



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:28 PM BST

PDB ID : 5AA0
EMDB ID: : EMD-6397
Title : Complex of Thermosus thermophilus ribosome (A-and P-site tRNA) bound to BipA-GDPCP
Authors : Kumar, V.; Chen, Y.; Ahmed, T.; Tan, J.; Ero, R.; Bhushan, S.; Gao, Y.-G.
Deposited on : 2015-07-23
Resolution : 5.00 Å(reported)
Based on PDB ID : 4V4Y

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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

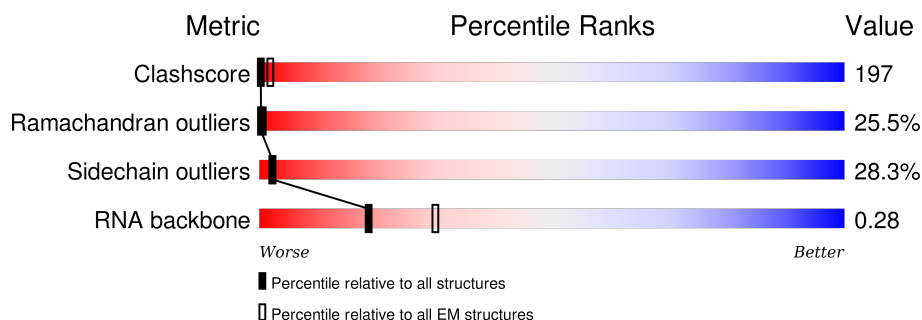
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.00 Å.

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







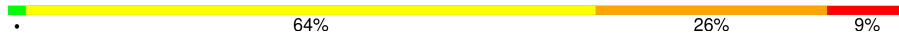
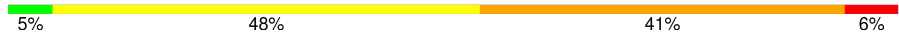

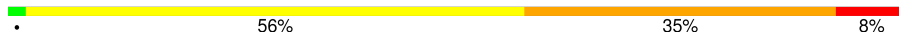

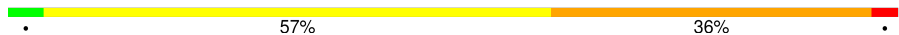
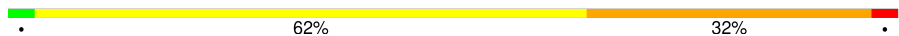
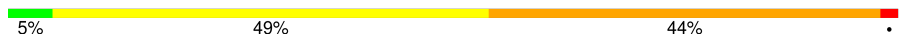
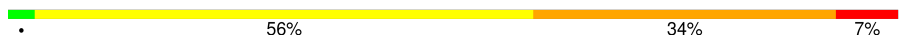
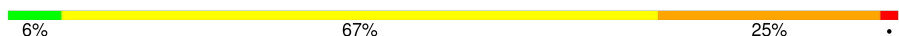




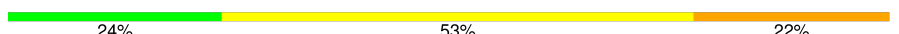





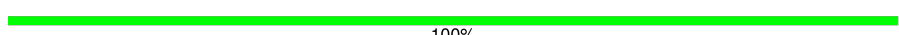
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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

Mol	Chain	Length	Quality of chain
1	AA	2889	
2	AB	123	
3	AC	228	
4	AD	272	
5	AE	206	
6	AF	208	
7	AG	182	
8	AH	174	


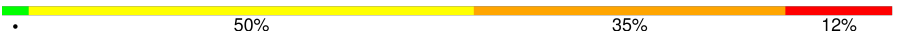
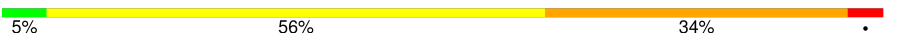


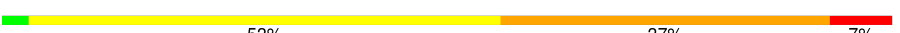
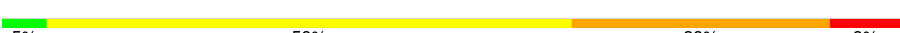




