R107	R112	L113	K114	D115	L116	F125	D126	K127	L128	T129	L134	H135	R136	T137
					</											

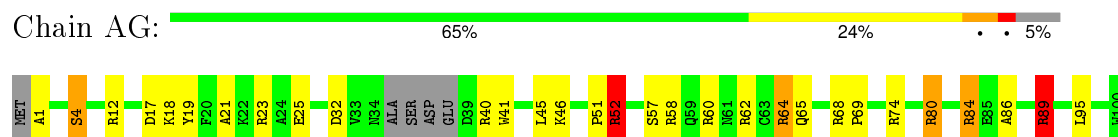
- Molecule 6: 30S ribosomal protein S12



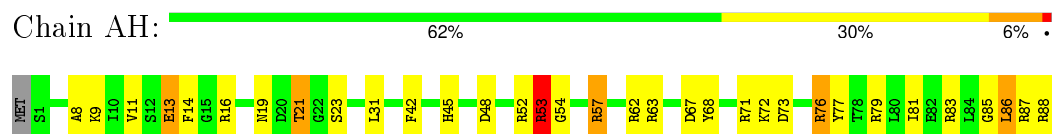
- Molecule 7: 30S ribosomal protein S13



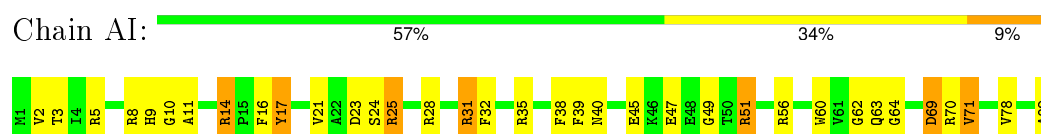
- Molecule 8: 30S ribosomal protein S14



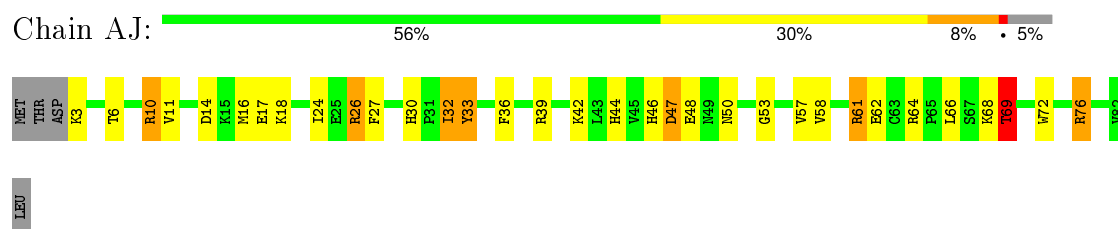
- Molecule 9: 30S ribosomal protein S15



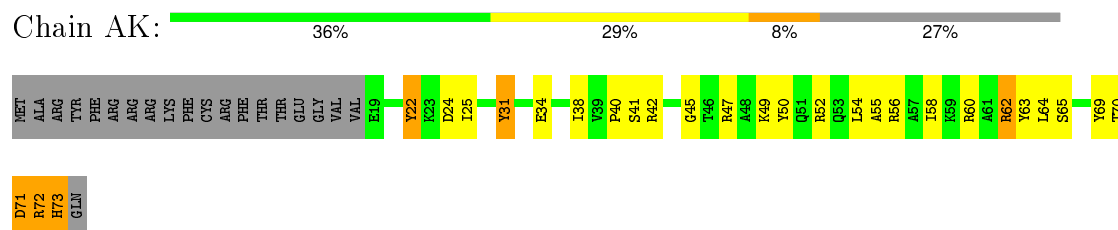
- Molecule 10: 30S ribosomal protein S16



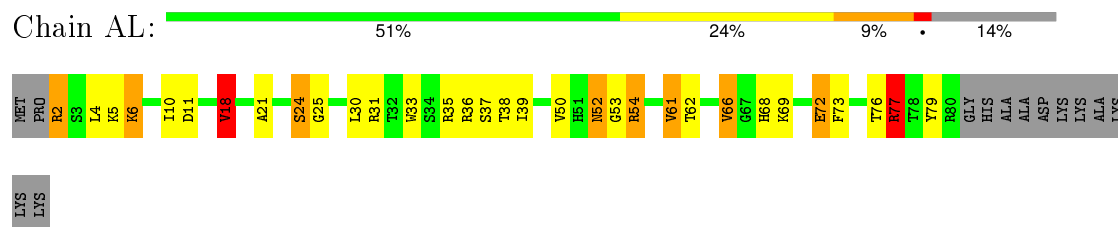
- Molecule 11: 30S ribosomal protein S17



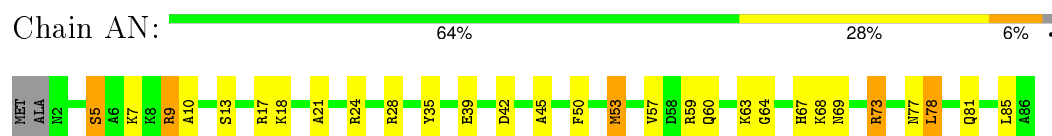
- Molecule 12: 30S ribosomal protein S18



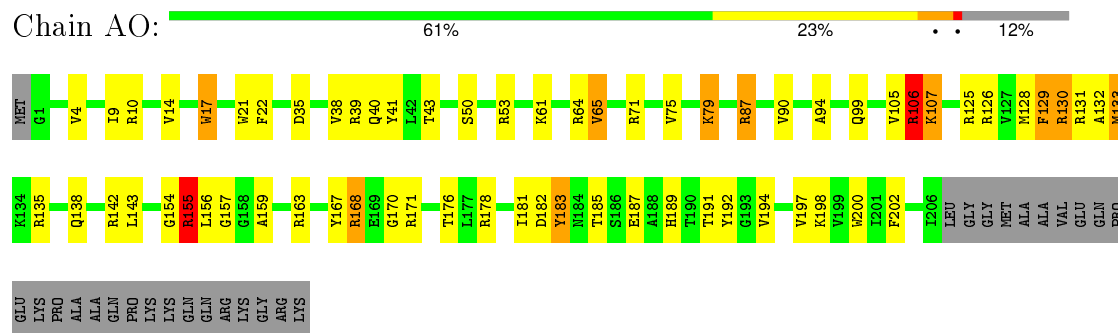
- Molecule 13: 30S ribosomal protein S19



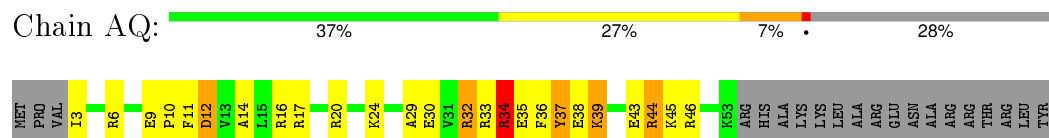
- Molecule 14: 30S ribosomal protein S20



