



wwPDB EM Map/Model Validation Report ⓘ

Jun 22, 2016 – 06:28 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 : 2016-03-06
Resolution : unknown (reported)
Based on PDB ID : 4W2E, 5AA0

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) : rb-20027790

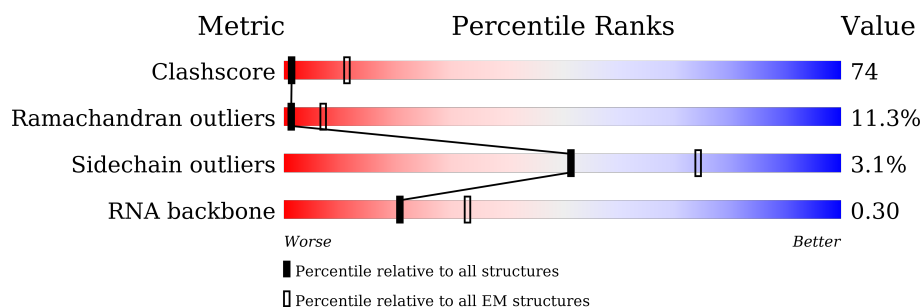
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is unknown.

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.




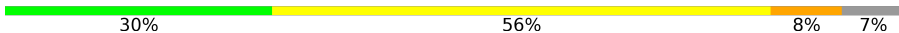
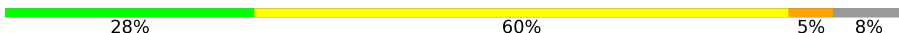

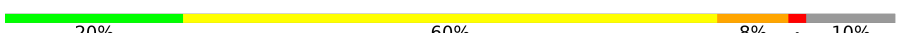
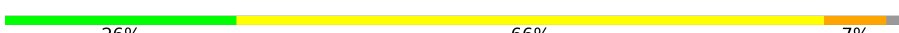
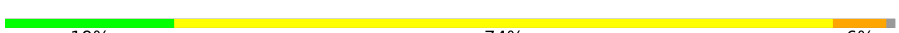




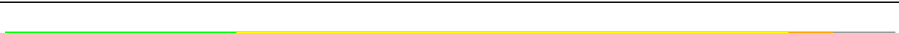













Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	A	1522	
2	F	256	
3	G	239	
4	H	209	
5	I	162	
6	J	101	
7	K	156	
8	L	138	











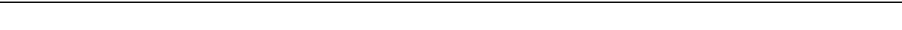

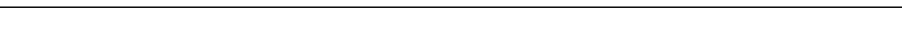
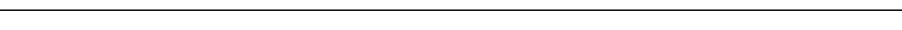
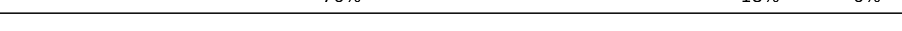








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Mol	Chain	Length	Quality of chain
9	M	128	
10	N	105	
11	O	129	
12	P	132	
13	Q	126	
14	R	61	
15	S	89	
16	T	88	
17	U	105	
18	V	88	
19	W	93	
20	X	106	
21	Y	27	
22	C	610	
23	D	2893	
24	E	123	
25	Z	229	
26	a	276	
27	b	206	
28	c	210	
29	d	182	
30	e	180	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

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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	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		

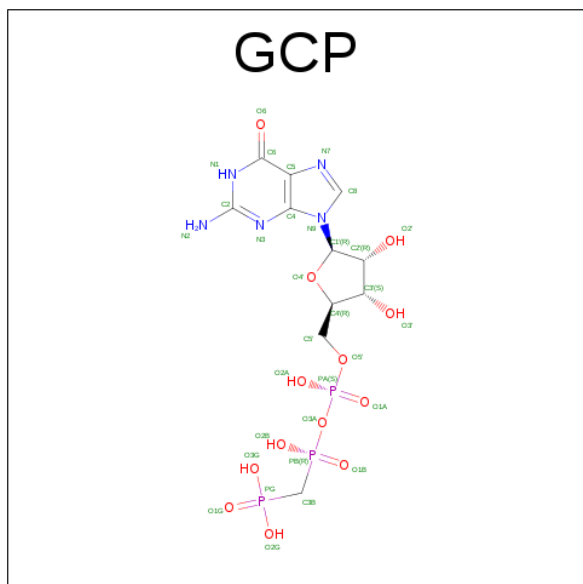
- Molecule 55 is a RNA chain called P site- tRNA.

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: $C_{11}H_{18}N_5O_{13}P_3$).



