



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jul 24, 2017 – 03:09 AM EDT

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

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)

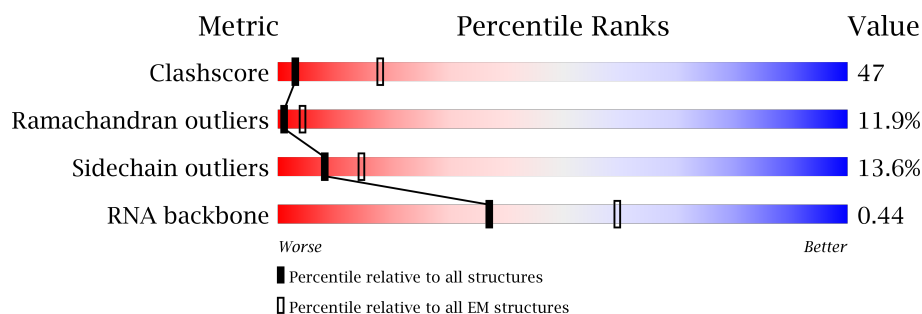
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

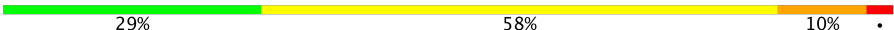
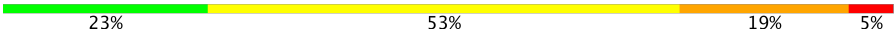
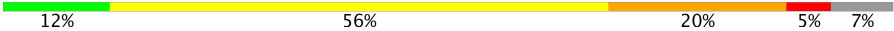

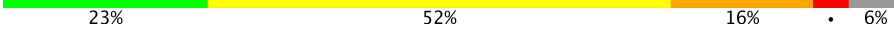
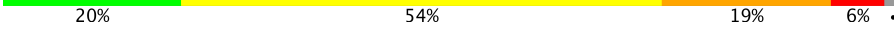
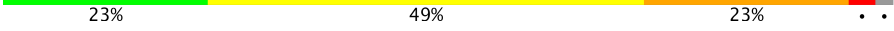

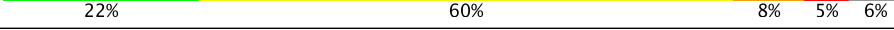


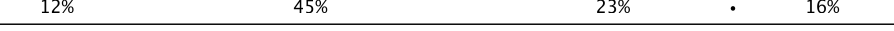




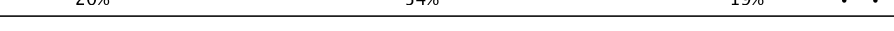


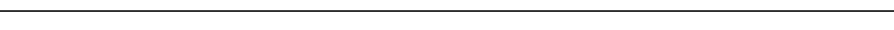

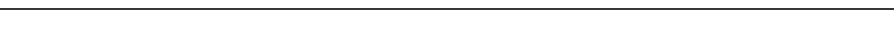
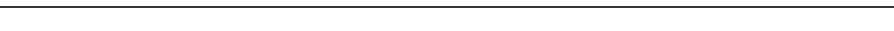


The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues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

Mol	Chain	Length	Quality of chain
1	AA	1522	
2	AB	256	
3	AC	239	
4	AD	209	
5	AE	162	
6	AF	101	
7	AG	156	

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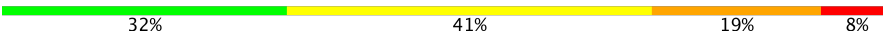



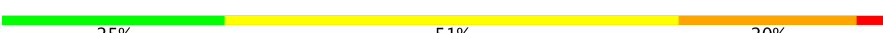
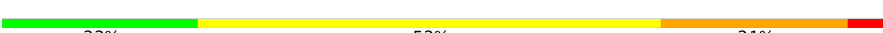




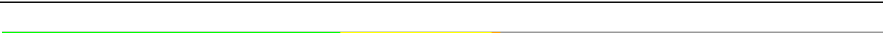




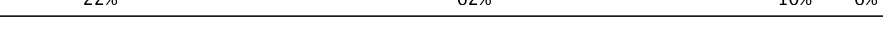
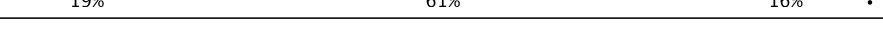


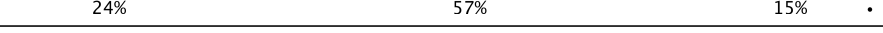

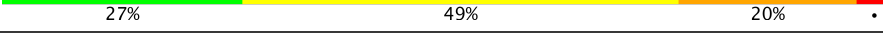


Validation Pipeline (wwPDB-VP) : rb-20029824

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Mol	Chain	Length	Quality of chain
8	AH	138	
9	AI	128	
10	AJ	105	
11	AK	129	
12	AL	132	
13	AM	126	
14	AN	61	
15	AO	89	
16	AP	88	
17	AQ	105	
18	AR	88	
19	AS	93	
20	AT	106	
21	AU	27	
22	AV	77	
23	AX	11	
24	AY	691	
25	B0	85	
26	B1	98	
27	B2	72	
28	B3	60	
29	B4	71	
30	B5	60	
31	B6	54	
32	B7	49	

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Mol	Chain	Length	Quality of chain
33	B8	65	
34	B9	37	
35	BA	2915	
36	BB	122	
37	BC	229	
38	BD	276	
39	BE	206	
40	BF	210	
41	BG	182	
42	BH	180	
43	BK	147	
44	BL	121	
45	BN	140	
46	BO	122	
47	BP	150	
48	BQ	141	
49	BR	118	
50	BS	112	
51	BT	146	
52	BU	118	
53	BV	101	
54	BW	113	
55	BX	96	
56	BY	110	
57	BZ	206	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 152777 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 22 is a RNA chain called TRNA.

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

- Molecule 23 is a RNA chain called MRNA.

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

- Molecule 24 is a protein called ELONGATION FACTOR G.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

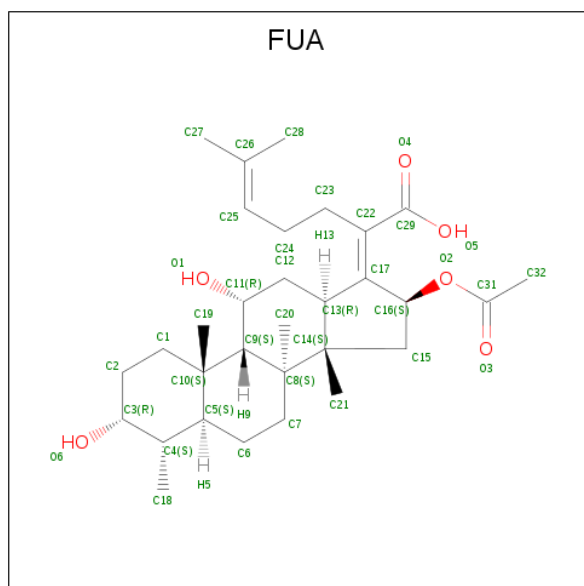
- Molecule 56 is a protein called 50S RIBOSOMAL PROTEIN L24.

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

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

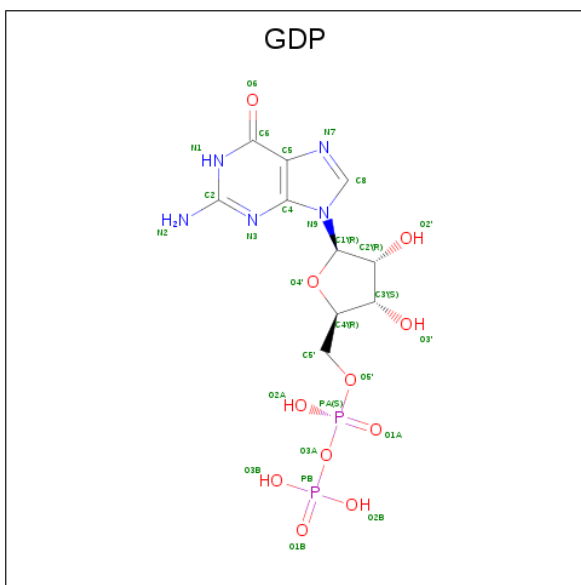
Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	184	Total	C	N	O	S	0	0
			1467	936	261	268	2		

