



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Sep 21, 2017 – 10:38 AM EDT

PDB ID : 5IMR
EMDB ID: : EMD-6585
Title : Structure of ribosome bound to cofactor at 5.7 angstrom resolution
Authors : Kumar, V.; Ero, R.; Jian, G.K.; Ahmed, T.; Zhan, Y.; Bhushan, S.; Gao, Y.G.
Deposited on : unknown
Resolution : 5.70 Å(reported)
Based on PDB ID : 4W2E, 5AA0

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.

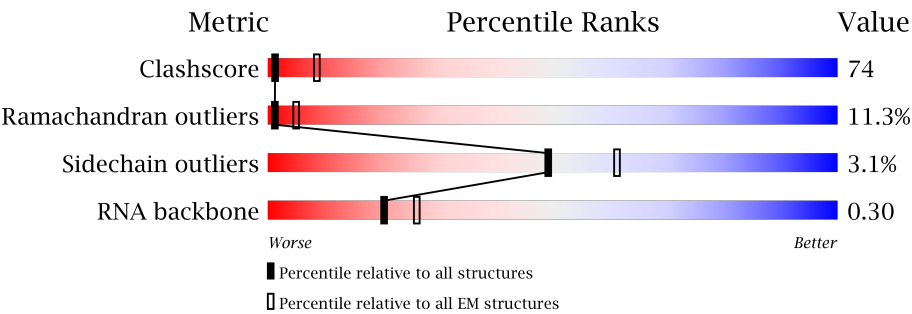
MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

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 5.70 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.




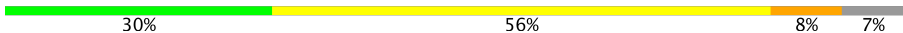
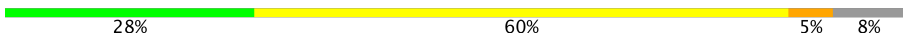

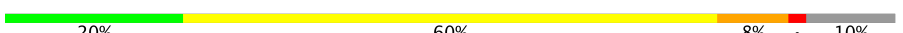
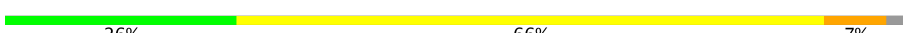
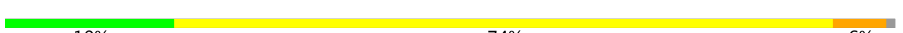




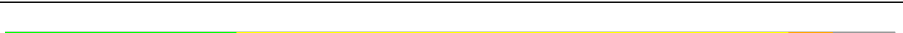













Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	A	1522	<div><div>55%41%</div><div></div></div>
2	F	256	<div><div>27%60%5%9%</div><div></div></div>
3	G	239	<div><div>24%59%14%</div><div></div></div>
4	H	209	<div><div>27%67%6%</div><div></div></div>
5	I	162	<div><div>22%68%7%</div><div></div></div>
6	J	101	<div><div>26%72%</div><div></div></div>
7	K	156	<div><div>33%65%</div><div></div></div>
8	L	138	<div><div>21%72%7%</div><div></div></div>











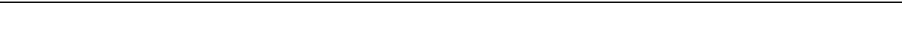

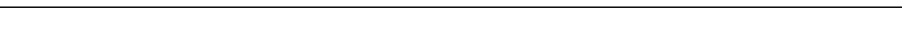
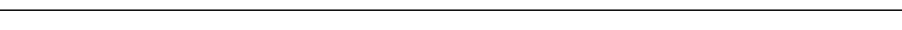
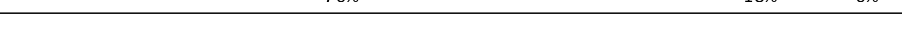








Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	M	128	
10	N	105	
11	O	129	
12	P	132	
13	Q	126	
14	R	61	
15	S	89	
16	T	88	
17	U	105	
18	V	88	
19	W	93	
20	X	106	
21	Y	27	
22	C	610	
23	D	2893	
24	E	123	
25	Z	229	
26	a	276	
27	b	206	
28	c	210	
29	d	182	
30	e	180	
31	f	140	
32	g	122	
33	h	150	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	i	141	 86% 10% . .
35	j	118	 92% 8% .
36	k	112	 89% 9% .
37	l	146	 70% 10% . 20%
38	m	118	 91% 8% .
39	n	101	 81% 18% .
40	o	113	 90% 6% . .
41	p	96	 91% 7% .
42	q	110	 78% 22%
43	r	206	 79% 8% 13%
44	s	85	 87% 6% 7%
45	t	67	 93% 7%
46	u	60	 92% 7% .
47	v	71	 76% 18% 6%
48	w	60	 82% 13% 5%
49	x	54	 69% 22% 9%
50	y	49	 86% 14%
51	z	65	 83% 14% . .
52	1	37	 30% 65% 5%
53	2	173	 50% 23% . 25%
54	3	147	 18% 48% 22% . 9%
55	4	77	 14% 51% 34% .
56	5	76	 5% 49% 45% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	GCP	C	701	-	-	X	-

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 152879 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1515	Total	C	N	O	P	0	0
			32554	14490	6022	10527	1515		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	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	G	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	H	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	I	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	J	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	K	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	L	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	M	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	N	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	O	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	P	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	Q	114	Total	C	N	O	S	0	0
			914	565	189	158	2		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	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	S	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	T	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	U	104	Total	C	N	O	S	0	0
			857	547	161	147	2		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	V	73	Total	C	N	O	0	0
			597	380	118	99		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	80	Total	C	N	O	S	0	0
			647	414	119	112	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	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	Y	24	Total	C	N	O	0	0
			208	128	50	30		

- Molecule 22 is a protein called Elongation factor 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	C	570	Total	C	N	O	S	0	0
			4461	2858	768	826	9		

- Molecule 23 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	D	2889	Total	C	N	O	P	0	0
			62218	27691	11629	20009	2889		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	E	123	Total	C	N	O	P	0	0
			2641	1175	488	855	123		

- Molecule 25 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	228	Total	C	N	O	S	0	0
			1742	1102	318	319	3		

- Molecule 26 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	272	Total	C	N	O	S	0	0
			2124	1339	424	358	3		

- Molecule 27 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	206	Total	C	N	O	S	0	0
			1578	997	302	273	6		

- Molecule 28 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	208	Total	C	N	O	S	0	0
			1625	1034	303	286	2		

- Molecule 29 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	182	Total	C	N	O	S	0	0
			1482	947	269	261	5		

- Molecule 30 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	174	Total	C	N	O	S	0	0
			1328	844	248	235	1		

- Molecule 31 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	139	Total	C	N	O	S	0	0
			1113	717	207	186	3		

- Molecule 32 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	122	Total	C	N	O	S	0	0
			932	587	171	170	4		

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	145	Total	C	N	O	S	0	0
			1106	688	226	190	2		

- Molecule 34 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	136	Total	C	N	O	S	0	0
			1080	688	204	183	5		

- Molecule 35 is a protein called 50S ribosomal protein L17.

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

- Molecule 36 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	k	110	Total	C	N	O	0	0
			877	553	175	149		

- Molecule 37 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	117	Total	C	N	O	S	0	0
			976	614	197	164	1		

- Molecule 38 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	117	Total	C	N	O	S	0	0
			964	610	202	151	1		

- Molecule 39 is a protein called 50S ribosomal protein L21.

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

- Molecule 40 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	110	Total	C	N	O	S	0	0
			876	552	171	151	2		

- Molecule 41 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	p	94	Total	C	N	O	0	0
			742	483	133	126		

- Molecule 42 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	110	Total	C	N	O	S	0	0
			844	539	158	141	6		

- Molecule 43 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	180	Total	C	N	O	S	0	0
			1435	916	256	260	3		

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	79	Total	C	N	O	S	0	0
			625	387	131	106	1		

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	67	Total	C	N	O	S	0	0
			567	350	116	99	2		

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	u	59	Total	C	N	O	0	0
			469	298	90	81		

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	v	71	Total	C	N	O	S	0	0
			581	364	108	104	5		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	w	57	Total	C	N	O	S	0	0
			445	279	87	74	5		

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	x	49	Total	C	N	O	S	0	0
			426	265	87	70	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	49	Total	C	N	O	S	0	0
			430	263	108	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	z	64	Total	C	N	O	S	0	0
			515	331	102	79	3		

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	1	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 53 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	130	Total	C	N	O		0	0
			641	381	130	130			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	3	134	Total	C	N	O	S	0	0
			993	632	175	181	5		

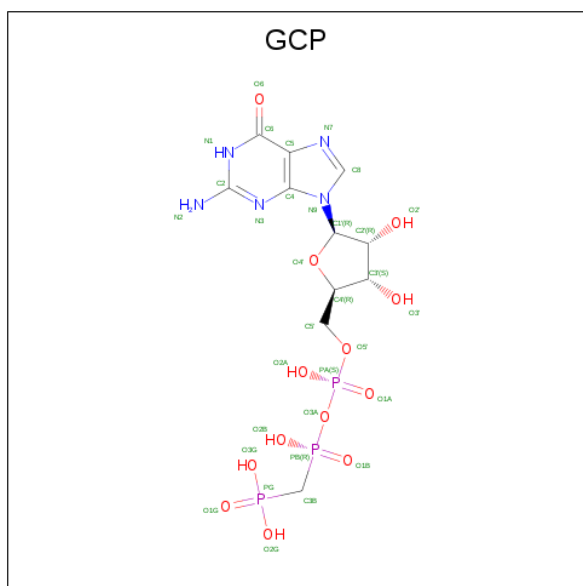
- Molecule 55 is a RNA chain called P site- tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	4	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 56 is a RNA chain called E site- tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	5	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 57 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: $\text{C}_{11}\text{H}_{18}\text{N}_5\text{O}_{13}\text{P}_3$).