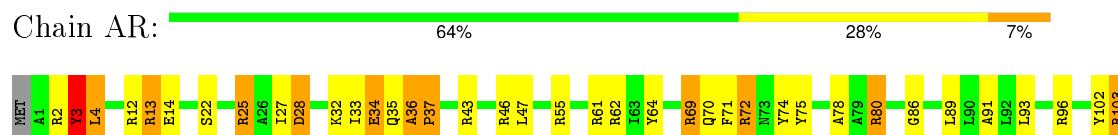
- Molecule 15: 30S ribosomal protein S3

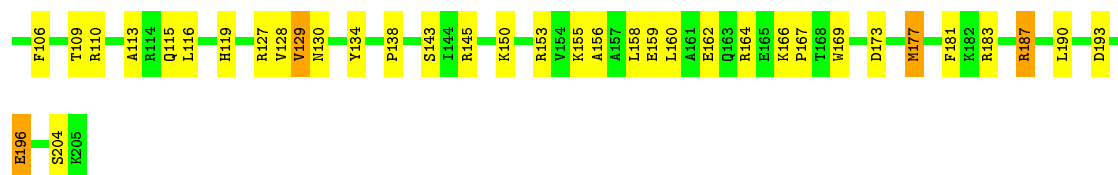


- Molecule 16: 30S ribosomal protein S21



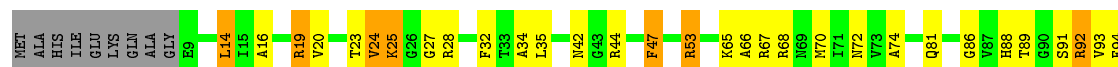
- Molecule 17: 30S ribosomal protein S4





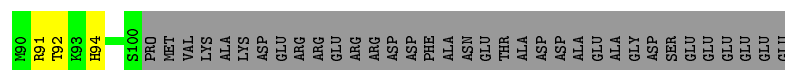
- Molecule 18: 30S ribosomal protein S5

Chain AS: 62% 25% 8% 6%



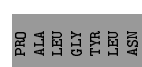
- Molecule 19: 30S ribosomal protein S6

Chain AT: 42% 24% 7% 26%



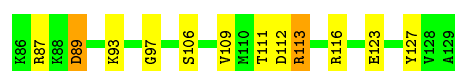
- Molecule 20: 30S ribosomal protein S7

Chain AU: 48% 29% 6% 16%



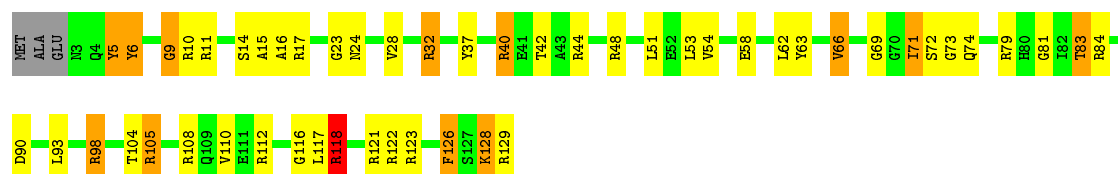
- Molecule 21: 30S ribosomal protein S8

Chain AV: 62% 31% 5% 2%



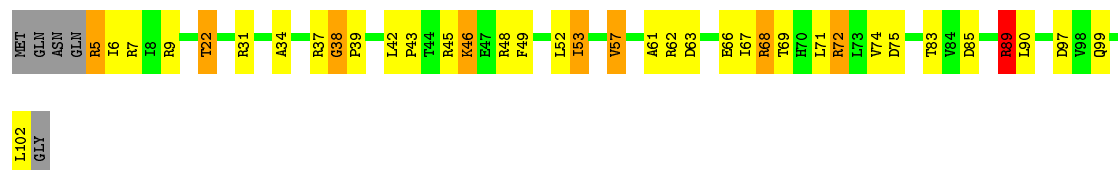
- Molecule 22: 30S ribosomal protein S9

Chain AW: 58% 29% 9% 4%



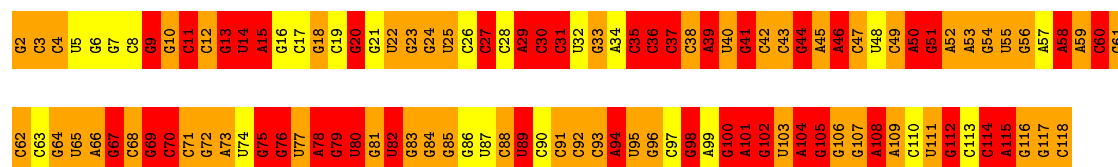
- Molecule 23: 30S ribosomal protein S10