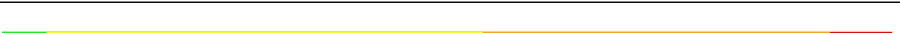













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Mol	Chain	Length	Quality of chain
9	AK	139	
10	AL	122	
11	AM	145	
12	AN	136	
13	AO	117	
14	AP	110	
15	AQ	117	
16	AR	117	
17	AS	101	
18	AT	110	
19	AU	94	
20	AV	110	
21	AW	180	
22	AX	85	
23	AY	67	
24	AZ	59	
25	Aa	71	
26	Ab	57	
27	Ac	49	
28	Ad	49	
29	Ae	64	
30	Af	37	
31	AI	153	
32	AJ	134	
33	Ag	128	

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Mol	Chain	Length	Quality of chain
34	BA	1515	
35	BF	234	
36	BG	206	
37	BH	208	
38	BI	150	
39	BJ	101	
40	BK	155	
41	BL	138	
42	BM	127	
43	BN	98	
44	BO	119	
45	BP	124	
46	BQ	114	
47	BR	60	
48	BS	88	
49	BT	83	
50	BU	104	
51	BV	73	
52	BW	80	
53	BX	99	
54	BY	24	
55	BC	76	
56	BD	75	
56	BE	75	
57	BZ	605	

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
58	NMY	AA	3001	-	-	X	-
59	8AN	AA	3002	-	-	X	-
59	8AN	AA	3003	-	-	X	-
60	GCP	BZ	701	-	-	X	-

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 155482 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 23S ribosomal RNA.

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

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	A	deletion	GB 37223181
AA	?	-	A	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	A	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	G	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	?	-	C	deletion	GB 37223181
AA	1134	G	UNK	conflict	GB 37223181

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 3 is a protein called 50S ribosomal protein L1.

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

- Molecule 4 is a protein called 50S ribosomal protein L2.

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

- Molecule 5 is a protein called 50S ribosomal protein L3.

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

- Molecule 6 is a protein called 50S ribosomal protein L4.

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

- Molecule 7 is a protein called 50S ribosomal protein L5.

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

- Molecule 8 is a protein called 50S ribosomal protein L6.

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

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

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

- Molecule 11 is a protein called 50S ribosomal protein L15.

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

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

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

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

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

- Molecule 20 is a protein called 50S ribosomal protein L24.

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

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AX	85	Total	C	N	O	S	0	0
			670	415	141	112	2		

- Molecule 23 is a protein called 50S ribosomal protein L29.

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

- Molecule 24 is a protein called 50S ribosomal protein L30.

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

- Molecule 25 is a protein called 50S ribosomal protein L31.

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

- Molecule 26 is a protein called 50S ribosomal protein L32.

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

- Molecule 27 is a protein called 50S ribosomal protein L33.

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

- Molecule 28 is a protein called 50S ribosomal protein L34.

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

- Molecule 29 is a protein called 50S ribosomal protein L35.

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

- Molecule 30 is a protein called 50S ribosomal protein L36.

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

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AI	153	Total	C	N	O		0	0
			752	446	153	153			

- Molecule 32 is a protein called 50S ribosomal protein L11.

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

- Molecule 33 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ag	128	Total	C	N	O		0	5
			620	369	128	123			

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

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

- Molecule 35 is a protein called 30S ribosomal protein S2.

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

- Molecule 36 is a protein called 30S ribosomal protein S3.

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

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

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

- Molecule 39 is a protein called 30S ribosomal protein S6.

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

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BM	127	Total	C	N	O		0	0
			1010	639	197	174			

- Molecule 43 is a protein called 30S ribosomal protein S10.

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

- Molecule 44 is a protein called 30S ribosomal protein S11.

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

- Molecule 45 is a protein called 30S ribosomal protein S12.

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

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BQ	114	Total	C	N	O	S	0	0
			914	565	189	158	2		

- Molecule 47 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BU	104	Total	C	N	O	S	0	0
			857	547	161	147	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BU	96	GLN	GLU	conflict	UNP Q5SHP7

- Molecule 51 is a protein called 30S ribosomal protein S18.

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

- Molecule 52 is a protein called 30S ribosomal protein S19.

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

- Molecule 53 is a protein called 30S ribosomal protein S20.

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

- Molecule 54 is a protein called 30S ribosomal protein Thx.