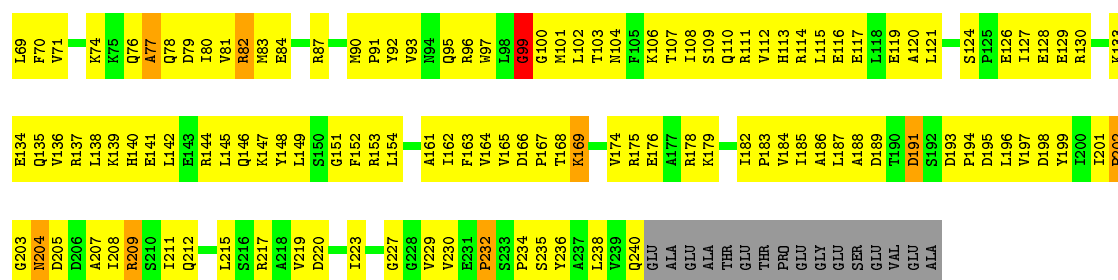
Mol	Chain	Residues	Atoms					AltConf
57	C	1	Total	C	N	O	P	0
			32	11	5	13	3	

C1527	C1466	C1401	C1342	C1282	G1222	C1161	A1101	C985	G925	A865	G799	C739
U1528	G1467	C1402	G1343	G1283	C1223	C1162	A1102	A986	G926	C866	G800	U740
G1529	A1468	C1403	C1344	C1284	G1224	C1163	C1103	G987	G927	C867	U801	G741
G1469	G1469	C1404	U1345	A1285	A1225	C1164	C1043	G988	G928	C868	A802	G742
A1531	G1470	G1405	A1346	A1286	C1226	G1165	A1105	G989	G929	C869	G803	U743
U1532	G1471	G1406	G1347	A1287	A1227	G1166	A1046	C990	G930	U870	U804	G744
C1533	G1472	C1407	U1348	A1288	C1228	A1167	G1047	U991	C931	U871	C805	G745
A1534	G1473	A1408	A1349	A1289	A1229	A1169	U1048	U992	C932	A872	C806	A746
C1535	G1474	C1409	A1350	G1290	C1230	A1170	U1049	U993	G933	A873	A807	G747
U1536	G1475	G1410	U1351	G1291	U1231	G1171	A1110	A994	G934	G874	C808	G748
U1537	C1476	C1411	C1352	U1292	U1232	C1172	A1111	C995	A935	C875	C809	G749
C1538	G1477	G1412	G1353	G1293	G1233	G1173	U1052		G936	G876	C810	G750
U1539	C1478	A1413	C1354	G1294	C1234	G1174	C1113		A937	C877	C811	U751
U1540	G1480	U1414	G1355	U1295	U1235	G1175	C1114	C998	A938	G878	C812	G752
U1541	G1481	G1415	G1356	C1296	C1236	A1176	C1054	C999	G939	C879	U813	A753
U1542	G1482	G1416	A1357	C1297	C1237	G1177	A1056	U999	C940	C880	A814	C754
C	A1483	G1417	U1358	A1298	A1238	G1178	G1057	G1001	G941	G881	A815	G755
U	C1484	A1418	C1359	A1299	A1239	A1179	G1058	G1002	G942	C882	A816	G756
	U1485	G1419	A1360	G1300	U1240	A1180	C1059	G1003	U943	C883	C817	U757
	G1486	C1420	G1361	U1301	G1241	G1181	G1120	A1004	G944	U884	G818	G758
	G1487	G1421	C1362	U1302	C1242	G1182	U1121	A1005	G945	G885	A819	A759
	G1488	G1422	C1363	G1303	C1243	A1183	U1122	C1006	A946	G886	U820	G760
	G1489	G1423	A1363	C1304	C1244	G1184	A1123	C1007	G947	G887	G821	G761
	C1490	C1424	U1364	G1305	A1245	G1185	G1124	G1008	C948	G888	C822	G762
	G1491	U1425	G1365	A1306	C1246	G1186	U1125	G1009	A949	A889	G823	G763
	A1492	C1426	C1366	U1307	U1247	G1187	U1126	G1010	U950	G890	C824	G764
	G1493	U1427	C1367	U1308	A1248	A1188	G1127	G1011	G951	U891	G825	G765
	G1494	A1428	G1368	C1309	G1249	C1189	C1128	U1012	U952	A892	C826	A766
	U1495	G1429	C1369	G1310	A1250	G1190	C1129	G1013	G953	C893	U827	A767
	C1496	C1430	G1370	G1311	A1251	A1191	U1070	A1014	G954	G894	A828	A768
	G1497	G1431	G1371	G1312	A1252	C1192	G1131	A1015	U955	G895	G829	G769
	U1498	G1432	U1372	U1313	G1253	G1193	C1132	A1016	U956	C896	G830	C770
	A1499	A1433	G1373	C1314	G1254	U1194	U1073	G1017	U957	C897	U831	G771
	C1500	A1434	A1374	U1315	G1255	C1195	G1133	C1018	A958	C898	C832	U772
	U1501	G1435	A1375	G1316	A1256	U1196	U1335	C1019	A959	C899	U833	G773
	A1502	U1436	U1376	G1317	U1257	G1197	U1336	U1020	U960	A900	C834	G774
	A1503	C1437	A1377	A1318	G1258	G1198	C137	G1021	U961	A901	U835	G775
	G1504	G1438	C1378	A1319	C1259	U1199	G138	G1022	C962	G902	G836	G776
	U1505	C1439	G1379	C1320	C1260	C1200	G1339	G1023	G963	G903	G837	A777
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	A1507	G1441	U1381	C1322	C1262	G1202	G1141	U1025	G965	U905	U841	C779
	G1508	G1442	C1382	G1323	G1263	C1203	G1142	G1026	G966	G906	C842	A780
	C1509	A1443	C1383	A1324	C1264	U1204	U1083	C1027	C967	A907	U843	A781
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	G1511	G1447	G1385	C1326	G1266	G1206	U1085	C1028A	A969	A909	C849	C783
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	G1525	G1464	C1399	A1340	A1280	U1220	U1159	C1039	U983	A923	U863	C797
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• Molecule 2: 30S ribosomal protein S2