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



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

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

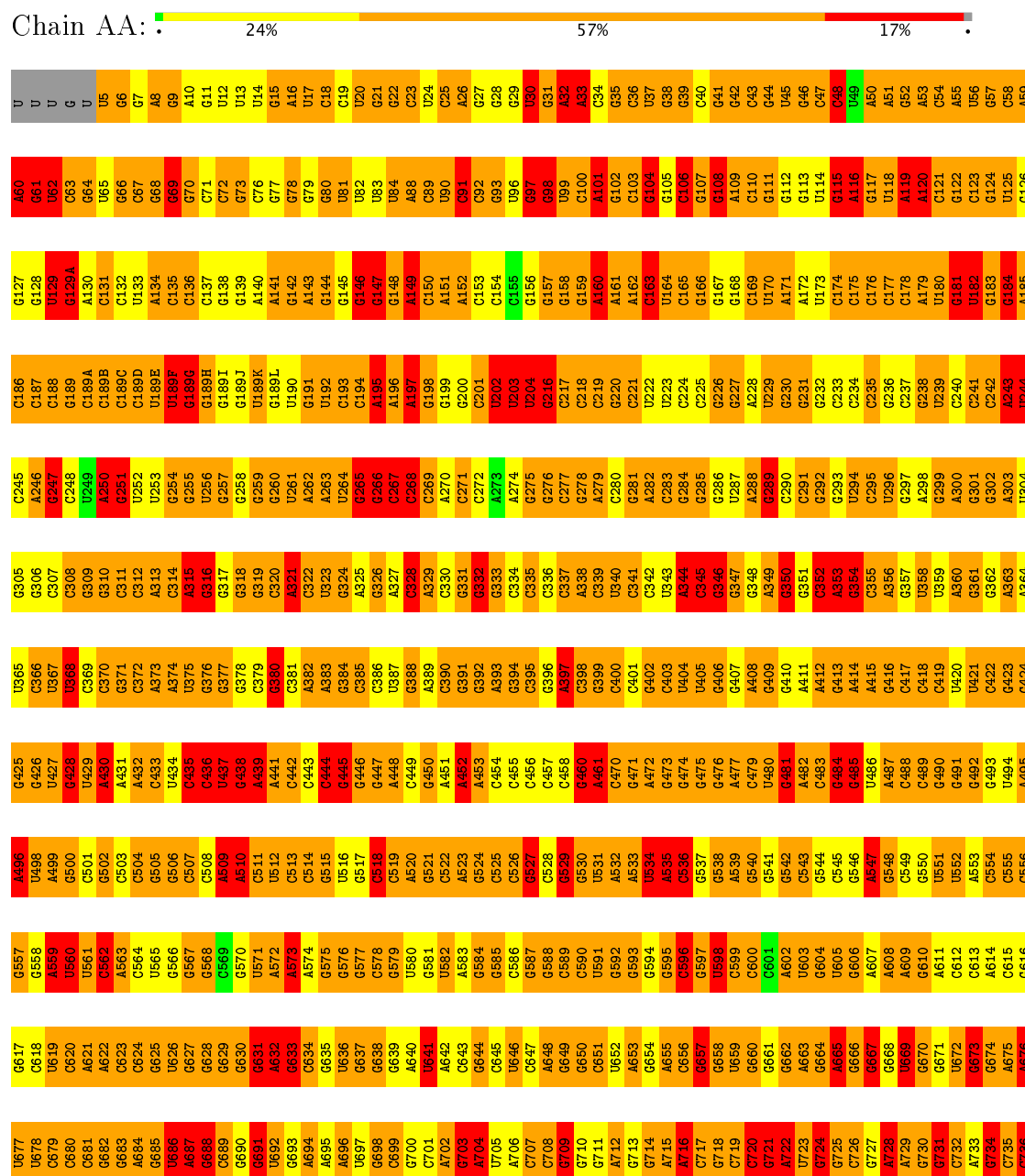


Mol	Chain	Residues	Atoms					AltConf
59	AY	1	Total	C	N	O	P	0
			28	10	5	11	2	

3 Residue-property plots

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

• Molecule 1: 16S rRNA

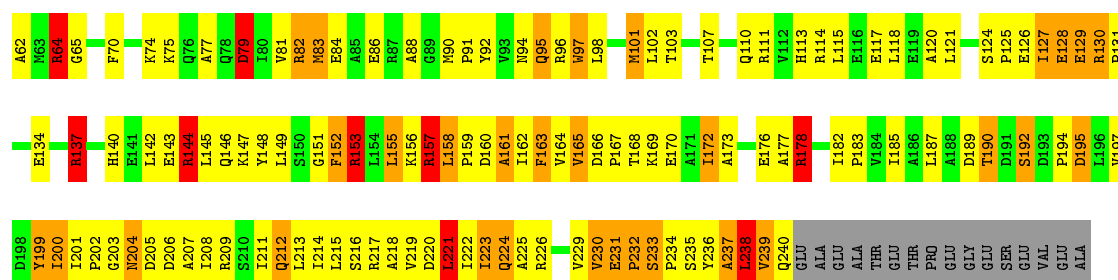


G1523	G1463	A1398	A1339	U1219	C1458	C1098	A983	A923	U863	C797	A737
C1524	G1464	C1399	A1340	G1220	U1159	G1099	C984	C924	A864	G798	C738
G1525	C1465	C1400	C1341	G1221	G1160	C1100	C985	G925	A865	G799	C739
G1526	C1466	G1401	C1342	G1222	C1161	A1101	A986	G926	C866	G800	U740
C1527	G1467	C1402	G1343	C1223	C1162	C1102	G987	G927	C867	U801	G741
U1528	A1468	C1403	C1344	G1224	C1163	A1103	G988	G928	C868	A802	G742
G1529	G1469	C1404	U1345	A1225	G1164	G1104	C989	G929	C869	G803	U743
G1530	G1470	A1405	A1346	C1226	C1165	A1105	C990	C930	U870	U804	C744
A1531	G1471	U1406	G1347	A1227	G1166	G1106	U991	C931	U871	C805	C745
U	U1472	A1407	A1348	C1228	C1167	G1107	U992	G932	A872	C806	A746
C	A1473	A1408	A1349	A1229	A1168	G1108	U993	G933	A873	A807	C747
A	G1474	C1409	A1350	G1230	A1169	C1109	A994	C934	G874	C808	C748
C	G1475	G1410	U1351	G1231	A1170	A1110	C995	A935	C875	G809	C749
C	G1476	C1411	C1352	U1232	C1172	A1111	A996	C936	G876	C810	G750
U	C1477	C1412	G1353	G1233	G1173	C1112	U997	C937	C877	C811	U751
C	C1478	A1413	C1354	C1234	G1174	C1113	G998	A938	G878	C812	G752
C	A1479	U1414	G1355	U1235	G1175	C1114	C999	G939	C879	U813	A753
U	G1480	G1415	G1356	A1236	A1176	C1115	U1000	C940	C880	A814	C754
U	U1481	G1416	A1357	C1237	G1177	C1116	A1001	G941	C881	A815	G755
U	G1417	G1417	A1358	A1238	G1178	G1117	G1001A	G942	C882	A816	C756
U	A1482	A1418	C1359	A1239	A1179	C1118	G1002	U943	C883	C817	U757
C	G1483	G1419	A1360	U1240	A1180	C1119	G1003	G944	U884	G818	G758
C	U1485	C1420	G1361	G1241	A1181	G1120	A1004	G945	U885	A819	A759
G1486	G1421	G1421	C1362	C1242	G1182	U1121	A1005	A946	G886	U820	G760
G1487	G1422	G1422	C1363	C1243	A1183	U1122	C1006	G947	C887	G821	G761
G1488	G1423	A1423	A1364	G1244	G1184	A1123	C1007	C948	G888	C822	G762
G1489	G1424	C1424	U1365	A1245	G1185	G1124	G1064	A949	A889	G823	G763
C1490	U1425	G1425	G1366	C1246	G1186	U1125	U1065	U950	C890	G824	C764
G1491	C1426	G1426	C1367	U1247	A1187	U1126	C1066	G951	U891	G825	G765
A1492	U1427	U1427	U1368	A1248	A1188	G1127	A1067	U952	A892	C826	A766
G1493	A1428	G1428	G1369	G1309	A1189	C1128	G893	G953	C893	U827	A767
G1494	C1429	C1429	G1370	G1310	G1190	C1129	G894	G954	G894	A828	A768
U1495	U1430	A1430	G1371	A1251	A1191	A1130	U955	U956	C896	G829	G769
C1496	C1431	G1431	U1372	G1252	C1192	G1131	A1015	C897	U957	G830	C770
G1497	G1432	A1432	G1373	C1253	G1193	C1132	A1016	U958	C898	U831	G771
U1498	G1433	A1434	A1374	C1254	U1194	G1133	G1017	A959	C899	C832	U772
A1499	A1434	G1435	G1375	G1255	C1195	G1134	C1018	U960	C899	U833	G773
A1500	G1435	G1435	U1376	A1256	U1196	U1135	C1019	U961	A900	C834	G774
C1501	U1436	U1436	U1377	U1257	G1197	U1136	U1020	C962	A901	U835	G775
A1502	A1437	A1437	A1378	G1258	G1198	C1137	G1077	G963	G902	G836	G776
A1503	G1438	G1438	G1379	C1259	U1199	G1138	G1078	G964	C904	G837	A777
G1504	C1439	C1439	U1380	C1320	C1200	G1139	G1079	A965	U905	G838	G778
G1505	C1440	G1440	U1381	C1321	A1201	C1140	A1080	G966	C910	U839	C779
U1506	G1441	C1441	C1382	G1322	C1202	C1141	G1081	C967	U907	C840	A780
A1507	G1442	G1442	C1383	C1263	G1203	G1142	G1082	C968	A908	U841	A781
G1508	G1442A	A1442A	C1384	G1264	A1204	G1143	C1027	A969	C848	C848	A782
A1509	A1442B	A1442B	G1385	G1265	U1205	G1144	G1084	C970	C849	C783	C783
U1510	G1443	G1443	G1386	G1266	G1206	C1145	C1029	G971	U911	U850	C784
G1511	C1444	C1444	G1387	C1267	G1207	A1146	U1086	G972	G912	G851	G785
U1512	C1445	U1445	G1388	A1268	C1208	C1147	G1087	C973	C912	G852	G786
A1513	U1446	U1446	C1389	A1269	C1209	U1148	G1088	G974	A913	G853	A787
C1514	A1447	A1447	U1390	G1270	C1210	U1149	G1089	A975	A914	G854	U788
C1515	T54	C1452	U1391	G1271	U1211	U1150	A1030D	G976	A915	G855	U789
G1516	G1456	G1456	G1392	G1272	A1151	U1091	G1031	G977	G916	C856	A790
G1517	G1457	G1457	G1393	G1273	A1152	A1092	G1032	A978	G917	C857	G791
A1518	G1458	G1458	U1394	G1274	C1213	C1153	A1093	C979	A918	G858	A792
A1519	C1459	C1459	A1395	A1275	G1215	G1154	G1034	C980	A919	A859	U793
G1520	A1460	A1460	C1396	G1276	G1216	G1155	G1035	U981	A920	A860	A794
G1521	A1461	A1461	C1397	C1277	C1217	G1156	G1036	U982	U921	G861	C795
U1522	G1462	G1462	C1397	U1278	C1218	A1157	C1037	U983	G922	C862	C796

