



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:46 PM BST

PDB ID : 4V5N
EMDB ID: : EMD-1799
Title : tRNA translocation on the 70S ribosome: the post- translocational translocation intermediate TI(POST)
Authors : Ratje, A.H.; Loerke, J.; Mikolajka, A.; Bruenner, M.; Hildebrand, P.W.; Starosta, A.L.; Doenhoefer, A.; Connell, S.R.; Fucini, P.; Mielke, T.; Whitford, P.C.; Onuchic, J.N.; Yu, Y.; Sanbonmatsu, K.Y.; Hartmann, R.K.; Penczek, P.A.; Wilson, D.N.; Spahn, C.M.T.
Deposited on : 2010-10-21
Resolution : 7.60 Å(reported)
Based on PDB ID : 2WRI,2WRJ

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

For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

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

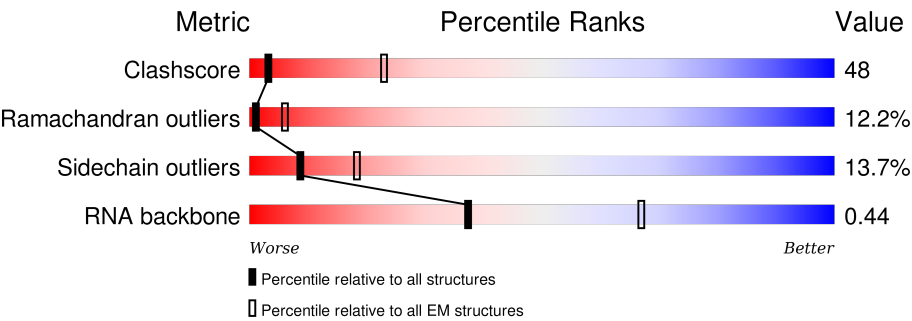
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

1 Overall quality at a glance i

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

The reported resolution of this entry is 7.60 Å.

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



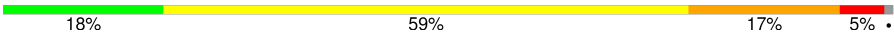


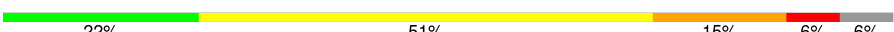
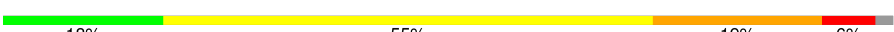
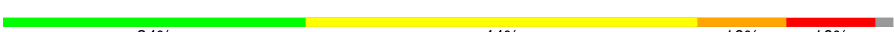
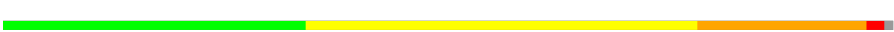





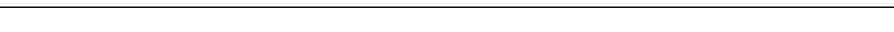

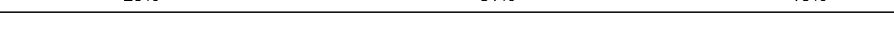

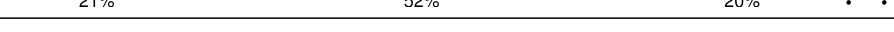







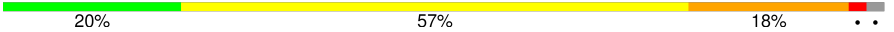
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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

Mol	Chain	Length	Quality of chain
1	AA	1522	<div><div>22%58%18%</div><div></div></div>
2	AB	256	<div><div>23%49%14%5%9%</div><div></div></div>
3	AC	239	<div><div>24%44%14%5%14%</div><div></div></div>
4	AD	209	<div><div>30%49%16%5%</div><div></div></div>
5	AE	162	<div><div>31%44%14%7%</div><div></div></div>
6	AF	101	<div><div>33%50%15%</div><div></div></div>
7	AG	156	<div><div>34%48%15%</div><div></div></div>
8	AH	138	<div><div>30%57%10%</div><div></div></div>

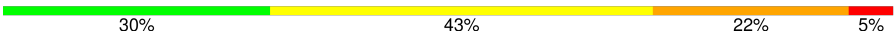
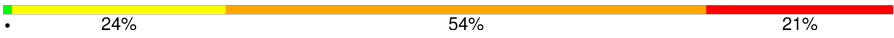
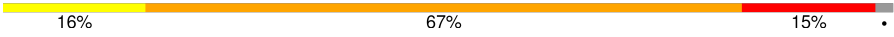

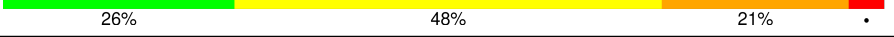
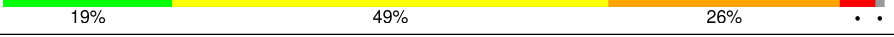
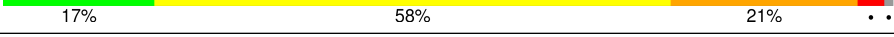

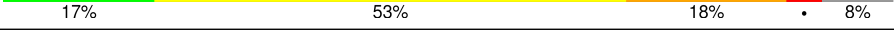
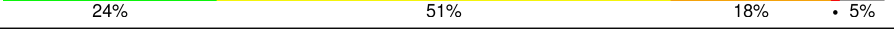
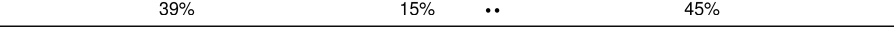
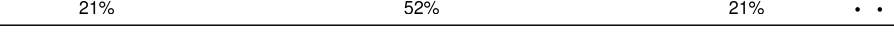
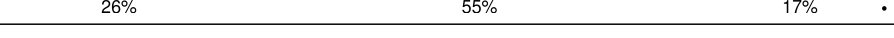
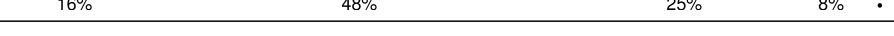
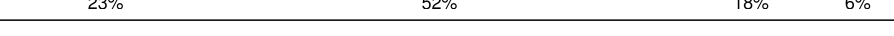
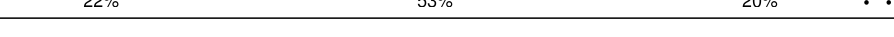

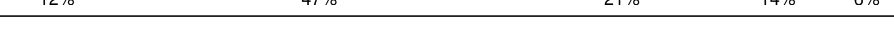
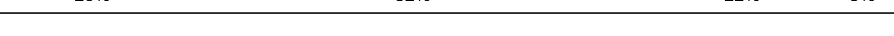

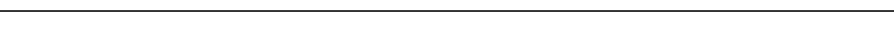

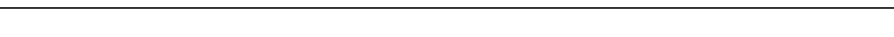
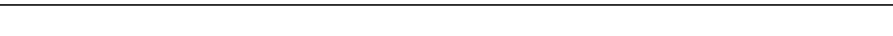
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Mol	Chain	Length	Quality of chain
9	AI	128	
10	AJ	105	
11	AK	129	
12	AL	132	
13	AM	126	
14	AN	61	
15	AO	89	
16	AP	88	
17	AQ	105	
18	AR	88	
19	AS	93	
20	AT	106	
21	AU	27	
22	AV	77	
23	AX	11	
24	AY	691	
25	B0	85	
26	B1	98	
27	B2	72	
28	B3	60	
29	B4	71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

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

2 Entry composition

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 22 is a RNA chain called TRNA.

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

- Molecule 23 is a RNA chain called MRNA.

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

- Molecule 24 is a protein called ELONGATION FACTOR G.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

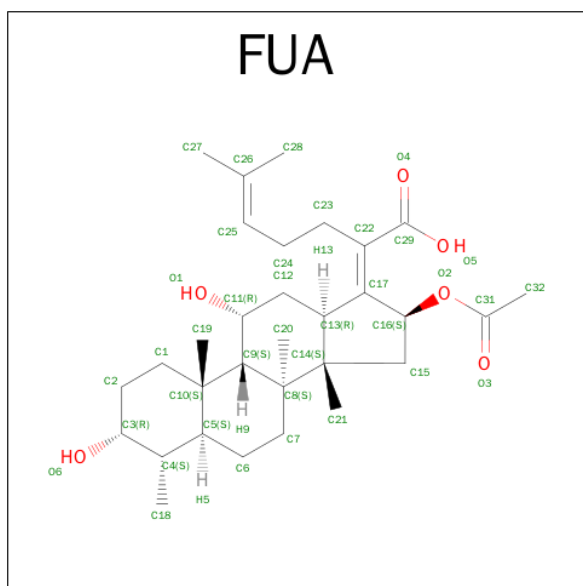
- Molecule 56 is a protein called 50S RIBOSOMAL PROTEIN L24.

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

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

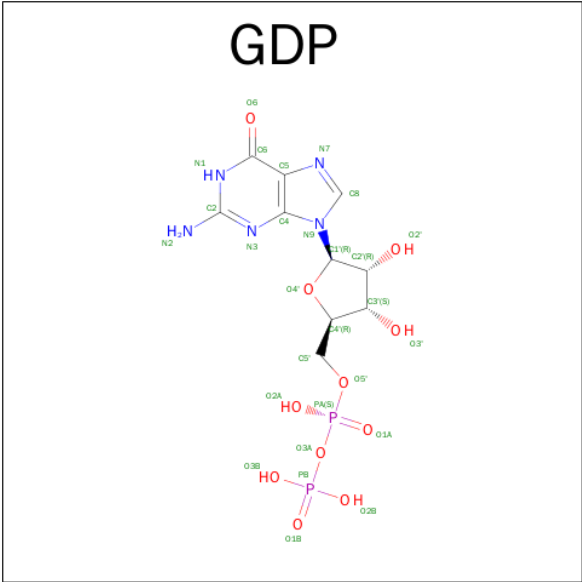
Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	184	Total	C	N	O	S	0	0
			1467	936	261	268	2		