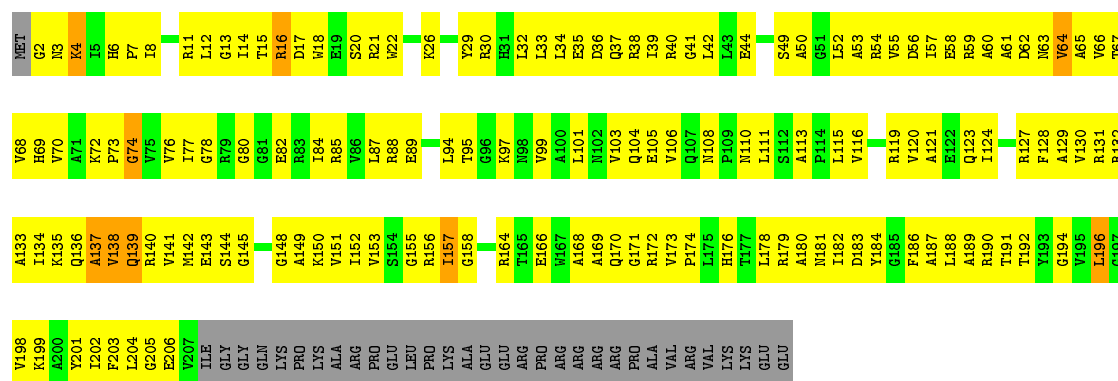
Chain F:  27% 60% 5% 9%

MET	F28	A29	I32	G38	I39	H40	I41	I42	D43	L44	Q45	T47	M49	E49	E50	I51	E52	R53	T54	F55	R56	F57	I58	E59	D60	L61	G62	R64	I68
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