● Molecule 2: 30S RIBOSOMAL PROTEIN S2

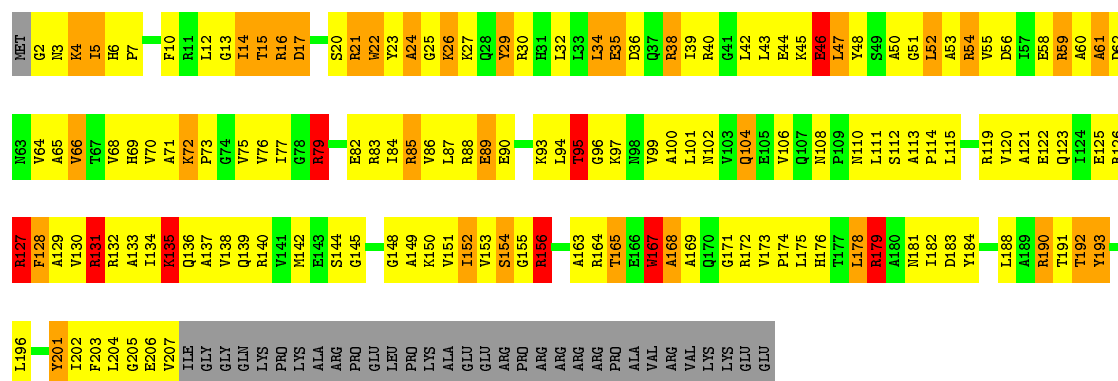
Chain AB:  23% 48% 16% 9%

MET	L10	L11	E12	A13	G14	V15	H16	F17	G18	H19	E20	R21	K22	R23	N24	P25	P26	K27	F28	A29	R30	Y31	I32	Y33	A34	E35	R36	I39	H40	I41	I42	D43	L44	Q45	K46	T47	M48	E49	E50	L51	E52	R53	T54	F55	R56	F57	I58	E59	D60	L61
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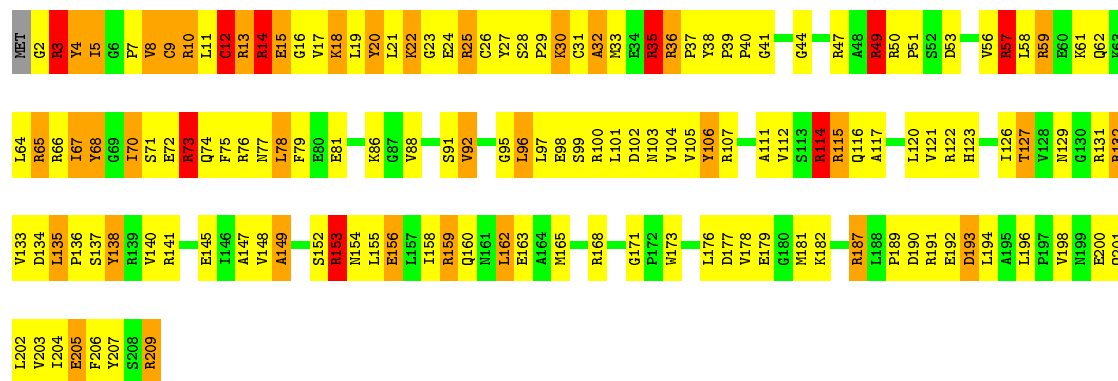
• Molecule 3: 30S RIBOSOMAL PROTEIN S3

Chain AC: 22% 46% 14% • 14%



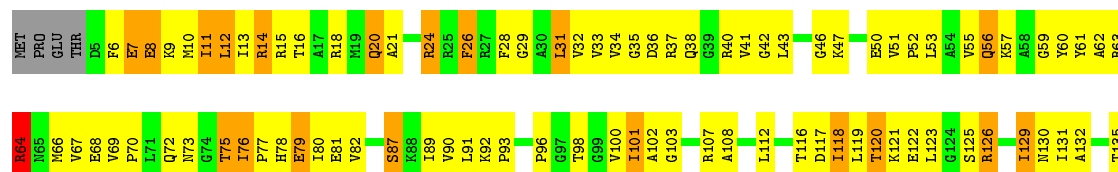
• Molecule 4: 30S RIBOSOMAL PROTEIN S4

Chain AD: 29% 49% 17% •



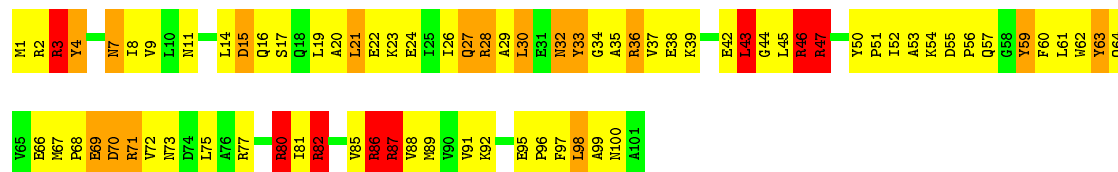
• Molecule 5: 30S RIBOSOMAL PROTEIN S5

Chain AE: 27% 52% 13% • 7%

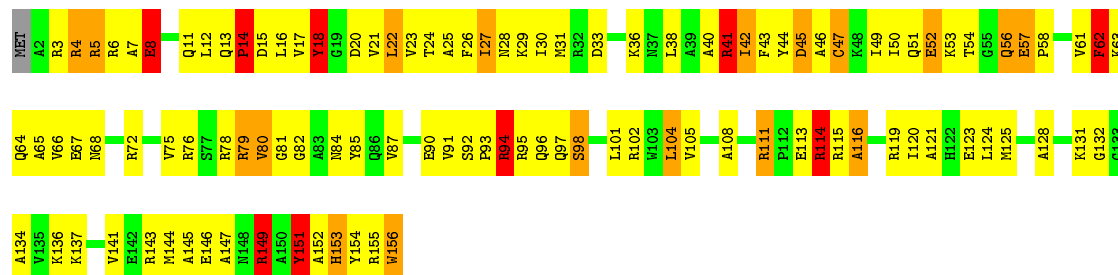




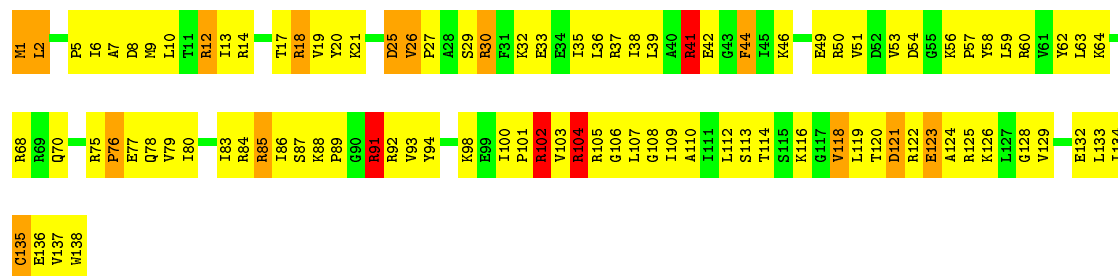
• Molecule 6: 30S RIBOSOMAL PROTEIN S6



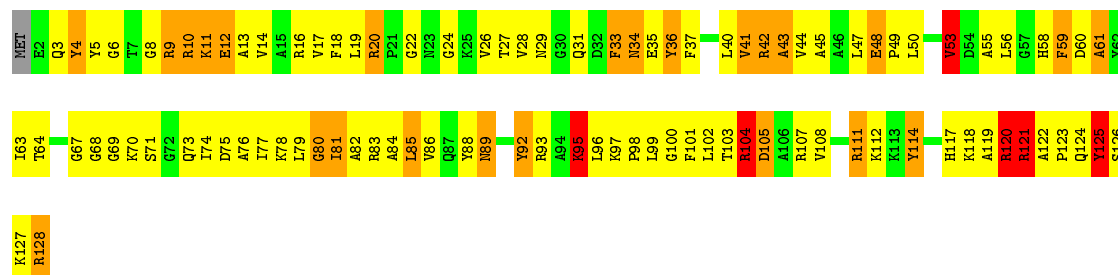
• Molecule 7: 30S RIBOSOMAL PROTEIN S7



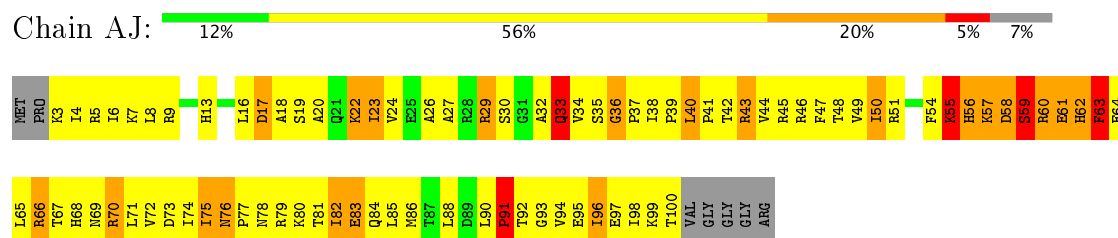
• Molecule 8: 30S RIBOSOMAL PROTEIN S8



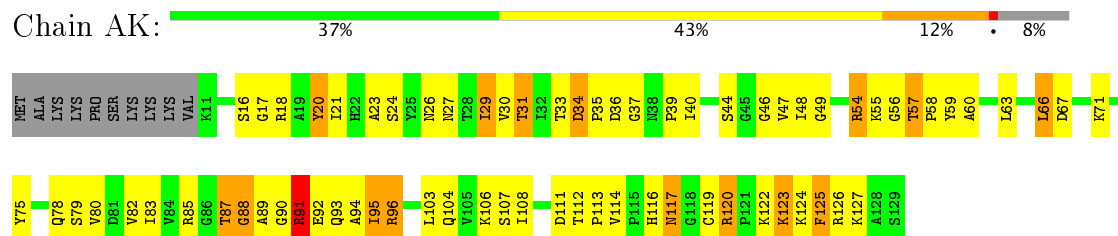
• Molecule 9: 30S RIBOSOMAL PROTEIN S9



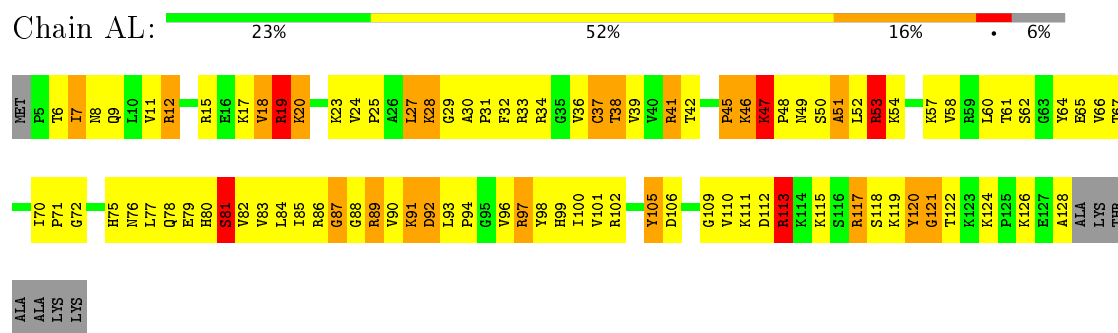
- Molecule 10: 30S RIBOSOMAL PROTEIN S10