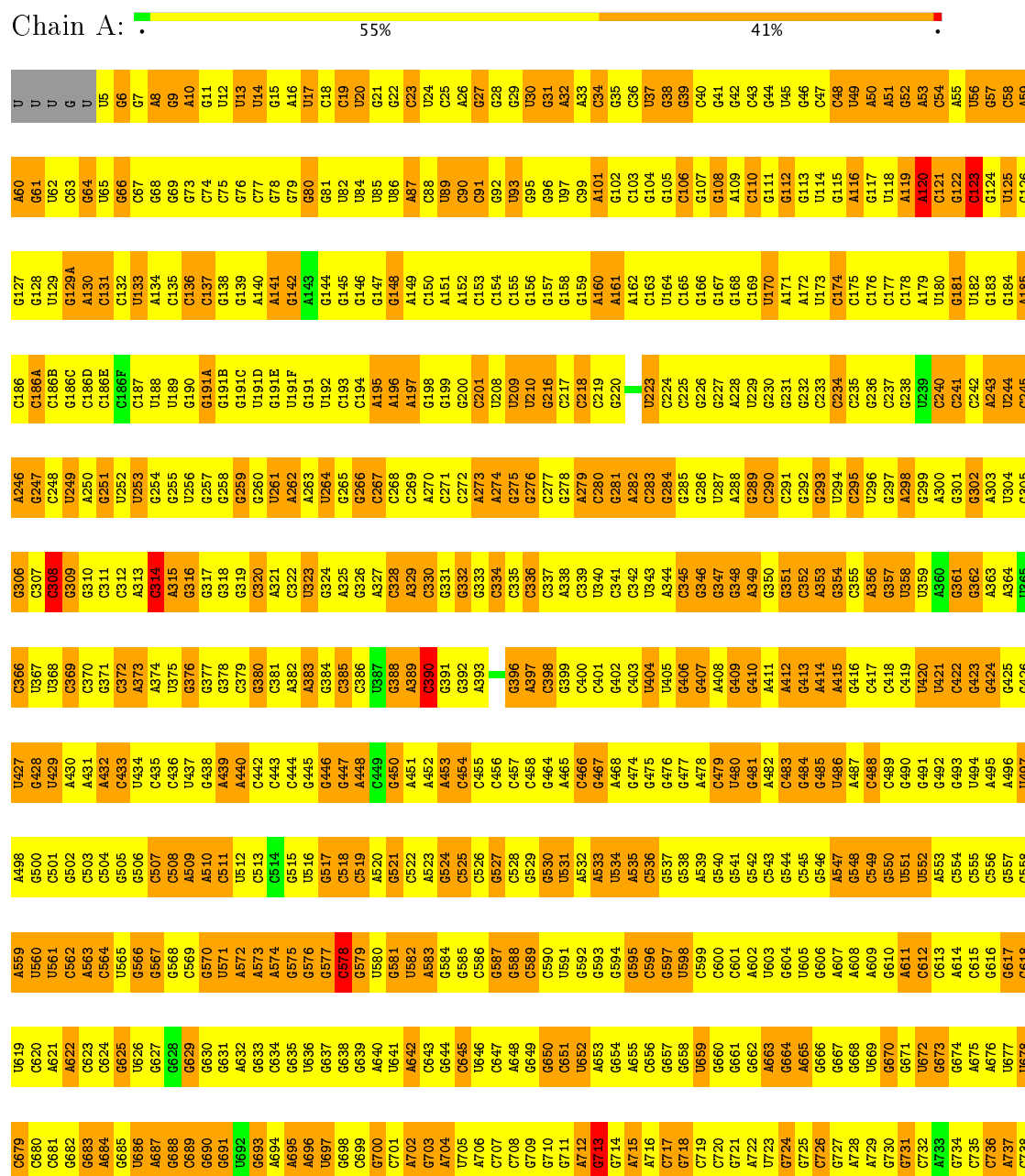


Mol	Chain	Residues	Atoms					AltConf
57	C	1	Total	C	N	O	P	0
			32	11	5	13	3	

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 ribosomal RNA

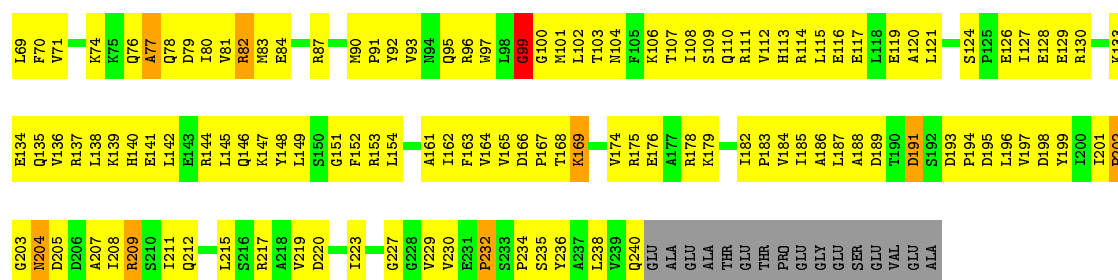


C1527	C1466	G1401	C1342	C1282	G1222	C1161	A1101	A1041	C985	G925	A865	G799	C739
U1528	A1467	C1402	C1343	C1283	C1223	C1162	A1102	C1042	A986	G926	C866	G800	U740
G1529	A1468	C1403	C1344	C1284	G1224	C1163	C1103	C1043	G987	G927	C867	U801	G741
G1530	G1469	U1345	A1285	A1285	A1225	G1164	G1404	A1044	G988	G928	C868	A802	G742
A1531	A1470	A1346	A1286	A1286	C1226	C1165	A1105	C1045	G989	G929	C869	G803	U743
U1532	U1406	G1347	A1287	A1227	G1166	G1166	G1106	A1046	C990	C930	U870	U804	C744
A1473	A1407	U1348	A1288	A1228	A1167	A1167	C1107	G1047	U991	C931	U871	C805	C745
A1474	A1408	A1349	A1289	A1229	A1168	A1168	A1108	G1048	U992	C932	A872	C806	A746
U1540	A1409	A1350	G1290	G1290	A1170	A1170	C1109	U1049	G993	G933	A873	A807	C747
G1475	G1476	U1351	G1291	G1231	A1171	A1171	A1110	G1050	A994	C934	G874	C808	G748
C1411	C1352	U1292	U1292	U1232	C1172	C1172	C1101	G1051	C995	A935	C875	G809	C749
C1412	G1353	G1293	G1293	G1233	G1173	C1112	C1112	U1052		C936	G876	C810	G750
A1413	A1354	G1294	C1234	C1234	G1174	C1113	C1113	G1053	G998	A937	C877	C811	U751
C1479	A1413	C1355	G1295	U1235	G1175	C1114	C1054	C1054	C998A	A938	C878	C812	G752
G1480	G1480	G1356	A1296	A1236	A1176	C1115	A1055	C879	U999	G939	C879	U813	A753
U1481	C1415	G1357	C1297	C1237	G1177	G1177	A1056	C880	A1000	C940	C880	A814	C754
G1416	G1417	U1358	C1298	A1238	G1178	G1178	G1107	G1057	G1001	G941	C881	A815	G755
C1417	C1359	A1299	A1239	A1239	A1179	C1118	C1118	G1058	G1002	G942	C882	A816	C756
U1418	A1360	G1300	U1240	A1240	A1180	C1119	C1119	C1059	G1003	U943	C883	C817	G757
C1420	C1361	U1301	G1241	A1241	G1181	G1120	A1004	C1060	U884	G944	U884	G818	U758
G1421	C1362	U1302	C1242	A1242	G1182	U1121	G1061	C1061	A1005	G945	C885	A819	A759
G1422	C1362A	C1303	C1243	C1243	A1183	U1122	U1062	C1062	G1006	A946	G886	U820	G760
A1423	A1363	G1304	C1244	A1244	G1184	A1123	C1063	C1063	C1007	G947	C887	G821	G761
C1424	U1364	G1305	A1245	A1245	G1185	G1124	C1064	C1064	C1008	G948	C888	C822	C762
U1425	G1365	A1306	C1246	A1246	G1186	U1125	U1065	C1065	G1009	A949	A889	G823	G763
C1426	C1366	U1307	U1247	A1247	G1187	U1126	C1066	C1066	G1010	U950	C890	C824	G764
U1427	C1367	U1308	A1248	A1248	A1188	G1127	A1067	C1067	G1011	G951	C891	G825	G765
A1428	G1368	G1309	A1249	A1249	G1189	C1128	G1068	C1068	U1012	U952	A892	C826	A766
C1429	C1369	G1310	A1250	A1250	G1190	C1129	C1069	C1069	G1013	G953	C893	U827	A767
C1430	G1370	G1311	A1251	A1251	A1191	A1130	U1070	C1070	A1014	G954	C894	A828	A768
C1431	G1371	A1312	A1252	A1252	C1192	C1131	C1071	C1071	A1015	U955	C895	G829	G769
G1432	G1372	U1313	G1253	G1253	C1193	C1132	G1072	C1072	A1016	U956	C896	G830	C770
A1433	G1373	C1314	C1254	C1254	U1194	G1133	U1073	G1073	G1017	U957	C897	U831	G771
A1500	A1434	A1374	G1255	G1255	U1195	G1134	G1074	C1074	G1018	A958	C898	C832	U772
G1435	A1435	A1375	A1256	A1256	U1196	U1135	C1075	C1075	C1019	A959	C899	U833	G773
A1502	U1436	U1376	C1337	U1257	G1197	U1136	C1076	C1076	U1020	U960	A900	C834	G774
A1503	C1437	A1377	A1318	G1258	G1198	C1137	G1077	C1077	G1021	U961	A901	U835	G775
G1504	A1438	C1378	A1319	A1259	U1199	G1138	U1078	C1078	G1022	C962	G902	C836	G776
G1505	C1439	G1379	C1320	C1260	G1200	G1139	G1079	G1079	G1023	G963	G903	C837	A777
U1506	C1440	U1380	A1261	A1261	A1201	C1140	A1080	C1079	G1024	A964	C904	C838	G778
A1507	G1441	U1381	C1322	C1262	G1202	C1141	G1081	C1081	U1025	A965	U905	U841	C779
U1508	C1442	C1382	G1323	C1263	C1203	G1142	G1082	C1082	G1026	G966	G906	C842	A780
C1509	G1443	C1383	A1324	C1264	A1204	C1143	U1083	C1083	C1027	C967	A907	U843	A781
U1510	A1446	C1384	C1325	G1265	U1205	G1144	A1084	C1084	C1028	A968	A908	C848	A782
G1447	G1448	G1385	A1326	G1266	G1206	C1145	U1085	C1085	C1028A	A969	A909	C849	C783
U1512	C1448	G1386	C1327	G1267	G1207	A1146	U1086	C1086	C1028B	C970	C910	U850	C784
A1513	C1449	G1387	C1328	A1268	C1208	C1147	G1087	C1087	G1029	C971	U911	C851	G785
C1514	U1450	C1388	A1329	A1269	C1209	U1148	G1088	C1088	C1030	C972	C912	G852	G786
U1515	A1451	C1389	U1330	C1270	C1210	C1149	G1089	C1089	G1031	G973	A913	G853	A787
G1516	C1452	U1390	A1331	G1271	U1211	U1090	U1090	A1090	A1032	A974	A914	C854	U788
C1517	G1453	C1391	A1332	G1272	U1212	A1151	U1091	C1091	G1032A	A975	A915	C855	U789
A1518	G1454	G1392	A1333	G1273	C1213	A1152	A1092	C1092	G1032B	G976	G916	C856	A790
A1519	G1455	U1393	G1334	G1274	C1214	C1153	A1093	C1093	G1033	A977	C857	G791	
G1520	C1459	A1394	C1335	A1275	G1215	G1154	G1094	C1094	G1034	A978	A918	C858	A792
U1521	G1460	C1395	G1336	G1276	G1216	G1155	U1095	C1095	A1035	C979	A919	A859	U793
U1522	C1461	A1396	G1337	C1277	C1217	G1156	U1096	C1096	G1036	C980	U920	A860	A794
G1523	C1462	C1397	G1338	A1278	A1157	C1097	C1097	C1097	C1037	U981	U921	C861	C795
A1463	C1463	A1398	A1339	A1279	C1218	C1158	C1098	C1098	G1038	U982	G922	C862	C796
G1525	C1464	C1399	U1280	A1280	U1219	C1159	G1099	C1099	C1039	A983	A923	C797	
C1526	G1465	C1400	U1281	U1281	G1220	C1160	C1100	C1100	U1040	C984	U924	A864	C798

- Molecule 2: 30S ribosomal protein S2

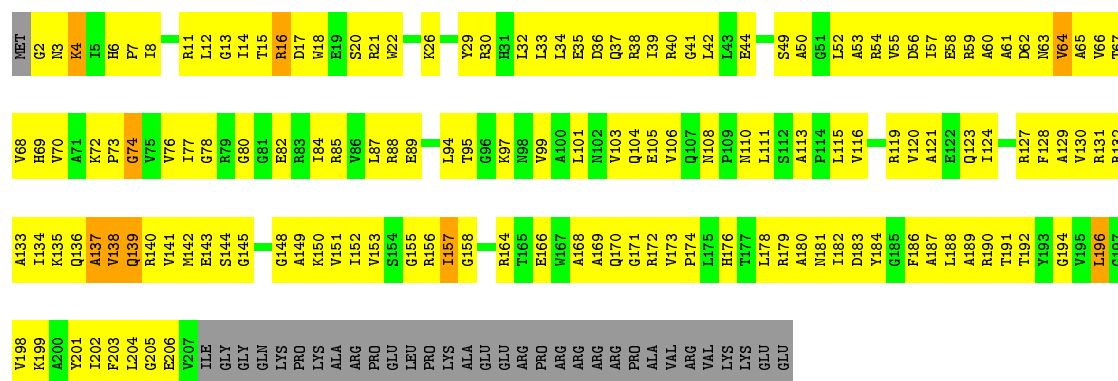
Chain F: 27% 60% 5% 9%

MET	PRO	VAL	GLU	ILE	THR	V7	K8	K8	L10	L11	V15	H16	F17	G18	H19	R20	R21	R22	R23	R24	F28	A29	I32	I32	Y33	A34	E35	R36	N37	G38	I39	H40	I41	I42	D43	L44	Q45	K46	T47	M48	E49	E50	F50	T54	F55	R56	F57	I58	E59	D60	L61	R64	T65
-----	-----	-----	-----	-----	-----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