• Molecule 3: 30S ribosomal protein S3

Chain G: 24% 59% 14%



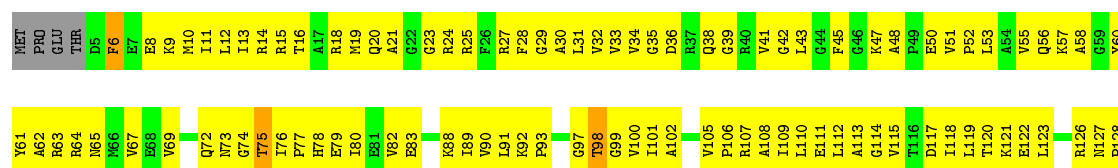
• Molecule 4: 30S ribosomal protein S4

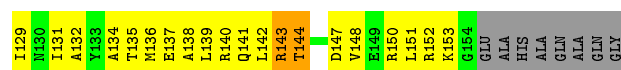
Chain H: 27% 67% 6%



• Molecule 5: 30S ribosomal protein S5

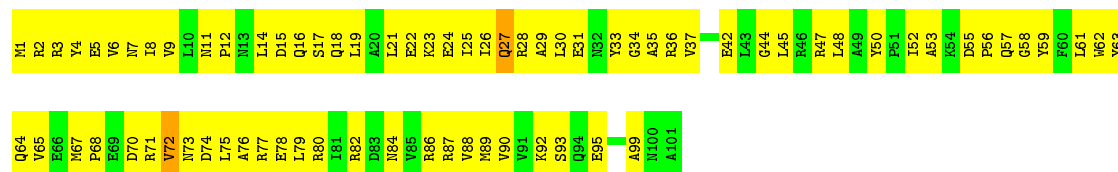
Chain I: 22% 68% 7%





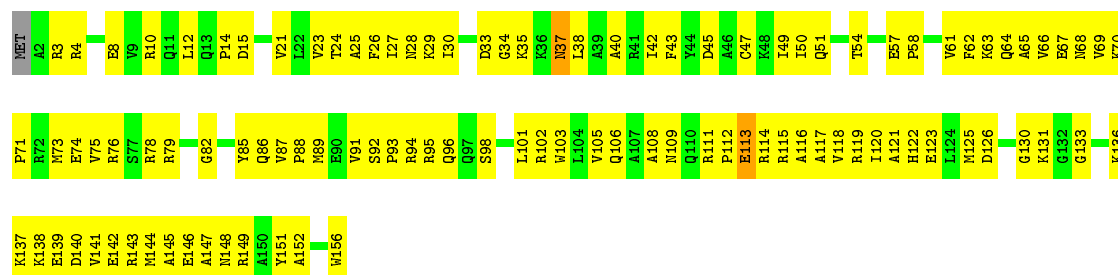
• Molecule 6: 30S ribosomal protein S6

Chain J: 26% 72%



• Molecule 7: 30S ribosomal protein S7

Chain K: 33% 65%



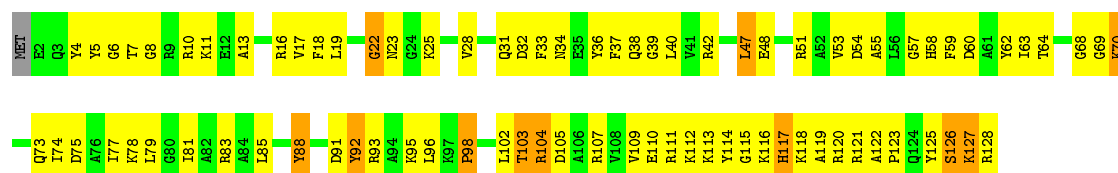
• Molecule 8: 30S ribosomal protein S8

Chain L: 21% 72% 7%



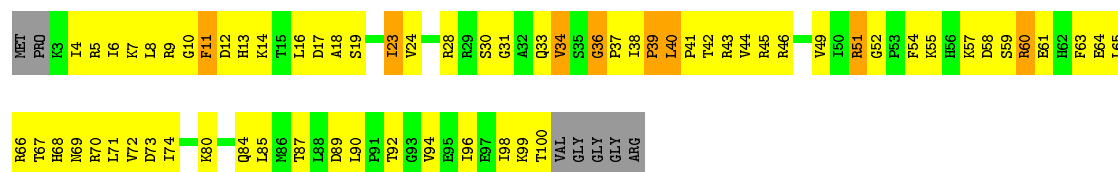
• Molecule 9: 30S ribosomal protein S9

Chain M: 35% 55% 9%



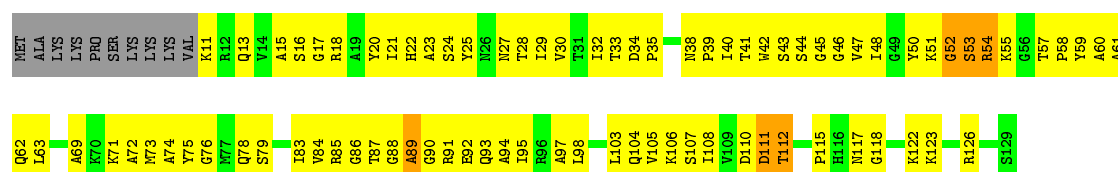
• Molecule 10: 30S ribosomal protein S10

Chain N: 

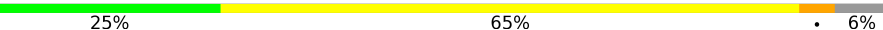


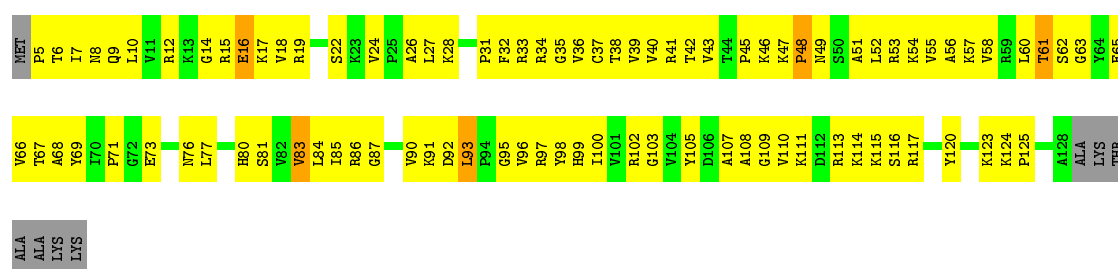
• Molecule 11: 30S ribosomal protein S11

Chain O: 



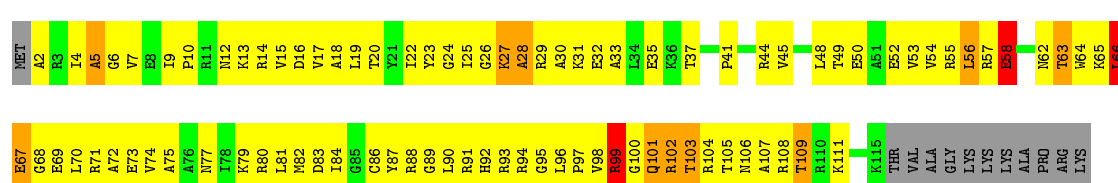
• Molecule 12: 30S ribosomal protein S12