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



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

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

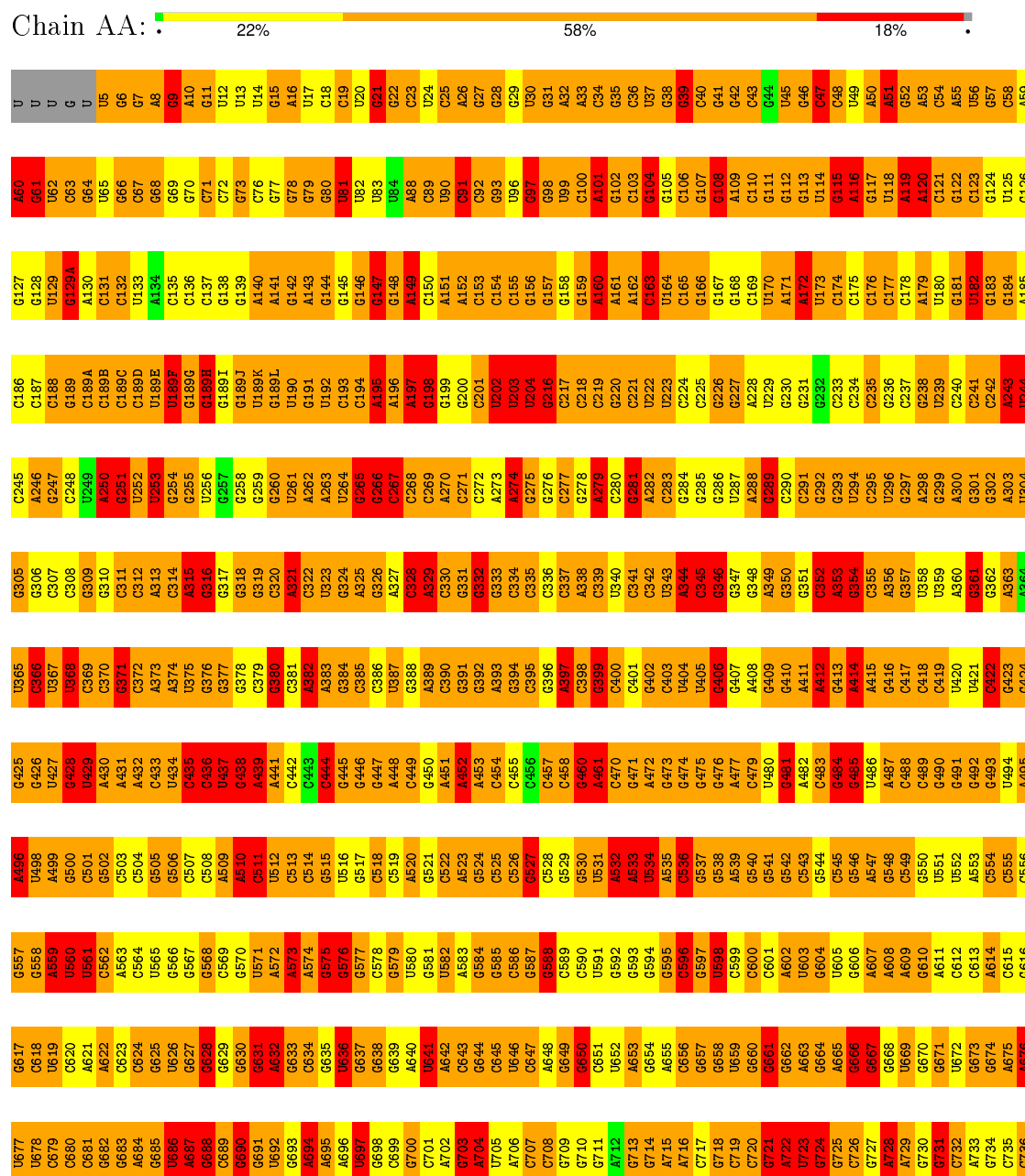


Mol	Chain	Residues	Atoms					AltConf
59	AY	1	Total	C	N	O	P	0
			28	10	5	11	2	

3 Residue-property plots

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

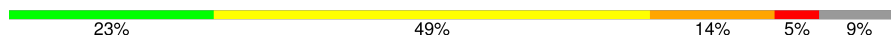
• Molecule 1: 16S rRNA



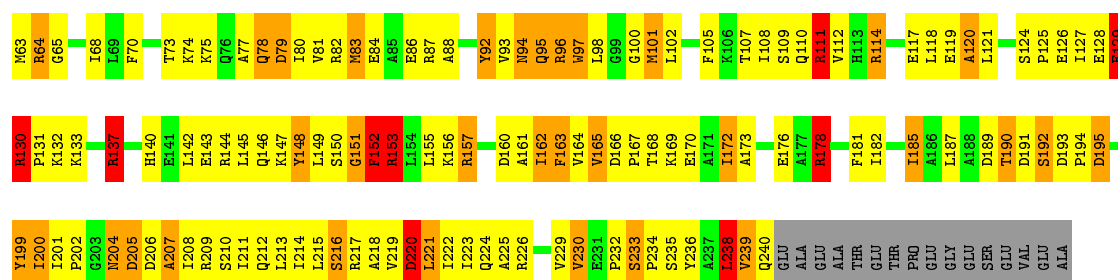
G1523	C1463	A1388	A1339	A1279	U1219	C1158	C1098	C1038	A983	A923	U863	C797	A737
G1524	G1464	C1399	A1340	A1280	G1220	U1159	G1099	C1039	C984	C924	A864	G798	C738
G1525	C1465	C1400	U1341	U1281	G1221	G1160	C1100	U1040	C985	G925	A865	G799	C739
G1526	C1466	G1401	C1342	U1282	G1222	C1161	A1041	A986	G986	G926	C866	G800	U740
G1527	G1467	C1402	G1343	G1283	C1223	C1163	A1042	G1042	G987	G927	C867	U801	G741
U1528	C1403	C1403	C1344	G1284	G1224	C1163	C1043	C1043	G988	G928	C868	A802	G742
G1529	G1468	C1404	U1345	A1285	A1225	G1164	G1044	A1044	C989	G929	C869	G803	U743
G1530	G1469	G1404	G1346	A1286	C1226	C1165	A1045	C1045	C990	C930	U870	U804	C744
G1531	G1405	G1405	G1347	A1287	C1227	G1166	A1046	A1046	U991	C931	C805	C745	C744
U	G1471	U1407	U1348	A1288	C1228	G1168	C1047	A872	U992	G932	A872	C806	A746
C	A1472	C1407	A1349	A1289	A1229	G1169	G1048	G1048	U993	G933	A873	A807	C747
A	G1473	A1408	A1350	G1290	C1230	A1170	U1049	U1049	A994	G934	G874	C808	C748
C	G1474	C1409	U1351	G1291	G1231	C1171	G1050	G1050	A995	A935	C875	C809	C749
C	G1475	G1410	C1352	U1292	U1232	C1172	A1111	C1051	A996	G936	G876	C810	G750
C	G1476	G1411	C1353	G1293	G1233	G1173	C1112	G1052	U997	A937	C877	C812	U751
C	G1477	C1412	G1354	G1294	C1234	G1174	C1113	G1053	A998	A938	C878	C813	G752
C	G1478	A1413	C1355	G1295	U1235	G1175	C1114	A1054	C999	G939	C879	U813	A753
C	G1479	U1414	G1356	C1296	A1236	A1176	C1115	A1055	C940	C940	C880	A814	C754
C	G1480	G1415	G1357	C1297	C1237	G1177	C1116	U1056	A1001	G941	G881	A815	G755
U	G1481	G1416	U1358	C1298	A1238	G1178	G1117	G1057	G942	G942	C882	A816	C756
C	G1482	G1417	C1359	A1299	U1239	A1179	C1118	G1058	U943	U943	C883	C817	U757
C	A1483	A1418	U1360	G1300	U1240	A1180	C1119	C1059	G944	G944	U884	G818	G758
C	G1484	G1419	G1361	U1301	G1241	G1181	G1120	C1060	G945	G945	G885	A819	A759
U	U1485	C1420	C1362	U1302	C1242	G1182	U121	G1061	A1005	A946	G886	U820	G760
P26	G1486	G1421	C1363	C1303	C1243	A1183	U122	G1062	C1006	G947	C887	G821	G761
G1487	G1487	G1422	G1364	G1304	G1244	G1184	A1123	C1063	C1007	C948	G888	C822	C762
G1488	G1488	G1423	U1365	A1245	A1245	G1185	G1124	G1064	A949	A949	A889	G823	G763
G1489	G1489	G1424	G1366	C1246	C1246	G1186	U125	U1065	G1008	U950	C884	G824	C764
A29	U1490	U1425	C1367	U1307	U1247	G1187	G1126	C1066	G1010	G951	C885	G825	G765
R30	G1491	C1426	C1367	U1308	U1248	A1188	G1127	A1067	G1011	U952	A892	C826	A766
Y31	A1492	U1427	G1368	G1309	G1249	C1189	C1128	C1068	U1012	G953	C893	U827	A767
I32	G1493	A1428	C1369	A1250	A1250	G1190	C1129	C1069	G1013	G954	C894	A828	A768
Y33	G1494	C1429	G1370	G1311	A1251	A1191	A1130	U1070	G1014	U955	C895	G829	G769
A34	U1495	C1430	U1371	G1312	A1252	C1192	G1131	C1071	A1015	U956	C896	G830	C770
E35	C1496	C1431	U1372	U1313	G1253	G1193	C1132	G1072	A1016	U957	C897	U831	G771
R36	G1497	A1432	G1373	C1314	C1254	U1194	G1133	U1073	G1017	A958	C898	C832	U772
N37	U1498	A1433	A1374	U1315	G1255	C1195	G1134	G1074	C1018	A959	C899	U833	G773
G38	A1499	A1434	A1375	G1316	A1256	U1196	U1135	C1075	C1019	U960	A900	C834	G774
I39	A1500	G1435	U1376	G1317	U1257	G1197	U1136	C1076	U1020	U961	A901	U835	G775
H40	C1501	U1436	A1377	C1318	G1258	G1198	C1137	G1077	G1021	C962	G902	G836	G776
I41	U1502	C1437	G1378	A1319	C1259	U1199	G1138	U1078	G1022	G963	C903	G837	A777
D43	G1503	G1438	C1379	C1320	C1260	C1200	G1139	G1079	G1023	A964	C904	G838	G778
D43	G1504	C1439	U1380	C1321	A1261	A1201	C1140	A1080	G1024	A965	U905	U839	C779
L44	C1440	G1441	U1381	C1322	C1262	C1202	C1141	G1081	U1025	G966	G906	C840	A780
Q45	U1506	G1442	C1382	G1323	C1263	C1203	G1142	G1082	G1026	C967	A907	U841	A781
K46	A1507	G1442	C1383	A1324	C1264	A1204	G1143	U1083	C1027	A968	A908	C848	A782
T47	G1508	G1442A	C1384	C1325	G1265	U1205	G1144	G1084	C1028	A969	A909	C849	C783
M48	C1509	A1442B	G1385	C1326	G1266	G1206	G1145	U1085	C1029	C970	C910	U850	C784
E49	U1510	G1443	G1386	C1327	C1267	G1207	A1146	U1086	G1030	G971	U911	G851	G785
E50	G1511	C1444	G1387	C1328	A1268	C1208	C1147	G1087	G1030A	C972	C912	G852	G786
L51	U1512	C1445	C1388	A1329	A1269	C1209	U1148	G1088	C1030B	G973	A913	G853	A787
E52	A1513	U1446	C1389	U1330	C1270	C1210	G1149	G1089	C1030C	A974	A914	G854	U788
R53	C1514	A1447	U1390	G1331	G1271	U1211	U1150	U1090	A1030D	A975	A915	G855	U789
T54	C1515	C1452	U1391	A1332	G1272	U1212	A1151	U1091	G1031	G976	G916	C856	A790
F55	G1516	G1456	G1392	G1333	G1273	A1213	A1152	A1092	G1032	A977	G917	C857	G791
F55	G1517	G1457	U1393	G1334	G1274	U1214	C1153	A1093	G1033	A978	A918	G858	A792
I58	A1518	G1458	U1394	C1335	A1275	G1215	G1154	G1094	G1034	C979	A919	A859	U793
E59	C1459	C1459	C1395	G1336	G1276	G1216	G1155	U1095	A1035	C980	U920	A860	A794
D60	A1460	C1396	G1337	C1277	G1217	C1217	G1156	C1096	G1036	U921	U921	G861	C795
L61	G1461	A1396	C1397	G1338	U1278	C1218	A1157	C1097	C1037	U922	G922	C862	C796

● Molecule 2: 30S RIBOSOMAL PROTEIN S2

Chain AB:

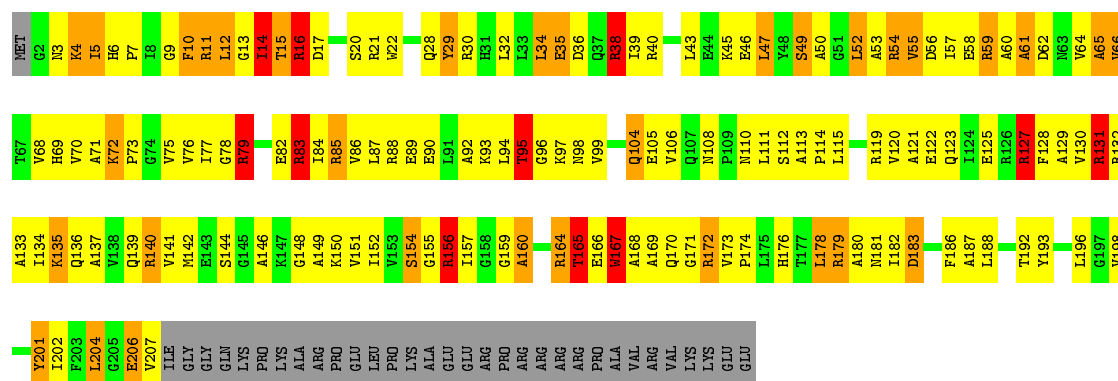


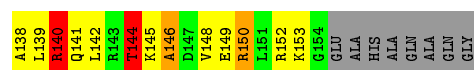
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-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