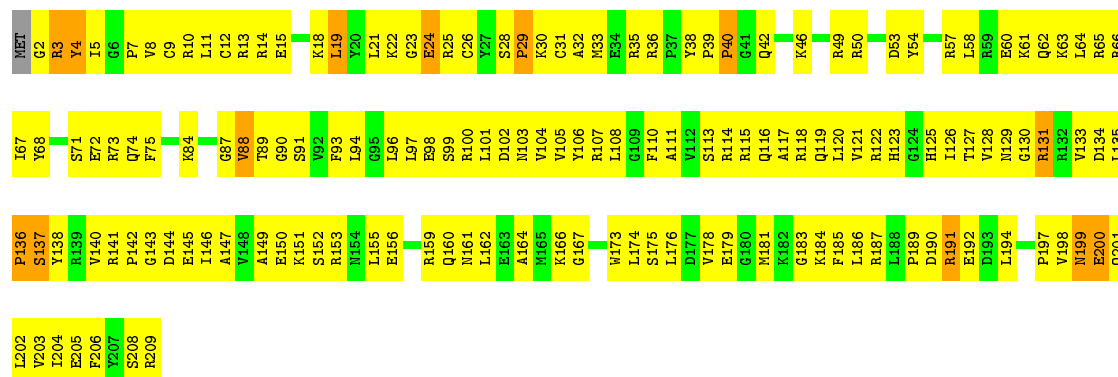
• Molecule 3: 30S ribosomal protein S3

Chain G: 24% 59% 14%



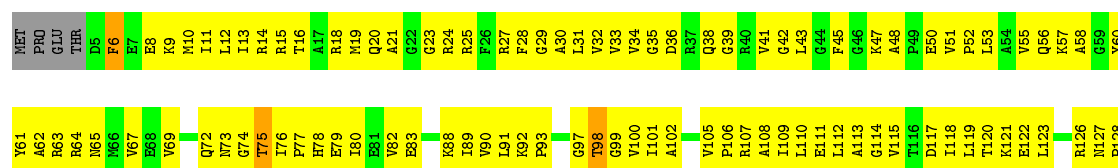
• Molecule 4: 30S ribosomal protein S4

Chain H: 27% 67% 6%



• Molecule 5: 30S ribosomal protein S5

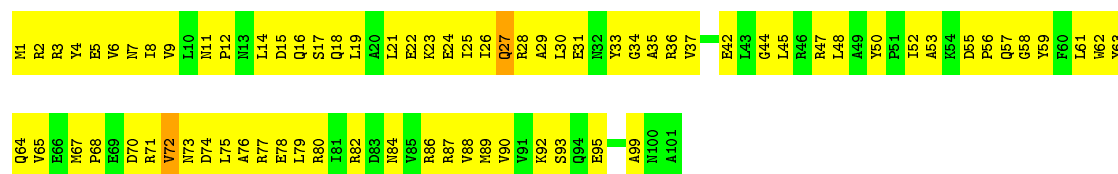
Chain I: 22% 68% 7%





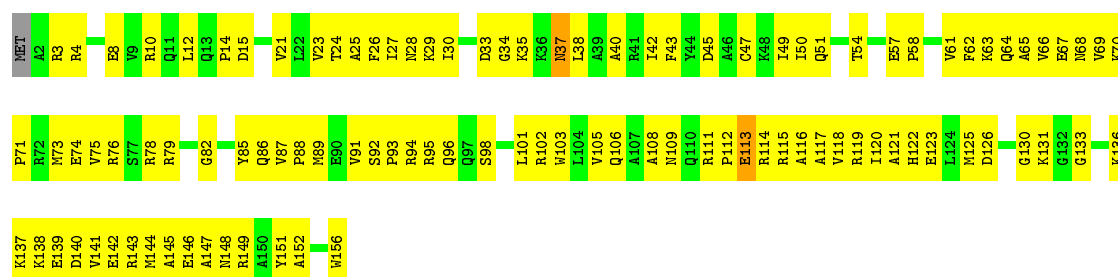
• Molecule 6: 30S ribosomal protein S6

Chain J: 26% 72%



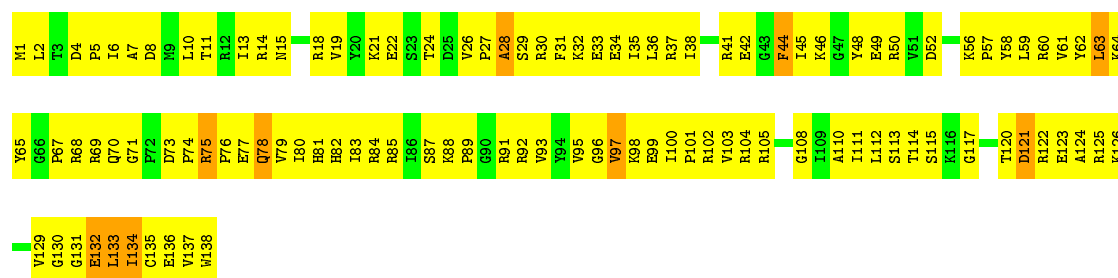
• Molecule 7: 30S ribosomal protein S7

Chain K: 33% 65%



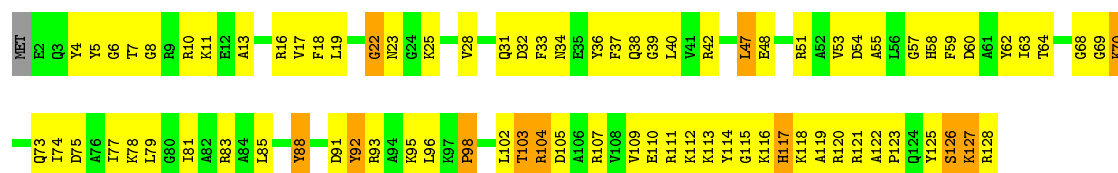
• Molecule 8: 30S ribosomal protein S8

Chain L: 21% 72%



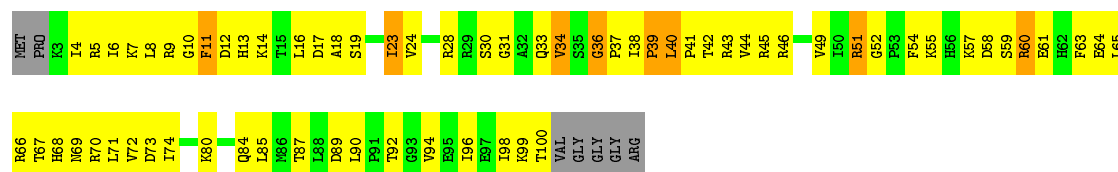
• Molecule 9: 30S ribosomal protein S9

Chain M: 35% 55%



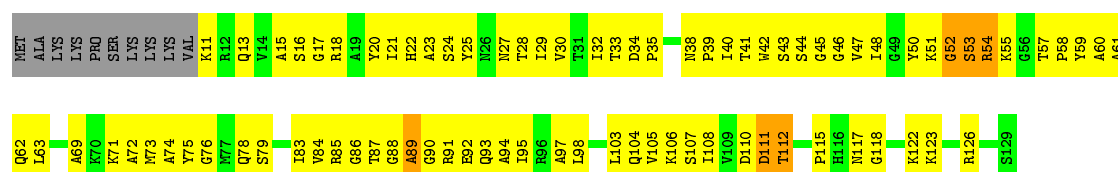
• Molecule 10: 30S ribosomal protein S10

Chain N: 

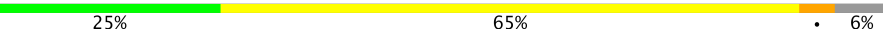


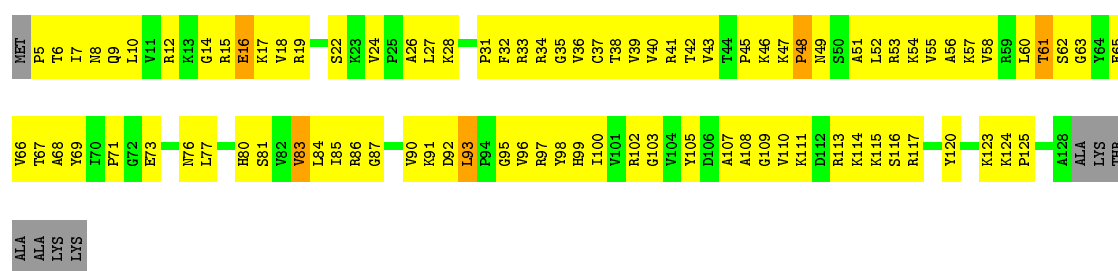
• Molecule 11: 30S ribosomal protein S11

Chain O: 



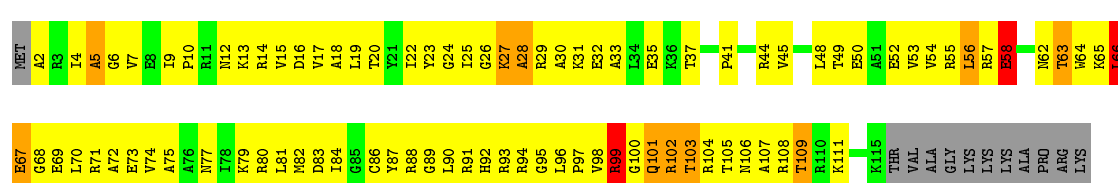
• Molecule 12: 30S ribosomal protein S12

Chain P: 



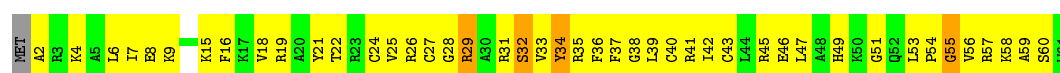
• Molecule 13: 30S ribosomal protein S13

Chain Q: 



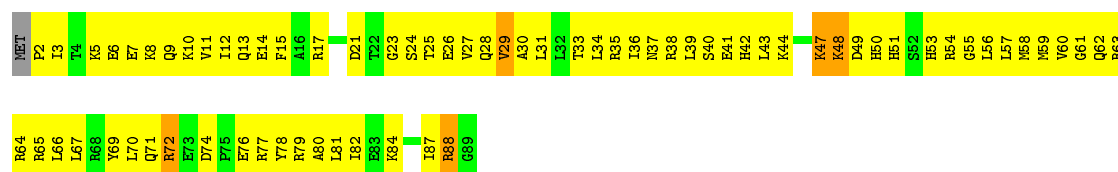
• Molecule 14: 30S ribosomal protein S14 type Z

Chain R: 



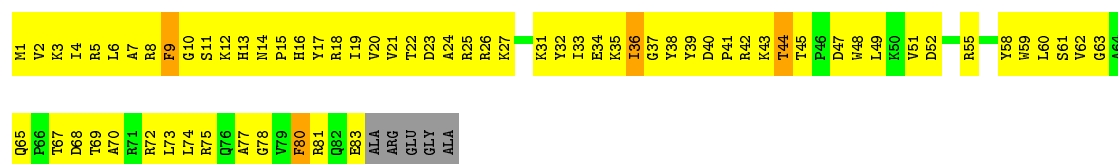
• Molecule 15: 30S ribosomal protein S15

Chain S: 



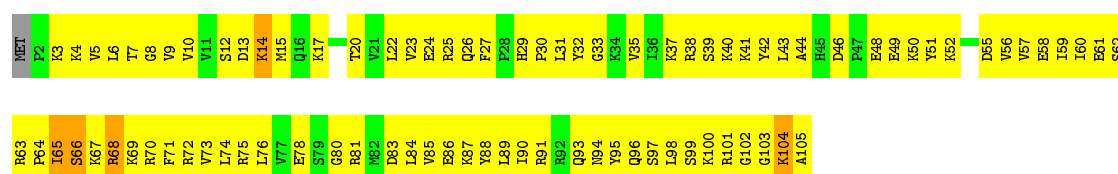
• Molecule 16: 30S ribosomal protein S16