Chain P: 



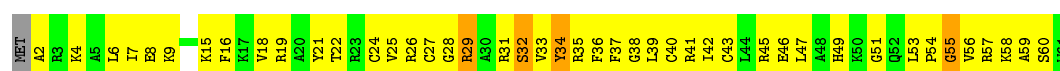
• Molecule 13: 30S ribosomal protein S13

Chain Q: 



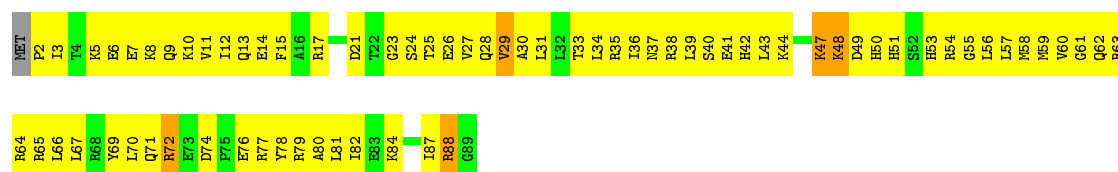
• Molecule 14: 30S ribosomal protein S14 type Z

Chain R: 



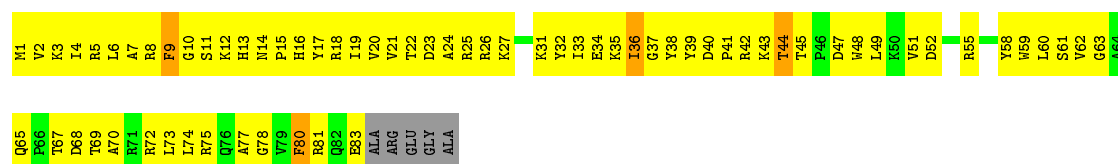
• Molecule 15: 30S ribosomal protein S15

Chain S: 



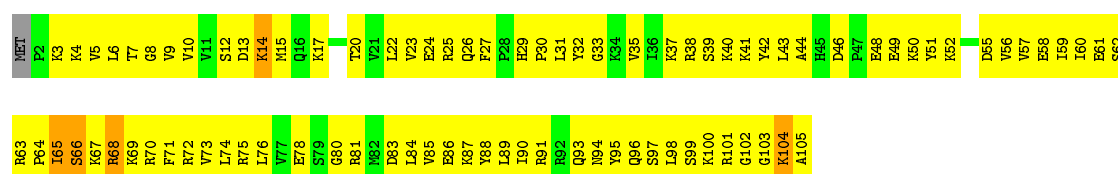
• Molecule 16: 30S ribosomal protein S16

Chain T: 17% 73% 5% 6%



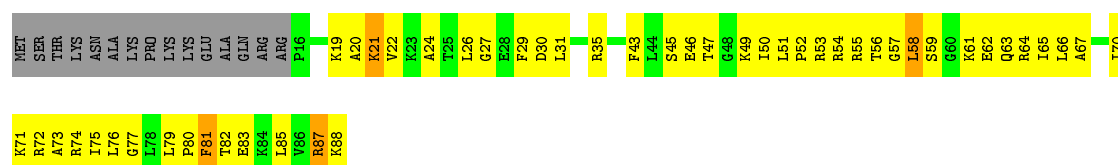
• Molecule 17: 30S ribosomal protein S17

Chain U: 16% 78% 5%



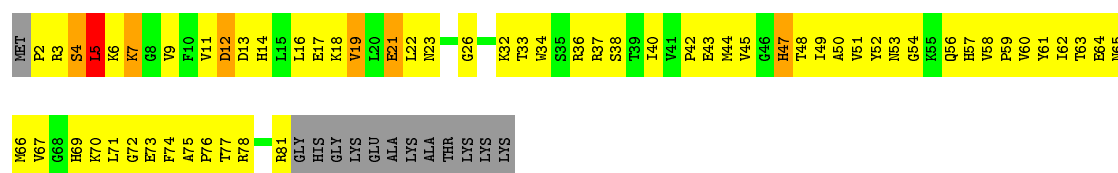
• Molecule 18: 30S ribosomal protein S18