Chain AX: 59% 27% 8% 5%



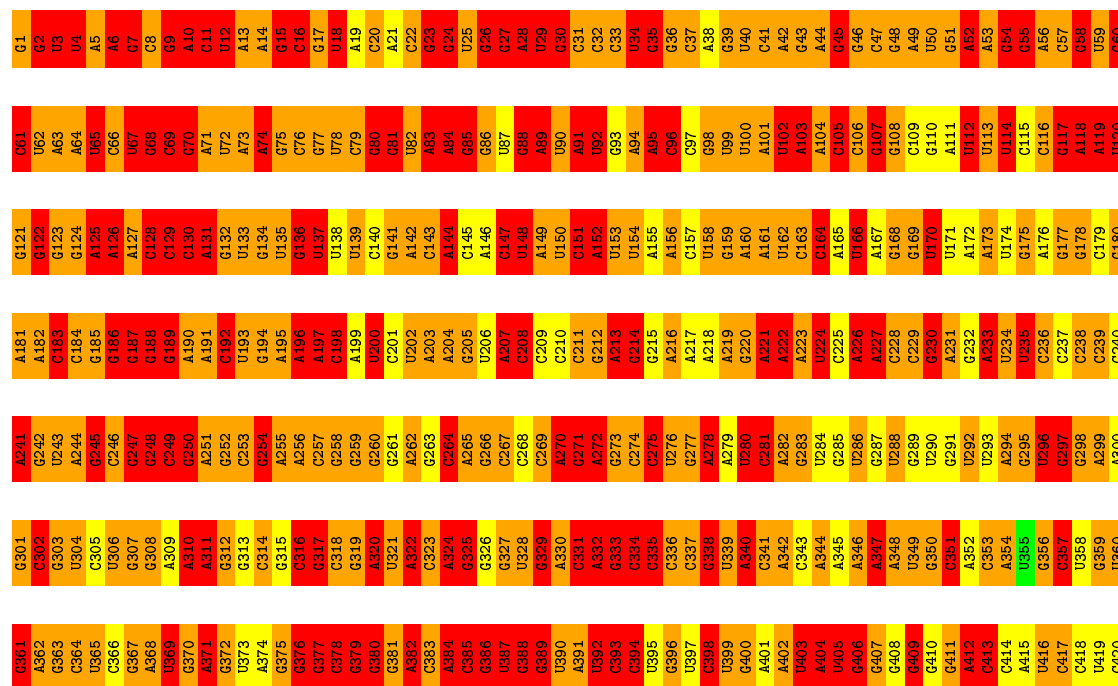
- Molecule 24: 5S rRNA

Chain BA: 20% 44% 36%



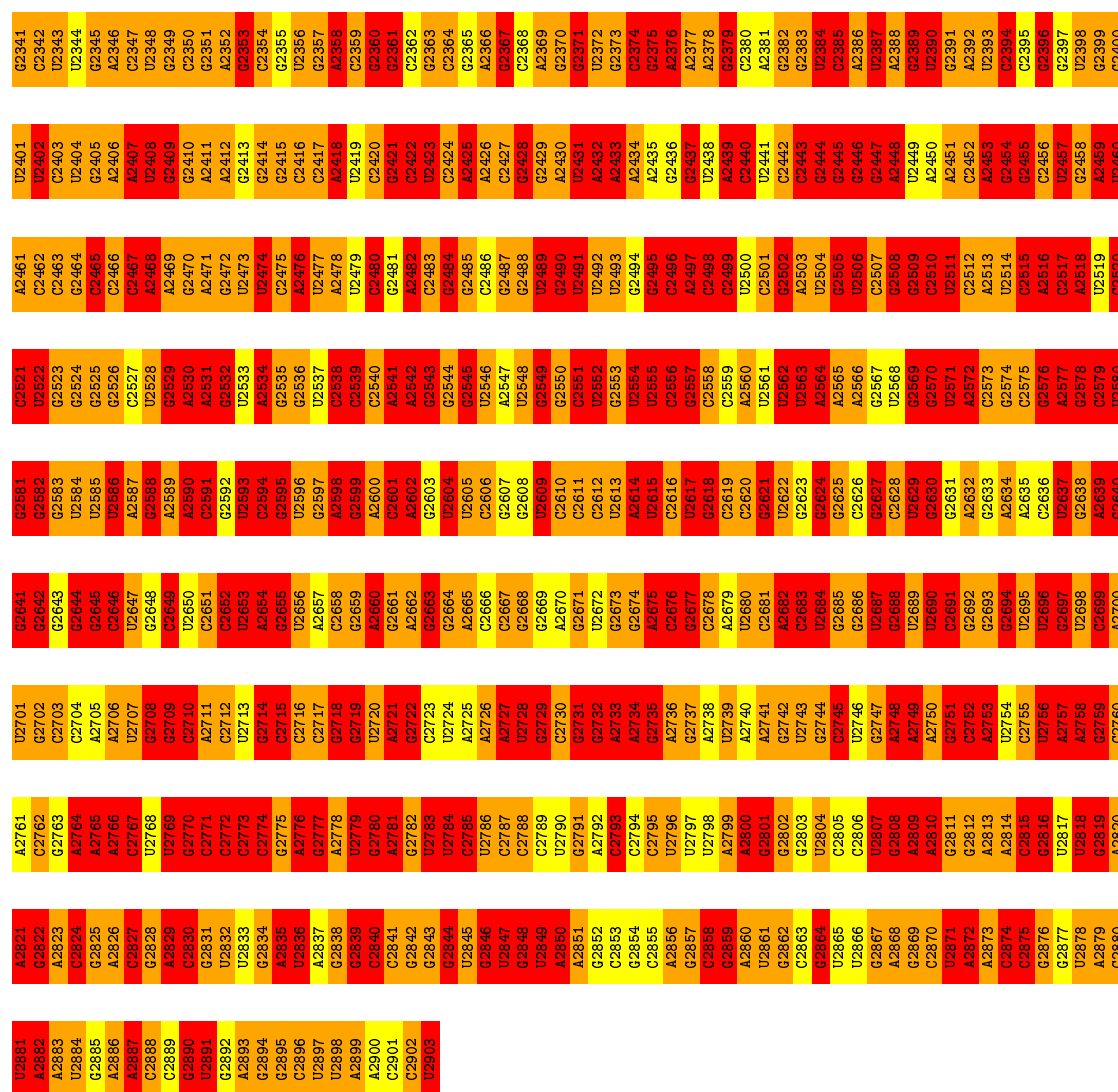
- Molecule 25: 23S rRNA

Chain BB: 15% 43% 42%

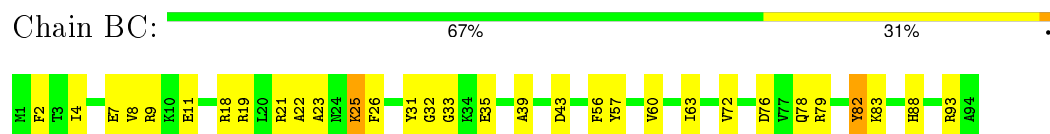


A1321	G1281	U1201	U1141	U1081	A1021	C961	C901	G841	A781	A721	A661	C601	A541	G481	C421
A1322	A1262	G1202	A1142	U1082	G1022	G962	C902	U842	A782	A722	A662	A602	A542	A482	A422
G1323	U1263	U1203	A1143	U1083	G1023	U963	C903	G843	A783	A723	A663	A603	A543	A483	A423
C1324	A1264	A1204	A1144	A1084	G1024	C964	G904	G844	G784	A724	A664	G604	A544	C484	G424
U1325	A1265	A1205	C1145	A1085	G1025	C965	A905	U845	G785	G725	A665	G605	U545	G485	G425
U1326	A1266	A1206	C1146	A1086	G1026	G966	U906	U846	G786	G726	A666	U606	U546	C486	C426
A1327	U1267	C1207	A1147	G1087	A1027	U967	G907	U847	C787	A727	U667	U607	U547	C487	U427
A1328	A1268	U1208	U1148	A1088	A1028	C968	C908	C848	A788	G728	A668	A608	A548	C488	A428
U1329	A1269	U1209	G1149	A1089	A1029	G969	A909	A849	A789	G729	A669	A609	A549	C489	A429
C1330	G1210	C1030	A1150	A1090	C1030	U970	A910	U850	U790	A730	A670	C610	C550	C490	A430
G1331	C1211	A1151	A1151	G1091	G1031	G971	A911	C851	C791	G731	C671	C611	C551	A491	U431
G1332	A1272	G1212	C1152	G1092	A1032	A972	C912	U852	A792	G732	C672	G612	U552	A492	A432
G1333	U1273	A1213	G1153	U1093	U1033	A973	C913	C853	A793	G733	C673	A613	C553	G493	C433
G1334	A1274	A1214	G1154	U1094	G1034	G974	G914	C854	A794	A734	A674	A614	U554	C494	U434
C1335	A1275	G1215	A1155	A1095	U1035	A975	C915	G855	C795	A735	A675	U615	G555	G495	C435
A1336	A1276	G1216	A1156	A1096	G1036	G976	G916	G856	A796	G736	A676	A616	A556	C496	C436
G1337	C1277	U1217	G1157	U1097	G1037	G977	A917	G857	G797	C737	C677	G617	C557	A497	U437
G1338	C1278	G1218	C1158	A1098	G1038	G978	A918	G858	G798	G738	C678	G618	U558	C498	G438
G1339	U1279	U1219	U1159	U1099	A1039	A979	U919	G859	G799	A739	C679	G619	G559	U499	A439
U1340	G1280	G1220	G1160	C1100	A1040	A980	A920	U860	A800	C740	C680	G620	C560	G500	C440
C1341	G1281	C1221	C1161	U1101	G1041	A981	C921	A861	A801	A741	C681	A621	A501	A501	U441
A1342	U1282	U1222	G1162	C1102	G1042	C982	C922	A862	A802	A742	C682	G622	U562	A502	G442
G1343	G1283	G1223	G1163	A1103	C1043	A983	G923	A863	U803	A743	C683	C623	A563	A503	A443
U1344	U1284	U1224	A1164	C1104	G1044	A984	G924	G864	A804	U744	C684	C624	C564	A504	C444
C1345	A1285	G1225	A1165	U1105	C1045	C985	A925	C865	G805	G745	A685	G625	C565	A505	C445
G1346	A1286	A1226	G1166	G1106	A1046	C986	G926	A866	C906	U746	U686	A626	U566	G506	G446
A1347	G1287	G1227	C1167	G1107	G1047	C987	A927	C867	U807	A747	C687	A627	U567	A507	A447
C1348	G1288	G1228	G1168	U1108	A1048	A988	A928	U868	A808	G748	U688	G628	U568	A508	U448
C1349	C1289	C1049	A1169	C1109	C1049	G989	U929	G869	G809	A749	A689	G629	U569	C509	A449
U1350	U1290	G1110	C1170	G1110	A1050	A990	G930	U870	U810	A750	G690	G630	C570	C510	G450
C1351	U1291	U1231	G1171	A1111	G1051	C991	U931	U871	U811	A751	C691	A631	U571	U511	U451
U1352	G1292	G1232	C1172	G1112	C1052	C992	U932	U872	C812	A752	C692	A632	A572	G512	G452
A1353	C1293	C1233	U1173	U1113	C1053	A993	A933	G873	A693	A753	C693	A633	U573	A513	A453
U1354	U1294	U1234	A1174	C1114	A1054	C994	U934	G874	C814	U754	C694	C634	A574	A514	A454
G1355	C1295	G1235	A1175	G1115	G1055	C995	C935	G875	C815	U755	C695	G635	A575	A515	C455
G1356	G1296	G1236	G1176	G1116	A1056	A996	A936	C876	C816	A756	G696	G636	U576	C516	C456
C1357	A1297	A1237	G1177	G1117	A1057	G997	C937	A877	C817	A757	G697	A637	A577	C517	A457
G1358	C1298	G1238	C1178	C1118	U1058	C998	G938	A878	G818	C758	C698	G638	A578	G518	G458
A1359	G1299	G1059	G1179	U1119	G1059	U999	G939	G879	A819	G759	A699	U639	G579	U519	U459
G1360	G1300	U1240	U1180	G1120	U1060	A1000	G940	G880	A920	G760	G700	C640	U580	G520	A460
C1361	A1301	A1241	U1181	C1121	U1061	A1001	A941	G881	A821	A761	C581	U641	C581	U521	C461
G1362	U1242	U1242	G1182	G1122	G1062	G1002	G942	G882	G822	U762	A582	U642	A582	A522	C462
C1363	G1303	C1243	U1183	C1123	G1063	G1003	A943	G883	C823	G763	U703	A643	G583	G523	G463
G1364	A1244	A1244	U1184	G1124	C1064	U1004	C944	U884	U824	A764	C584	A644	G584	G524	U464
A1365	G1245	G1245	G1185	G1125	U1065	C1005	A945	C885	A825	C765	A705	C645	G585	U525	G465
C1366	A1246	A1246	G1186	A1126	U1066	C1006	C946	A886	U826	U766	A706	U646	A586	A526	A466
A1367	A1247	A1247	G1187	A1127	A1067	C1007	A947	U887	U827	U767	G707	G647	C587	C527	G467
G1368	G1248	G1248	U1188	G1128	G1068	A1008	C948	C888	U828	G768	U708	G648	U588	A528	G468
G1369	U1249	U1249	A1189	A1129	A1069	A1009	G949	C889	A829	U769	U709	G649	U589	A529	G469
C1370	G1310	G1250	G1190	U1130	A1070	A1010	G950	C890	G830	G770	U710	C650	A590	G530	A470
G1371	G1311	C1251	G1191	G1131	G1071	G1011	C951	G891	G831	G771	G711	G651	U591	C531	A471
U1372	G1312	G1252	G1192	U1132	C1072	U1012	G952	A892	U832	G772	G712	U652	A592	A532	A472
A1373	U1313	A1253	G1193	A1133	A1073	C1013	G953	C893	A833	G773	G713	U653	U593	G533	G473
G1374	C1314	A1254	A1194	A1134	G1074	A1014	G954	U894	G834	G774	U714	A654	U594	U534	G474
G1375	G1315	U1255	G1195	C1075	C1075	U1015	U955	U895	C835	G775	A715	A655	C595	G535	C475
C1376	U1316	G1256	G1196	G1136	C1076	G1016	G956	A896	G836	G776	A716	G656	U596	G536	G476
G1377	G1317	C1257	G1197	G1137	A1077	G1017	C957	C897	C837	G777	C717	U657	G597	G537	A477
U1378	U1318	U1258	U1198	G1138	U1078	U1018	U958	C898	C838	G778	A718	U658	U598	A538	A478
U1379	C1319	G1259	U1199	G1139	U1079	U1019	A959	C899	U839	G779	A719	G659	A599	G539	A479
G1380	C1320	A1260	C1200	C1140	A1080	A1020	A960	A900	C940	G780	U720	C660	G600	C540	A480