Chain T: 17% 73% 5% 6%



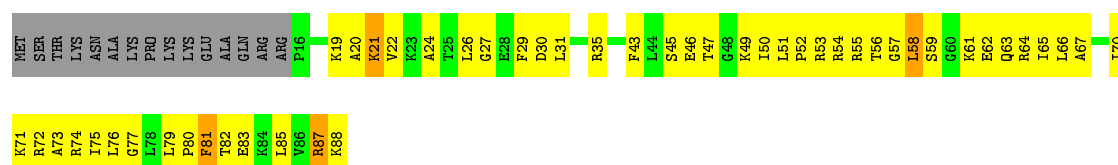
• Molecule 17: 30S ribosomal protein S17

Chain U: 16% 78% 5%



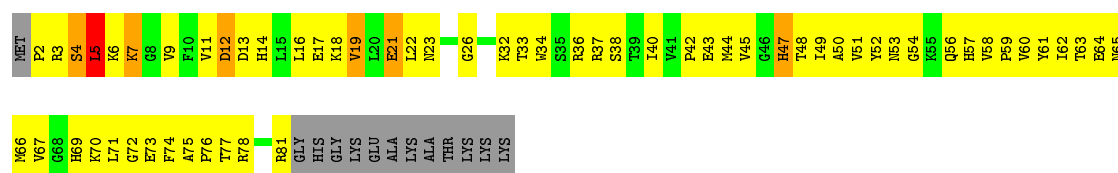
• Molecule 18: 30S ribosomal protein S18

Chain V: 27% 51% 5% 17%



• Molecule 19: 30S ribosomal protein S19

Chain W: 20% 58% 6% 14%



• Molecule 20: 30S ribosomal protein S20

Chain X: 26% 62% 5% 7%

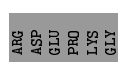
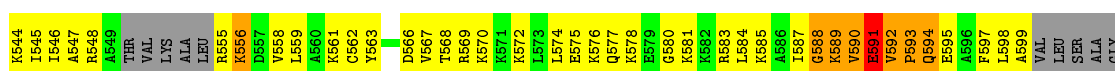
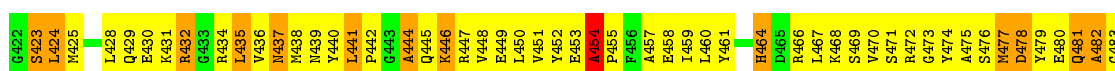
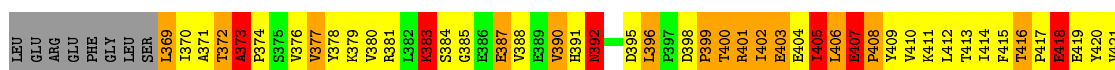
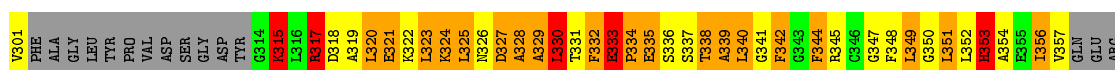
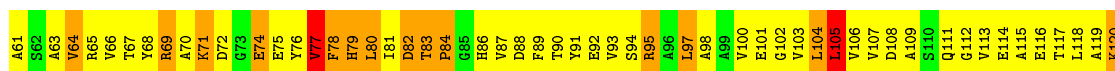




- Molecule 21: 30S ribosomal protein Thx



- Molecule 22: Elongation factor 4



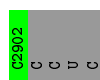
- Molecule 23: 23S ribosomal RNA



G939	U877	C817	U757	C697	A837	G579	C517	C456	U395	G338	A278	C253	U193	G124	U63	G1
G940	A878	G818	G758	C698	G638	C580	C518	A457	G396	U339	C279	G254	G194	G125	A64	
G941	G879	A819	G759	A699	U639	C581	U519	G458	G397	A340	C280	A255	A195	A126	C65	C4
G942	G880	A820	G760	G700	C640	G582	G520	U459	G398	G341	G281	A256	A196	A127	C66	A5
U943	G881	A821	A761	G701	C641	G583	G521	A460	G399	G342	A282	A257	A197	C128	U67	A6
G944	G882	U822	A762	G702	G642	C584	G522	C461	G400	C343	A283	G258	A198	C129	G68	G7
A945	G883	G823	G763	U703	A643	G585	C523	C462	A401	G344	U284	G259	A199	C130	C69	A8
G946	C884	A824	A764	A644	A586	U524	U524	C285	A402	A345	G286	G260	U200	G131	G70	U9
G947	C885	C825	G765	A705	C645	C587	U525	U464	U403	A346	C286	G261	C201	G132	A71	G10
G948	C886	U826	G766	A706	U588	U588	A526	G465	U404	A347	C287	A262	U202	G133	U72	G11
G949	A887	U827	A767	G707	G647	C589	C527	A466	U405	G348	C288	C263	C203	C134	A73	U12
G950	C888	U828	G768	G708	G648	A590	A528	G467	G406	G349	A289	C264	A204	G135	A74	U13
G951	C889	A829	G769	U709	G649	C591	C529	G468	G407	U350	G290	A265	G205	G136	G75	A14
G952	A890	G819	G770	G710	C650	G592	C530	G469	A408	G351	C291	G266	U206	C137	C76	G15
A953	G892	G831	G771	G711	C651	A593	C531	A470	C409	G352	C292	C267	A207	G137A	C77	G16
G954	C893	G832	G772	G712	C652	U594	A532	A471	G410	G353	U293	C268	C208	G138	A78	G17
C955	C894	U833	G773	G713	G653	C595	G533	A472	G411	G354	U294	U269	C209	G139	G79	C18
G956	U895	C834	A774	U714	A654	G596	U534	G473	A412	G355	G295	A270	C210	A140	G80	C19
A957	A896	A835	G775	G715	A655	U597	C535	G474	C413	G356	C296	A270A	A211	A141	G81	C20
U958	C897	G836	G776	A716	G598	G598	C536	U475	A415	U357	C297	A270B	G212	C141A	G82	A21
A959	A898	G837	A777	G717	U657	G599	C537	G476	A416	U358	G298	C270C	A213	G142	G83	C22
A960	A899	C838	G778	A718	C658	G600	A539	A477	A359	A359	A299	C270D	G214	C143	A84	G23
C961	A900	U839	U779	G719	C659	C601	G540	A478	C417	G360	A300	G270E	G215	C144	G85	G24
G962	A901	C840	G780	C720	G660	G602	C541	A479	G418	G361	G301	U270F	A216	G145	C86	U25
G963	C902	A841	A781	C721	C661	A603	C542	A480	C419	U362	C302	C270G	G217	G146	C87	G26
C964	C903	G842	A782	G722	G662	G604	C543	A481	C420	G363	U303	C270H	A218	U147	G88	G27
C965	C904	G843	A783	G723	C663	C605	C544	A482	U421	A363A	G304	G270I	G219	C148	G89	A28
G966	U905	C844	A784	U724	C664	U606	C545	A483	A422	G363B	U305	G270J	G220	A149	U90	U29
G967	G906	G845	G785	G725	C665	U607	C546	A484	A423	C363C	U306	C270K	A221	C150	A91	G30
G968	U907	C846	G786	G726	G666	A608	A547	C485	G424	G363D	G307	U270L	A222	C151	G92	C31
U969	C908	U847	U787	U667	A609	A609	C548	C486	G425	U363E	G308	U270M	A223	G152	G93	C32
C970	A909	A848	A788	G728	G668	G609A	A549	G487	C426	A363F	G309	G270N	G224	C153	C94	U33
A910	A849	A789	G729	G669	C610	G550	C550	G488	U427	C364	A310	U270O	A225	G154	G95	C34
G971	C911	C850	C790	G730	A670	C611	G551	G489	A428	C365	A311	C270P	G226	C155	G96	G35
A973	C912	U851	G791	C731	C671	G612	G552	G491	A429	C366	G312	C270Q	A227	U161	C97	G36
U913	U913	G852	G792	C732	C672	U613	U553	A492	G430	G370	C313	G270R	A228	U162	G98	C37
C974A	C914	G853	A793	G733	C673	U614	U554	G493	U431	A371	A314	G270S	A229	U163	U99	A38
G975	C915	G854	G794	A674	G674	G615	G556	G494	A432	G372	G320	G270T	G230	U164	G101	C39
C976	C916	G855	C795	A735	A675	A616	U557	G495	C433	U373	C316	C270U	C231	G171	G102	C40
G977	A917	C856	G796	G736	A676	G558	G558	G496	U434	A374	G317	G270V	G232	G172	A103	C41
G978	A918	C857	G797	C737	A677	G618	G559	A497	C435	C318	C318	G270W	A233	G173	U104	G43
G979	G919	U858	G798	G738	C678	C618A	C560	G498	C436	C376	G319	G270X	C234	G174	C105	A44
A980	G920	G859	G799	G739	C679	G619	G561	U499	G438	C377	A320	G270Y	U235	G175	C106	G45
A981	G921	U860	A800	U740	G680	G620	U562	G500	G439	C378	G321	U270Z	C236	G176	C107	C46
C982	U922	A861	G801	G741	G681	A621	G563	A442	G440	G379	A322	C271A	C237	G177	U108	C47
A983	C923	G862	A802	G742	G682	G622	C564	A502	U441	U380	G323	G271B	C238	G178	G109	G48
C924	C924	A863	U803	G743	C683	G623	C565	A503	G442	G381	A324	U271C	U239	G179	G110	A49
G985	C925	G864	A804	G744	G684	C624	U566	U504	A443	G382	G325	G271	G240	A111	A111	U50
C986	A926	C865	G805	G745	A685	G625	A567	A505	C444	U383	G326	G272	A241	G180	G180	G51
G987	G928	A866	C806	U746	G686	U626	U568	G506	C445	U384	A327	G273A	G242	A182	G113	A52
A988	G929	C867	U807	U747	C687	A627	U569	A507	G446	C385	U328	G273B	U243	C183	U114	A53
G989	U930	U868	G808	G748	U688	G628	G570	G508	U447	G386	G329	A244	G245	G184	C115	G54
A990	G931	C869	A809	G749	A689	G629	A571	C509	A448	U387	A330	C273C	G246	U185	C116	G55
C991	C932	A870	U810	A750	G890	G630	A572	C510	A449	G388	A331	C273D	C246	G186	G117	A56
G992	A933	U871	U811	A751	C691	A631	C573	G512	G450	G389	A332	U273E	G247	G187	A118	C57
C993	G934	A872	C812	A752	C692	A632	C574	G512	C451	A390	G333	C273F	G248	G188	A119	G58
C994	C935	G873	U813	C763	A633	A575	A575	G453	A391	G391	C334	G274	C249	G189	U120	U59
G995	C936	C874	C814	C764	U694	C634	U576	A514	C453	C392	G275	G275	G250	A190	G121	G60
A996	U937	G875	C815	C765	G695	C635	G577	A515	A454	C393	C336	A276	A251	G122	G61	G61
C998	C938	C876	C816	C766	G696	C636	A578	A516	C455	A394	C337	C277	C252	C122	C62	C62