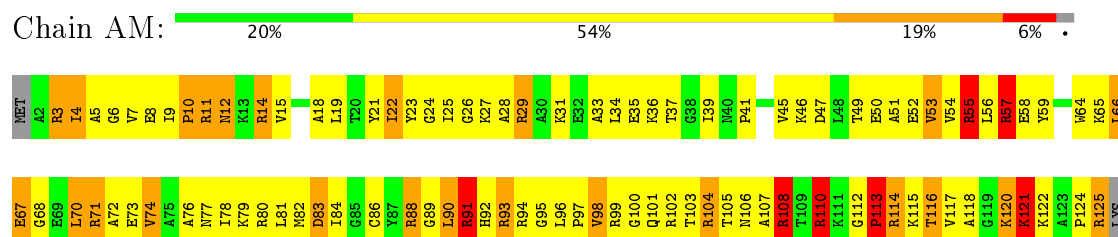
- Molecule 11: 30S RIBOSOMAL PROTEIN S11



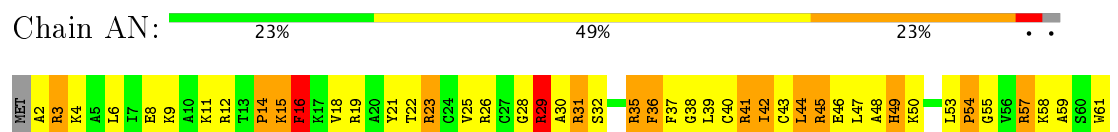
- Molecule 12: 30S RIBOSOMAL PROTEIN S12



- Molecule 13: 30S RIBOSOMAL PROTEIN S13

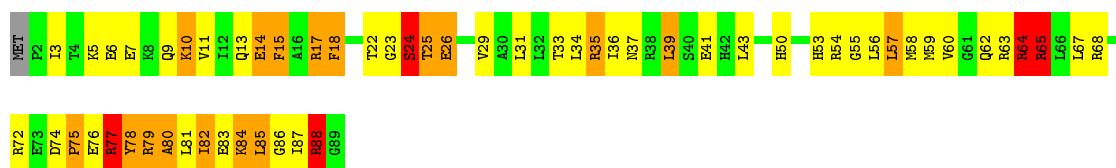


- Molecule 14: 30S RIBOSOMAL PROTEIN S14 TYPE Z



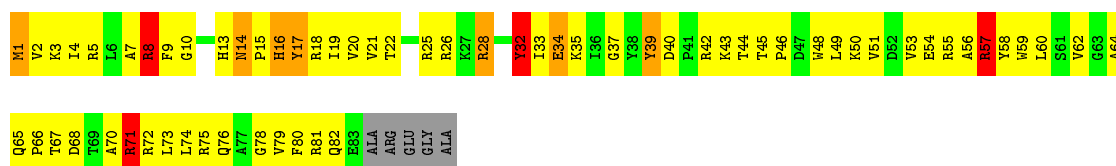
- Molecule 15: 30S RIBOSOMAL PROTEIN S15





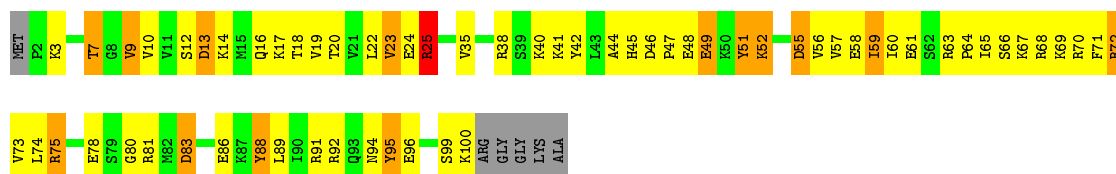
• Molecule 16: 30S RIBOSOMAL PROTEIN S16

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



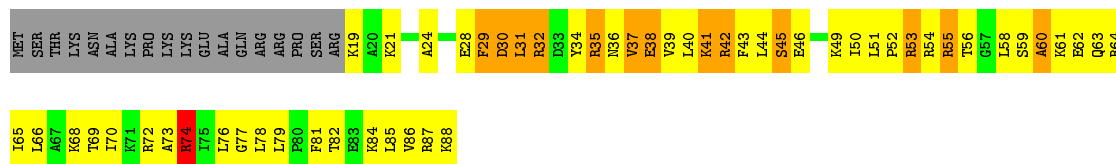
• Molecule 17: 30S RIBOSOMAL PROTEIN S17

Chain AQ: 34% 46% 13% 6%



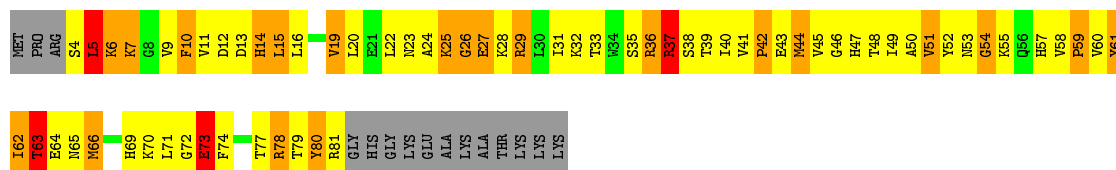
• Molecule 18: 30S RIBOSOMAL PROTEIN S18

Chain AR: 17% 47% 15% 20%



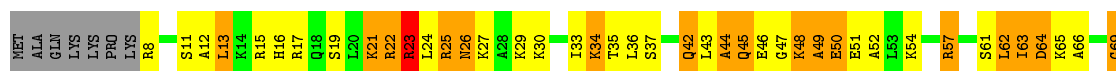
• Molecule 19: 30S RIBOSOMAL PROTEIN S19

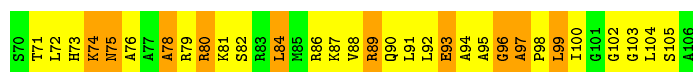
Chain AS: 12% 45% 23% 16%



• Molecule 20: 30S RIBOSOMAL PROTEIN S20

Chain AT: 25% 42% 25% 7%





• Molecule 21: 30S RIBOSOMAL PROTEIN THX

Chain AU: 26% 37% 22% • 11%



• Molecule 22: TRNA

Chain AV: 14% 64% 22%



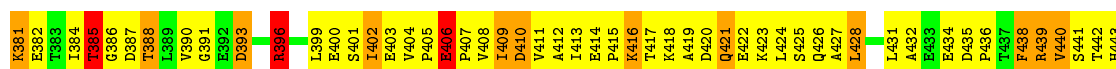
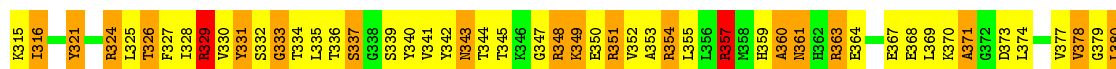
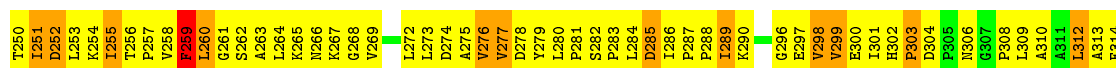
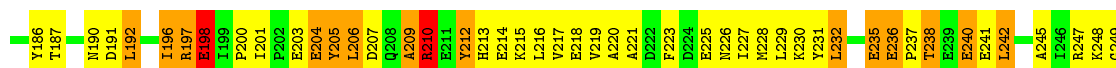
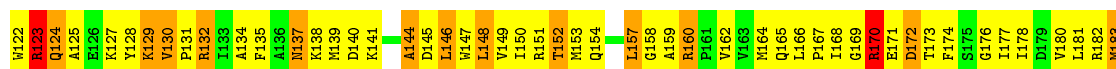
• Molecule 23: MRNA

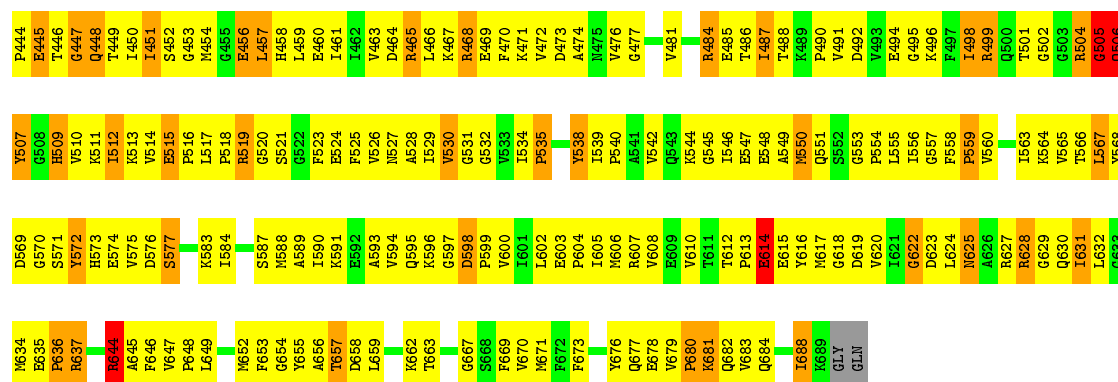
Chain AX: 9% 55% 36%



• Molecule 24: ELONGATION FACTOR G

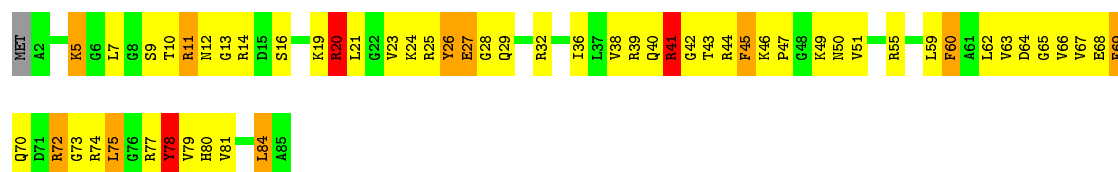
Chain AY: 20% 54% 19% • •





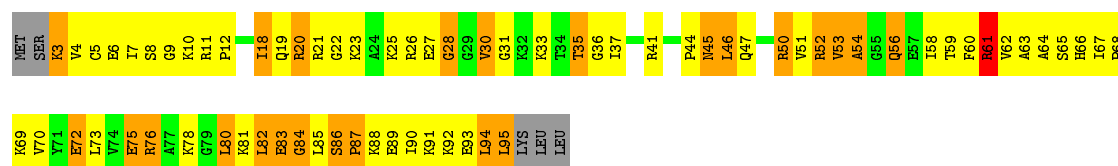
• Molecule 25: 50S RIBOSOMAL PROTEIN L27

Chain B0: 33% 51% 12% . .