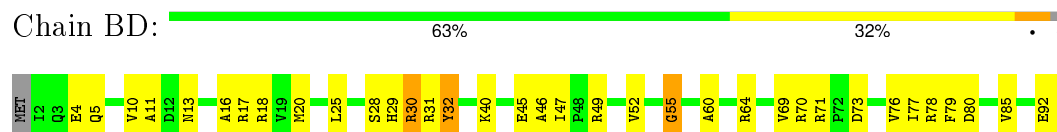
A2281	G2221	C2161	A2101	U2041	A1981	G1921	G1861	A1801	C1741	G1681	U1621	C1561	G1501	U1441	G1381
G2282	C2222	G2162	G2102	A2042	U1982	G1922	G1862	A1802	U1742	G1682	G1622	U1562	A1502	U1442	G1382
C2283	G2223	A2163	C2103	A2043	G1983	G1923	G1863	A1803	G1743	G1683	U1623	U1563	A1503	U1443	A1383
A2284	C2224	C2164	C2104	G2044	G1984	G1924	U1864	C1804	A1744	G1684	U1624	C1564	A1504	G1444	A1384
C2285	A2225	U2165	U2105	G2045	C1985	G1925	U1865	A1805	A1745	C1685	C1625	C1565	A1505	G1445	C1385
G2286	C2226	U2166	U2106	G2046	G1986	G1926	A1866	C1806	A1746	C1686	A1626	A1566	U1506	C1446	C1386
A2287	A2227	U2167	G2107	C2047	A1987	A1927	G1867	A1807	U1747	G1687	G1627	G1567	C1507	G1447	A1387
G2288	G2228	G2168	A2108	G2048	G1988	A1928	C1868	A1808	C1748	U1688	G1628	G1568	A1508	U1448	G1388
C2289	U2229	A2169	U2109	G2049	G1989	G1929	G1869	A1809	A1749	A1689	U1629	A1569	A1509	G1449	G1389
G2290	G2230	A2170	G2110	C2050	C1990	G1930	C1870	A1810	G1750	A1690	A1630	A1570	G1510	G1450	U1390
U2291	U2231	A2171	U2111	A2051	U1991	G1931	A1871	A1811	U1751	C1691	G1631	A1571	G1511	C1451	U1391
C2292	C2232	U2172	G2112	A2052	G1992	A1932	A1872	U1812	G1752	U1692	A1632	G1572	C1512	G1452	A1392
G2293	G2233	U2173	U2113	G2053	C1993	G1933	G1873	U1813	G1753	U1693	G1633	A1573	U1513	G1453	A1393
A2294	G2234	A2174	A2114	A2054	C1994	C1934	C1874	G1814	A1754	C1694	A1634	C1574	G1514	C1454	U1394
C2295	G2235	G2175	G2115	C2055	U1995	G1935	A1875	A1815	A1755	G1695	A1635	A1575	A1515	G1455	A1395
U2296	U2236	A2176	G2116	G2056	C1996	A1936	A1876	C1816	G1756	G1696	G1636	U1576	G1516	G1456	U1396
A2297	G2237	C2177	A2117	G2057	G1997	A1937	A1877	U1817	A1757	G1697	A1637	U1577	C1517	U1457	U1397
C2298	U2238	C2178	U2118	A2058	A1998	A1938	G1878	U1818	U1758	A1698	C1638	U1578	C1518	U1458	C1398
U2299	G2239	C2179	A2119	A2059	C1999	U1939	C1879	A1819	A1759	G1699	C1639	A1579	G1519	G1459	C1399
C2300	U2240	U2180	G2120	A2060	C2000	U1940	U1880	A1820	C1760	A1700	A1640	U1580	U1520	U1460	U1400
G2301	A2241	U2181	G2121	C2061	C2001	G1941	C1881	A1821	C1761	A1701	A1641	G1581	G1521	C1461	G1401
U2302	G2242	U2182	U2122	A2062	G2002	C1942	U1882	C1822	A1762	G1702	G1642	C1582	A1522	C1462	U1402
C2303	U2243	A2183	G2123	C2063	A2003	U1943	U1883	C1823	G1763	G1703	G1643	C1583	U1523	C1463	A1403
U2304	U2244	G2184	G2124	C2064	G2004	U1944	G1884	G1824	C1764	C1704	C1644	U1584	G1524	G1464	C1404
G2305	U2245	U2185	G2125	C2065	A2005	G1945	A1885	U1825	U1765	A1705	G1645	C1585	A1525	G1465	U1405
C2306	G2246	G2186	A2126	C2066	C2006	U1946	U1886	G1826	G1766	C1706	C1646	A1586	C1526	U1466	U1406
G2307	A2247	U2187	G2127	G2067	U2007	C1947	C1887	U1827	C1767	G1707	U1647	G1587	G1527	U1467	G1407
C2308	G2248	U2188	C2128	C2068	C2008	G1948	G1888	G1828	C1768	A1708	G1648	U1588	A1528	U1468	A1408
A2309	U2249	U2189	C2129	C2069	A2009	G1949	A1889	A1829	U1769	U1709	G1649	U1589	G1529	U1469	U1409
C2310	G2250	G2190	U2130	A2070	G2010	U1950	A1890	C1830	G1770	G1710	A1650	A1590	G1530	A1470	G1410
A2311	G2251	A2191	U2131	A2071	U2011	U1951	G1891	G1831	C1771	G1711	G1651	A1591	C1531	G1471	U1411
U2312	U2252	U2192	U2132	C2072	G2012	A1952	C1892	C1832	A1772	U1712	A1652	C1592	A1532	C1472	U1412
G2313	G2253	G2193	G2133	C2073	A2013	A1953	C1893	C1833	A1773	U1713	G1653	A1593	C1533	G1473	A1413
A2314	C2254	U2194	A2134	U2074	A2014	G1954	C1894	C1834	C1774	U1714	A1654	U1594	U1534	U1474	C1414
G2315	G2255	A2195	A2135	U2075	A2015	U1955	C1895	G1835	U1775	G1715	A1655	C1595	A1535	G1475	U1415
C2316	G2256	G2196	G2136	U2076	U2016	U1956	G1896	C1836	G1776	U1716	C1656	A1596	C1536	U1476	G1416
A2317	U2257	U2197	U2137	A2077	U2017	C1957	G1897	C1837	U1777	A1717	U1657	A1597	G1537	A1477	C1417
G2318	G2258	A2198	G2138	C2078	G2018	C1958	U1898	C1838	U1778	G1718	C1658	A1598	G1538	G1478	G1418
U2319	U2259	A2199	U2139	U2079	A2019	G1959	A1899	G1839	U1779	G1719	G1659	U1599	U1539	G1479	A1419
C2320	C2260	C2200	G2140	A2080	A2020	A1960	A1900	G1840	A1780	U1720	G1660	C1600	G1540	C1480	A1420
U2321	C2261	G2201	C2141	U2081	C2021	C1961	A1901	U1841	U1781	G1721	G1661	G1601	C1541	U1481	G1421
A2322	U2262	U2202	A2142	A2082	U2022	C1962	C1902	G1842	U1782	A1722	U1662	U1602	U1542	G1482	G1422
G2323	C2263	G2203	C2143	G2083	C2023	U1963	G1903	C1843	A1783	G1723	G1663	A1603	G1543	G1483	G1423
U2324	G2264	U2204	G2144	C2084	G2024	G1964	G1904	C1844	A1784	G1724	A1664	C1604	A1544	U1484	G1424
C2325	U2265	A2205	C2145	U2085	C2025	C1965	C1905	G1845	A1785	U1725	A1665	C1605	A1545	U1485	G1425
A2326	A2266	C2206	C2146	U2086	U2026	A1966	G1906	G1846	A1786	C1726	G1666	C1606	G1546	U1486	G1426
U2327	A2267	G2207	A2147	G2087	G2027	C1967	G1907	A1847	A1787	C1727	G1667	C1607	C1547	U1487	A1427
A2328	G2268	G2208	G2148	A2088	U2028	G1968	C1908	A1848	C1788	G1728	A1668	A1608	A1548	C1488	C1428
U2329	U2269	G2209	U2149	C2089	G2029	A1969	C1909	G1849	A1789	U1729	A1669	A1609	A1549	C1489	G1429
G2330	A2270	C2210	C2150	A2090	A2030	U1970	G1910	G1850	C1790	G1730	C1670	A1610	C1550	A1490	G1430
C2331	G2271	A2211	U2151	C2091	A2031	U1971	U1911	U1851	A1791	G1731	U1671	C1611	A1551	G1491	A1431
U2332	U2272	G2212	G2152	G2092	G2032	G1972	A1912	G1852	G1792	C1732	A1672	C1612	A1552	G1492	G1432
A2333	A2273	C2213	C2153	G2093	A2033	G1973	A1913	A1853	G1793	G1733	G1673	C1613	A1553	C1493	A1433
U2334	G2274	A2154	U2154	U2094	U2034	C1974	A1914	A1854	A1794	G1734	G1674	A1614	U1554	A1494	A1434
A2335	C2275	G2215	U2155	A2095	G2035	G1975	U1915	U1855	C1795	A1735	C1675	C1615	G1555	A1495	G1435
G2336	G2276	G2216	G2156	C2096	G2036	U1976	A1916	U1856	U1796	U1736	A1676	A1616	C1556	A1496	G1436
C2337	G2277	G2217	G2157	A2097	A2037	A1977	U1917	G1857	G1797	G1737	A1677	C1617	C1557	U1497	C1437
U2338	A2278	G2218	A2158	U2098	C2038	A1978	A1918	A1858	U1798	G1738	A1678	A1618	U1558	C1498	U1438
G2339	G2279	U2219	G2159	U2099	U2039	U1979	A1919	U1859	G1799	G1739	A1679	A1619	U1559	C1499	G1439
A2340	G2280	U2220	C2160	G2100	G2040	G1980	C1920	G1860	C1800	G1740	U1680	G1620	G1560	G1500	U1440