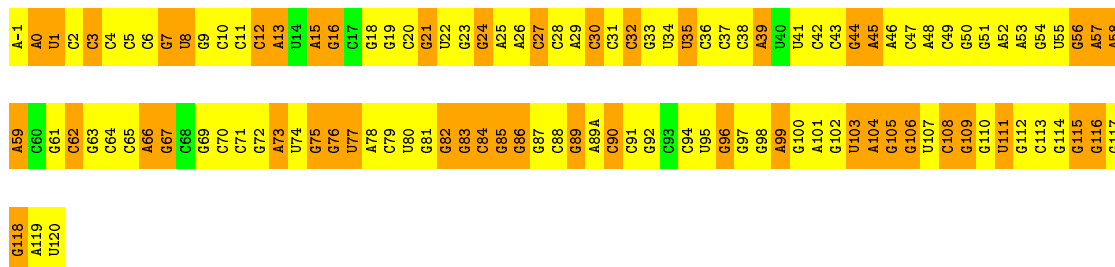
G1855	G1795	G1728	G1658	C1599	G1539	A1477	G1418	G1358	C1298	G1238	C1178	C1118	G1058	C998
G1856	G1796	A1729	G1659	C1600	G1540	G1478	A1419	A1359	G1299	G1239	C1179	C1119	G1059	U999
G1857	G1797	U1730	G1660	G1601	U1541	G1479	U1420	A1360	A1360	U1240	C1180	C1120	U1060	A1000
G1858	G1798	G1731	G1661	U1602	G1542	G1480	G1421	G1361	A1301	A1241	C1181	C1121	U1061	A1001
A1859	G1799	A1732	C1662	G1603	A1543	U1482	G1422	C1362	G1302	A1242	A1182	G1122	G1062	G1002
G1860	C1800	G1733	C1663	C1604	C1544	G1483	G1423	C1363	G1303	G1243	G1183	C1123	G1063	G1003
G1861	G1801	C1734	A1664	C1605	A1545	G1484	G1424	G1364	C1304	G1244	G1184	C1124	C1064	C1004
G1862	A1802	C1735	A1665	G1606	A1545A	G1485	G1425	G1365	C1305	G1245	C1185	G1125	U1065	C1005
G1863	C1803	C1741	G1666	C1607	C1546	A1486	G1426	A1366	C1306	A1246	G1186	A1126	G1066	C1006
G1864	C1804	G1742	G1667	A1608	C1548	G1487	A1427	G1367	A1307	A1247	G1187	A1127	A1067	C1007
G1865	U1805	G1743	A1668	A1609	C1548	G1488	C1428	G1368	A1308	G1248	G1188	A1128	G1068	C1008
G1866	C1806	G1746	A1669	A1610	C1549	U1489	G1429	G1369	G1309	U1249	A1189	A1129	A1069	A1009
A1870	G1807	G1747	C1670	C1611	C1550	A1490	C1430	C1370	G1310	G1250	G1190	U1130	A1070	A1010
A1871	U1808	G1748	U1671	C1612	C1551	G1491	U1431	G1371	G1311	C1251	G1191	G1131	G1071	G1011
A1872	A1809	C1749	C1672	G1613	G1552	G1492	C1432	U1372	U1312	G1252	G1192	A1132	C1072	U1012
G1878	A1810	G1750	U1673	A1614	G1553	C1493	U1433	A1373	U1313	A1253	G1193	A1133	C1073	C1013
G1879	C1810	G1751	G1674	A1615	G1554	A1494	A1434	G1374	C1314	A1254	A1194	G1134	G1074	U1014
G1880	G1811	C1752	C1675	A1616	G1555	A1495	G1435	C1375	C1315	U1255	G1195	C1135	C1075	G1015
G1881	A1812	G1753	A1676	C1617	C1556	A1496	G1436	G1376	U1316	G1256	C1196	G1136	G1076	G1016
G1882	G1813	G1754	A1677	A1618	C1557	U1497	C1437	G1377	A1317	C1257	G1197	G1137	A1077	G1017
G1883	A1814	C1755	G1678	G1619	G1558	C1498	U1438	A1378	C1318	G1258	G1198	G1138	U1078	C1018
A1884	C1815	A1756	A1679	G1620	G1559	A1499	A1439	A1379	G1319	G1259	U1199	G1139	C1079	U1019
A1885	G1816	G1756	U1679	G1621	C1560	G1500	G1440	G1380	C1320	G1260	C1200	C1140	C1080	A1020
G1886	C1817	U1757	G1680	U1621	G1561	C1501	G1441	G1381	A1321	C1261	C1201	U1141	U1081	A1021
G1887	U1818	G1758	G1681	G1622	A1562	C1502	G1442	G1382	A1322	A1262	C1202	U1142	U1082	G1022
G1888	A1819	A1759	G1682	G1623	G1563	U1503	G1443	C1383	U1323	U1263	G1203	A1142A	U1083	U1023
A1889	U1820	A1760	C1683	G1624	G1564	C1504	G1444	A1384	G1324	G1264	A1204	A1143	A1084	G1024
G1890	A1821	C1761	G1684	C1625	C1565	C1505	A1444A	G1385	G1325	A1265	U1205	A1144	A1085	G1025
G1891	C1822	A1762	C1685	G1626	C1566	C1506	G1445	G1386	G1326	G1266	G1206	C1145	A1086	U1026
C1892	G1823	G1763	G1686	G1627	A1567	C1507	G1446	C1387	C1327	U1267	C1207	C1146	G1087	A1027
G1893	G1824	G1764	G1687	G1628	A1568	A1508	G1447	G1388	G1328	A1268	C1208	C1147	A1088	A1028
C1894	A1825	C1765	U1688	G1629	G1569	A1509	G1448	G1389	U1329	A1269	G1209	A1148	G1089	A1029
G1895	G1826	U1766	G1689	G1630	A1570	A1510	A1449	U1390	C1330	C1270	A1210	C1150	U1090	G1030
G1896	C1827	C1767	A1690	G1630A	A1571	A1511	G1449A	U1391	A1331	G1271	U1211	C1151	G1091	G1031
G1897	G1828	U1768	G1691	A1631	A1572	G1512	C1450	A1392	G1332	A1272	G1212	C1152	C1092	A1032
U1898	A1829	G1769	G1692	C1632	C1573	C1513	C1451	A1393	G1333	U1273	A1213	C1153	G1093	U1033
G1899	C1830	G1770	G1693	A1633	G1574	U1514	A1453	U1394	G1334	A1274	A1214	C1154	U1094	G1034
A1900	G1831	C1771	G1695	A1634	C1575	C1515	U1454	A1395	U1335	A1275	G1215	G1154	A1095	U1035
A1901	C1832	G1772	G1696	G1635	C1576	U1516	G1455	U1396	A1336	A1276	G1216	A1155	A1096	G1036
C1902	U1833	A1773	G1697	C1636	U1576	G1517	G1456	U1397	G1337	G1277	C1217	A1156	U1097	G1037
G1903	U1834	C1774	A1698	A1637	C1577	C1518	A1457	C1398	G1338	A1278	G1218	C1157	A1098	C1038
G1904	G1835	U1775	G1699	C1638	A1578	G1519	C1458	C1399	G1339	G1279	G1219	C1158	G1099	G1039
C1905	C1836	G1776	A1700	U1639	U1579	U1520	G1459	G1400	U1340	G1280	A1220	U1159	C1100	C1040
G1906	C1837	U1777	G1701	C1640	A1580	U1521	A1460	G1401	U1341	G1281	C1221	G1160	U1101	G1041
G1907	G1838	U1778	G1702	A1641	C1581	G1522	G1461	C1402	A1342	U1282	C1222	C1161	C1102	G1042
C1908	C1839	U1779	G1703	G1642	C1582	U1523	C1462	C1403	G1343	G1283	C1223	G1162	A1103	C1043
G1909	G1840	A1780	G1704	G1643	A1583	G1524	C1463	C1404	G1344	A1284	G1224	G1163	C1104	G1044
G1910	U1841	C1781	G1705	C1644	C1585	G1525	C1464	U1405	C1345	G1285	C1225	G1164	U1105	A1045
G1911	G1842	C1782	U1706	G1645	A1586	G1526	G1465	U1406	G1346	A1286	G1226	U1165	G1106	A1046
A1912	C1843	A1783	G1707	C1646	A1587	G1527	G1466	C1407	G1347	A1287	A1227	C1166	G1107	G1047
A1913	G1844	A1784	C1708	G1647	C1588	G1528	G1467	C1408	G1348	U1288	G1228	U1167	U1108	A1048
C1914	G1845	A1785	U1709	C1648	C1589	A1529	C1468	C1409	A1349	U1289	G1229	G1168	C1109	G1049
U1915	A1846	A1786	C1710	G1649	U1590	A1530	G1469	G1410	C1350	C1290	G1230	G1169	A1050	A1050
A1918	C1847	C1787	G1711	G1650	G1591	G1531	G1470	C1411	C1351	C1291	G1231	G1170	G1051	A1051
A1919	G1848	A1788	C1712	G1651	C1592	C1532	G1471	A1412	U1352	U1292	G1232	G1171	C1052	G1052
C1920	C1849	U1789	U1716	A1652	G1593	C1533	A1472	G1413	C1353	C1293	G1233	G1172	C1053	C1053
G1921	G1850	G1717	G1717	G1653	G1594	G1534	G1473	G1414	A1354	U1294	U1234	A1174	G1114	A1054
G1922	U1851	A1791	G1718	A1654	G1595	G1535	G1474	U1415	G1355	C1295	G1235	U1175	G1115	G1055
C1923	C1852	G1792	G1726	A1655	A1596	G1537	G1475	G1416	G1356	C1296	G1236	G1176	C1116	G1056
U1923	A1853	C1793	G1727	C1656	A1597	U1538	C1476	C1417	U1357	C1297	A1237	A1177	G1117	A1057
C1924	A1854	U1794	U1727	C1657	C1598	G1538	C1476	C1417	U1357	C1297	A1237	A1177	G1117	A1057