• Molecule 3: 30S RIBOSOMAL PROTEIN S3

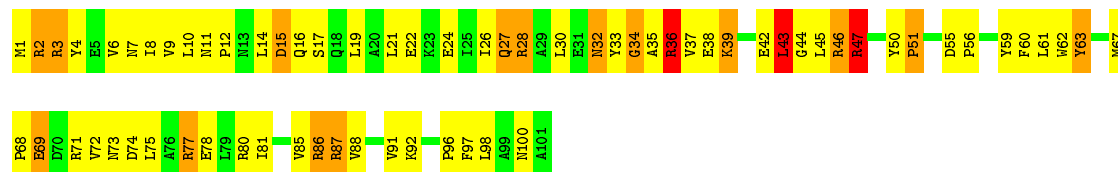
Chain AC: 24% 44% 14% 5% 14%





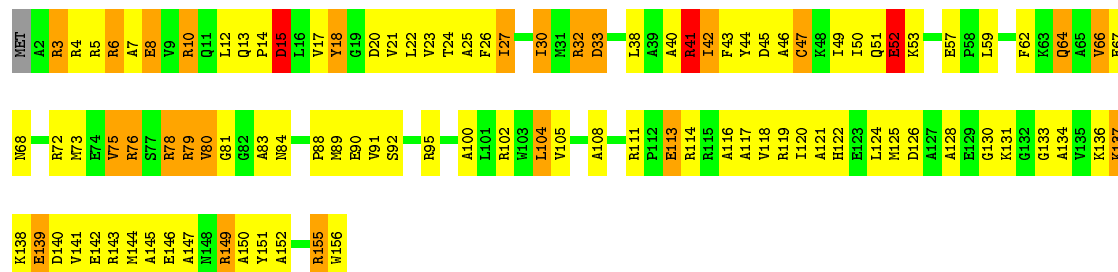
• Molecule 6: 30S RIBOSOMAL PROTEIN S6

Chain AF: 33% 50% 15%

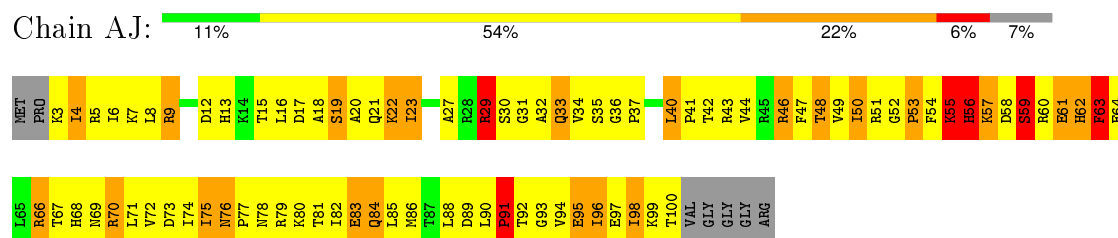


• Molecule 7: 30S RIBOSOMAL PROTEIN S7

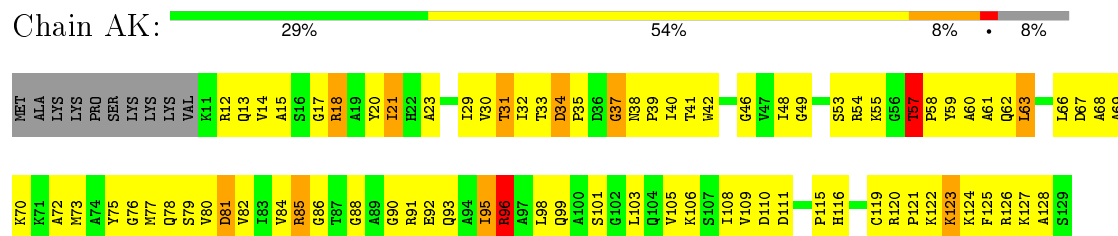
Chain AG: 34% 48% 15%



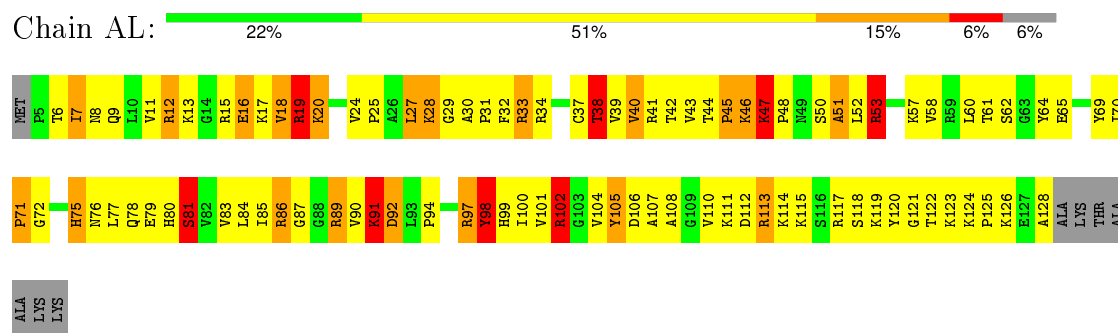
- Molecule 10: 30S RIBOSOMAL PROTEIN S10



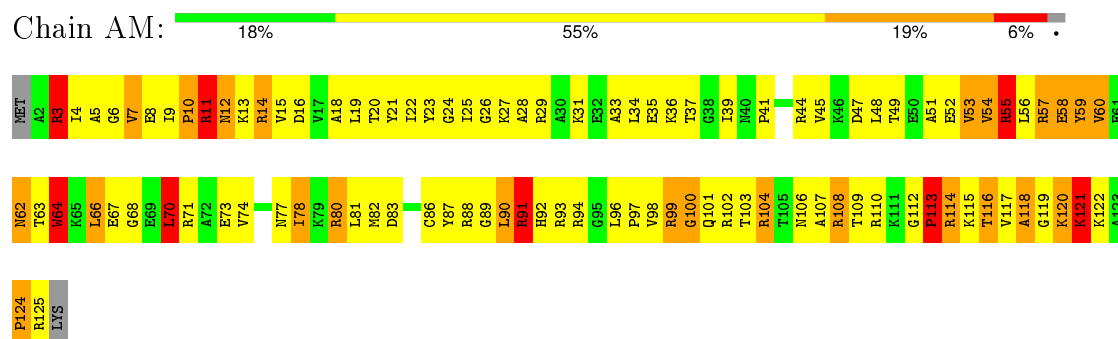
- Molecule 11: 30S RIBOSOMAL PROTEIN S11



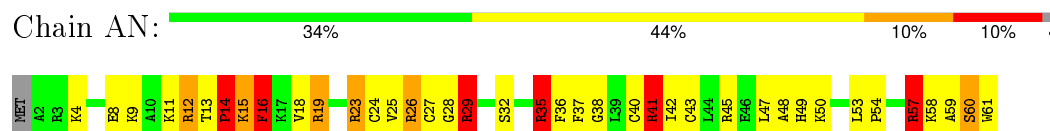
- Molecule 12: 30S RIBOSOMAL PROTEIN S12



- Molecule 13: 30S RIBOSOMAL PROTEIN S13

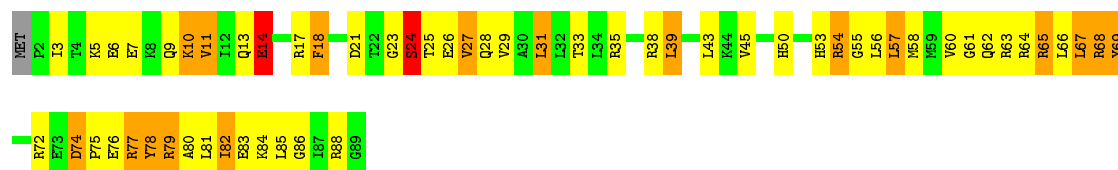


- Molecule 14: 30S RIBOSOMAL PROTEIN S14 TYPE Z




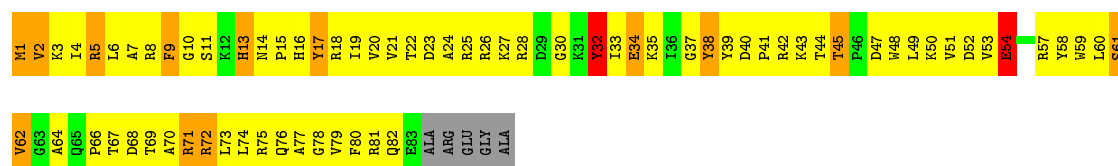
- Molecule 15: 30S RIBOSOMAL PROTEIN S15

Chain AO: 



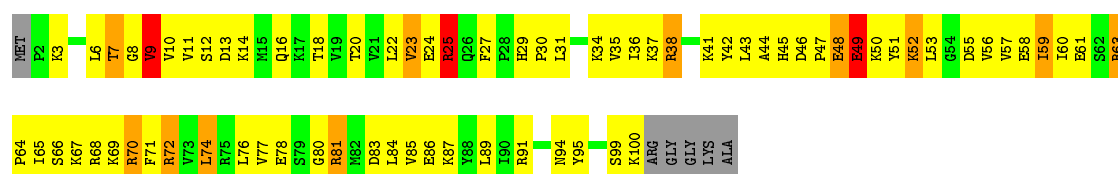
- Molecule 16: 30S RIBOSOMAL PROTEIN S16

Chain AP: 




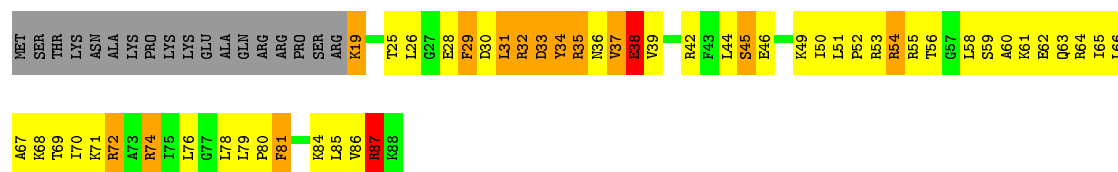
- Molecule 17: 30S RIBOSOMAL PROTEIN S17

Chain AQ: 



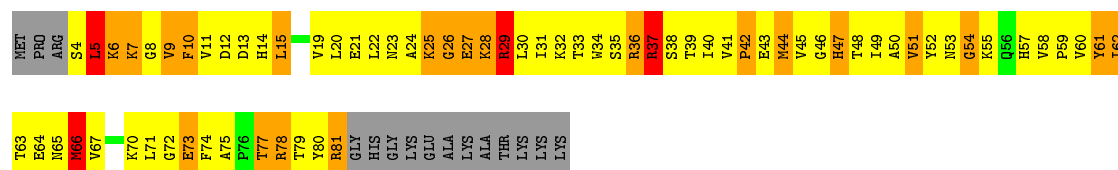
- Molecule 18: 30S RIBOSOMAL PROTEIN S18

Chain AR: 

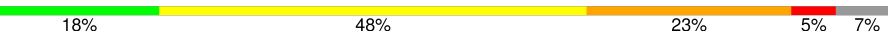


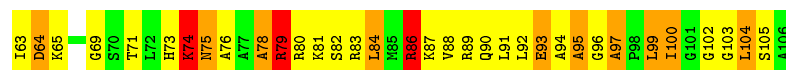
- Molecule 19: 30S RIBOSOMAL PROTEIN S19

Chain AS: 