- Molecule 26: 50S ribosomal protein L25

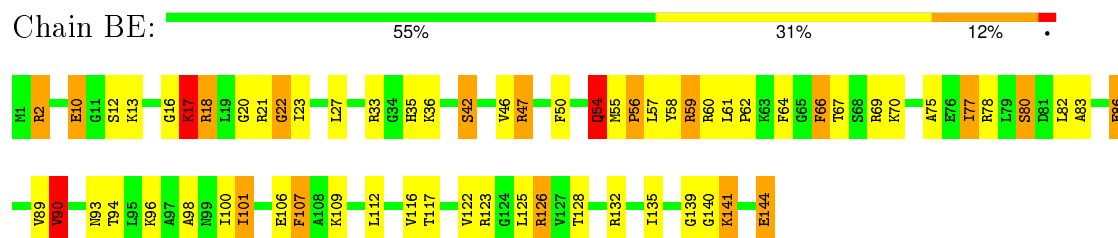


- Molecule 27: 50S ribosomal protein L14

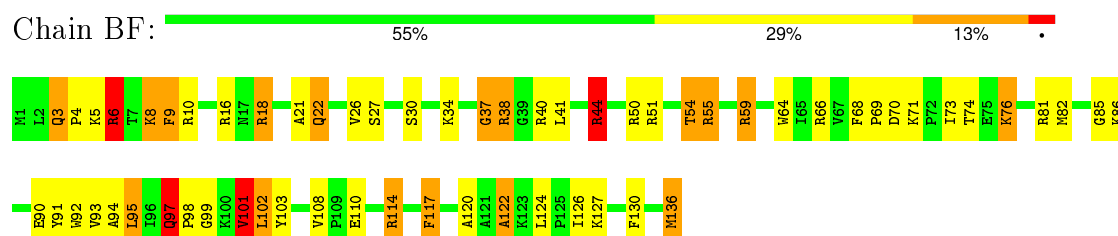


- Molecule 28: 50S ribosomal protein L15

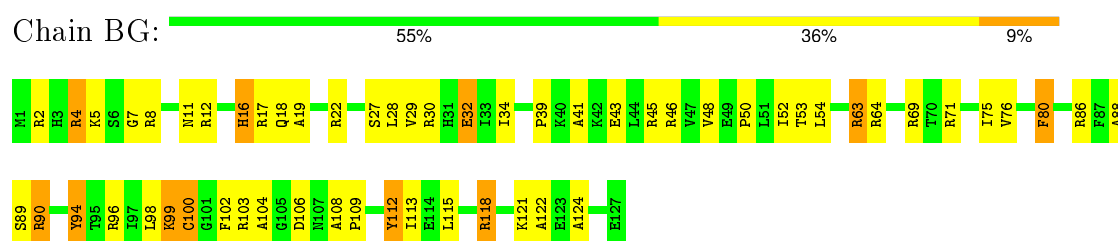




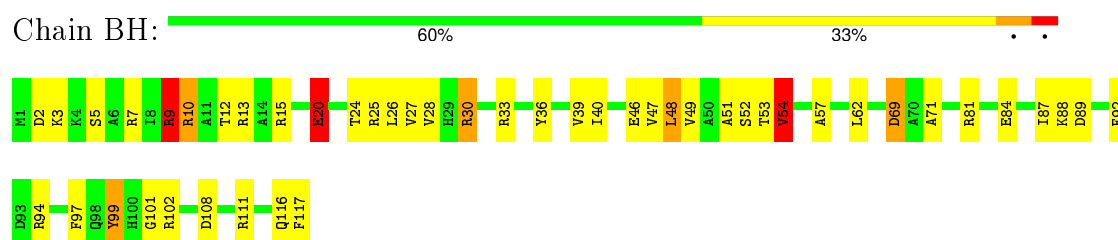
- Molecule 29: 50S ribosomal protein L16



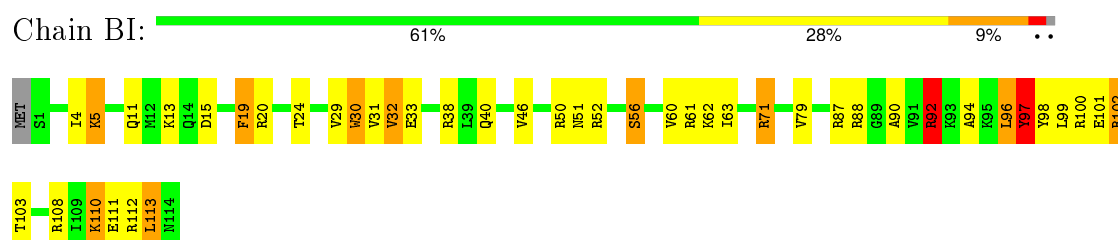
- Molecule 30: 50S ribosomal protein L17



- Molecule 31: 50S ribosomal protein L18



- Molecule 32: 50S ribosomal protein L19



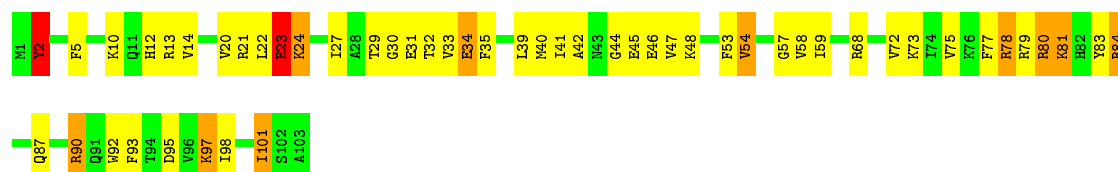
- Molecule 33: 50S ribosomal protein L20





- Molecule 34: 50S ribosomal protein L21

Chain BK:



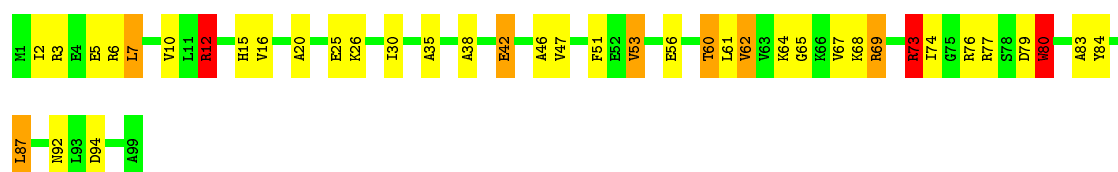
- Molecule 35: 50S ribosomal protein L22

Chain BL:



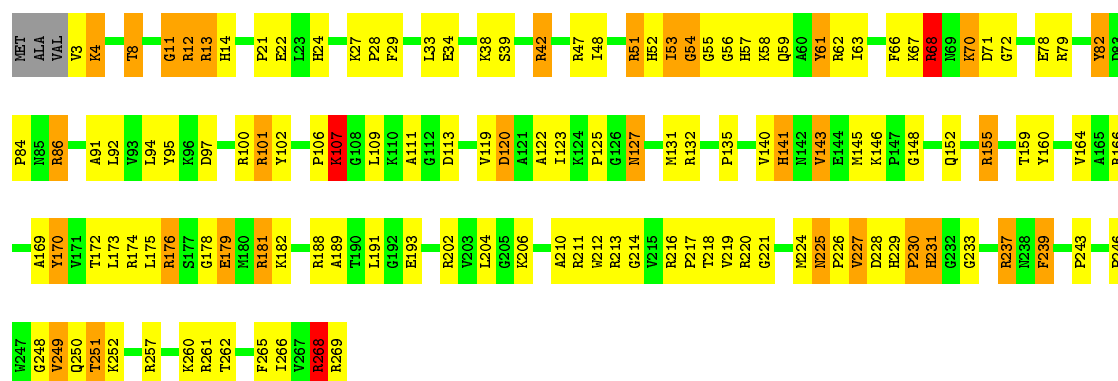
- Molecule 36: 50S ribosomal protein L23

Chain BM:

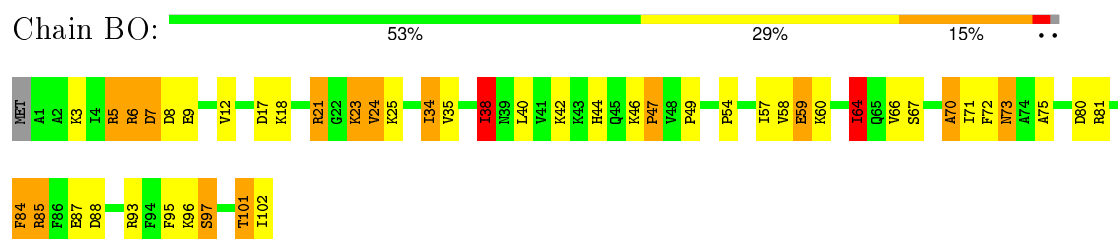


- Molecule 37: 50S ribosomal protein L2

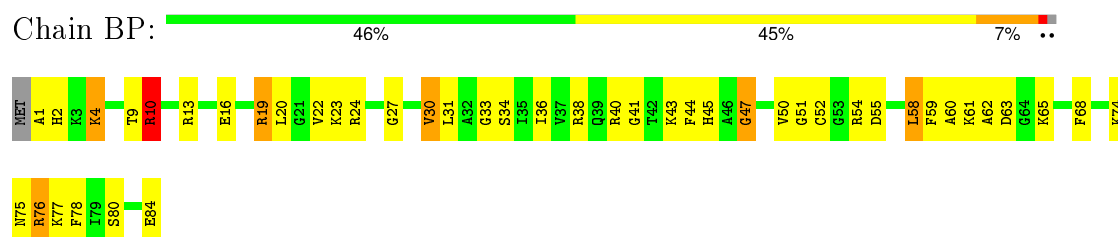
Chain BN:



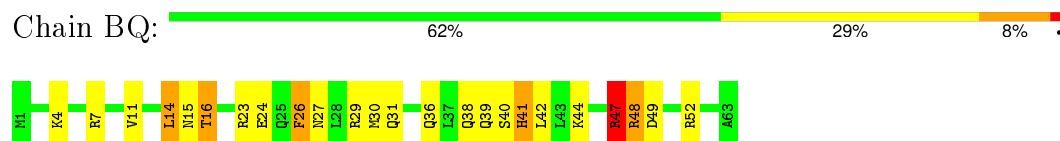
- Molecule 38: 50S ribosomal protein L24



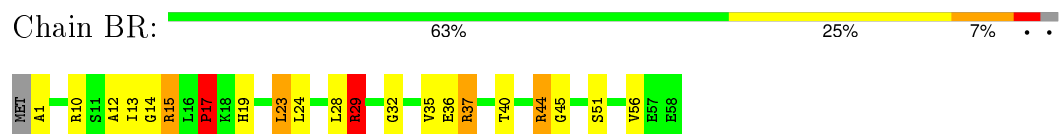
- Molecule 39: 50S ribosomal protein L27