Chain V: 27% 51% 5% 17%



• Molecule 19: 30S ribosomal protein S19

Chain W: 20% 58% 6% 14%



• Molecule 20: 30S ribosomal protein S20

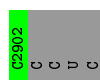
Chain X: 26% 62% 5% 7%



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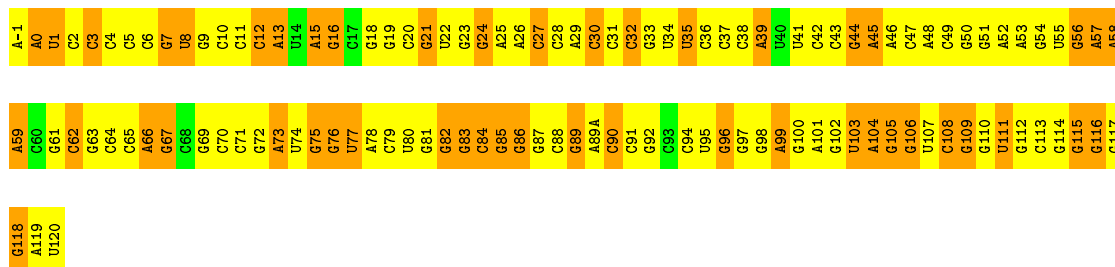
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A1890	A1821	C1761	C1684	C1625	C1564	C1504	G1444	A1384	G1324	G1264	A1204	A1143	A1084	G1024
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G1893	G1824	G1764	G1687	G1628	A1567	C1507	C1446	C1387	C1327	U1267	C1207	C1146	G1087	A1027
C1894	A1825	C1765	U1688	G1629	G1568	A1508	G1447	G1388	G1328	A1268	C1208	C1147	A1088	A1028
C1895	G1826	U1766	A1689	G1630	A1569	C1509	G1448	G1389	U1329	A1269	G1209	A1148	C1089	A1029
G1896	C1827	C1767	A1690	G1630A	A1570	U1510	A1449	U1390	C1330	C1270	A1210	G1150	U1090	G1030
C1897	G1828	U1768	A1691	A1631	A1571	A1511	G1449A	U1391	A1331	G1271	U1211	C1151	G1091	G1031
U1898	A1829	G1769	C1692	A1632	A1572	G1512	C1450	A1392	G1332	A1272	G1212	G1152	C1092	A1032
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A1900	G1831	G1771	G1695	A1634	G1574	U1514	A1453	U1394	G1334	A1274	A1214	C1153	U1094	G1034
A1901	C1832	G1772	G1696	G1635	C1575	C1515	U1454	A1395	U1335	A1275	G1215	G1154	A1095	U1035
C1902	U1833	A1773	G1697	C1636	U1576	U1516	G1455	U1396	A1336	A1276	G1216	A1155	A1096	G1036
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G1904	G1835	U1775	G1699	C1638	A1578	C1518	A1457	C1398	G1338	A1278	G1218	G1157	A1098	C1038
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G1906	C1837	U1777	A1701	U1640	A1580	U1520	A1459	G1400	U1340	G1280	A1220	U1159	C1100	C1040
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G2901	C2840	U2656	G2536	U2656	U2596	G2536	A2476	C2416	C2356	U2296	G2236	G2166	G2104	C2044	G1984



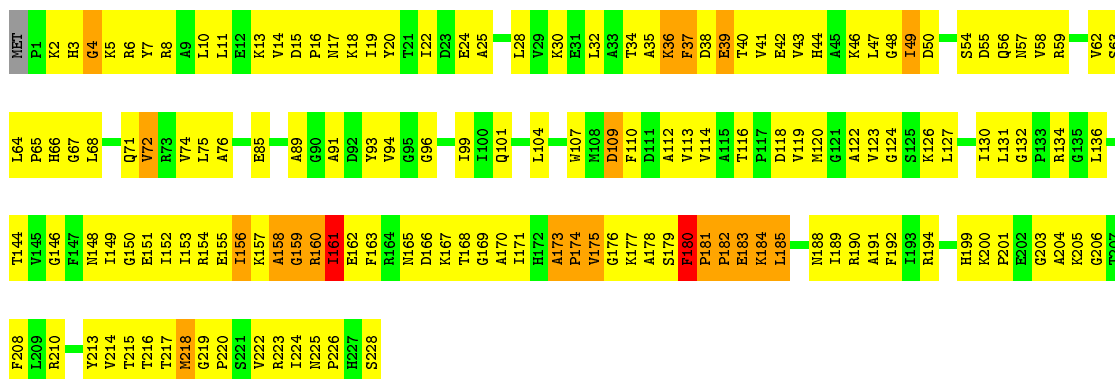
- Molecule 24: 5S ribosomal RNA

Chain E: 5% 56% 39%



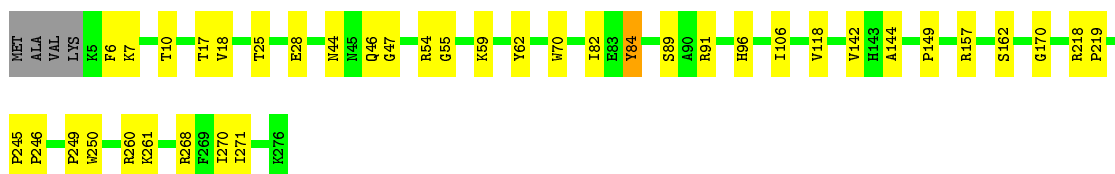
- Molecule 25: 50S ribosomal protein L1

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%




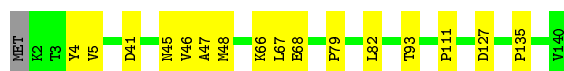
- Molecule 30: 50S ribosomal protein L6

Chain e:  82% 13%




- Molecule 31: 50S ribosomal protein L13

Chain f:  88% 11%




- Molecule 32: 50S ribosomal protein L14

Chain g:  89% 11%




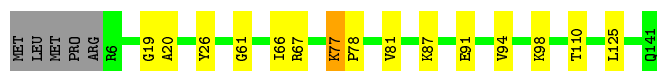
- Molecule 33: 50S ribosomal protein L15