G2841	G2777	G2717	A2657	G2597	U2537	C2477	C2417	U2357	C2297	G2237	U2167	C2105	C2045	G1985	G1925
G2842	A2778	G2718	C2658	A2596	C2536	A2478	A2418	G2356	A2296	G2236	G2166	G2106	G2046	A1986	U1926
G2843	G2779	G2719	G2659	G2599	C2539	G2479	U2419	G2359	G2299	G2239	G2169	C2107	U2047	A1987	A1927
G2844	G2780	G2720	A2660	A2600	C2540	G2480	C2420	A2360	G2300	C2240	A2170	G2108	G2048	C1988	A1928
G2845	A2781	G2721	G2661	G2601	A2541	G2481	G2421	G2361	G2301	G2241	A2171	G2109	G2049	G1989	G1929
G2846	G2782	G2722	A2662	A2602	A2542	G2482	A2422	G2362	G2302	G2242	A2172	G2110	C2050	G1990	G1930
U2847	G2783	G2723	G2663	G2603	G2543	G2483	U2423	G2363	G2303	U2243	A2173	C2111	A2051	U1991	U1931
G2848	G2784	C2724	G2664	U2604	G2544	G2484	C2424	G2364	G2304	U2244	C2174	G2112	G2052	U1992	U1932
U2849	A2785	A2725	G2665	U2605	G2545	G2485	A2425	G2365	G2305	G2245	C2175	G2113	G2053	U1993	G1933
A2850	G2786	G2726	G2666	G2606	U2546	G2486	A2426	A2366	G2306	G2246	A2176	G2114	A2054	C1994	C1934
A2851	G2787	G2727	G2667	G2607	U2547	G2487	C2427	G2367	G2307	A2247	C2177	G2115	C2055	U1995	G1935
G2852	G2788	U2728	G2668	G2608	G2548	A2488	G2428	G2368	G2308	C2248	C2178	G2116	G2056	G1996	A1936
G2853	G2789	U2729	G2669	U2609	G2549	G2489	G2429	A2369	A2309	U2249	C2179	A2117	U2057	G1997	A1937
G2854	A2790	C2730	A2670	C2610	G2550	G2490	A2430	G2370	A2310	G2250	U2180	U2118	A2058	G1998	A1938
G2855	G2791	G2731	G2671	U2611	C2551	U2491	U2431	G2371	A2311	G2251	G2181	A2119	A2059	G1999	U1939
G2856	G2792	G2732	G2672	G2612	U2552	U2492	A2432	G2372	U2312	G2252	G2182	G2120	A2060	G2000	U1940
G2857	A2793	A2733	G2673	U2613	G2553	U2493	A2433	G2373	C2313	G2253	C2183	G2121	G2061	A2001	C1941
G2858	A2794	A2734	G2674	A2614	U2554	G2494	A2434	G2374	C2314	G2254	G2184	U2122	A2062	G2002	C1942
G2859	G2795	G2735	G2675	U2615	U2555	G2495	A2435	G2375	G2315	G2255	C2185	G2123	C2063	G2003	U1943
A2860	G2796	G2736	G2676	C2616	C2556	G2496	G2436	A2376	C2316	G2256	G2186	G2124	C2064	G2004	U1944
G2861	G2797	C2737	G2677	C2617	U2557	A2497	U2437	A2377	C2317	U2257	G2187	G2125	C2065	A2005	G1945
G2862	A2798	G2738	G2678	G2618	C2558	C2498	U2438	A2378	G2318	C2258	C2188	A2126	C2066	C2006	U1946
G2863	G2800	U2739	C2679	G2619	C2559	C2499	A2439	G2379	G2319	G2259	U2189	G2127	G2067	C2007	C1947
G2864	C2801	C2740	C2680	C2620	C2560	U2500	C2440	C2380	A2320	C2260	G2190	C2128	U2068	C2008	G1948
U2865	C2802	A2741	C2681	A2621	A2561	C2501	C2441	C2381	G2321	C2261	G2191	C2129	G2069	G2009	G1949
G2866	G2803	G2742	U2682	C2622	U2562	G2502	C2442	G2382	A2322	U2262	G2192		G2070	G2010	G1950
G2867	G2804	G2743	G2683	G2623	U2563	A2503	G2443	G2383	C2323	C2263	G2193	U2132	A2071	U2011	U1951
A2868	U2805	G2744	G2684	G2624	A2564	U2504	G2444	G2384	C2324	C2264	G2194	G2133	G2072	G2012	A1952
G2869	G2806	G2745	G2685	G2625	A2565	G2505	G2445	G2385	G2325	U2265	C2195	A2134	C2073	A2013	A1953
G2870	G2807	U2746	U2686	C2626	A2566	U2506	G2446	C2386	G2326	A2266	C2196	A2135	U2074	A2014	G1954
G2871	G2808	G2747	U2687	G2627	G2567	C2507	G2447	U2387	A2327	A2267	U2197	C2136	U2075	A2015	U1955
G2872	G2809	A2748	U2688	C2628	C2568	G2508	A2448	A2388	A2328	A2268	A2198	C2137	U2076	U2016	U1956
A2873	G2810	G2749	G2689	G2629	C2569	G2509	U2449	G2389	G2329	A2269	A2199	C2138	U2077	U2017	C1957
C2874	G2811	U2750	G2690	G2630	G2570	C2510	A2450	G2390	G2330	G2270	C2205	C2139	C2078	G2018	G1958
G2875	C2812	G2751	C2691	G2631	C2571	U2511	A2451	G2391	G2331	G2271	C2206	G2140	U2079	A2019	G1959
G2876	G2813	G2752	G2692	A2632	C2572	A2512	C2452	A2392	U2332	U2272	C2207	G2141	G2080	A2020	A1960
G2877	G2814	A2753	G2693	G2633	C2573	G2513	A2453	A2393	G2333	G2273	U2208	C2142	C2081	C2021	C1961
U2878	G2815	U2754	G2694	G2634	G2574	U2514	G2454	C2394	G2334	A2274	C2209	C2143	A2082	U2022	C1962
G2879	G2816	C2755	U2695	C2635	C2575	G2515	G2455	G2395	A2335	G2275	G2210	U2144	G2083	G2023	U1963
G2880	A2817	G2756	G2696	U2636	C2576	G2516	C2456	G2396	A2336	G2276	G2211	C2145	C2084	G2024	G1964
C2881	G2818	U2757	U2697	G2637	A2577	A2517	U2457	G2397	G2337	G2277	U2212	G2146	C2085	C2025	C1965
A2882	G2819	G2758	G2698	G2638	G2578	A2518	G2458	U2398	G2338	G2278	U2213	G2147	U2086	C2026	A1966
A2883	G2820	G2759	C2700	A2639	C2579	U2519	A2459	G2399	G2339	G2279	G2215	G2148	G2087	G2027	C1967
U2884	G2821	G2760	G2701	G2640	U2580	C2520	U2460	G2400	G2340	G2280	G2216	U2150	G2088	U2028	G1968
C2885	G2822	G2761	U2702	G2641	G2581	C2521	C2461	U2401	G2341	C2281	G2217	G2151	U2089	G2029	A1969
G2886	A2823	G2762	C2703	G2642	C2582	U2522	U2462	C2402	C2342	G2282	G2218		G2090	A2030	A1970
G2887	G2824	G2763	G2704	G2643	G2583	G2523	C2463	C2403	G2343	C2283	G2219	G2152	U2091	A2031	A1971
G2888	G2825	G2764	A2705	G2644	U2584	G2524	C2464	C2404	U2344	C2284	G2224	G2153	U2092	G2032	A1972
G2889	C2826	G2765	G2706	G2645	U2585	G2525	C2465	G2405	G2345	C2285	A2225	G2155	G2093	A2033	G1973
G2890	G2827	G2766	G2707	C2646	C2586	G2526	C2466	U2406	A2346	A2286	C2226	G2156	G2094	U2034	C1974
A2891	U2828	C2767	G2708	U2647	A2587	G2527	C2467	G2407	C2347	A2287	A2227	G2157	C2095	G2035	U1975
G2892	G2829	G2768	G2709	G2648	G2588	U2528	G2468	U2408	G2348	A2288	G2228	A2158	U2096	C2036	G1976
G2893	G2830	C2769	C2710	U2649	A2589	G2529	A2469	G2409	G2349	C2289	C2229	G2159	C2097	G2037	A1977
G2894	G2831	G2770	A2711	U2650	A2590	G2530	G2470	G2410	C2350	G2290	G2230	G2160	U2098	G2038	A1978
U2895	G2832	G2771	U2712	C2651	C2591	A2531	C2471	A2411	G2351	U2291	G2231	G2161	U2099	C2039	G1979
G2896	G2833	C2772	G2713	G2652	G2592	G2532	G2472	A2412	A2352	C2292	U2232	G2162	G2100	C2040	G1980
U2897	G2834	G2773	A2714	U2653	U2593	A2533	U2473	G2413	G2353	C2293	U2233	C2163	G2101	U2041	A1981
G2898	G2835	G2774	G2715	A2654	C2594	A2534	C2474	G2414	G2354	C2294	G2234	C2164	U2102	A2042	C1982
G2899	G2836	U2775	C2716	G2655	G2595	G2535	C2475	G2415	C2355	G2295	G2235	C2165	C2103	C2043	C1983
A2900	G2837	A2776	U2717	U2656	U2596	G2536	A2476	C2416	C2356	U2296	G2236	G2166	G2104	C2044	G1984



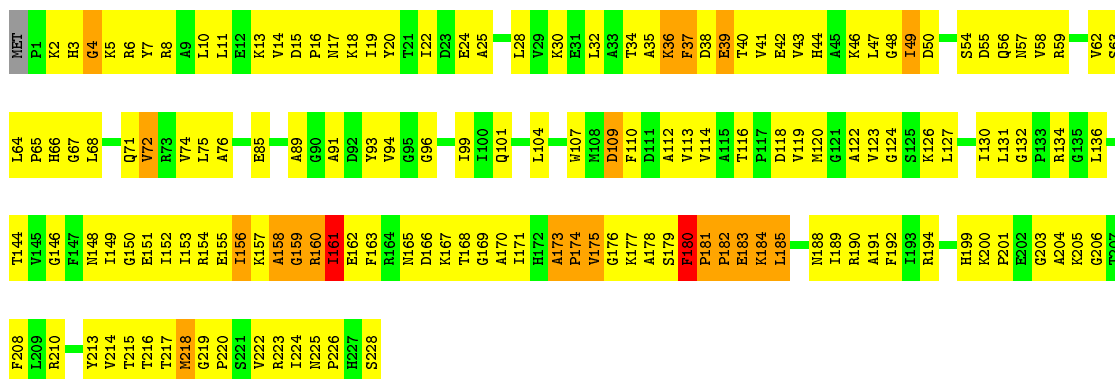
- Molecule 24: 5S ribosomal RNA

Chain E: 5% 56% 39%



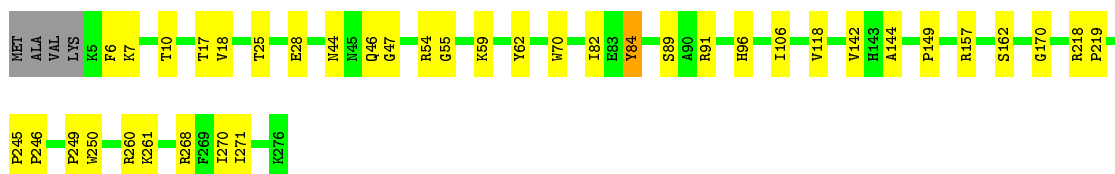
- Molecule 25: 50S ribosomal protein L1

Chain Z: 33% 57% 9%



- Molecule 26: 50S ribosomal protein L2

Chain a: 84% 14%




- Molecule 27: 50S ribosomal protein L3

Chain b: 85% 15%




- Molecule 28: 50S ribosomal protein L4

Chain c:  90% 9% .




- Molecule 29: 50S ribosomal protein L5

Chain d:  86% 13% .




- Molecule 30: 50S ribosomal protein L6

Chain e:  82% 13% . .




- Molecule 31: 50S ribosomal protein L13

Chain f:  88% 11% .




- Molecule 32: 50S ribosomal protein L14

Chain g:  89% 11% .




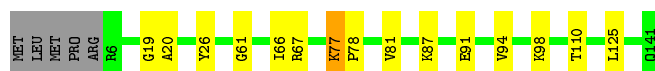
- Molecule 33: 50S ribosomal protein L15

Chain h:  83% 14% .



- Molecule 34: 50S ribosomal protein L16

Chain i:  86% 10% . .



- Molecule 35: 50S ribosomal protein L17

Chain j:  92% 8% .



- Molecule 36: 50S ribosomal protein L18

Chain k: 89% 9%



- Molecule 37: 50S ribosomal protein L19

Chain l: 70% 10% 20%



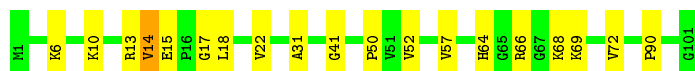
- Molecule 38: 50S ribosomal protein L20

Chain m: 91% 8%



- Molecule 39: 50S ribosomal protein L21

Chain n: 81% 18%



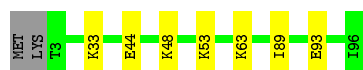
- Molecule 40: 50S ribosomal protein L22

Chain o: 90% 6%



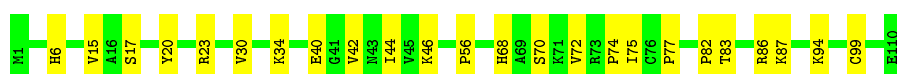
- Molecule 41: 50S ribosomal protein L23

Chain p: 91% 7%

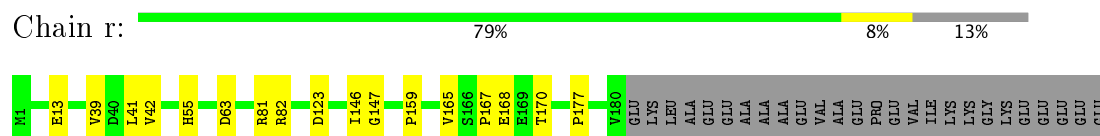


- Molecule 42: 50S ribosomal protein L24

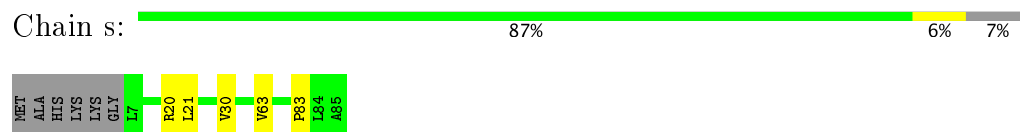
Chain q: 78% 22%



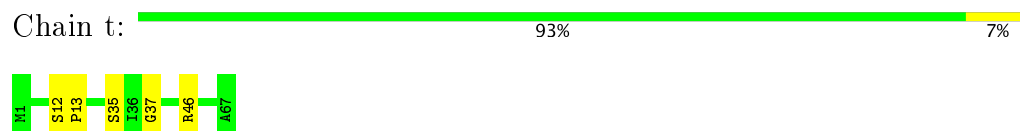
- Molecule 43: 50S ribosomal protein L25