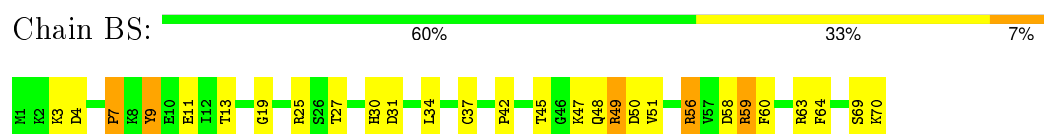
- Molecule 40: 50S ribosomal protein L29



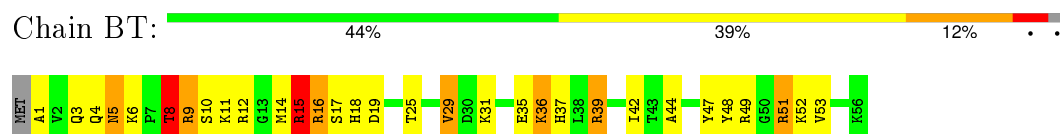
- Molecule 41: 50S ribosomal protein L30



- Molecule 42: 50S ribosomal protein L31



- Molecule 43: 50S ribosomal protein L32

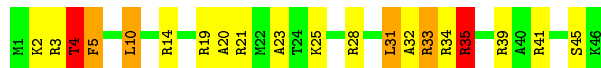


- Molecule 44: 50S ribosomal protein L33





- Molecule 45: 50S ribosomal protein L34



- Molecule 46: 50S ribosomal protein L35



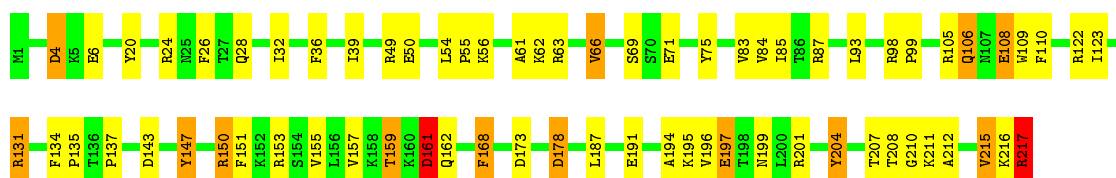
- Molecule 47: 50S ribosomal protein L36



- Molecule 48: 50S ribosomal protein L3

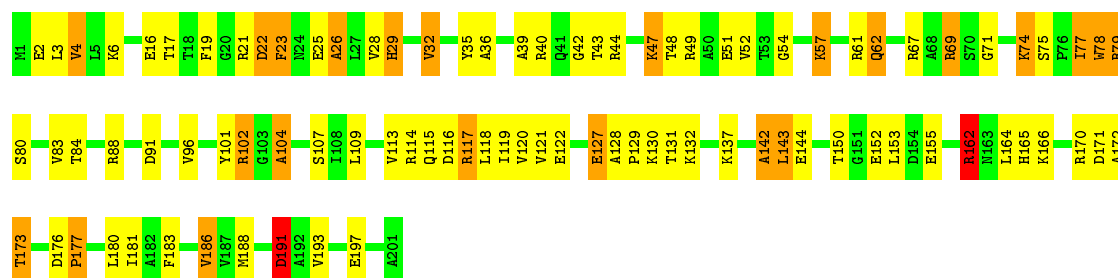


- Molecule 49: 50S ribosomal protein L1P



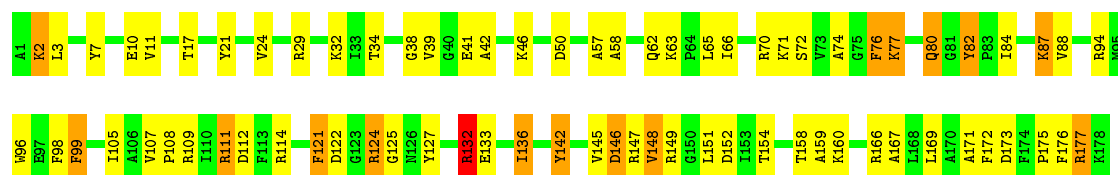
- Molecule 50: 50S ribosomal protein L4





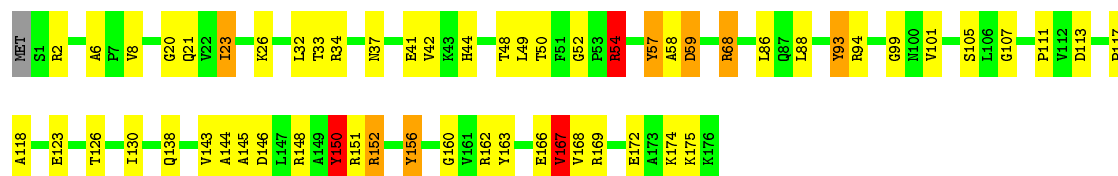
- Molecule 51: 50S ribosomal protein L5

Chain B2: 58% 33% 8% .



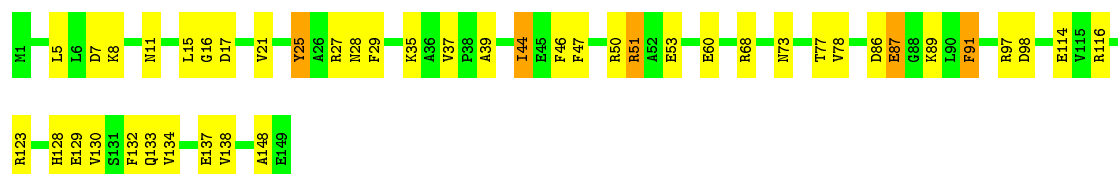
- Molecule 52: 50S ribosomal protein L6

Chain B3: 67% 27% . . .



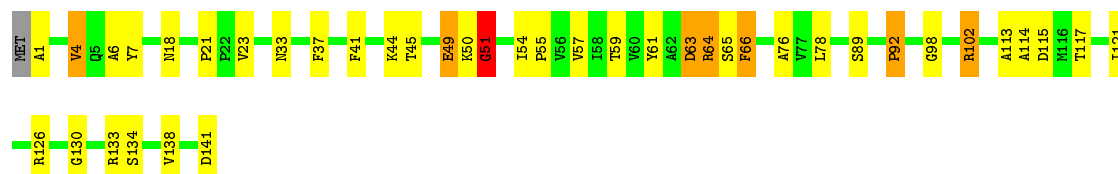
- Molecule 53: 50S ribosomal protein L9

Chain B4: 70% 26% .

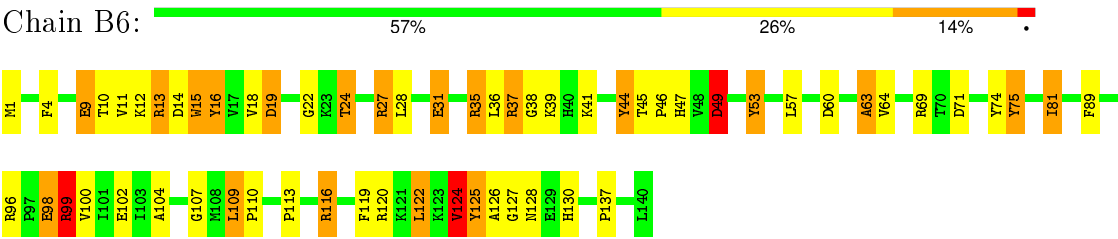


- Molecule 54: 50S ribosomal protein L11

Chain B5: 70% 23% 5% . .