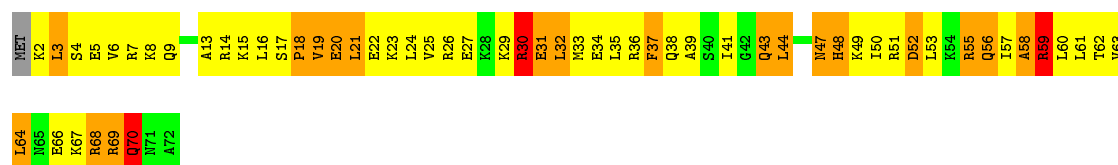
• Molecule 26: 50S RIBOSOMAL PROTEIN L28

Chain B1: 22% 47% 24% . 5%



• Molecule 27: 50S RIBOSOMAL PROTEIN L29

Chain B2: 17% 51% 26% . .



• Molecule 28: 50S RIBOSOMAL PROTEIN L30

Chain B3: 22% 62% 13% . .



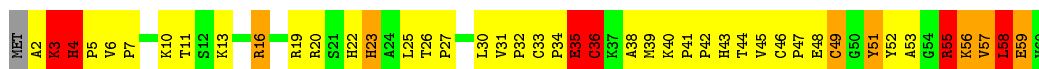
• Molecule 29: 50S RIBOSOMAL PROTEIN L31

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



- Molecule 30: 50S RIBOSOMAL PROTEIN L32

Chain B5: 25% 52% 12% 10% .



- Molecule 31: 50S RIBOSOMAL PROTEIN L33

Chain B6: 43% 33% 15% 7% .



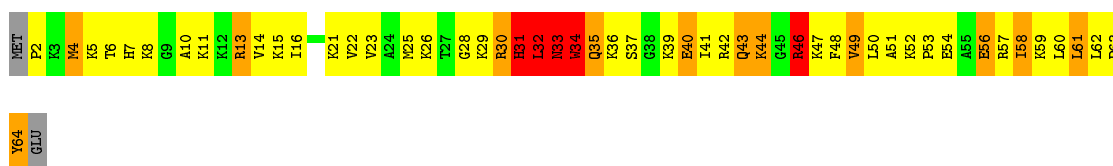
- Molecule 32: 50S RIBOSOMAL PROTEIN L34

Chain B7: 20% 51% 24% . .



- Molecule 33: 50S RIBOSOMAL PROTEIN L35

Chain B8: 18% 52% 18% 8% .



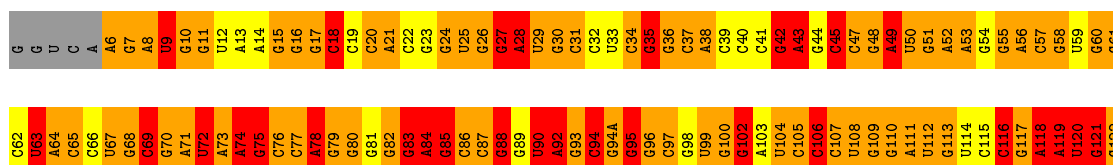
- Molecule 34: 50S RIBOSOMAL PROTEIN L36