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%



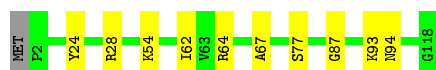
- Molecule 37: 50S ribosomal protein L19

Chain l: 70% 10% 20%



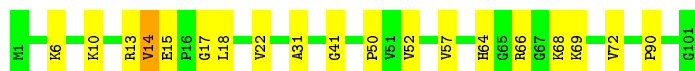
- Molecule 38: 50S ribosomal protein L20

Chain m: 91% 8%



- Molecule 39: 50S ribosomal protein L21

Chain n: 81% 18%



- Molecule 40: 50S ribosomal protein L22

Chain o: 90% 6%



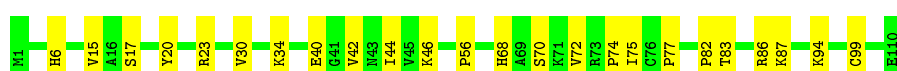
- Molecule 41: 50S ribosomal protein L23

Chain p: 91% 7%

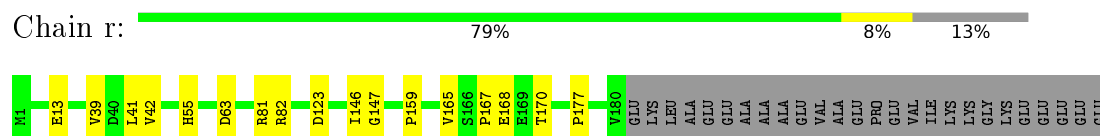


- Molecule 42: 50S ribosomal protein L24

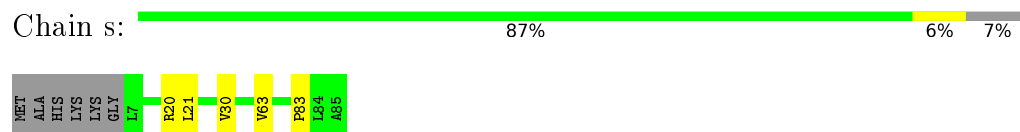
Chain q: 78% 22%



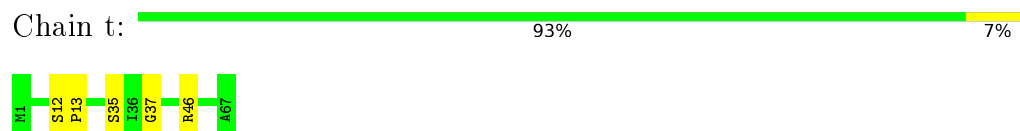
- Molecule 43: 50S ribosomal protein L25



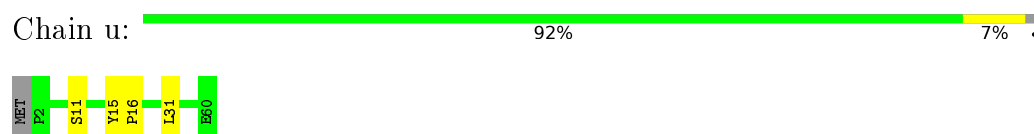
- Molecule 44: 50S ribosomal protein L27



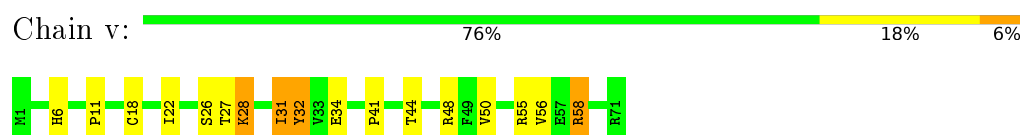
- Molecule 45: 50S ribosomal protein L29



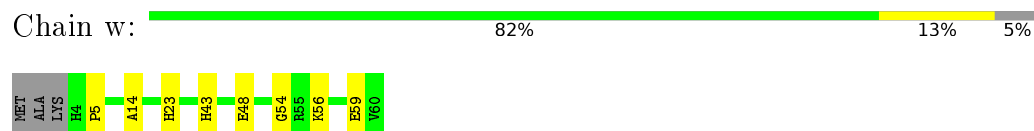
- Molecule 46: 50S ribosomal protein L30



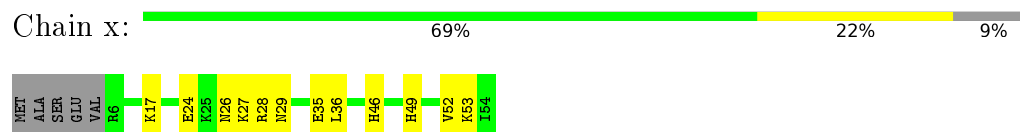
- Molecule 47: 50S ribosomal protein L31