- Molecule 55: 50S ribosomal protein L13



4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	Not provided	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	3.40	236/1789 (13.2%)	4.38	561/2788 (20.1%)
1	AE	3.39	235/1814 (13.0%)	4.16	549/2827 (19.4%)
1	AP	4.04	200/1789 (11.2%)	4.62	517/2788 (18.5%)
10	AI	1.65	6/658 (0.9%)	2.62	33/884 (3.7%)
11	AJ	1.59	5/657 (0.8%)	2.37	33/881 (3.7%)
12	AK	1.77	5/462 (1.1%)	2.48	33/621 (5.3%)
13	AL	1.63	3/652 (0.5%)	2.09	19/877 (2.2%)
14	AN	1.53	3/670 (0.4%)	2.09	21/888 (2.4%)
15	AO	1.66	19/1651 (1.2%)	2.22	58/2225 (2.6%)
16	AQ	1.74	6/430 (1.4%)	2.77	30/570 (5.3%)
17	AR	1.65	17/1664 (1.0%)	2.37	81/2227 (3.6%)
18	AS	1.67	10/1118 (0.9%)	2.31	38/1504 (2.5%)
19	AT	1.63	5/835 (0.6%)	2.30	36/1128 (3.2%)
2	AM	2.83	38/436 (8.7%)	3.84	119/672 (17.7%)
20	AU	1.68	10/1187 (0.8%)	2.46	56/1591 (3.5%)
21	AV	1.64	7/988 (0.7%)	2.27	43/1326 (3.2%)
22	AW	1.78	14/1033 (1.4%)	2.59	48/1375 (3.5%)
23	AX	1.57	4/796 (0.5%)	2.46	38/1077 (3.5%)
24	BA	3.32	357/2800 (12.8%)	4.36	854/4367 (19.6%)
25	BB	15.87	8884/69795 (12.7%)	4.40	21260/108884 (19.5%)
26	BC	1.63	10/765 (1.3%)	2.11	24/1025 (2.3%)
27	BD	1.69	7/939 (0.7%)	2.47	44/1258 (3.5%)
28	BE	1.68	9/1061 (0.8%)	2.33	37/1413 (2.6%)
29	BF	1.62	6/1092 (0.5%)	2.24	37/1460 (2.5%)
3	A1	3.49	4705/36759 (12.8%)	4.27	10939/57346 (19.1%)
30	BG	1.70	10/1020 (1.0%)	2.53	58/1364 (4.3%)
31	BH	1.69	11/909 (1.2%)	2.40	43/1219 (3.5%)
32	BI	1.71	8/928 (0.9%)	2.37	36/1242 (2.9%)
33	BJ	1.71	15/959 (1.6%)	2.50	62/1278 (4.9%)
34	BK	1.62	5/828 (0.6%)	2.36	35/1107 (3.2%)
35	BL	1.52	4/863 (0.5%)	2.38	33/1156 (2.9%)
36	BM	1.54	4/784 (0.5%)	2.16	28/1048 (2.7%)
37	BN	1.74	26/2092 (1.2%)	2.34	97/2813 (3.4%)
38	BO	1.59	2/787 (0.3%)	2.39	37/1051 (3.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	BP	1.71	7/641 (1.1%)	2.42	28/848 (3.3%)
4	AB	1.61	8/1735 (0.5%)	2.18	57/2338 (2.4%)
40	BQ	1.67	5/509 (1.0%)	2.16	15/677 (2.2%)
41	BR	1.60	5/452 (1.1%)	2.10	15/605 (2.5%)
42	BS	1.65	8/558 (1.4%)	2.43	20/745 (2.7%)
43	BT	1.77	7/449 (1.6%)	2.34	22/599 (3.7%)
44	BU	1.61	3/447 (0.7%)	2.19	18/594 (3.0%)
45	BV	1.74	3/379 (0.8%)	2.64	22/498 (4.4%)
46	BW	1.55	3/512 (0.6%)	2.18	20/676 (3.0%)
47	BX	1.56	2/302 (0.7%)	2.90	18/397 (4.5%)
48	BY	1.69	11/1585 (0.7%)	2.23	58/2134 (2.7%)
49	BZ	1.57	8/1711 (0.5%)	2.13	57/2305 (2.5%)
5	AC	1.67	7/892 (0.8%)	2.45	47/1205 (3.9%)
50	B1	1.66	15/1570 (1.0%)	2.30	70/2113 (3.3%)
51	B2	1.67	11/1443 (0.8%)	2.29	62/1937 (3.2%)
52	B3	1.60	9/1342 (0.7%)	2.13	50/1816 (2.8%)
53	B4	1.61	11/1121 (1.0%)	2.08	27/1515 (1.8%)
54	B5	1.51	4/1045 (0.4%)	2.16	35/1410 (2.5%)
55	B6	1.69	9/1135 (0.8%)	2.39	60/1529 (3.9%)
6	AD	1.69	12/968 (1.2%)	2.37	39/1300 (3.0%)
7	AF	1.58	5/892 (0.6%)	2.47	46/1193 (3.9%)
8	AG	1.66	9/785 (1.1%)	2.56	33/1046 (3.2%)
9	AH	1.80	12/723 (1.7%)	2.44	37/966 (3.8%)
All	All	10.61	15060/162206 (9.3%)	3.93	36793/242726 (15.2%)

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	52
1	AE	0	46
1	AP	2	51
10	AI	0	9
11	AJ	0	4
12	AK	0	3
13	AL	0	8
14	AN	1	0
15	AO	0	9
16	AQ	0	5
17	AR	0	5

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
18	AS	0	2
19	AT	0	9
2	AM	0	12
20	AU	0	8
21	AV	0	4
22	AW	0	9
23	AX	0	2
24	BA	0	81
25	BB	3	1853
26	BC	0	2
27	BD	0	4
28	BE	0	5
29	BF	0	9
3	A1	4	995
30	BG	0	5
31	BH	0	7
32	BI	0	6
33	BJ	0	3
34	BK	0	11
35	BL	0	4
36	BM	0	3
37	BN	0	12
38	BO	0	4
39	BP	0	7
4	AB	0	8
41	BR	0	4
42	BS	0	7
43	BT	0	3
44	BU	0	3
45	BV	0	4
46	BW	0	7
47	BX	0	1
48	BY	0	8
49	BZ	0	9
5	AC	0	4
50	B1	0	9
51	B2	0	7
52	B3	0	7
53	B4	0	3
54	B5	0	3
55	B6	0	12
6	AD	0	9

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
7	AF	0	8
8	AG	0	3
9	AH	0	2
All	All	10	3370

The worst 5 of 15060 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BB	995	C	C4-C5	2385.00	20.50	1.43
25	BB	995	C	C2-N3	2363.63	20.26	1.35
25	BB	995	C	C4-N4	2355.33	22.53	1.33
3	A1	1429	A	P-O5'	178.05	3.37	1.59
3	A1	1340	A	C3'-O3'	103.07	2.86	1.42

The worst 5 of 36793 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BB	995	C	C5-C4-N4	-167.42	3.01	120.20
25	BB	995	C	C4-C5-C6	-165.92	34.44	117.40
25	BB	995	C	N1-C2-N3	-110.87	41.59	119.20
1	AP	74	C	P-O3'-C3'	-90.94	10.58	119.70
25	BB	995	C	N3-C4-C5	-73.62	92.45	121.90

5 of 10 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AP	31	A	C2',C1'
3	A1	13	U	C2',C1'
3	A1	1198	G	C4'
3	A1	1483	A	C2'
14	AN	13	SER	CA

5 of 3370 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	G	Sidechain
1	AA	3	G	Sidechain
1	AA	4	G	Sidechain
1	AA	5	A	Sidechain
1	AA	6	U	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	1600	0	754	13	0
1	AE	1622	0	773	5	0
1	AP	1600	0	756	42	0
2	AM	397	0	202	4	0
3	A1	32828	0	15398	147	0
4	AB	1704	0	1732	7	0
5	AC	876	0	887	5	0
6	AD	954	0	1019	5	0
7	AF	883	0	944	5	0
8	AG	773	0	824	4	0
9	AH	715	0	742	3	0
10	AI	648	0	666	0	0
11	AJ	648	0	691	2	0
12	AK	455	0	478	1	0
13	AL	637	0	665	5	0
14	AN	664	0	714	5	0
15	AO	1624	0	1699	2	0
16	AQ	425	0	449	1	0
17	AR	1642	0	1710	6	0
18	AS	1105	0	1148	3	0
19	AT	817	0	808	2	0
20	AU	1174	0	1230	0	0
21	AV	978	0	1034	3	0
22	AW	1021	0	1070	0	0
23	AX	786	0	828	7	0
24	BA	2504	0	1160	13	0
25	BB	62317	0	29301	262	0
26	BC	752	0	780	2	0
27	BD	930	0	1000	1	0
28	BE	1052	0	1129	6	0
29	BF	1073	0	1157	8	0
30	BG	1007	0	1045	5	0
31	BH	899	0	935	2	0
32	BI	916	0	965	6	0
33	BJ	946	0	1022	3	0
34	BK	815	0	839	5	0
35	BL	856	0	922	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	BM	777	0	840	5	0
37	BN	2053	0	2122	10	0
38	BO	779	0	834	8	0
39	BP	633	0	656	0	0
40	BQ	508	0	543	5	0
41	BR	448	0	491	0	0
42	BS	548	0	552	0	0
43	BT	443	0	461	1	0
44	BU	440	0	485	1	0
45	BV	376	0	418	5	0
46	BW	503	0	574	3	0
47	BX	301	0	343	0	0
48	BY	1564	0	1616	7	0
49	BZ	1687	0	1814	4	0
50	B1	1551	0	1619	6	0
51	B2	1419	0	1460	6	0
52	B3	1322	0	1374	4	0
53	B4	1110	0	1148	1	0
54	B5	1031	0	1088	2	0
55	B6	1112	0	1147	1	0
All	All	149248	0	97061	544	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 2.