Chain B9: 32% 41% 19% 8%



- Molecule 35: 23S RIBOSOMAL RNA

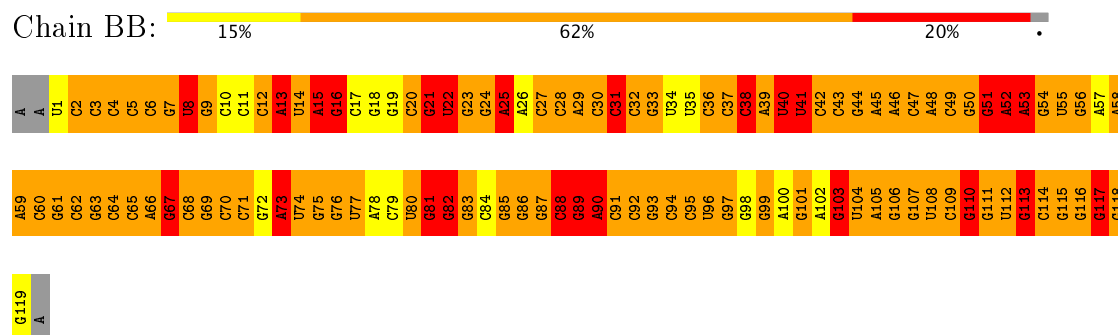
Chain BA: 21% 57% 21%

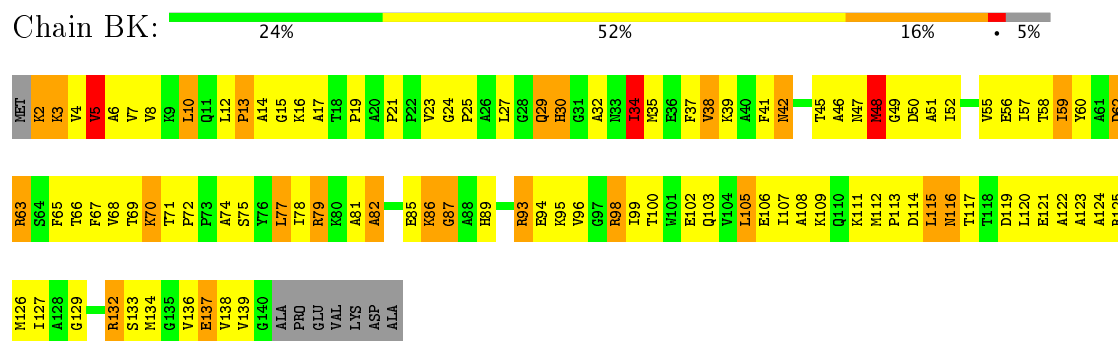


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G1036	C976	G916	G855	C795	A735	A675	A637	G579	C517	C486	U395	G338	A278	G253	U193	G124
G1037	G977	A917	C856	C796	C736	A676	G638	C580	U518	A487	G396	U339	C279	G254	U193	G125
G1038	G978	A918	C857	C797	C737	A677	U639	C581	U519	G488	G397	A340	C280	G255	A195	A126
G1039	G979	G919	U858	C798	G738	G678	C640	G582	G520	U489	G398	G341	G281	A256	A196	A127
G1040	G980	G920	G859	C799	G739	C679	C641	G583	G521	U490	G399	G342	A282	A257	A197	G128
G1041	A981	G921	U860	A800	U740	G680	G642	C584	G522	C461	G400	C343	A283	G258	C198	G129
G1042	C982	U922	A861	G801	G741	G681	A643	G585	G523	C462	A401	G344	U284	G259	C199	G130
G1043	A983	G923	G862	A802	G742	G682	A644	A586	U524	G463	A345	G345	C285	G260	U200	G131
G1044	A984	C924	A863	U803	G743	G683	C645	U525	U525	U464	U403	A346	C286	G261	C201	G132
G1045	C985	C925	G864	A804	G744	G684	A646	U588	A526	G465	A404	A347	C287	A262	U202	C133
G1046	C986	A926	G865	G805	G745	G685	G647	C589	C527	A466	U405	G348	C288	C263	C203	G134
G1047	G987	G927	A866	C806	A746	G686	G648	A590	U528	G467	G406	G349	A289	C264	A204	G135
A1048	A988	G928	C867	U807	U747	C687	G649	C591	A529	G468	G407	U850	G290	A265	G205	G136
G1049	G989	U930	U868	G808	G748	U688	C650	G592	G530	G469	G408	G351	C291	G266	U206	G137
A1050	A990	G931	G869	G809	C749	A689	G651	G593	C531	A470	C409	G352	C292	C267	A207	G139
G1051	C991	G932	A870	U810	A750	G690	C652	U594	A532	A471	G410	G353	U293	C268	C208	G139A
G1052	C992	A933	U871	U811	A751	C691	A653	C595	G533	A472	G411	G354	A294	U269	C209	G140
C1053	G993	G934	A872	C812	A752	C692	A654	C596	U534	G473	A412	G355	G295	A270	C210	A141
A1054	C994	C935	G873	U813	C753	C693	G654A	U597	C535	G474	C413	G356	C296	A271	A211	A142
G1055	C995	G936	G874	C814	C754	U694	C654B	U598	A536	G475	C414	A357	C297	A271A	G212	C142A
A1056	A996	U937	G875	C815	C755	G695	G654C	G599	C537	G476	A415	U858	G298	C271B	A213	G143
G1057	G997	G938	C876	C816	C756	G696	G654D	G600	U538	A477	C416	A359	A299	C271C	G214	C143A
G1058	C998	G939	U877	C817	U757	C697	G654E	G601	C539	A478	G417	G360	A300	G271D	G215	C144
G1059	U999	G940	A878	G818	C758	C698	C654F	G602	C540	A479	G418	G361	G301	U271E	A216	G145
U1060	A1000	A941	G879	A819	G759	A699	C654G	A603	C541	A480	C419	U862	C302	C271F	G217	G146
A1061	A1001	G942	G880	A820	G760	G700	G654H	G604	C542	A481	C420	G363	U303	C271G	A218	U147
G1062	G1002	U943	G881	A821	A761	G701	C654I	C605	C543	A482	U421	A364	G312	C271H	G225	G148
G1063	G1003	G944	G882	U822	G762	G702	G654J	U606	G544	A483	A422	G363B	U306	G271I	G220	A149
C1064	A1004	A945	G883	G823	G763	G703	G654K	U607	C545	C484	A423	G363C	U305	C271J	A221	C150
U1065	G1005	G946	G884	A824	A764	G704	G654L	A608	A547	C485	G424	G363D	G307	U271K	A222	C151
U1066	C1006	G947	C885	C825	G765	A705	G654M	A609	A548	C486	G425	U863E	G308	U271L	G223	G152
A1067	C1007	G948	C886	U826	C766	A706	G654N	G610	G549	C487	C426	A363F	G309	G271M	G224	C153
G1068	A1008	C949	A887	U827	G767	G707	G654O	C611	G551	G488	U427	C364	A310	U271N	A225	G154
A1069	G1009	G950	C888	U828	G768	G708	C654P	C612	G552	G489	A428	C365	A311	C271O	G226	C154A
G1070	C951	G951	G889	A829	G769	U709	G654Q	G613	G553	G491	A429	C366	G312	C271P	A227	U155
G1071	G952	A953	G890	G830	G770	G710	C654R	U614	U554	A492	G430	G370	C313	G271Q	A228	U156
C1072	A953	G953	G892	G831	G771	G711	G654S	U614A	U555	G493	U431	A371	A314	G271R	A229	U157
A1073	G954	G954	C893	G832	C772	G712	C654T	G614B	G556	G494	A432	G372	G315	G271S	U230	U158
G1074	U1014	C955	C894	U833	U773	G713	A654U	A614C	U557	G495	C433	U373	C316	C271T	C231	C172
G1075	G1015	G956	U895	C834	A774	G715	A654V	G615	G558	G496	U434	A374	G317	G271U	A232	G173
G1076	G1016	A957	A896	A835	G775	G716	A655	G616	C559	A497	C435	C375	C318	G271V	A233	G174
A1077	G1017	U958	C897	G836	G776	A716	G656	C618	C560	G498	G436	C376	C319	G271W	C234	G175
C1078	C1018	A959	C898	C837	A777	G717	U657	G619	G561	U499	G437	C377	A320	G271X	U235	G176
G1079	U1019	A960	A899	C838	G778	A718	C658	G620	U562	G500	G438	C378	G321	U271Y	C236	G177
C1080	A1020	C961	A900	U839	U779	C719	C659	A621	G563	A501	G440	G379	A322	C271Z	C237	G178
U1081	A1021	G962	A901	C840	G780	C720	G660	G622	C564	A502	U441	U380	G323	G272	C238	G179
G1082	G1022	U963	C902	A841	A781	A721	C661	G623	C565	A503	G442	G381	A324	U272A	U239	G180
U1083	C903	C964	C903	G842	A782	A722	G662	G624	U566	U504	A443	G382	G325	G272B	G240	G181
A1084	G1024	C965	C904	G843	A783	G723	G663	G625	A567	A505	C444	U383	G326	G272C	A241	A182
A1085	G1025	G966	U905	C844	A784	U724	C664	U626	U568	G506	C445	U384	G327	G272D	G242	A183
A1086	U1026	C967	G906	G845	G785	G725	C665	A627	U569	A507	G446	C385	U328	G272E	U243	C184
G1087	A1027	G968	U907	C846	C786	G726	G666	G628	G570	G508	A447	G386	A329	C272F	A244	U185
A1088	A1028	U969	C908	U847	U787	A727	U667	G629	A571	C509	U448	U387	A330	C272G	G245	U186
G1089	A1029	C970	A909	G848	A788	G728	G668	G630	G572	C510	A449	G388	A331	C272H	G246	G187
U1090	G1030	C971	A910	A849	A789	G729	G669	A631	G573	U511	G450	G389	A332	U272I	G247	G188
G1091	G1031	G972	A911	C850	C790	C730	A670	A632	C574	G512	C451	A390	G333	C272J	G248	G189
C1092	A1032	A973	C912	U851	C791	G731	C671	A633	A575	A513	G452	C391	G334	G274	C249	A190
G1093	G974	C974	U913	G852	G792	C732	C672	C634	U576	A514	C453	C392	C335	G275	G250	G191
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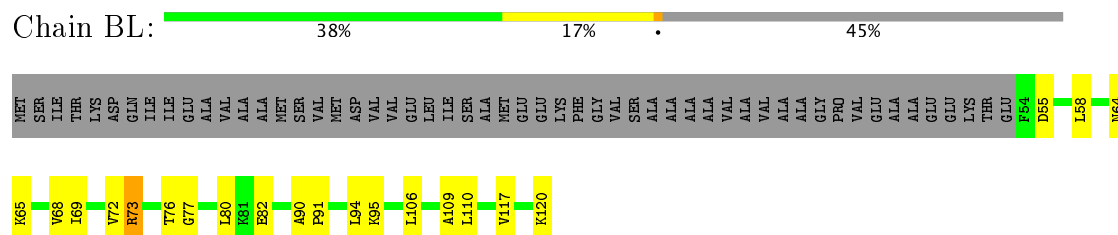
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G1899	A1900	A1901	C1902	G1903	G1904	C1905	C1906	G1907	G1908	G1909	G1910	U1911	A1912	A1913	C1914	U1915	A1916	U1917	A1918	A1919	G1920	G1921	G1922	U1923	G1924	G1925	U1926	G1927	G1928	A1929	G1930	U1931	G1932	G1933	C1934	G1935	G1936	A1937	A1938	G1939	U1940	C1941	C1942	U1943	U1944	G1945	U1946	C1947	G1948	G1949	U1950	G1951	A1952	A1953	G1954	U1955	U1956	C1957	C1958									
C1830	G1831	C1832	U1833	U1834	G1835	C1836	C1837	G1838	G1839	G1840	G1841	G1842	C1843	C1844	G1845	G1846	A1847	A1848	G1849	G1850	U1851	C1852	A1853	G1854	G1855	G1856	G1857	G1858	G1859	G1860	G1861	G1862	G1863	U1864	G1865	G1866	A1867	G1868	G1869	G1870	G1871	G1872	G1873	G1874	G1875	G1876	G1877	G1878	G1879	G1880	G1881	G1882	G1883	A1884	G1885	G1886	G1887	G1888	A1889	A1890	G1891	C1892	C1893	G1894	C1895	G1896	G1897	U1898
G1770	C1771	G1772	A1773	C1774	G1775	G1776	G1777	G1778	G1779	A1780	G1781	G1782	A1783	A1784	G1785	A1786	G1787	G1788	A1789	G1790	U1791	G1792	C1793	U1794	G1795	G1796	G1797	G1798	G1799	G1800	G1801	A1802	G1803	G1804	U1805	G1806	G1807	U1808	A1809	A1810	G1811	A1812	G1813	G1814	A1815	G1816	G1817	G1818	A1819	A1820	A1821	G1822	G1823	G1824	A1825	G1826	G1827	G1828	A1829									
G1694	G1695	G1696	G1697	A1698	G1699	G1700	A1640	A1641	G1702	G1703	G1704	G1705	G1706	G1707	G1647	G1648	U1709	G1710	G1711	G1712	G1713	G1714	G1715	G1716	G1717	G1718	G1719	U1720	G1721	A1722	G1661	C1662	G1663	A1664	G1665	G1666	G1667	G1668	A1669	U1670	U1671	G1672	G1673	G1674	G1675	G1676	G1677	G1678	U1679	G1680	G1681	G1682	G1683	A1684	A1685	G1686	G1687	G1688	U1689	A1690	C1691	U1692	U1693					
C1574	C1575	U1576	C1577	U1578	U1579	A1580	G1581	C1582	A1583	C1584	A1586	A1587	C1588	C1589	C1590	G1591	C1592	G1593	G1594	G1595	A1596	C1597	C1598	C1599	C1600	G1601	U1602	A1603	C1604	C1605	G1606	G1607	C1608	A1609	A1610	C1611	C1612	G1613	A1614	C1615	A1616	C1617	A1618	G1619	G1620	U1621	G1622	G1623	G1624	C1625	G1626	G1627	G1628	U1629	G1630	C1631	A1631A	A1632	G1633	U1634								
A1634	G1635	A1636	A1637	C1638	U1639	G1640	A1641	C1642	A1643	C1644	A1645	C1646	G1647	C1648	G1649	G1650	G1651	A1652	G1653	A1654	A1655	C1656	C1657	C1658	U1659	C1660	G1661	G1662	C1663	G1664	G1665	G1666	G1667	A1668	A1669	C1670	U1671	C1672	U1673	C1674	G1675	C1676	A1677	G1678	U1679	G1680	G1681	G1682	C1683	C1684	C1685	C1686	G1687	U1688	G1689	A1690	C1691	U1692	U1693									
G1513	U1514	G1515	C1516	G1517	U1518	G1519	G1520	G1521	U1523	G1524	G1525	G1526	G1527	A1528	A1528A	G1529	C1530	G1531	G1532	G1533	U1534	A1535	C1536	G1537	G1538	G1539	U1540	U1541	U1542	G1543	C1544	A1545	C1546	C1547	G1548	C1549	G1550	C1551	G1552	A1553	A1554	G1555	C1556	C1557	A1558	G1559	G1560	G1561	A1562	G1563	C1564	C1565	G1566	A1567	G1568	A1569	A1570	U1571	A1572	G1573								
U1453	G1453	G1456	G1457	C1458	G1459	A1460	G1461	C1462	C1463	G1464	G1465	G1466	C1467	C1468	C1469	A1469	C1470	A1471	A1472	G1473	C1474	G1475	C1476	A1477	G1478	G1479	U1480	U1481	G1482	G1483	G1484	A1485	A1486	G1487	G1488	U1489	A1490	G1491	G1492	C1493	A1494	A1495	A1496	U1497	C1498	C1499	G1500	C1501	C1502	G1503	C1504	C1505	C1506	A1507	A1508	C1509	A1509A	A1509B	G1510	C1511	A1512	U1513						
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U1335	A1336	G1337	G1338	G1339	G1340	U1341	A1342	G1343	G1344	C1345	G1346	G1347	G1348	A1349	C1350	C1351	U1352	A1353	A1354	G1355	G1356	G1357	G1358	A1359	A1360	G1361	G1362	G1363	G1364	C1365	A1366	A1367	G1368	G1369	C1370	G1371	U1372	U1373	A1374	C1375	G1376	G1377	A1378	A1379	G1380	G1381	A1382	G1383	A1384	G1385	C1386	C1387	G1388	G1389	U1390	U1391	A1392	C1393	U1394									
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G1216	C1217	G1218	G1219	G1220	C1221	C1221A	C1222	G1223	C1224	G1225	A1226	G1227	G1228	G1229	C1230	G1231	G1232	G1233	U1234	G1235	G1236	G1237	G1238	G1239	U1240	A1241	A1242	G1243	G1244	G1245	A1246	A1247	U1248	U1249	G1250	C1251	G1252	A1253	A1254	U1255	G1256	G1257	C1258	G1259	G1260	C1261	A1262	U1263	G1264	A1265	G1266	C1267	A1268	G1269	A1270	U1271	G1272	A1273	A1274									
A1155	A1156	G1157	G1158	U1159	G1160	U1161	G1162	G1163	G1164	U1165	G1166	U1167	G1168	G1169	G1170	G1171	G1172	G1173	A1174	U1175	G1176	A1177	C1178	G1179	C1180	C1181	A1182	G1183	G1184	C1185	G1186	G1187	U1188	A1189	G1190	G1191	G1192	G1193	A1194	C1195	G1196	G1197	U1198	U1199	C1200	U1141	C1202	G1203	A1204	U1205	G1206	C1207	C1208	G1209	A1210	U1211	G1212	A1213	G1214	G1215	G1216							
A1095	A1096	U1097	A1098	G1099	C1100	U1101	C1102	A1103	C1104	U1105	G1106	G1107	U1108	C1109	G1110	G1111	G1112	G1113	U1114	G1115	C1116	G1117	G1118	C1119	G1120	C1121	A1122	G1123	C1124	G1125	A1126	A1127	A1128	G1129	U1130	G1131	A1132	U1133	G1135	G1136	G1137	U1138	G1139	C1140	U1141	U1142	A1142A	A1143	G1144	C1145	G1146	C1147	A1148	G1149	C1150	G1151	C1152	C1153	G1154									