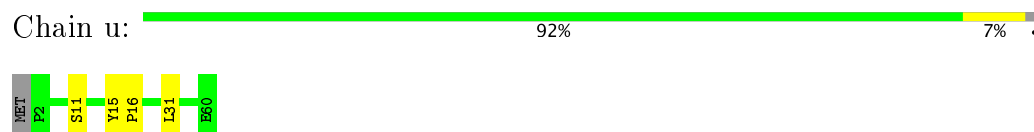
- Molecule 44: 50S ribosomal protein L27



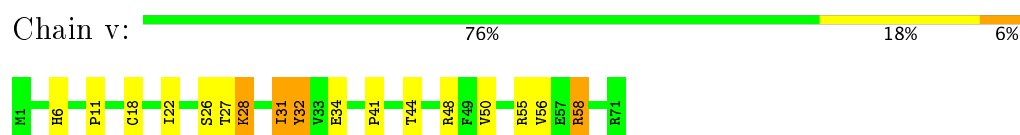
- Molecule 45: 50S ribosomal protein L29



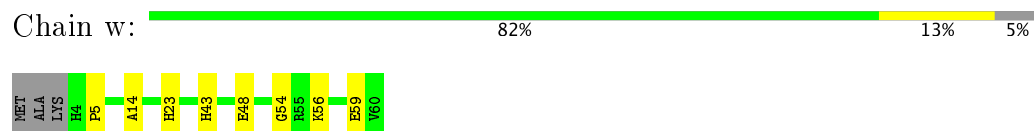
- Molecule 46: 50S ribosomal protein L30



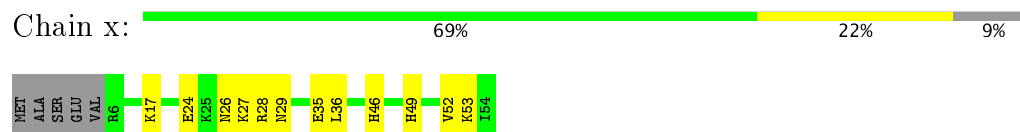
- Molecule 47: 50S ribosomal protein L31



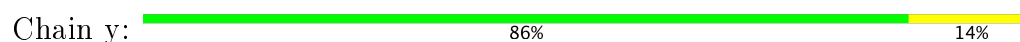
- Molecule 48: 50S ribosomal protein L32



- Molecule 49: 50S ribosomal protein L33



- Molecule 50: 50S ribosomal protein L34





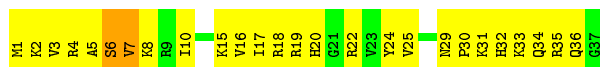
- Molecule 51: 50S ribosomal protein L35

Chain z: 83% 14% ..



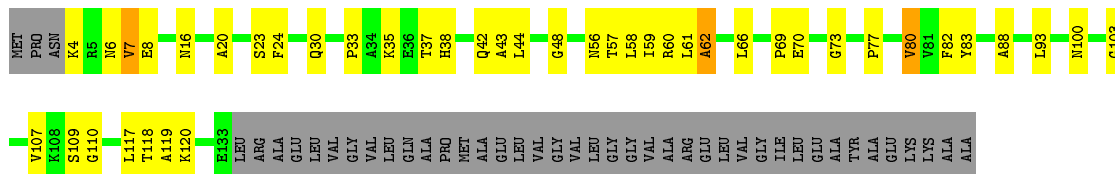
- Molecule 52: 50S ribosomal protein L36

Chain 1: 30% 65% 5%



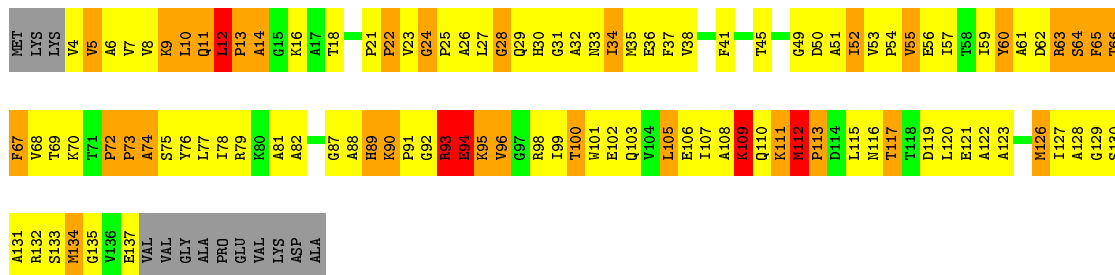
- Molecule 53: 50S ribosomal protein L10

Chain 2: 50% 23% 25%



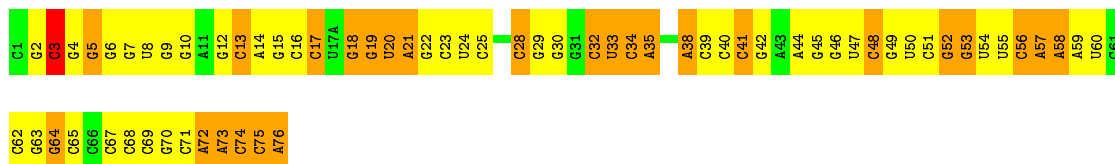
- Molecule 54: 50S ribosomal protein L11

Chain 3: 18% 48% 22% 9%



- Molecule 55: P site- tRNA

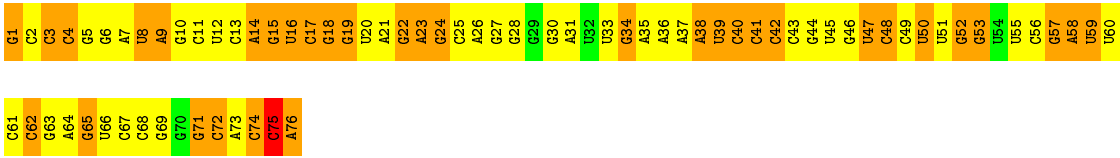
Chain 4: 14% 51% 34%



- Molecule 56: E site- tRNA



Chain 5: 5%49%45%.



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	22	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	A	0.78	1/36438 (0.0%)	1.10	50/56869 (0.1%)
10	N	0.34	0/807	0.67	0/1085
11	O	0.39	0/900	0.63	0/1213
12	P	0.54	0/986	0.79	0/1320
13	Q	0.35	0/924	0.67	1/1238 (0.1%)
14	R	0.42	0/501	0.69	0/664
15	S	0.56	0/745	0.78	0/992
16	T	0.53	0/716	0.75	0/963
17	U	0.48	0/870	0.71	0/1159
18	V	0.41	0/603	0.72	1/799 (0.1%)
19	W	0.39	0/661	0.67	0/890
2	F	0.44	0/1935	0.72	1/2609 (0.0%)
20	X	0.50	0/765	0.79	0/1007
21	Y	0.36	0/212	0.66	0/277
22	C	0.44	0/4545	0.57	25/6155 (0.4%)
23	D	0.97	10/69685 (0.0%)	1.24	293/108786 (0.3%)
24	E	0.82	1/2954 (0.0%)	1.09	2/4606 (0.0%)
25	Z	0.33	0/1775	0.58	2/2393 (0.1%)
26	a	0.57	1/2174 (0.0%)	0.80	1/2927 (0.0%)
27	b	0.54	0/1611	0.85	2/2171 (0.1%)
28	c	0.56	0/1660	0.78	0/2247
29	d	0.39	0/1507	0.73	2/2027 (0.1%)
3	G	0.42	0/1636	0.66	0/2205
30	e	0.47	0/1354	0.75	1/1831 (0.1%)
31	f	0.53	0/1140	0.79	2/1537 (0.1%)
32	g	0.52	0/942	0.80	0/1268
33	h	0.48	0/1123	0.85	1/1493 (0.1%)
34	i	0.55	0/1100	0.81	1/1470 (0.1%)
35	j	0.52	0/974	0.73	0/1302
36	k	0.48	0/887	0.78	0/1180
37	l	0.52	0/990	0.81	1/1325 (0.1%)
38	m	0.60	0/982	0.79	0/1306

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	n	0.45	0/790	0.78	0/1057
4	H	0.49	0/1733	0.71	1/2318 (0.0%)
40	o	0.52	0/886	0.71	0/1189
41	p	0.47	0/756	0.71	0/1015
42	q	0.43	0/857	0.78	0/1142
43	r	0.41	0/1467	0.70	0/1992
44	s	0.48	0/633	0.71	0/843
45	t	0.50	0/569	0.72	0/751
46	u	0.56	0/474	0.77	0/635
47	v	0.51	0/594	0.85	1/795 (0.1%)
48	w	0.56	0/459	0.76	0/621
49	x	0.49	0/433	0.87	0/576
5	I	0.49	0/1162	0.76	0/1564
50	y	0.58	0/438	0.78	0/575
51	z	0.57	0/523	0.83	0/690
52	1	0.46	0/310	0.72	0/407
53	2	0.23	0/640	0.45	0/889
54	3	0.43	0/1012	0.70	2/1373 (0.1%)
55	4	0.57	0/1832	0.96	1/2855 (0.0%)
56	5	1.93	7/1813 (0.4%)	1.02	3/2823 (0.1%)
6	J	0.40	0/856	0.63	0/1154
7	K	0.38	0/1276	0.67	0/1709
8	L	0.48	0/1136	0.77	1/1527 (0.1%)
9	M	0.38	0/1029	0.65	0/1379
All	All	0.81	20/165780 (0.0%)	1.07	395/247193 (0.2%)

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
2	F	0	1
26	a	0	5
28	c	0	3
30	e	0	1
31	f	0	1
32	g	0	1
37	l	0	2
38	m	0	1
39	n	0	1
40	o	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
41	p	0	1
42	q	0	1
46	u	0	1
47	v	0	1
49	x	0	1
51	z	0	1
54	3	0	2
8	L	0	1
All	All	0	26

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	5	75	C	N3-C4	39.72	1.61	1.33
56	5	75	C	N1-C6	36.95	1.59	1.37
56	5	75	C	C2-N3	36.64	1.65	1.35
56	5	75	C	C4-C5	26.84	1.64	1.43
56	5	75	C	N1-C2	25.86	1.66	1.40

The worst 5 of 395 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	D	2075	U	N1-C2-O2	10.51	130.16	122.80
23	D	1498	C	C2-N1-C1'	10.33	130.16	118.80
23	D	2498	C	N1-C2-O2	9.67	124.70	118.90
23	D	2498	C	N3-C2-O2	-9.54	115.22	121.90
23	D	1937	A	N1-C6-N6	-9.37	112.98	118.60

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	F	99	GLY	Peptide
8	L	28	ALA	Peptide
26	a	46	GLN	Peptide
26	a	82	ILE	Peptide
26	a	96	HIS	Peptide

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	A	32554	0	16432	3234	0
2	F	1900	0	1951	189	0
3	G	1612	0	1677	179	0
4	H	1703	0	1763	200	0
5	I	1146	0	1207	149	0
6	J	843	0	857	106	0
7	K	1257	0	1296	115	0
8	L	1116	0	1177	144	0
9	M	1010	0	1037	108	0
10	N	794	0	840	87	0
11	O	885	0	904	98	0
12	P	970	0	1057	130	0
13	Q	914	0	969	194	0
14	R	492	0	529	88	0
15	S	734	0	771	106	0
16	T	700	0	720	104	0
17	U	857	0	930	116	0
18	V	597	0	668	71	0
19	W	647	0	673	104	0
20	X	763	0	861	91	0
21	Y	208	0	221	33	0
22	C	4461	0	4547	2055	0
23	D	62218	0	31357	6715	0
24	E	2641	0	1337	207	0
25	Z	1742	0	1794	264	0
26	a	2124	0	2207	0	0
27	b	1578	0	1647	0	0
28	c	1625	0	1666	0	0
29	d	1482	0	1546	0	0
30	e	1328	0	1407	0	0
31	f	1113	0	1183	0	0
32	g	932	0	994	0	0
33	h	1106	0	1183	0	0
34	i	1080	0	1127	0	0
35	j	960	0	1021	0	0
36	k	877	0	938	0	0
37	l	976	0	1033	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	964	0	1022	0	0
39	n	779	0	852	0	0
40	o	876	0	941	0	0
41	p	742	0	800	0	0
42	q	844	0	930	0	0
43	r	1435	0	1463	0	0
44	s	625	0	647	0	0
45	t	567	0	621	0	0
46	u	469	0	518	0	0
47	v	581	0	576	0	0
48	w	445	0	459	0	0
49	x	426	0	452	0	0
50	y	430	0	480	0	0
51	z	515	0	587	0	0
52	1	307	0	335	52	0
53	2	641	0	309	31	0
54	3	993	0	1030	295	0
55	4	1640	0	837	128	0
56	5	1623	0	821	116	0
57	C	32	0	13	17	0
All	All	152879	0	105220	14713	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 74.