The worst 5 of 544 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BB:1687:G:C2'	25:BB:1687:G:C3'	1.94	1.42
25:BB:1687:G:C2'	25:BB:1687:G:C1'	1.98	1.40
1:AP:31:A:C2'	3:A1:1340:A:H3'	1.50	1.40
25:BB:1687:G:C4'	25:BB:1687:G:C3'	1.99	1.37
1:AP:31:A:C1'	1:AP:31:A:C2'	2.04	1.35

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	
4	AB	216/241 (90%)	173 (80%)	35 (16%)	8 (4%)	4	38
5	AC	115/129 (89%)	85 (74%)	26 (23%)	4 (4%)	4	39
6	AD	121/124 (98%)	71 (59%)	35 (29%)	15 (12%)	0	8
7	AF	112/118 (95%)	76 (68%)	27 (24%)	9 (8%)	1	19
8	AG	94/101 (93%)	71 (76%)	18 (19%)	5 (5%)	2	29
9	AH	86/89 (97%)	67 (78%)	14 (16%)	5 (6%)	2	27
10	AI	80/82 (98%)	56 (70%)	15 (19%)	9 (11%)	0	10
11	AJ	78/84 (93%)	51 (65%)	22 (28%)	5 (6%)	2	25
12	AK	53/75 (71%)	40 (76%)	9 (17%)	4 (8%)	1	21
13	AL	77/92 (84%)	57 (74%)	13 (17%)	7 (9%)	1	17
14	AN	83/87 (95%)	68 (82%)	12 (14%)	3 (4%)	4	38
15	AO	204/233 (88%)	157 (77%)	33 (16%)	14 (7%)	1	23
16	AQ	49/71 (69%)	38 (78%)	7 (14%)	4 (8%)	1	18
17	AR	203/206 (98%)	165 (81%)	29 (14%)	9 (4%)	3	33
18	AS	148/159 (93%)	111 (75%)	26 (18%)	11 (7%)	1	21
19	AT	98/135 (73%)	76 (78%)	15 (15%)	7 (7%)	1	22
20	AU	148/179 (83%)	118 (80%)	20 (14%)	10 (7%)	1	23
21	AV	127/130 (98%)	102 (80%)	17 (13%)	8 (6%)	2	25
22	AW	125/130 (96%)	96 (77%)	22 (18%)	7 (6%)	2	28
23	AX	96/103 (93%)	73 (76%)	15 (16%)	8 (8%)	1	18
26	BC	92/94 (98%)	70 (76%)	16 (17%)	6 (6%)	1	25
27	BD	119/123 (97%)	84 (71%)	25 (21%)	10 (8%)	1	18
28	BE	142/144 (99%)	90 (63%)	27 (19%)	25 (18%)	0	4
29	BF	134/136 (98%)	74 (55%)	37 (28%)	23 (17%)	0	4
30	BG	125/127 (98%)	82 (66%)	32 (26%)	11 (9%)	1	17

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	BH	115/117 (98%)	78 (68%)	27 (24%)	10 (9%)	1	17
32	BI	112/115 (97%)	67 (60%)	32 (29%)	13 (12%)	0	9
33	BJ	115/118 (98%)	84 (73%)	19 (16%)	12 (10%)	1	12
34	BK	101/103 (98%)	57 (56%)	32 (32%)	12 (12%)	0	9
35	BL	108/110 (98%)	71 (66%)	18 (17%)	19 (18%)	0	4
36	BM	97/99 (98%)	70 (72%)	19 (20%)	8 (8%)	1	18
37	BN	265/270 (98%)	167 (63%)	49 (18%)	49 (18%)	0	3
38	BO	100/103 (97%)	51 (51%)	31 (31%)	18 (18%)	0	4
39	BP	82/85 (96%)	42 (51%)	26 (32%)	14 (17%)	0	4
40	BQ	61/63 (97%)	44 (72%)	13 (21%)	4 (7%)	1	24
41	BR	56/59 (95%)	39 (70%)	10 (18%)	7 (12%)	0	8
42	BS	68/70 (97%)	47 (69%)	14 (21%)	7 (10%)	1	12
43	BT	54/57 (95%)	37 (68%)	11 (20%)	6 (11%)	0	11
44	BU	52/54 (96%)	35 (67%)	14 (27%)	3 (6%)	2	27
45	BV	44/46 (96%)	33 (75%)	9 (20%)	2 (4%)	3	33
46	BW	62/64 (97%)	31 (50%)	16 (26%)	15 (24%)	0	2
47	BX	36/38 (95%)	23 (64%)	6 (17%)	7 (19%)	0	3
48	BY	207/209 (99%)	120 (58%)	54 (26%)	33 (16%)	0	5
49	BZ	211/213 (99%)	169 (80%)	33 (16%)	9 (4%)	3	34
50	B1	199/201 (99%)	117 (59%)	53 (27%)	29 (15%)	0	6
51	B2	176/178 (99%)	125 (71%)	35 (20%)	16 (9%)	1	17
52	B3	174/177 (98%)	145 (83%)	19 (11%)	10 (6%)	2	28
53	B4	147/149 (99%)	109 (74%)	31 (21%)	7 (5%)	3	32
54	B5	139/142 (98%)	116 (84%)	17 (12%)	6 (4%)	3	34
55	B6	138/140 (99%)	78 (56%)	40 (29%)	20 (14%)	0	6
All	All	5844/6172 (95%)	4106 (70%)	1175 (20%)	563 (10%)	2	15

5 of 563 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AB	21	TYR
4	AB	97	GLY
4	AB	169	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	AC	118	ASN
6	AD	15	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AB	180/199 (90%)	167 (93%)	13 (7%)	18	55
5	AC	90/99 (91%)	81 (90%)	9 (10%)	9	38
6	AD	103/104 (99%)	91 (88%)	12 (12%)	7	32
7	AF	92/96 (96%)	82 (89%)	10 (11%)	8	35
8	AG	79/84 (94%)	76 (96%)	3 (4%)	40	73
9	AH	76/77 (99%)	71 (93%)	5 (7%)	21	57
10	AI	65/65 (100%)	61 (94%)	4 (6%)	23	60
11	AJ	74/78 (95%)	69 (93%)	5 (7%)	20	57
12	AK	48/66 (73%)	42 (88%)	6 (12%)	6	30
13	AL	70/79 (89%)	62 (89%)	8 (11%)	7	33
14	AN	65/66 (98%)	58 (89%)	7 (11%)	8	35
15	AO	170/190 (90%)	158 (93%)	12 (7%)	18	55
16	AQ	44/61 (72%)	39 (89%)	5 (11%)	7	33
17	AR	172/173 (99%)	156 (91%)	16 (9%)	11	42
18	AS	113/119 (95%)	97 (86%)	16 (14%)	4	26
19	AT	87/116 (75%)	78 (90%)	9 (10%)	9	37
20	AU	123/147 (84%)	109 (89%)	14 (11%)	7	33
21	AV	104/105 (99%)	98 (94%)	6 (6%)	25	61
22	AW	105/107 (98%)	95 (90%)	10 (10%)	11	41
23	AX	86/90 (96%)	81 (94%)	5 (6%)	25	61
26	BC	78/78 (100%)	76 (97%)	2 (3%)	54	80
27	BD	102/104 (98%)	94 (92%)	8 (8%)	16	51

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	BE	103/103 (100%)	84 (82%)	19 (18%)	2	14
29	BF	109/109 (100%)	94 (86%)	15 (14%)	4	27
30	BG	103/103 (100%)	94 (91%)	9 (9%)	13	45
31	BH	87/87 (100%)	82 (94%)	5 (6%)	25	62
32	BI	99/100 (99%)	95 (96%)	4 (4%)	38	71
33	BJ	89/90 (99%)	79 (89%)	10 (11%)	7	33
34	BK	84/84 (100%)	73 (87%)	11 (13%)	5	28
35	BL	93/93 (100%)	83 (89%)	10 (11%)	8	35
36	BM	83/83 (100%)	71 (86%)	12 (14%)	4	24
37	BN	213/215 (99%)	188 (88%)	25 (12%)	7	32
38	BO	83/84 (99%)	74 (89%)	9 (11%)	8	35
39	BP	62/63 (98%)	53 (86%)	9 (14%)	4	24
40	BQ	55/55 (100%)	45 (82%)	10 (18%)	2	15
41	BR	48/49 (98%)	45 (94%)	3 (6%)	22	59
42	BS	62/62 (100%)	58 (94%)	4 (6%)	21	58
43	BT	47/48 (98%)	34 (72%)	13 (28%)	0	4
44	BU	48/48 (100%)	43 (90%)	5 (10%)	9	36
45	BV	38/38 (100%)	32 (84%)	6 (16%)	3	21
46	BW	51/51 (100%)	41 (80%)	10 (20%)	1	12
47	BX	34/34 (100%)	32 (94%)	2 (6%)	24	61
48	BY	164/164 (100%)	150 (92%)	14 (8%)	13	48
49	BZ	187/187 (100%)	172 (92%)	15 (8%)	15	50
50	B1	165/165 (100%)	143 (87%)	22 (13%)	5	28
51	B2	149/149 (100%)	133 (89%)	16 (11%)	8	36
52	B3	137/138 (99%)	123 (90%)	14 (10%)	9	37
53	B4	114/114 (100%)	104 (91%)	10 (9%)	12	45
54	B5	109/110 (99%)	100 (92%)	9 (8%)	14	49
55	B6	114/114 (100%)	102 (90%)	12 (10%)	8	36
All	All	4856/5043 (96%)	4368 (90%)	488 (10%)	14	38

5 of 488 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	BG	32	GLU
36	BM	42	GLU
52	B3	68	ARG
30	BG	121	LYS
34	BK	23	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
30	BG	16	HIS
30	BG	73	ASN
37	BN	162	GLN
27	BD	90	ASN
28	BE	99	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	75/76 (98%)	21 (28%)	10 (13%)
1	AE	75/76 (98%)	12 (16%)	5 (6%)
1	AP	74/76 (97%)	10 (13%)	9 (12%)
2	AM	20/20 (100%)	10 (50%)	8 (40%)
24	BA	116/117 (99%)	36 (31%)	18 (15%)
25	BB	2901/2903 (99%)	1500 (51%)	494 (17%)
3	A1	1529/1530 (99%)	730 (47%)	270 (17%)
All	All	4790/4798 (99%)	2319 (48%)	814 (16%)

5 of 2319 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	C
1	AA	3	G
1	AA	10	G
1	AA	16	U
1	AA	17	U

5 of 814 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	BB	250	G
25	BB	774	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
25	BB	2497	A
25	BB	331	C
25	BB	549	G

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
25	BB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	1959:G	O3'	1960:A	P	3.49