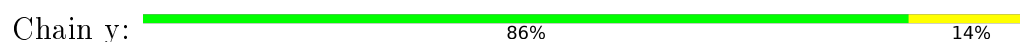
- Molecule 48: 50S ribosomal protein L32



- Molecule 49: 50S ribosomal protein L33



- Molecule 50: 50S ribosomal protein L34





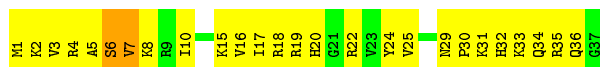
- Molecule 51: 50S ribosomal protein L35

Chain z: 83% 14% ..



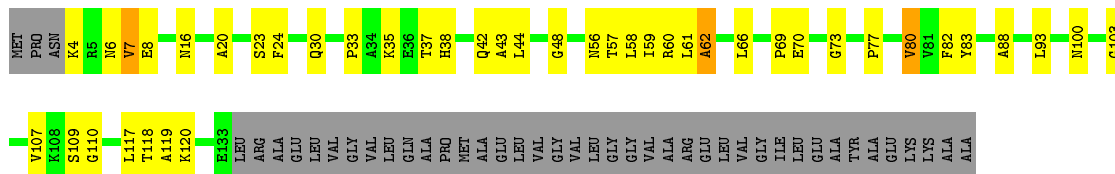
- Molecule 52: 50S ribosomal protein L36

Chain 1: 30% 65% 5%



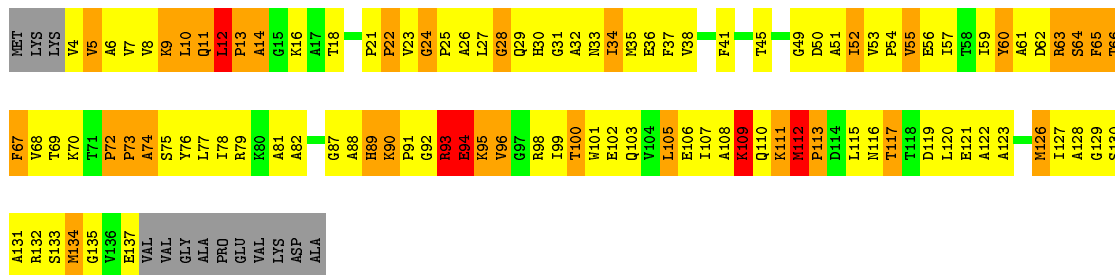
- Molecule 53: 50S ribosomal protein L10

Chain 2: 50% 23% • 25%



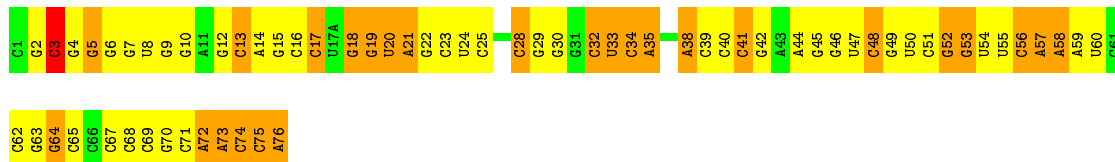
- Molecule 54: 50S ribosomal protein L11

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	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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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

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

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

5 of 735 Ramachandran outliers are listed below:

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

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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%)	82	82
13	Q	92/101 (91%)	87 (95%)	5 (5%)	27	27
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%)	51	51
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	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	Z	180/181 (99%)	174 (97%)	6 (3%)	45	45
26	a	215/218 (99%)	213 (99%)	2 (1%)	84	84
27	b	166/166 (100%)	165 (99%)	1 (1%)	90	90
28	c	164/166 (99%)	164 (100%)	0	100	100
29	d	156/156 (100%)	153 (98%)	3 (2%)	65	65
30	e	143/148 (97%)	141 (99%)	2 (1%)	74	74
31	f	118/119 (99%)	118 (100%)	0	100	100
32	g	100/100 (100%)	99 (99%)	1 (1%)	82	82
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%)	31	31
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%)	4	4
All	All	5373/5618 (96%)	5206 (97%)	167 (3%)	51	47

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

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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	29,34,34	3.49	11 (37%)	31,54,54	1.46	4 (12%)

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 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	C	701	GCP	C3'-C4'	-8.99	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

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	C	701	GCP	O4'-C1'	-4.18	1.31	1.42
57	C	701	GCP	C8-N9	-3.98	1.34	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	C	701	GCP	O6-C6-N1	-2.87	119.03	122.80
57	C	701	GCP	C3'-C2'-C1'	2.51	106.49	101.44
57	C	701	GCP	C4-C5-N7	3.52	108.16	102.67
57	C	701	GCP	C8-N9-C4	3.90	109.23	104.78

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.