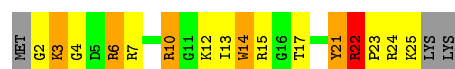


- Molecule 20: 30S RIBOSOMAL PROTEIN S20

Chain AT: 



• Molecule 21: 30S RIBOSOMAL PROTEIN THX



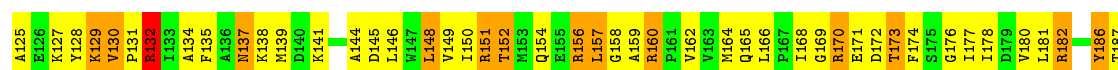
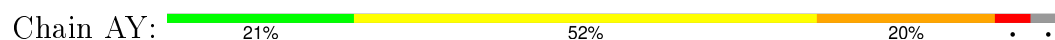
• Molecule 22: TRNA

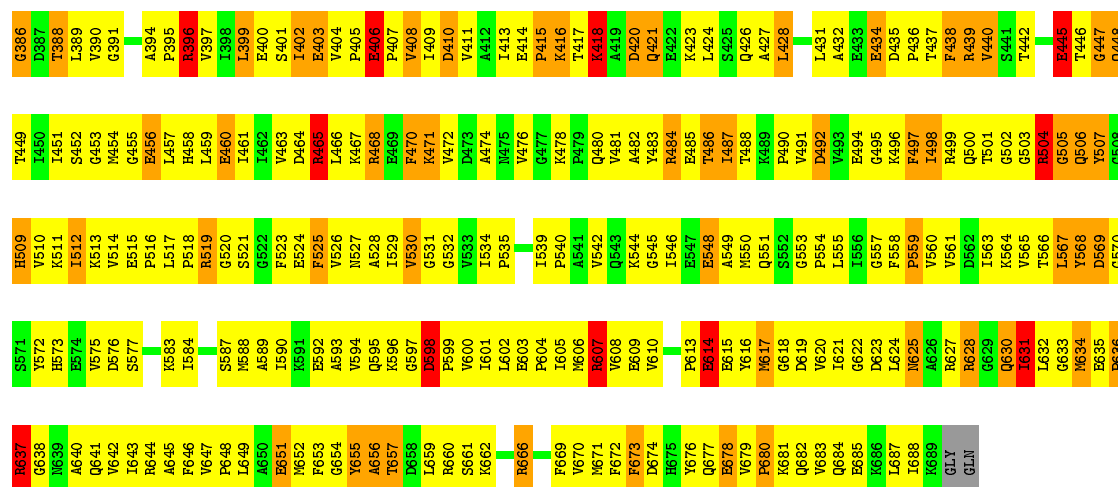


• Molecule 23: MRNA

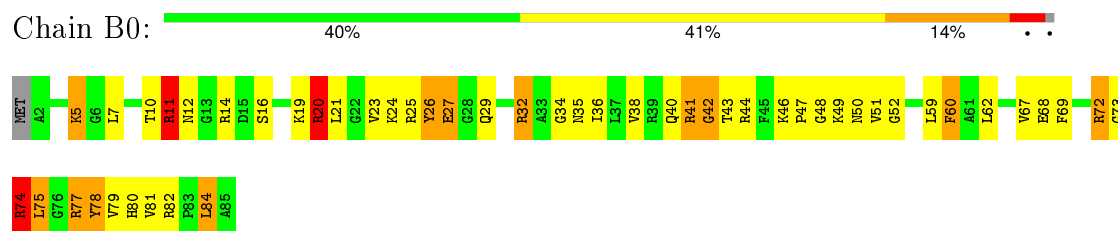


• Molecule 24: ELONGATION FACTOR G

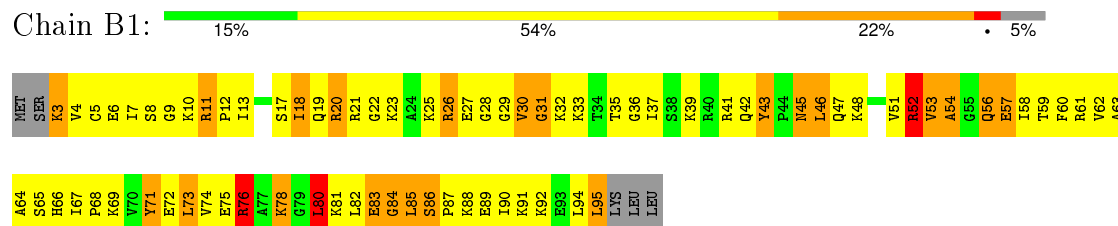




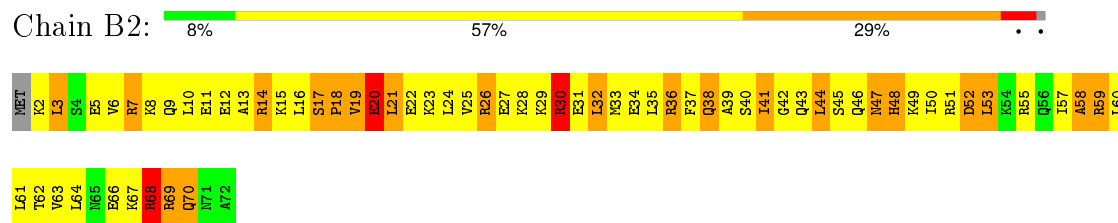
• Molecule 25: 50S RIBOSOMAL PROTEIN L27



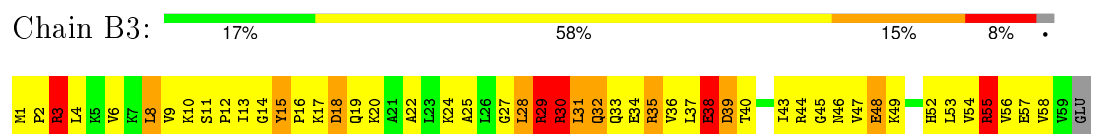
• Molecule 26: 50S RIBOSOMAL PROTEIN L28



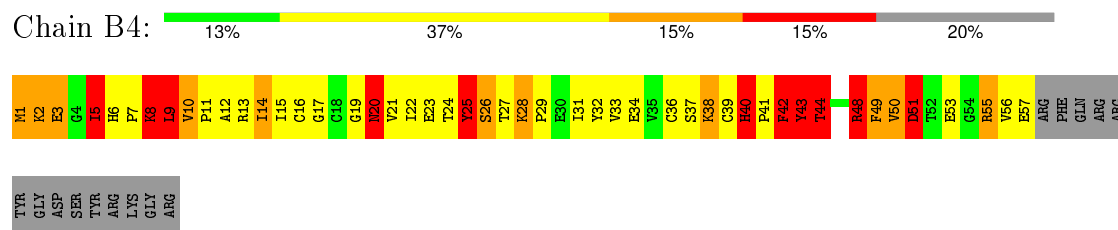
• Molecule 27: 50S RIBOSOMAL PROTEIN L29



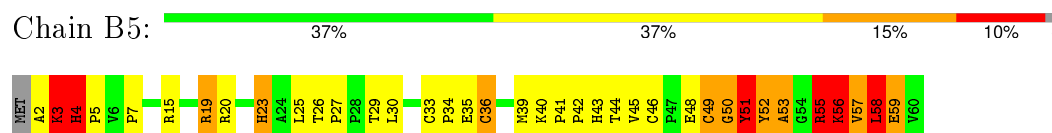
• Molecule 28: 50S RIBOSOMAL PROTEIN L30



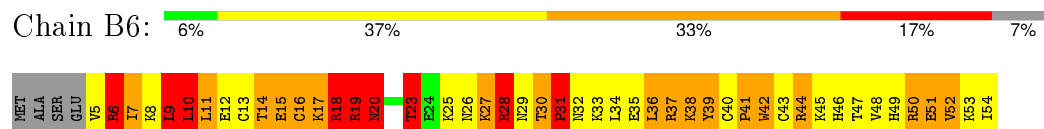
• Molecule 29: 50S RIBOSOMAL PROTEIN L31



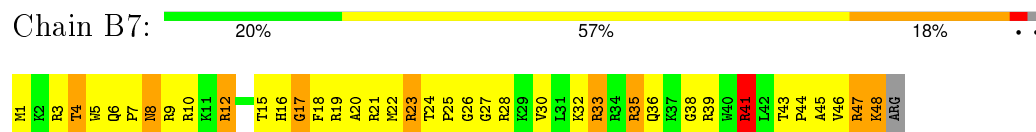
- Molecule 30: 50S RIBOSOMAL PROTEIN L32



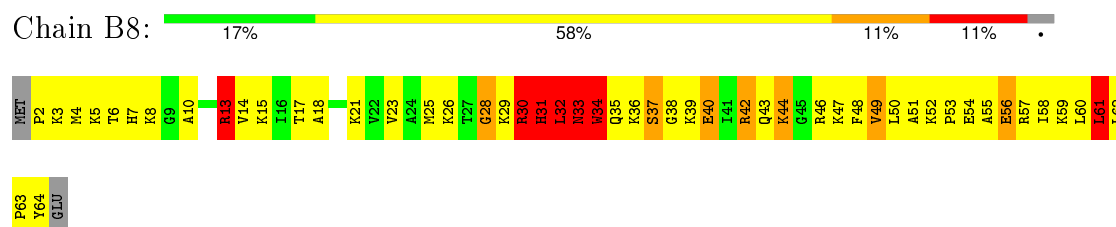
- Molecule 31: 50S RIBOSOMAL PROTEIN L33



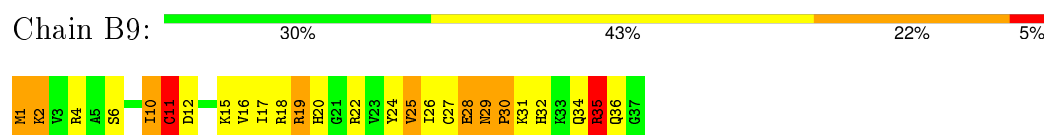
- Molecule 32: 50S RIBOSOMAL PROTEIN L34



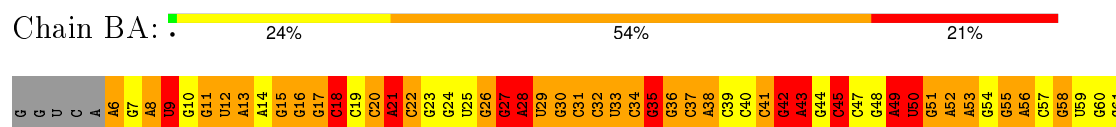
- Molecule 33: 50S RIBOSOMAL PROTEIN L35