The worst 5 of 14713 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)
22:C:116:GLU:HB3	22:C:120:LYS:CE	1.19	1.66
22:C:41:MET:HB3	22:C:45:PHE:CD1	1.31	1.62
23:D:1064:C:C2	54:3:91:PRO:HD3	1.30	1.62
22:C:493:ASN:HA	22:C:505:THR:CG2	1.26	1.62
22:C:25:LEU:CD2	22:C:174:VAL:HG21	1.19	1.61

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	F	232/256 (91%)	181 (78%)	33 (14%)	18 (8%)	1	17
3	G	204/239 (85%)	157 (77%)	33 (16%)	14 (7%)	1	20
4	H	206/209 (99%)	168 (82%)	21 (10%)	17 (8%)	1	16
5	I	148/162 (91%)	122 (82%)	19 (13%)	7 (5%)	3	28
6	J	99/101 (98%)	85 (86%)	11 (11%)	3 (3%)	5	37
7	K	153/156 (98%)	130 (85%)	16 (10%)	7 (5%)	3	28
8	L	136/138 (99%)	107 (79%)	19 (14%)	10 (7%)	1	18
9	M	125/128 (98%)	96 (77%)	14 (11%)	15 (12%)	0	7
10	N	96/105 (91%)	73 (76%)	11 (12%)	12 (12%)	0	7
11	O	117/129 (91%)	96 (82%)	15 (13%)	6 (5%)	2	26
12	P	122/132 (92%)	79 (65%)	33 (27%)	10 (8%)	1	16
13	Q	112/126 (89%)	80 (71%)	19 (17%)	13 (12%)	0	8
14	R	58/61 (95%)	40 (69%)	12 (21%)	6 (10%)	0	11
15	S	86/89 (97%)	70 (81%)	9 (10%)	7 (8%)	1	16
16	T	81/88 (92%)	65 (80%)	10 (12%)	6 (7%)	1	18
17	U	102/105 (97%)	82 (80%)	13 (13%)	7 (7%)	1	20
18	V	71/88 (81%)	57 (80%)	9 (13%)	5 (7%)	1	19
19	W	78/93 (84%)	53 (68%)	17 (22%)	8 (10%)	0	11
20	X	97/106 (92%)	85 (88%)	7 (7%)	5 (5%)	2	26
21	Y	22/27 (82%)	17 (77%)	2 (9%)	3 (14%)	0	5
22	C	562/610 (92%)	244 (43%)	187 (33%)	131 (23%)	0	2
25	Z	226/229 (99%)	180 (80%)	26 (12%)	20 (9%)	1	15
26	a	270/276 (98%)	188 (70%)	51 (19%)	31 (12%)	0	8
27	b	204/206 (99%)	147 (72%)	29 (14%)	28 (14%)	0	5
28	c	206/210 (98%)	160 (78%)	29 (14%)	17 (8%)	1	16

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	d	180/182 (99%)	119 (66%)	39 (22%)	22 (12%)	0	7
30	e	172/180 (96%)	121 (70%)	27 (16%)	24 (14%)	0	5
31	f	137/140 (98%)	106 (77%)	18 (13%)	13 (10%)	1	13
32	g	120/122 (98%)	86 (72%)	22 (18%)	12 (10%)	1	12
33	h	143/150 (95%)	98 (68%)	25 (18%)	20 (14%)	0	5
34	i	134/141 (95%)	89 (66%)	30 (22%)	15 (11%)	0	9
35	j	115/118 (98%)	93 (81%)	13 (11%)	9 (8%)	1	17
36	k	108/112 (96%)	78 (72%)	20 (18%)	10 (9%)	1	14
37	l	115/146 (79%)	70 (61%)	32 (28%)	13 (11%)	0	8
38	m	115/118 (98%)	87 (76%)	19 (16%)	9 (8%)	1	17
39	n	99/101 (98%)	59 (60%)	21 (21%)	19 (19%)	0	3
40	o	108/113 (96%)	82 (76%)	18 (17%)	8 (7%)	1	18
41	p	92/96 (96%)	74 (80%)	12 (13%)	6 (6%)	1	21
42	q	108/110 (98%)	61 (56%)	24 (22%)	23 (21%)	0	2
43	r	178/206 (86%)	128 (72%)	33 (18%)	17 (10%)	1	12
44	s	77/85 (91%)	60 (78%)	12 (16%)	5 (6%)	1	21
45	t	65/67 (97%)	58 (89%)	2 (3%)	5 (8%)	1	17
46	u	57/60 (95%)	43 (75%)	11 (19%)	3 (5%)	2	25
47	v	69/71 (97%)	39 (56%)	14 (20%)	16 (23%)	0	2
48	w	55/60 (92%)	35 (64%)	12 (22%)	8 (14%)	0	5
49	x	47/54 (87%)	21 (45%)	15 (32%)	11 (23%)	0	2
50	y	47/49 (96%)	30 (64%)	10 (21%)	7 (15%)	0	5
51	z	62/65 (95%)	38 (61%)	14 (23%)	10 (16%)	0	4
52	1	35/37 (95%)	25 (71%)	8 (23%)	2 (6%)	2	24
53	2	128/173 (74%)	95 (74%)	21 (16%)	12 (9%)	1	14
54	3	132/147 (90%)	82 (62%)	20 (15%)	30 (23%)	0	2
All	All	6511/6972 (93%)	4639 (71%)	1137 (18%)	735 (11%)	1	8

5 of 735 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	191	ASP
2	F	209	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	G	64	VAL
4	H	30	LYS
4	H	191	ARG

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	F	202/220 (92%)	202 (100%)	0	100	100
3	G	160/188 (85%)	160 (100%)	0	100	100
4	H	180/181 (99%)	180 (100%)	0	100	100
5	I	115/123 (94%)	115 (100%)	0	100	100
6	J	90/90 (100%)	90 (100%)	0	100	100
7	K	126/127 (99%)	126 (100%)	0	100	100
8	L	119/119 (100%)	119 (100%)	0	100	100
9	M	98/99 (99%)	98 (100%)	0	100	100
10	N	88/92 (96%)	88 (100%)	0	100	100
11	O	90/99 (91%)	90 (100%)	0	100	100
12	P	104/109 (95%)	103 (99%)	1 (1%)	80	90
13	Q	92/101 (91%)	87 (95%)	5 (5%)	26	58
14	R	49/50 (98%)	49 (100%)	0	100	100
15	S	79/80 (99%)	79 (100%)	0	100	100
16	T	72/74 (97%)	72 (100%)	0	100	100
17	U	96/97 (99%)	96 (100%)	0	100	100
18	V	64/77 (83%)	64 (100%)	0	100	100
19	W	71/80 (89%)	69 (97%)	2 (3%)	49	74
20	X	76/82 (93%)	76 (100%)	0	100	100
21	Y	19/22 (86%)	19 (100%)	0	100	100
22	C	473/505 (94%)	347 (73%)	126 (27%)	0	4

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	Z	180/181 (99%)	174 (97%)	6 (3%)	43	70
26	a	215/218 (99%)	213 (99%)	2 (1%)	82	91
27	b	166/166 (100%)	165 (99%)	1 (1%)	89	94
28	c	164/166 (99%)	164 (100%)	0	100	100
29	d	156/156 (100%)	153 (98%)	3 (2%)	62	82
30	e	143/148 (97%)	141 (99%)	2 (1%)	71	86
31	f	118/119 (99%)	118 (100%)	0	100	100
32	g	100/100 (100%)	99 (99%)	1 (1%)	80	90
33	h	111/116 (96%)	111 (100%)	0	100	100
34	i	106/111 (96%)	106 (100%)	0	100	100
35	j	100/101 (99%)	100 (100%)	0	100	100
36	k	87/88 (99%)	87 (100%)	0	100	100
37	l	105/127 (83%)	105 (100%)	0	100	100
38	m	93/94 (99%)	93 (100%)	0	100	100
39	n	82/82 (100%)	82 (100%)	0	100	100
40	o	90/92 (98%)	90 (100%)	0	100	100
41	p	76/78 (97%)	76 (100%)	0	100	100
42	q	91/91 (100%)	91 (100%)	0	100	100
43	r	159/179 (89%)	159 (100%)	0	100	100
44	s	63/67 (94%)	63 (100%)	0	100	100
45	t	62/62 (100%)	62 (100%)	0	100	100
46	u	51/52 (98%)	51 (100%)	0	100	100
47	v	63/63 (100%)	60 (95%)	3 (5%)	30	62
48	w	50/52 (96%)	50 (100%)	0	100	100
49	x	48/52 (92%)	48 (100%)	0	100	100
50	y	42/42 (100%)	42 (100%)	0	100	100
51	z	54/55 (98%)	54 (100%)	0	100	100
52	1	34/34 (100%)	34 (100%)	0	100	100
54	3	101/111 (91%)	86 (85%)	15 (15%)	3	20
All	All	5373/5618 (96%)	5206 (97%)	167 (3%)	49	71

5 of 167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	C	294	PHE
22	C	377	VAL
54	3	12	LEU
22	C	315	LYS
22	C	332	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 111 such sidechains are listed below:

Mol	Chain	Res	Type
22	C	538	GLN
27	b	129	HIS
49	x	46	HIS
22	C	594	GLN
25	Z	172	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1514/1522 (99%)	640 (42%)	80 (5%)
23	D	2888/2893 (99%)	1464 (50%)	169 (5%)
24	E	122/123 (99%)	47 (38%)	4 (3%)
55	4	76/77 (98%)	30 (39%)	0
56	5	75/76 (98%)	36 (48%)	4 (5%)
All	All	4675/4691 (99%)	2217 (47%)	257 (5%)

5 of 2217 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	8	A
1	A	9	G
1	A	10	A
1	A	14	U

5 of 257 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	D	574	C
23	D	973	A
23	D	2660	A
23	D	616	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
23	D	822	U

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](#)

1 ligand is 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	$\# Z > 2$
57	GCP	C	701	22	25,34,34	3.73	10 (40%)	28,54,54	1.44	3 (10%)

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
57	GCP	C	701	22	-	0/18/38/38	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	C	701	GCP	C3'-C4'	-9.21	1.28	1.53
57	C	701	GCP	C4-N9	-8.71	1.36	1.47
57	C	701	GCP	C5-C6	-7.54	1.39	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	C	701	GCP	O4'-C1'	-4.27	1.31	1.42
57	C	701	GCP	C8-N9	-4.05	1.34	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	C	701	GCP	PA-O3A-PB	-4.80	116.91	132.39
57	C	701	GCP	O6-C6-N1	-2.75	119.03	122.70
57	C	701	GCP	C3'-C2'-C1'	2.63	106.49	101.43

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	C	701	GCP	17	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.