- Molecule 36: 5S RIBOSOMAL RNA

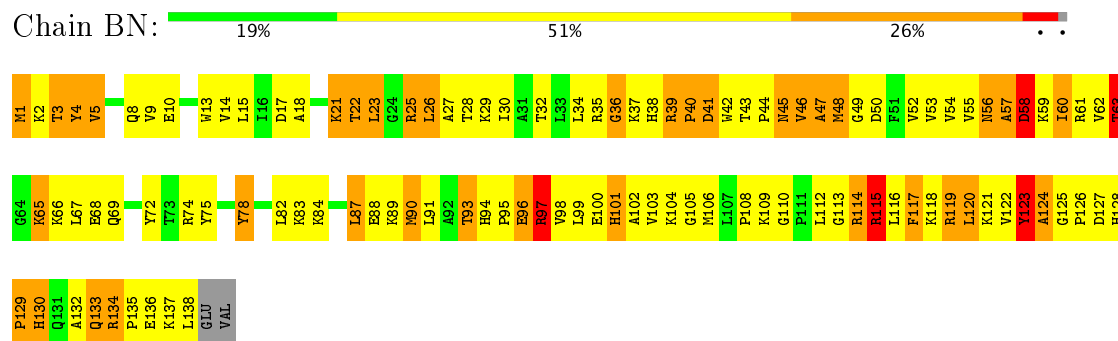




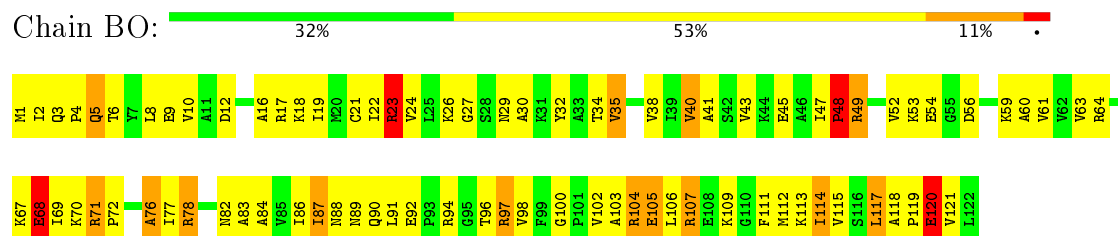
• Molecule 44: 50S RIBOSOMAL PROTEIN L7/L12



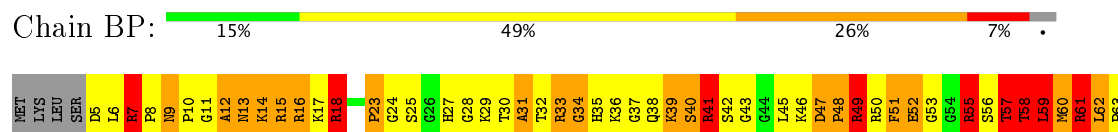
• Molecule 45: 50S RIBOSOMAL PROTEIN L13

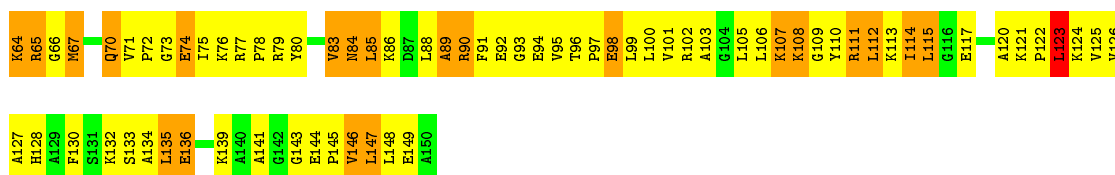


• Molecule 46: 50S RIBOSOMAL PROTEIN L14



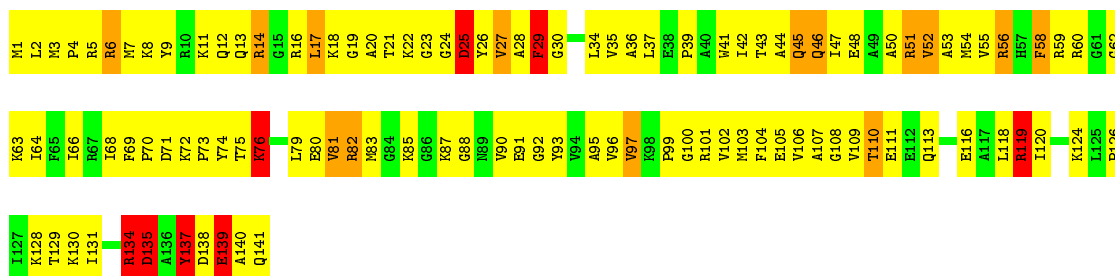
• Molecule 47: 50S RIBOSOMAL PROTEIN L15





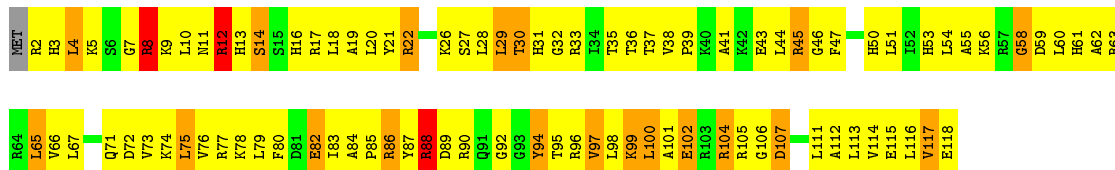
• Molecule 48: 50S RIBOSOMAL PROTEIN L16

Chain BQ: 22% 62% 10% 6%



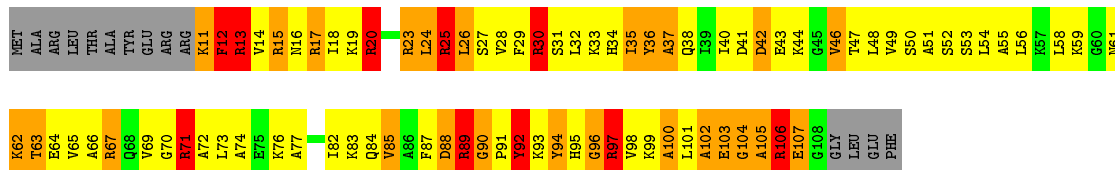
• Molecule 49: 50S RIBOSOMAL PROTEIN L17

Chain BR: 19% 61% 16% ..



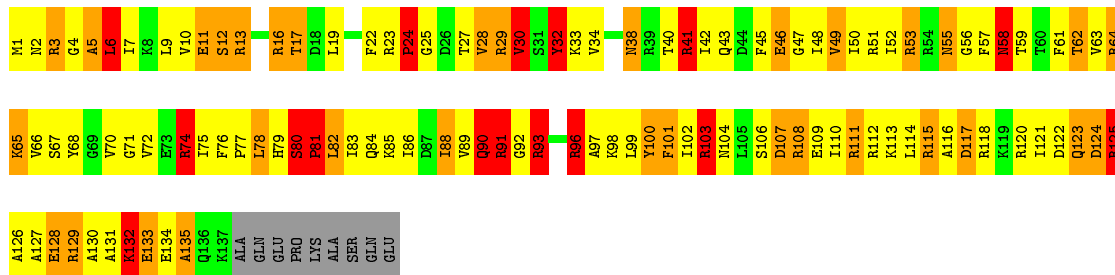
• Molecule 50: 50S RIBOSOMAL PROTEIN L18

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



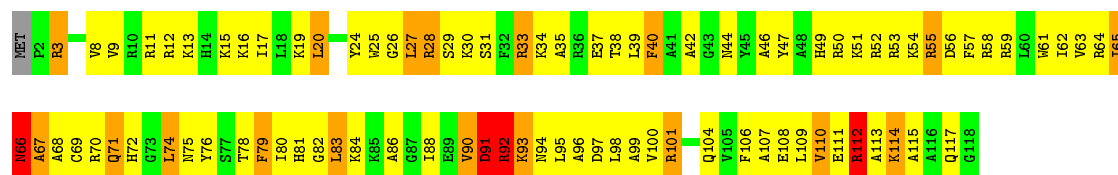
• Molecule 51: 50S RIBOSOMAL PROTEIN L19

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



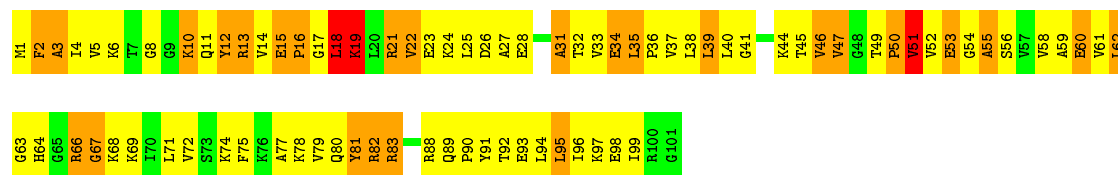
● Molecule 52: 50S RIBOSOMAL PROTEIN L20

Chain BU:  24% 57% 15% 4%



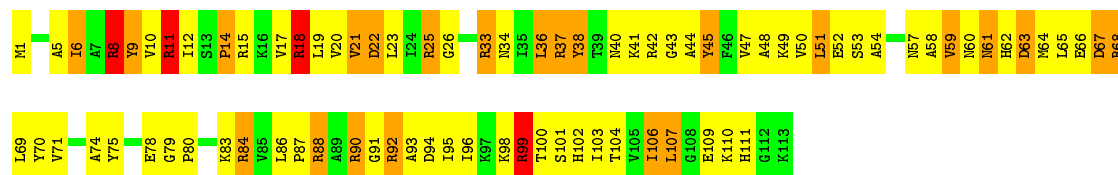
- Molecule 53: 50S RIBOSOMAL PROTEIN L21

Chain BV: 



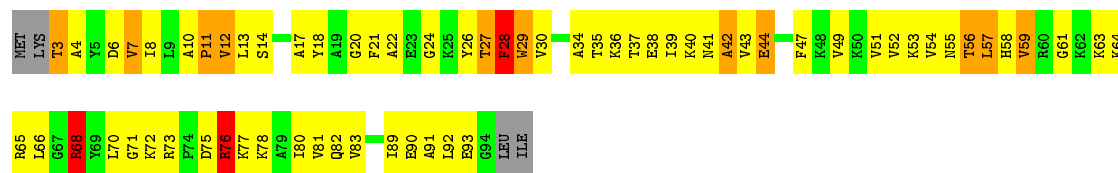
- Molecule 54: 50S RIBOSOMAL PROTEIN L22

Chain BW: 



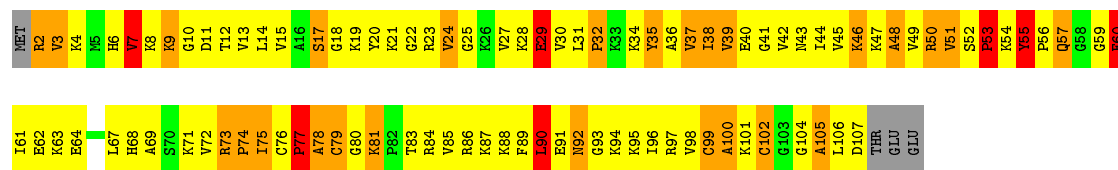
• Molecule 55: 50S RIBOSOMAL PROTEIN L23

Chain BX: 27% 54% 11% . .