- Molecule 34: 50S RIBOSOMAL PROTEIN L36



- Molecule 35: 23S RIBOSOMAL RNA

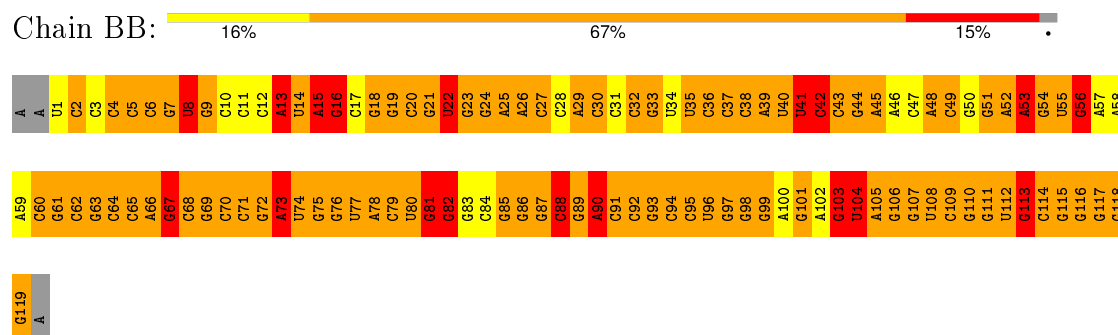


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C916	G916	G855	C795	A735	A675	A637	G579	C517	C456	U395	G338	A278	C283	U193	G124	C63
G917	C917	C856	C796	A736	A676	G638	G581	U519	A457	G397	U339	C279	G284	U194	G125	C64
G918	A918	C857	C797	A737	A677	U639	C581	U519	G458	G397	A340	C280	A285	A195	A126	C65
G919	G919	U858	C798	G738	C678	C640	G582	G521	U459	G399	G341	G381	A286	A196	A127	C66
A980	G920	G859	G799	G739	C679	C641	G583	G522	A460	G400	G342	A282	A287	A197	G128	C67
A981	U921	U860	A800	U740	G680	G642	C584	C523	C461	G401	C343	A383	C288	C198	C129	C68
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A983	C923	G862	A802	G742	G682	A644	A586	U524	C463	A403	A345	C285	G290	U200	G131	G70
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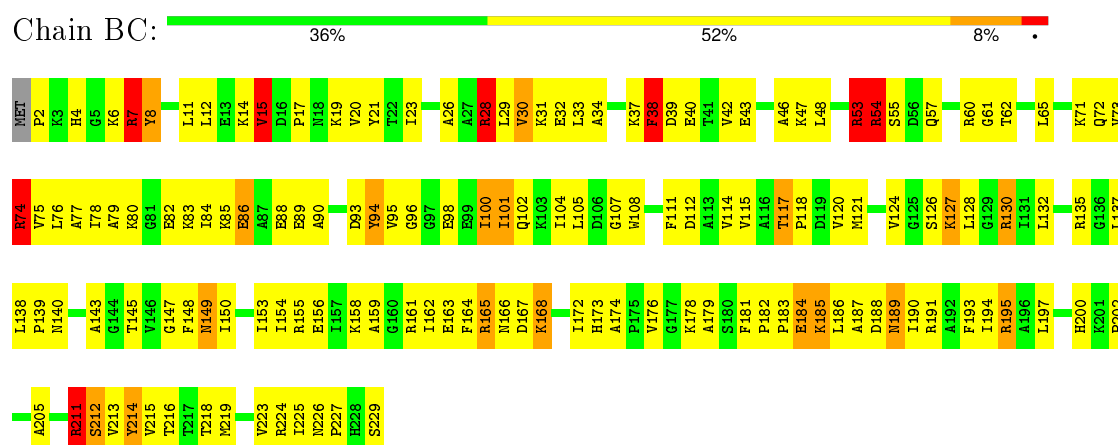
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U	G2844	A2602	A2721	G2542	C2482	A2422	G2362	G2302	G2242	U2172	G2112	G2052	U1992
U	G2845	G2603	G2722	G2543	C2483	U2423	C2363	G2303	U2243	A2173	U2113	G2053	U1993
U	U2846	C2604	C2723	G2544	G2484	C2424	C2364	G2304	U2244	C2174	A2114	A2054	C1994
U	G2847	U2605	G2724	G2545	G2485	A2425	G2365	A2305	U2245	C2175	G2115	G2055	U1995
U	U2848	C2606	A2725	U2546	G2486	A2426	A2366	C2306	G2246	A2176	G2116	G2056	C1996
U	A2849	G2607	U2726	U2547	G2487	C2427	G2367	G2307	A2247	C2177	A2117	A2057	G1997
U	C2850	G2608	G2727	G2548	A2488	G2428	C2368	G2308	C2248	C2178	U2118	A2058	G1998
U	A2851	U2609	U2728	G2549	G2489	G2429	A2369	A2309	U2249	C2179	A2119	A2059	C1999
U	G2852	C2610	G2729	C2550	G2490	A2430	G2370	A2310	G2250	U2180	G2120	A2060	G2000
U	C2853	U2611	C2730	C2551	U2491	A2431	G2371	A2311	G2251	G2181	G2121	G2061	A2001
U	G2854	G2612	G2731	U2552	U2492	A2432	G2372	U2312	G2252	G2182	U2122	A2062	G2002
U	C2855	U2613	G2732	G2553	U2493	A2433	G2373	C2313	G2253	C2183	G2123	C2063	G2003
U	U2856	A2614	A2733	U2554	G2494	A2434	C2374	G2314	C2254	G2184	G2124	C2064	G2004
U	C2857	G2615	C2734	U2555	G2495	A2435	G2375	G2315	G2255	C2185	G2125	C2065	A2005
U	G2858	C2616	G2735	C2556	C2496	G2436	A2376	C2316	G2256	A2186	A2126	C2066	C2006
U	C2859	G2617	U2736	G2557	A2497	U2437	A2377	C2317	U2257	G2187	G2127	G2067	G2007
U	A2860	G2618	C2737	C2558	C2498	U2438	A2378	G2318	C2258	C2188	C2128	U2068	C2008
U	G2861	C2619	U2738	C2559	C2499	A2439	G2379	G2319	G2259	U2189	C2129	G2069	G2009
U	C2862	G2620	U2739	G2560	U2500	C2440	C2380	A2320	G2260	U2190	U2130	G2070	G2010
U	U2863	A2621	C2740	A2561	C2501	C2441	C2381	A2321	C2261	G2191	A2071	A2071	U2011
U	C2864	C2622	U2741	U2562	G2502	C2442	G2382	A2322	U2262	G2192	U2132	G2072	G2012
U	U2865	G2623	C2742	C2563	A2503	C2443	C2383	A2323	G2263	G2193	G2133	C2073	A2013
U	C2866	G2624	C2743	U2564	U2504	G2444	G2384	C2324	C2264	G2194	A2134	U2074	A2014
U	G2867	U2625	U2744	A2565	G2505	G2445	C2385	C2325	U2265	C2195	A2135	U2075	A2015
U	A2868	G2626	C2745	A2566	U2506	G2446	C2386	C2326	A2266	C2196	C2136	U2076	U2016
U	C2869	G2627	U2746	G2567	C2507	G2447	U2387	A2327	A2267	U2197	C2137	A2077	U2017
U	C2870	C2628	G2747	C2568	G2508	A2448	A2388	A2328	A2268	U2198	C2138	C2078	G2018

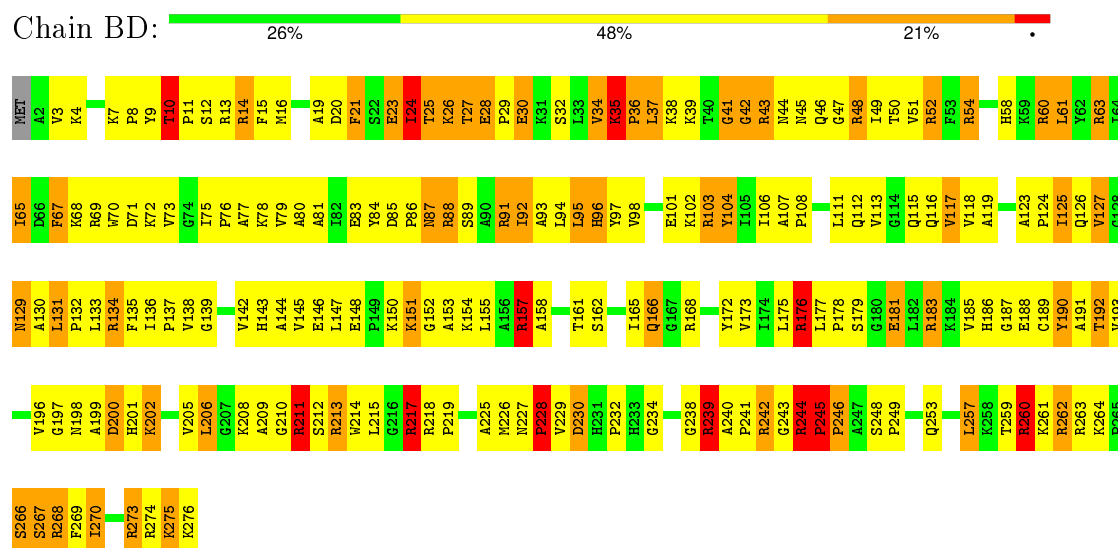
- Molecule 36: 5S RIBOSOMAL RNA



- Molecule 37: 50S RIBOSOMAL PROTEIN L1

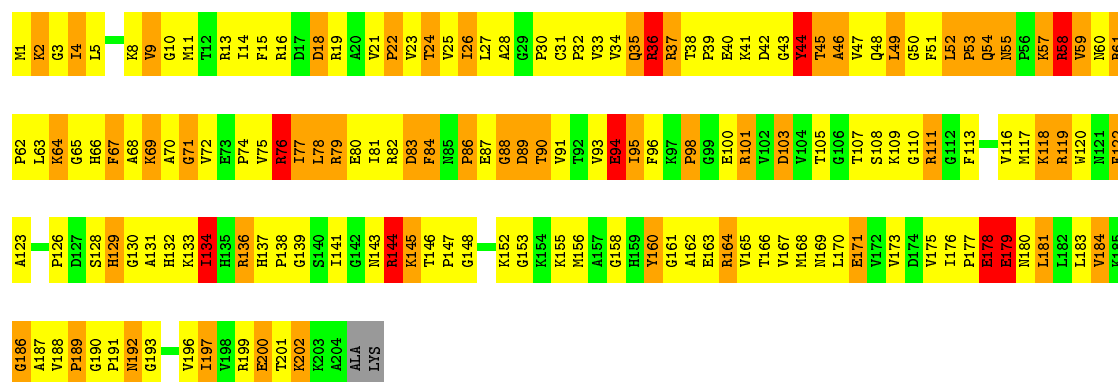


- Molecule 38: 50S RIBOSOMAL PROTEIN L2



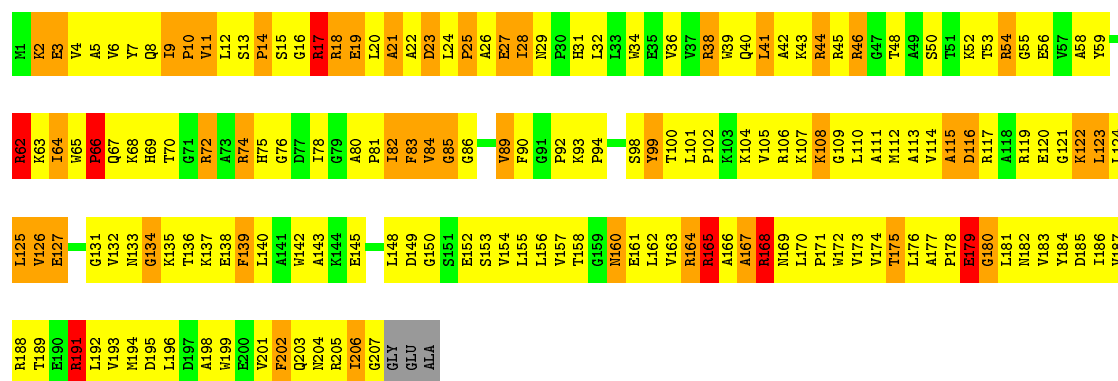
- Molecule 39: 50S RIBOSOMAL PROTEIN L3





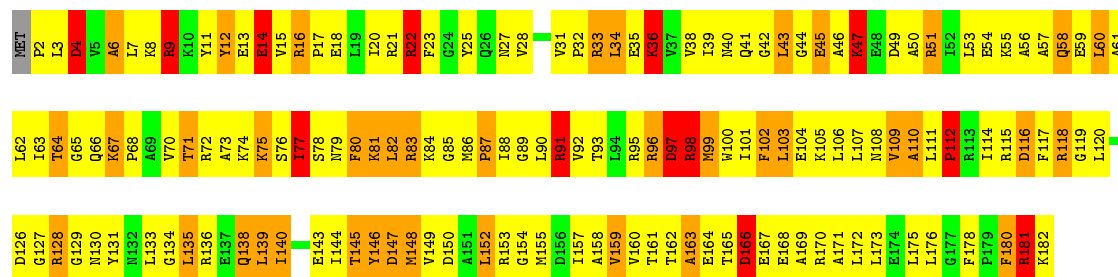
• Molecule 40: 50S RIBOSOMAL PROTEIN L4

Chain BF: 17% 58% 21%



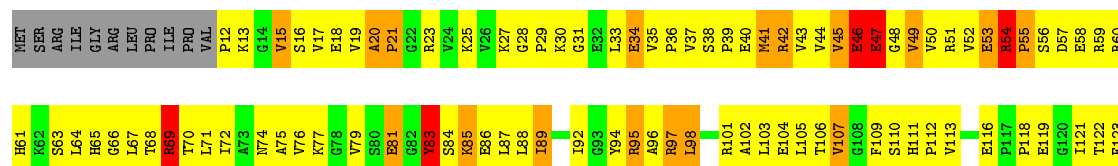
• Molecule 41: 50S RIBOSOMAL PROTEIN L5

Chain BG: 15% 55% 22% 7%



• Molecule 42: 50S RIBOSOMAL PROTEIN L6

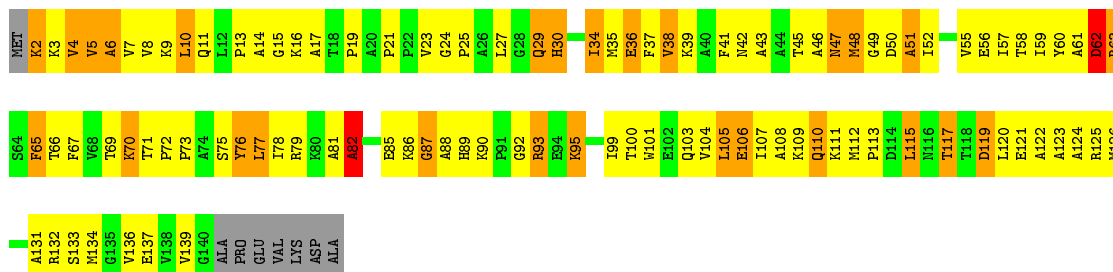
Chain BH: 17% 53% 18% 8%





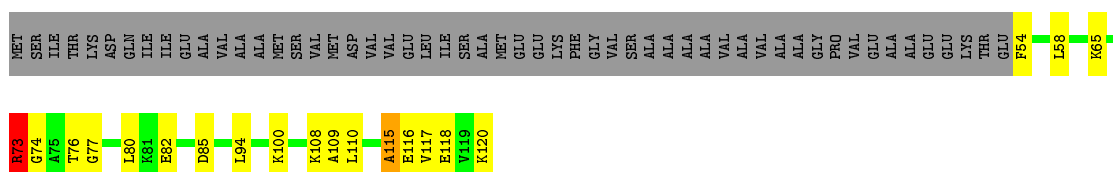
- Molecule 43: 50S RIBOSOMAL PROTEIN L11

Chain BK: 24% 51% 18% 5%



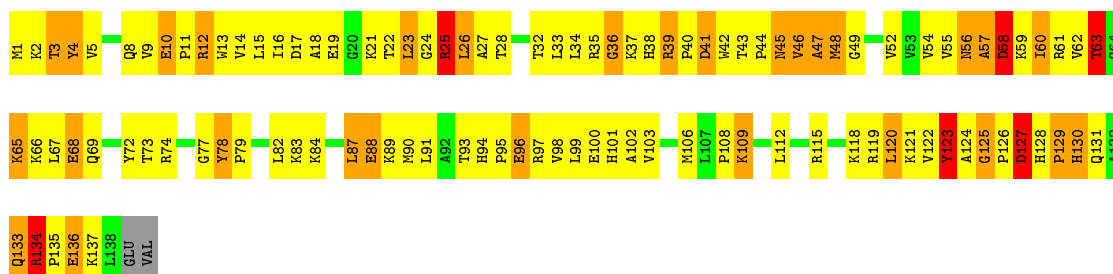
- Molecule 44: 50S RIBOSOMAL PROTEIN L7/L12

Chain BL:  39% 15% .. 45%



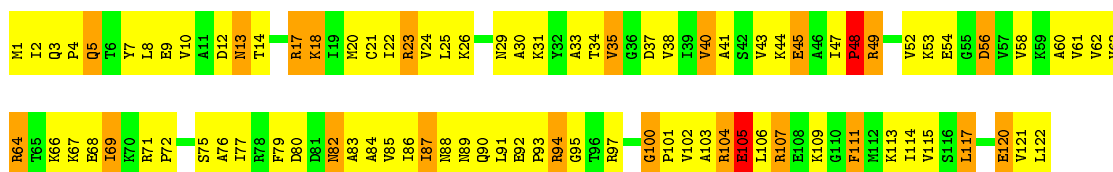
● Molecule 45: 50S RIBOSOMAL PROTEIN L13

Chain BN: 21% 52% 21% .

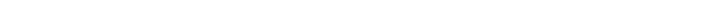


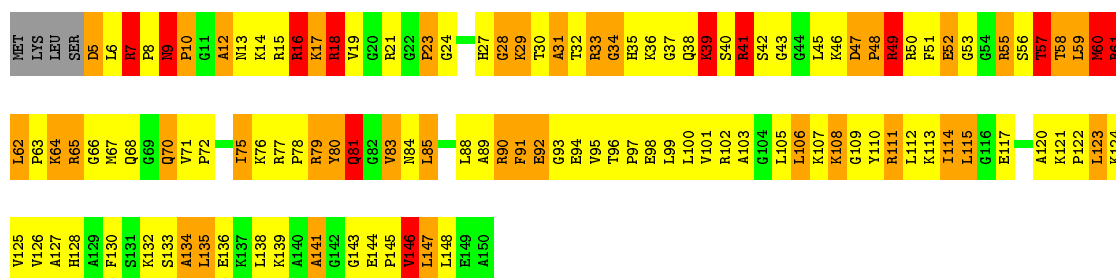
- Molecule 46: 50S RIBOSOMAL PROTEIN L14

Chain BO:  26% 55% 17%

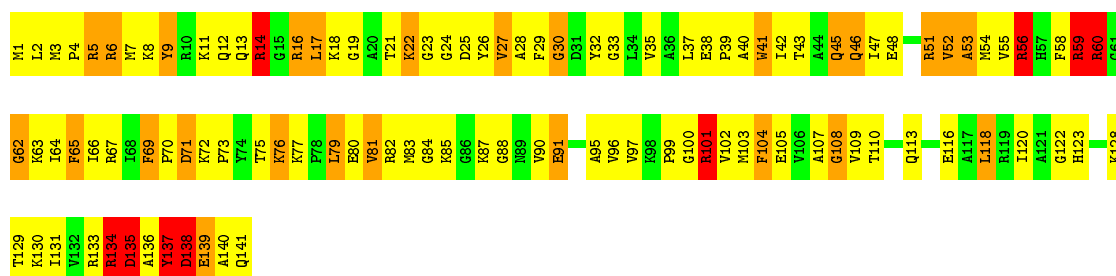


● Molecule 47: 50S RIBOSOMAL PROTEIN L15

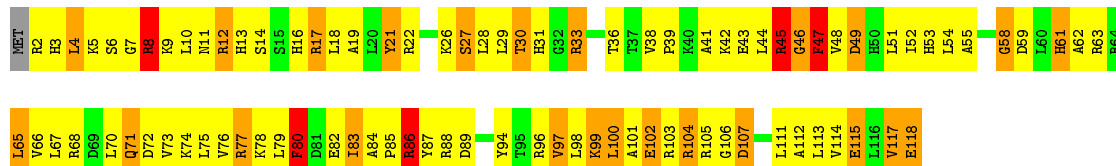
Chain BP: 



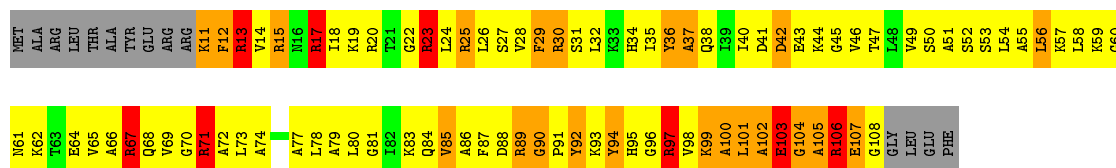
• Molecule 48: 50S RIBOSOMAL PROTEIN L16



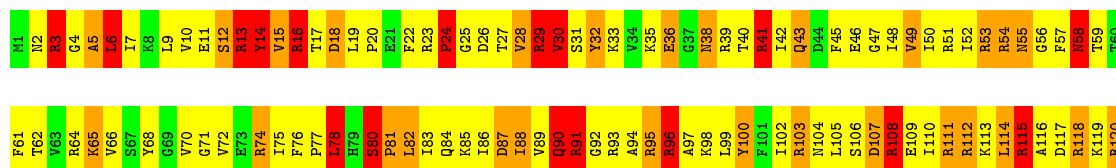
• Molecule 49: 50S RIBOSOMAL PROTEIN L17

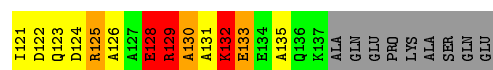


• Molecule 50: 50S RIBOSOMAL PROTEIN L18



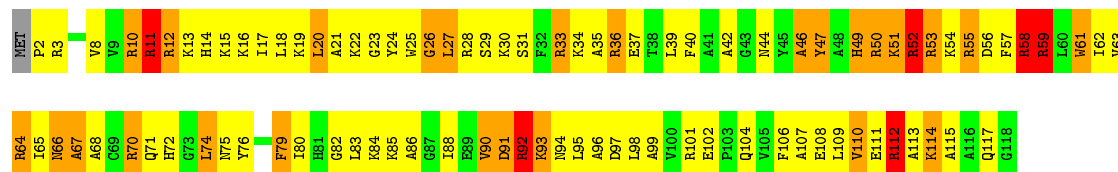
• Molecule 51: 50S RIBOSOMAL PROTEIN L19





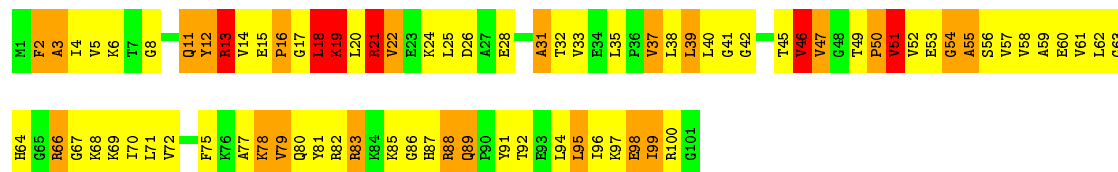
• Molecule 52: 50S RIBOSOMAL PROTEIN L20

Chain BU: 20% 52% 22% 5%



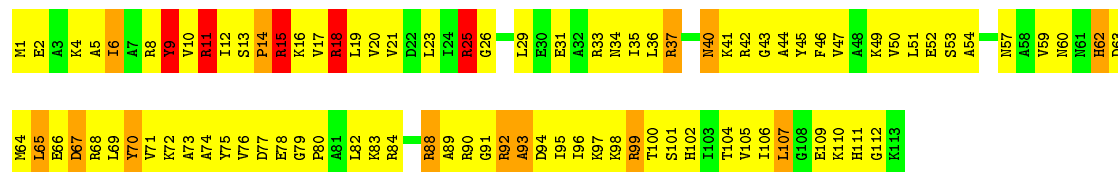
• Molecule 53: 50S RIBOSOMAL PROTEIN L21

Chain BV: 21% 51% 22% 6%



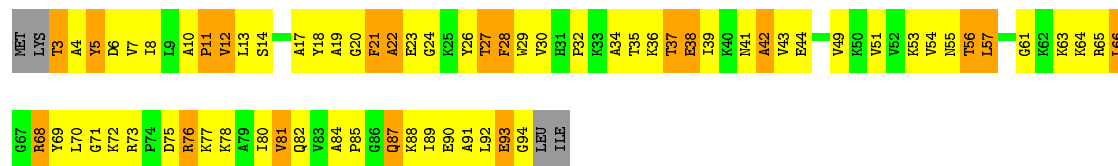
• Molecule 54: 50S RIBOSOMAL PROTEIN L22