● Molecule 56: 50S RIBOSOMAL PROTEIN L24

Chain BY: 9% 57% 24% 6% .



• Molecule 57: 50S RIBOSOMAL PROTEIN L25

Chain BZ: 



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	DEFOCUS GROUPS	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO-163 FILM	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

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

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

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	107
10	AJ	0	2
11	AK	0	2
12	AL	0	3
13	AM	0	3
14	AN	0	2
15	AO	0	3
16	AP	0	6
17	AQ	0	3

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

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

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

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

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

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

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
35	BA	1992	G	C3'

5 of 457 planarity outliers are listed below:

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

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32329	0	16041	1543	0
2	AB	1900	0	1951	244	0
3	AC	1612	0	1677	208	0
4	AD	1703	0	1767	205	0
5	AE	1146	0	1207	140	0
6	AF	843	0	857	95	0
7	AG	1257	0	1296	119	0
8	AH	1116	0	1177	110	0
9	AI	1010	0	1037	142	0
10	AJ	794	0	840	185	0
11	AK	885	0	904	92	0
12	AL	970	0	1057	144	0
13	AM	987	0	1059	139	0
14	AN	492	0	533	78	0
15	AO	734	0	771	74	0
16	AP	700	0	720	83	0
17	AQ	823	0	891	68	0
18	AR	574	0	644	77	0
19	AS	629	0	652	116	0
20	AT	763	0	861	112	0
21	AU	208	0	221	28	0
22	AV	1640	0	831	100	0
23	AX	230	0	114	17	0
24	AY	5214	0	5288	791	0
25	B0	662	0	688	91	0
26	B1	731	0	808	116	0
27	B2	598	0	653	94	0
28	B3	467	0	523	53	0
29	B4	450	0	449	93	0
30	B5	459	0	480	98	0
31	B6	433	0	461	148	0
32	B7	418	0	467	58	0
33	B8	507	0	576	103	0
34	B9	307	0	338	35	0
35	BA	62474	0	31032	3276	0
36	BB	2551	0	1281	164	0
37	BC	1742	0	1798	171	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	BD	2145	0	2234	305	0
39	BE	1563	0	1629	246	0
40	BF	1623	0	1677	283	0
41	BG	1474	0	1535	287	0
42	BH	1268	0	1337	232	0
43	BK	1025	0	1066	177	0
44	BL	477	0	509	14	0
45	BN	1104	0	1180	202	0
46	BO	933	0	996	124	0
47	BP	1114	0	1187	295	0
48	BQ	1122	0	1179	166	0
49	BR	960	0	1021	158	0
50	BS	770	0	832	168	0
51	BT	1141	0	1202	228	0
52	BU	958	0	1015	170	0
53	BV	779	0	852	148	0
54	BW	896	0	953	103	0
55	BX	725	0	778	93	0
56	BY	810	0	901	186	0
57	BZ	1467	0	1492	230	0
58	AY	37	0	47	12	0
59	AY	28	0	12	7	0
All	All	152777	0	105584	12183	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 47.

The worst 5 of 12183 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:509:A:H5'	1:AA:510:A:OP2	1.26	1.30
24:AY:496:LYS:HE2	24:AY:498:ILE:CD1	1.66	1.25
53:BV:15:GLU:HB3	53:BV:16:PRO:HD2	1.23	1.20
41:BG:63:ILE:HA	41:BG:143:GLU:HG3	1.22	1.19
35:BA:996:A:H4'	52:BU:92:ARG:HE	1.01	1.18

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	232/256 (91%)	146 (63%)	55 (24%)	31 (13%)	0	6
3	AC	204/239 (85%)	129 (63%)	58 (28%)	17 (8%)	1	16
4	AD	206/209 (99%)	133 (65%)	52 (25%)	21 (10%)	1	11
5	AE	148/162 (91%)	116 (78%)	27 (18%)	5 (3%)	4	35
6	AF	99/101 (98%)	78 (79%)	15 (15%)	6 (6%)	2	22
7	AG	153/156 (98%)	107 (70%)	34 (22%)	12 (8%)	1	18
8	AH	136/138 (99%)	106 (78%)	23 (17%)	7 (5%)	2	26
9	AI	125/128 (98%)	84 (67%)	26 (21%)	15 (12%)	0	7
10	AJ	96/105 (91%)	64 (67%)	19 (20%)	13 (14%)	0	6
11	AK	117/129 (91%)	93 (80%)	18 (15%)	6 (5%)	2	26
12	AL	122/132 (92%)	81 (66%)	26 (21%)	15 (12%)	0	7
13	AM	122/126 (97%)	77 (63%)	25 (20%)	20 (16%)	0	4
14	AN	58/61 (95%)	48 (83%)	6 (10%)	4 (7%)	1	20
15	AO	86/89 (97%)	53 (62%)	25 (29%)	8 (9%)	1	14
16	AP	81/88 (92%)	58 (72%)	19 (24%)	4 (5%)	2	27
17	AQ	97/105 (92%)	76 (78%)	16 (16%)	5 (5%)	2	26
18	AR	68/88 (77%)	51 (75%)	11 (16%)	6 (9%)	1	15
19	AS	76/93 (82%)	39 (51%)	20 (26%)	17 (22%)	0	2
20	AT	97/106 (92%)	52 (54%)	30 (31%)	15 (16%)	0	4
21	AU	22/27 (82%)	14 (64%)	6 (27%)	2 (9%)	1	15
24	AY	662/691 (96%)	442 (67%)	135 (20%)	85 (13%)	0	6
25	B0	82/85 (96%)	64 (78%)	16 (20%)	2 (2%)	7	42
26	B1	91/98 (93%)	60 (66%)	20 (22%)	11 (12%)	0	7
27	B2	69/72 (96%)	34 (49%)	22 (32%)	13 (19%)	0	3
28	B3	57/60 (95%)	41 (72%)	12 (21%)	4 (7%)	1	19

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

5 of 792 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	13	ALA

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

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	202/220 (92%)	178 (88%)	24 (12%)	6	27
3	AC	160/188 (85%)	133 (83%)	27 (17%)	2	16
4	AD	180/181 (99%)	158 (88%)	22 (12%)	6	26
5	AE	115/123 (94%)	101 (88%)	14 (12%)	6	26
6	AF	90/90 (100%)	80 (89%)	10 (11%)	7	29
7	AG	126/127 (99%)	113 (90%)	13 (10%)	8	32
8	AH	119/119 (100%)	106 (89%)	13 (11%)	7	30
9	AI	98/99 (99%)	88 (90%)	10 (10%)	8	33
10	AJ	88/92 (96%)	75 (85%)	13 (15%)	3	20
11	AK	90/99 (91%)	82 (91%)	8 (9%)	11	39
12	AL	104/109 (95%)	93 (89%)	11 (11%)	8	31
13	AM	99/101 (98%)	86 (87%)	13 (13%)	5	24
14	AN	49/50 (98%)	42 (86%)	7 (14%)	4	22
15	AO	79/80 (99%)	70 (89%)	9 (11%)	7	28
16	AP	72/74 (97%)	69 (96%)	3 (4%)	34	64
17	AQ	94/97 (97%)	86 (92%)	8 (8%)	12	42
18	AR	61/77 (79%)	58 (95%)	3 (5%)	29	61
19	AS	69/80 (86%)	59 (86%)	10 (14%)	4	21
20	AT	76/82 (93%)	66 (87%)	10 (13%)	5	24
21	AU	19/22 (86%)	19 (100%)	0	100	100

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	BZ	162/179 (90%)	134 (83%)	28 (17%)	2	14
All	All	5586/5868 (95%)	4824 (86%)	762 (14%)	8	23

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

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

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

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

5.3.3 RNA ⓘ

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

5 of 959 RNA backbone outliers are listed below:

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

5 of 126 RNA pucker outliers are listed below:

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

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
58	FUA	AY	701	-	37,40,40	2.21	9 (24%)	45,64,64	1.86	10 (22%)
59	GDP	AY	702	-	25,30,30	1.46	4 (16%)	26,47,47	2.35	9 (34%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	FUA	AY	701	-	-	0/10/92/92	0/4/4/4
59	GDP	AY	702	-	-	0/12/32/32	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	AY	701	FUA	C23-C22	-7.88	1.37	1.51
58	AY	701	FUA	C23-C24	-4.07	1.39	1.53
58	AY	701	FUA	C15-C14	-3.90	1.46	1.54
58	AY	701	FUA	C19-C10	-3.71	1.47	1.54
58	AY	701	FUA	C24-C25	-3.40	1.38	1.50

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	AY	701	FUA	C8-C9-C10	-6.57	109.63	116.44
59	AY	702	GDP	C4-C5-N7	-5.01	104.57	109.41
59	AY	702	GDP	C4'-O4'-C1'	-5.00	104.45	109.77
59	AY	702	GDP	N3-C2-N1	-4.27	121.22	127.46
58	AY	701	FUA	C6-C5-C10	-4.11	106.16	111.57

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 19 short contacts:

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

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.