Chain BW: 19% 65% 12%



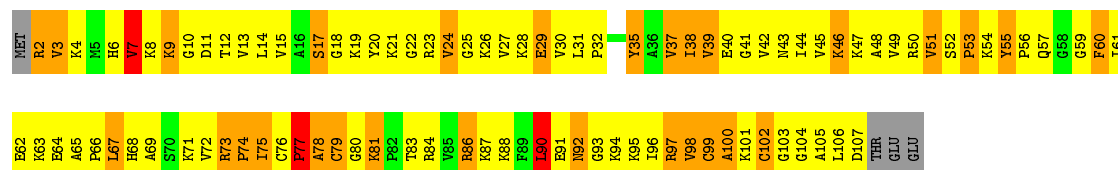
• Molecule 55: 50S RIBOSOMAL PROTEIN L23

Chain BX: 23% 53% 20%

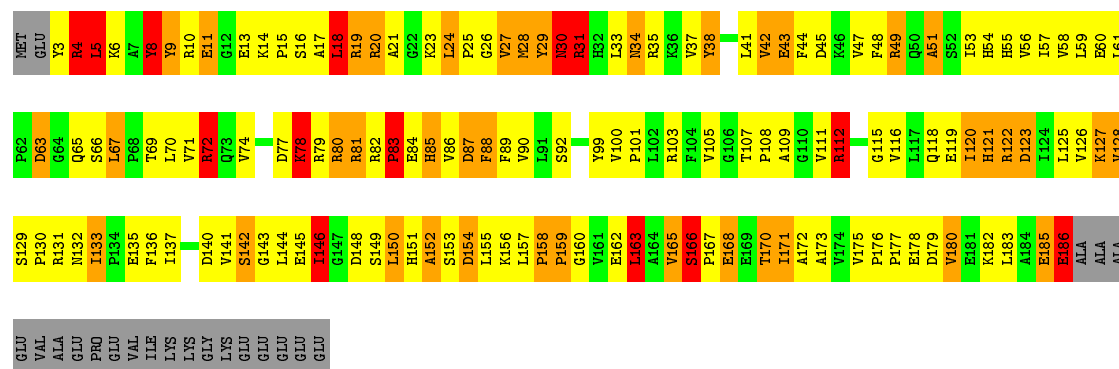


• Molecule 56: 50S RIBOSOMAL PROTEIN L24

Chain BY: 9% 58% 26%



Chain BZ:



4 Experimental information

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	AA	2.73	2519/36190 (7.0%)	2.44	3195/56486 (5.7%)
10	AJ	1.33	0/807	1.53	8/1085 (0.7%)
11	AK	1.40	1/900 (0.1%)	1.50	6/1213 (0.5%)
12	AL	1.42	1/986 (0.1%)	1.58	13/1320 (1.0%)
13	AM	1.33	0/998	1.68	17/1336 (1.3%)
14	AN	1.52	1/501 (0.2%)	1.72	9/664 (1.4%)
15	AO	1.36	1/745 (0.1%)	1.58	9/992 (0.9%)
16	AP	1.47	1/716 (0.1%)	1.59	11/963 (1.1%)
17	AQ	1.43	1/836 (0.1%)	1.57	11/1117 (1.0%)
18	AR	1.41	1/579 (0.2%)	1.56	12/768 (1.6%)
19	AS	1.30	0/642	1.50	6/865 (0.7%)
2	AB	1.36	3/1935 (0.2%)	1.50	19/2609 (0.7%)
20	AT	1.32	0/765	1.53	10/1007 (1.0%)
21	AU	1.50	1/212 (0.5%)	1.82	8/277 (2.9%)
22	AV	2.70	127/1832 (6.9%)	2.42	155/2855 (5.4%)
23	AX	2.50	14/257 (5.4%)	2.35	20/398 (5.0%)
24	AY	1.35	3/5312 (0.1%)	1.53	54/7193 (0.8%)
25	B0	1.32	0/671	1.75	11/892 (1.2%)
26	B1	1.34	1/738 (0.1%)	1.58	9/981 (0.9%)
27	B2	1.32	2/600 (0.3%)	1.60	9/793 (1.1%)
28	B3	1.42	0/472	1.51	5/634 (0.8%)
29	B4	1.28	0/460	1.67	9/621 (1.4%)
3	AC	1.44	1/1636 (0.1%)	1.59	20/2205 (0.9%)
30	B5	1.26	0/473	1.57	6/639 (0.9%)
31	B6	1.29	0/440	1.71	9/586 (1.5%)
32	B7	1.37	0/426	1.76	9/561 (1.6%)
33	B8	1.35	0/515	1.68	7/679 (1.0%)
34	B9	1.36	1/310 (0.3%)	1.54	3/407 (0.7%)
35	BA	2.69	4845/69972 (6.9%)	2.42	5972/109237 (5.5%)
36	BB	2.63	174/2853 (6.1%)	2.36	226/4451 (5.1%)
37	BC	1.32	1/1774 (0.1%)	1.51	18/2391 (0.8%)
38	BD	1.40	5/2195 (0.2%)	1.62	27/2955 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	BE	1.37	3/1596 (0.2%)	1.52	17/2153 (0.8%)
4	AD	1.38	0/1733	1.56	26/2318 (1.1%)
40	BF	1.36	1/1658 (0.1%)	1.64	27/2244 (1.2%)
41	BG	1.34	1/1499 (0.1%)	1.97	24/2016 (1.2%)
42	BH	1.32	4/1292 (0.3%)	1.50	11/1744 (0.6%)
43	BK	1.27	1/1044 (0.1%)	1.39	8/1416 (0.6%)
44	BL	1.08	0/478	1.54	3/640 (0.5%)
45	BN	1.34	2/1131 (0.2%)	1.52	11/1525 (0.7%)
46	BO	1.40	2/943 (0.2%)	1.55	9/1269 (0.7%)
47	BP	1.38	1/1131 (0.1%)	1.64	20/1504 (1.3%)
48	BQ	1.43	3/1143 (0.3%)	1.59	18/1527 (1.2%)
49	BR	1.35	2/974 (0.2%)	1.57	14/1302 (1.1%)
5	AE	1.45	1/1162 (0.1%)	1.44	9/1564 (0.6%)
50	BS	1.36	1/778 (0.1%)	1.71	13/1036 (1.3%)
51	BT	1.32	0/1155	1.77	33/1542 (2.1%)
52	BU	1.35	1/975 (0.1%)	1.59	18/1297 (1.4%)
53	BV	1.27	0/790	1.55	9/1057 (0.9%)
54	BW	1.33	0/907	1.59	11/1216 (0.9%)
55	BX	1.37	0/739	1.39	5/993 (0.5%)
56	BY	1.29	0/823	1.43	4/1098 (0.4%)
57	BZ	1.41	2/1499 (0.1%)	1.54	16/2035 (0.8%)
6	AF	1.39	0/856	1.57	12/1154 (1.0%)
7	AG	1.34	1/1276 (0.1%)	1.51	12/1709 (0.7%)
8	AH	1.41	1/1136 (0.1%)	1.60	15/1527 (1.0%)
9	AI	1.48	4/1029 (0.4%)	2.08	17/1379 (1.2%)
All	All	2.35	7735/165495 (4.7%)	2.21	10265/246445 (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	1	111
10	AJ	0	3
11	AK	0	3
12	AL	0	3
13	AM	0	6
14	AN	0	3
15	AO	0	2
16	AP	0	2
18	AR	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	10
20	AT	0	7
21	AU	0	1
22	AV	0	4
23	AX	0	2
24	AY	0	19
25	B0	0	3
26	B1	0	3
27	B2	0	5
28	B3	0	4
29	B4	0	1
3	AC	0	1
30	B5	0	1
31	B6	0	3
32	B7	0	2
33	B8	0	3
35	BA	2	161
36	BB	0	2
37	BC	0	7
38	BD	0	8
39	BE	0	6
4	AD	0	14
40	BF	0	4
41	BG	0	4
42	BH	0	5
43	BK	0	5
44	BL	0	3
45	BN	0	5
46	BO	0	4
47	BP	0	6
48	BQ	0	4
49	BR	0	3
5	AE	0	3
50	BS	0	3
51	BT	0	10
52	BU	0	4
53	BV	0	3
54	BW	0	5
55	BX	0	1
56	BY	0	2
57	BZ	0	6
6	AF	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	AG	0	11
8	AH	0	8
9	AI	0	9
All	All	3	514

The worst 5 of 7735 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	BA	1696	G	N7-C5	-15.22	1.30	1.39
1	AA	607	A	N7-C5	-14.64	1.30	1.39
35	BA	406	G	N7-C5	-14.28	1.30	1.39
1	AA	1144	G	C8-N7	-14.17	1.22	1.30
1	AA	1129	C	N3-C4	-13.63	1.24	1.33

The worst 5 of 10265 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	BG	112	PRO	O-C-N	-44.90	50.85	122.70
9	AI	53	VAL	O-C-N	-38.46	61.16	122.70
9	AI	104	ARG	O-C-N	-29.23	75.94	122.70
41	BG	112	PRO	CA-C-N	20.32	161.90	117.20
1	AA	1463	C	C6-N1-C2	18.92	127.87	120.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	575	G	C3'
35	BA	1799	G	C3'
35	BA	1992	G	C3'

5 of 514 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	108	G	Sidechain
1	AA	21	G	Sidechain
1	AA	37	U	Sidechain
1	AA	39	G	Sidechain
1	AA	5	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	32329	0	16035	1572	0
2	AB	1900	0	1951	268	0
3	AC	1612	0	1677	202	0
4	AD	1703	0	1767	195	0
5	AE	1146	0	1207	147	0
6	AF	843	0	857	95	0
7	AG	1257	0	1296	109	0
8	AH	1116	0	1177	98	0
9	AI	1010	0	1037	148	0
10	AJ	794	0	840	178	0
11	AK	885	0	904	79	0
12	AL	970	0	1057	149	0
13	AM	987	0	1059	140	0
14	AN	492	0	533	56	0
15	AO	734	0	771	71	0
16	AP	700	0	720	91	0
17	AQ	823	0	891	71	0
18	AR	574	0	644	92	0
19	AS	629	0	652	142	0
20	AT	763	0	861	124	0
21	AU	208	0	221	15	0
22	AV	1640	0	820	94	0
23	AX	230	0	119	17	0
24	AY	5214	0	5288	759	0
25	B0	662	0	688	86	0
26	B1	731	0	808	132	0
27	B2	598	0	653	123	0
28	B3	467	0	523	75	0
29	B4	450	0	449	101	0
30	B5	459	0	480	97	0
31	B6	433	0	461	177	0
32	B7	418	0	467	45	0
33	B8	507	0	576	112	0
34	B9	307	0	338	41	0
35	BA	62474	0	31032	3261	0
36	BB	2551	0	1278	167	0
37	BC	1742	0	1798	183	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	BD	2145	0	2234	311	0
39	BE	1563	0	1629	273	0
40	BF	1623	0	1677	288	0
41	BG	1474	0	1535	278	0
42	BH	1268	0	1337	209	0
43	BK	1025	0	1066	184	0
44	BL	477	0	509	17	0
45	BN	1104	0	1180	154	0
46	BO	933	0	996	116	0
47	BP	1114	0	1187	270	0
48	BQ	1122	0	1179	151	0
49	BR	960	0	1021	157	0
50	BS	770	0	832	177	0
51	BT	1141	0	1202	266	0
52	BU	958	0	1015	166	0
53	BV	779	0	852	142	0
54	BW	896	0	953	123	0
55	BX	725	0	778	97	0
56	BY	810	0	901	174	0
57	BZ	1467	0	1492	249	0
58	AY	37	0	46	17	0
59	AY	28	0	12	6	0
All	All	152777	0	105568	12278	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 48.

The worst 5 of 12278 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)
24:AY:252:ASP:CB	24:AY:254:LYS:HE3	1.55	1.36
37:BC:118:PRO:HA	37:BC:121:MET:CG	1.60	1.31
53:BV:18:LEU:HD22	53:BV:19:LYS:N	1.45	1.30
1:AA:1158:C:C5'	2:AB:133:LYS:HE2	1.62	1.28
53:BV:18:LEU:CD2	53:BV:19:LYS:H	1.50	1.25

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%)	149 (64%)	49 (21%)	34 (15%)	0	6
3	AC	204/239 (85%)	129 (63%)	56 (28%)	19 (9%)	1	16
4	AD	206/209 (99%)	138 (67%)	49 (24%)	19 (9%)	1	17
5	AE	148/162 (91%)	113 (76%)	25 (17%)	10 (7%)	1	23
6	AF	99/101 (98%)	77 (78%)	18 (18%)	4 (4%)	4	35
7	AG	153/156 (98%)	108 (71%)	35 (23%)	10 (6%)	1	25
8	AH	136/138 (99%)	110 (81%)	23 (17%)	3 (2%)	8	49
9	AI	125/128 (98%)	85 (68%)	24 (19%)	16 (13%)	0	8
10	AJ	96/105 (91%)	60 (62%)	23 (24%)	13 (14%)	0	7
11	AK	117/129 (91%)	91 (78%)	21 (18%)	5 (4%)	3	34
12	AL	122/132 (92%)	82 (67%)	23 (19%)	17 (14%)	0	6
13	AM	122/126 (97%)	73 (60%)	26 (21%)	23 (19%)	0	3
14	AN	58/61 (95%)	49 (84%)	5 (9%)	4 (7%)	1	23
15	AO	86/89 (97%)	55 (64%)	24 (28%)	7 (8%)	1	19
16	AP	81/88 (92%)	56 (69%)	19 (24%)	6 (7%)	1	21
17	AQ	97/105 (92%)	78 (80%)	15 (16%)	4 (4%)	3	35
18	AR	68/88 (77%)	49 (72%)	15 (22%)	4 (6%)	2	27
19	AS	76/93 (82%)	37 (49%)	21 (28%)	18 (24%)	0	2
20	AT	97/106 (92%)	49 (50%)	31 (32%)	17 (18%)	0	4
21	AU	22/27 (82%)	13 (59%)	8 (36%)	1 (4%)	3	33
24	AY	662/691 (96%)	440 (66%)	137 (21%)	85 (13%)	0	8
25	B0	82/85 (96%)	66 (80%)	13 (16%)	3 (4%)	4	38
26	B1	91/98 (93%)	65 (71%)	16 (18%)	10 (11%)	0	11
27	B2	69/72 (96%)	32 (46%)	24 (35%)	13 (19%)	0	3
28	B3	57/60 (95%)	41 (72%)	11 (19%)	5 (9%)	1	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	B4	55/71 (78%)	28 (51%)	12 (22%)	15 (27%)	0	0
30	B5	57/60 (95%)	36 (63%)	11 (19%)	10 (18%)	0	4
31	B6	48/54 (89%)	23 (48%)	11 (23%)	14 (29%)	0	0
32	B7	46/49 (94%)	38 (83%)	5 (11%)	3 (6%)	1	25
33	B8	61/65 (94%)	34 (56%)	16 (26%)	11 (18%)	0	4
34	B9	35/37 (95%)	21 (60%)	9 (26%)	5 (14%)	0	6
37	BC	226/229 (99%)	161 (71%)	55 (24%)	10 (4%)	3	33
38	BD	273/276 (99%)	192 (70%)	47 (17%)	34 (12%)	0	8
39	BE	202/206 (98%)	120 (59%)	49 (24%)	33 (16%)	0	5
40	BF	205/210 (98%)	141 (69%)	37 (18%)	27 (13%)	0	7
41	BG	179/182 (98%)	113 (63%)	41 (23%)	25 (14%)	0	6
42	BH	164/180 (91%)	85 (52%)	43 (26%)	36 (22%)	0	2
43	BK	137/147 (93%)	87 (64%)	41 (30%)	9 (7%)	1	24
44	BL	65/121 (54%)	57 (88%)	8 (12%)	0	100	100
45	BN	136/140 (97%)	90 (66%)	28 (21%)	18 (13%)	0	7
46	BO	120/122 (98%)	95 (79%)	16 (13%)	9 (8%)	1	21
47	BP	144/150 (96%)	78 (54%)	40 (28%)	26 (18%)	0	4
48	BQ	139/141 (99%)	103 (74%)	23 (16%)	13 (9%)	1	16
49	BR	115/118 (98%)	80 (70%)	20 (17%)	15 (13%)	0	7
50	BS	96/112 (86%)	46 (48%)	30 (31%)	20 (21%)	0	3
51	BT	135/146 (92%)	76 (56%)	32 (24%)	27 (20%)	0	3
52	BU	115/118 (98%)	75 (65%)	27 (24%)	13 (11%)	0	10
53	BV	99/101 (98%)	71 (72%)	11 (11%)	17 (17%)	0	4
54	BW	111/113 (98%)	78 (70%)	22 (20%)	11 (10%)	1	14
55	BX	90/96 (94%)	58 (64%)	24 (27%)	8 (9%)	1	17
56	BY	104/110 (94%)	50 (48%)	30 (29%)	24 (23%)	0	2
57	BZ	182/206 (88%)	113 (62%)	41 (22%)	28 (15%)	0	5
All	All	6645/7104 (94%)	4394 (66%)	1440 (22%)	811 (12%)	1	8

5 of 811 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	20	GLU

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Mol	Chain	Res	Type
2	AB	195	ASP
2	AB	233	SER
2	AB	239	VAL
3	AC	12	LEU

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%)	177 (88%)	25 (12%)	6	30
3	AC	160/188 (85%)	134 (84%)	26 (16%)	3	20
4	AD	180/181 (99%)	162 (90%)	18 (10%)	9	38
5	AE	115/123 (94%)	100 (87%)	15 (13%)	5	28
6	AF	90/90 (100%)	81 (90%)	9 (10%)	9	38
7	AG	126/127 (99%)	116 (92%)	10 (8%)	15	51
8	AH	119/119 (100%)	105 (88%)	14 (12%)	6	32
9	AI	98/99 (99%)	88 (90%)	10 (10%)	9	37
10	AJ	88/92 (96%)	73 (83%)	15 (17%)	2	18
11	AK	90/99 (91%)	85 (94%)	5 (6%)	26	62
12	AL	104/109 (95%)	90 (86%)	14 (14%)	5	27
13	AM	99/101 (98%)	87 (88%)	12 (12%)	6	31
14	AN	49/50 (98%)	45 (92%)	4 (8%)	14	49
15	AO	79/80 (99%)	69 (87%)	10 (13%)	5	29
16	AP	72/74 (97%)	67 (93%)	5 (7%)	19	56
17	AQ	94/97 (97%)	82 (87%)	12 (13%)	5	29
18	AR	61/77 (79%)	58 (95%)	3 (5%)	31	67
19	AS	69/80 (86%)	57 (83%)	12 (17%)	2	17
20	AT	76/82 (93%)	67 (88%)	9 (12%)	6	32
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%)	478 (85%)	85 (15%)	3	23
25	B0	66/67 (98%)	58 (88%)	8 (12%)	6	31
26	B1	78/83 (94%)	61 (78%)	17 (22%)	1	9
27	B2	66/67 (98%)	58 (88%)	8 (12%)	6	31
28	B3	51/52 (98%)	44 (86%)	7 (14%)	4	27
29	B4	51/63 (81%)	34 (67%)	17 (33%)	0	2
30	B5	51/52 (98%)	45 (88%)	6 (12%)	6	32
31	B6	49/52 (94%)	35 (71%)	14 (29%)	0	3
32	B7	41/42 (98%)	36 (88%)	5 (12%)	6	31
33	B8	53/55 (96%)	45 (85%)	8 (15%)	3	23
34	B9	34/34 (100%)	29 (85%)	5 (15%)	4	24
37	BC	180/181 (99%)	166 (92%)	14 (8%)	16	51
38	BD	217/218 (100%)	179 (82%)	38 (18%)	2	16
39	BE	165/166 (99%)	135 (82%)	30 (18%)	2	15
40	BF	165/166 (99%)	151 (92%)	14 (8%)	13	48
41	BG	155/156 (99%)	121 (78%)	34 (22%)	1	9
42	BH	136/148 (92%)	124 (91%)	12 (9%)	12	45
43	BK	104/111 (94%)	88 (85%)	16 (15%)	3	22
44	BL	46/85 (54%)	43 (94%)	3 (6%)	21	58
45	BN	117/119 (98%)	98 (84%)	19 (16%)	3	20
46	BO	100/100 (100%)	90 (90%)	10 (10%)	9	38
47	BP	112/116 (97%)	89 (80%)	23 (20%)	1	10
48	BQ	111/111 (100%)	94 (85%)	17 (15%)	3	22
49	BR	100/101 (99%)	85 (85%)	15 (15%)	3	23
50	BS	77/88 (88%)	67 (87%)	10 (13%)	5	28
51	BT	120/127 (94%)	97 (81%)	23 (19%)	2	13
52	BU	92/94 (98%)	84 (91%)	8 (9%)	13	45
53	BV	82/82 (100%)	71 (87%)	11 (13%)	5	27
54	BW	91/92 (99%)	82 (90%)	9 (10%)	10	39
55	BX	74/78 (95%)	62 (84%)	12 (16%)	3	20
56	BY	87/91 (96%)	75 (86%)	12 (14%)	4	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	BZ	162/179 (90%)	133 (82%)	29 (18%)	2	15
All	All	5586/5868 (95%)	4819 (86%)	767 (14%)	9	27

5 of 767 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	B3	8	LEU
38	BD	61	LEU
54	BW	52	GLU
29	B4	10	VAL
31	B6	42	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 173 such sidechains are listed below:

Mol	Chain	Res	Type
25	B0	70	GLN
33	B8	43	GLN
53	BV	11	GLN
26	B1	56	GLN
30	B5	23	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1503/1522 (98%)	277 (18%)	43 (2%)
22	AV	76/77 (98%)	16 (21%)	0
23	AX	10/11 (90%)	4 (40%)	0
35	BA	2900/2915 (99%)	637 (21%)	77 (2%)
36	BB	118/122 (96%)	25 (21%)	0
All	All	4607/4647 (99%)	959 (20%)	120 (2%)

5 of 959 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	7	G
1	AA	9	G
1	AA	31	G
1	AA	32	A
1	AA	33	A

5 of 120 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BA	363(F)	A
35	BA	1052	C
35	BA	2690	C
35	BA	474	G
35	BA	728	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](#)

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	2.17	12 (32%)	51,64,64	1.95	15 (29%)
59	GDP	AY	702	-	24,30,30	1.92	8 (33%)	26,47,47	2.07	4 (15%)

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 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	AY	701	FUA	C23-C22	-6.74	1.39	1.51
58	AY	701	FUA	C14-C8	-4.51	1.50	1.58
58	AY	701	FUA	C23-C24	-4.34	1.38	1.53
58	AY	701	FUA	C24-C25	-3.32	1.38	1.50
59	AY	702	GDP	PA-O2A	-3.29	1.41	1.55

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AY	702	GDP	C4'-O4'-C1'	-6.61	102.64	109.64
59	AY	702	GDP	N3-C2-N1	-5.26	120.40	127.56
58	AY	701	FUA	C13-C12-C11	-4.46	106.07	111.98
59	AY	702	GDP	C5-C6-N1	-3.49	118.97	123.52
58	AY	701	FUA	C18-C4-C3	-3.36	107.46	111.42

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	AY	701	FUA	17	0
59	AY	702	GDP	6	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.