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

- Molecule 55 is a RNA chain called tRNA chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BC	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

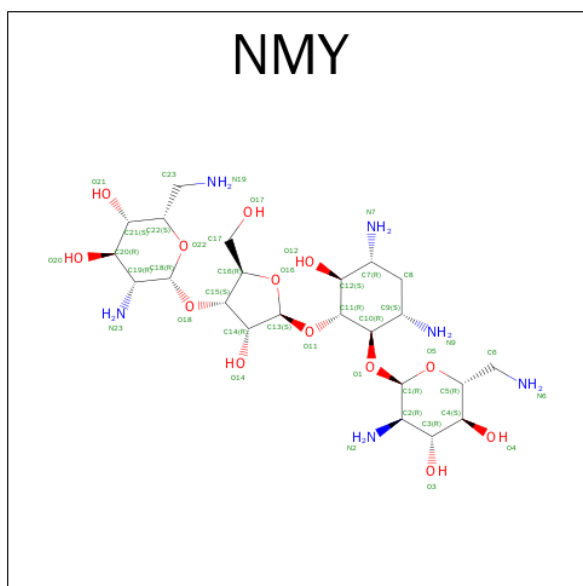
- Molecule 56 is a RNA chain called tRNA chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BD	75	Total	C	N	O	P	0	0
			1597	713	285	525	74		
56	BE	75	Total	C	N	O	P	0	0
			1597	713	285	525	74		

- Molecule 57 is a protein called GTP-binding protein.

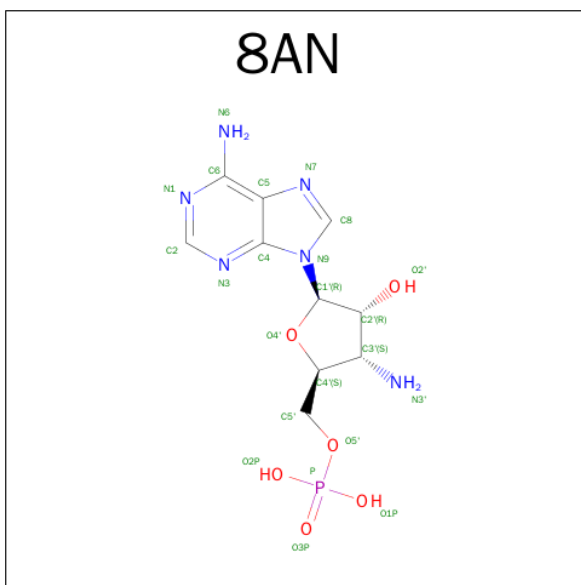
Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	605	Total	C	N	O	S	0	0
			4610	2902	807	883	18		

- Molecule 58 is NEOMYCIN (three-letter code: NMY) (formula: $\text{C}_{23}\text{H}_{46}\text{N}_6\text{O}_{13}$).



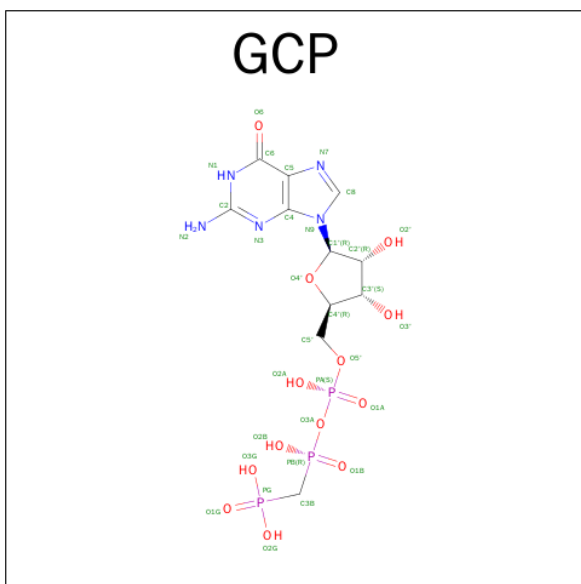
Mol	Chain	Residues	Atoms				AltConf
58	AA	1	Total 42	C 23	N 6	O 13	0
58	BA	1	Total 42	C 23	N 6	O 13	0

- Molecule 59 is 3'-amino-3'-deoxyadenosine 5'-(dihydrogen phosphate) (three-letter code: 8AN) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_6\text{O}_6\text{P}$).



Mol	Chain	Residues	Atoms					AltConf
59	AA	1	Total	C	N	O	P	0
			44	20	12	10	2	
59	AA	1	Total	C	N	O	P	0
			44	20	12	10	2	

- Molecule 60 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

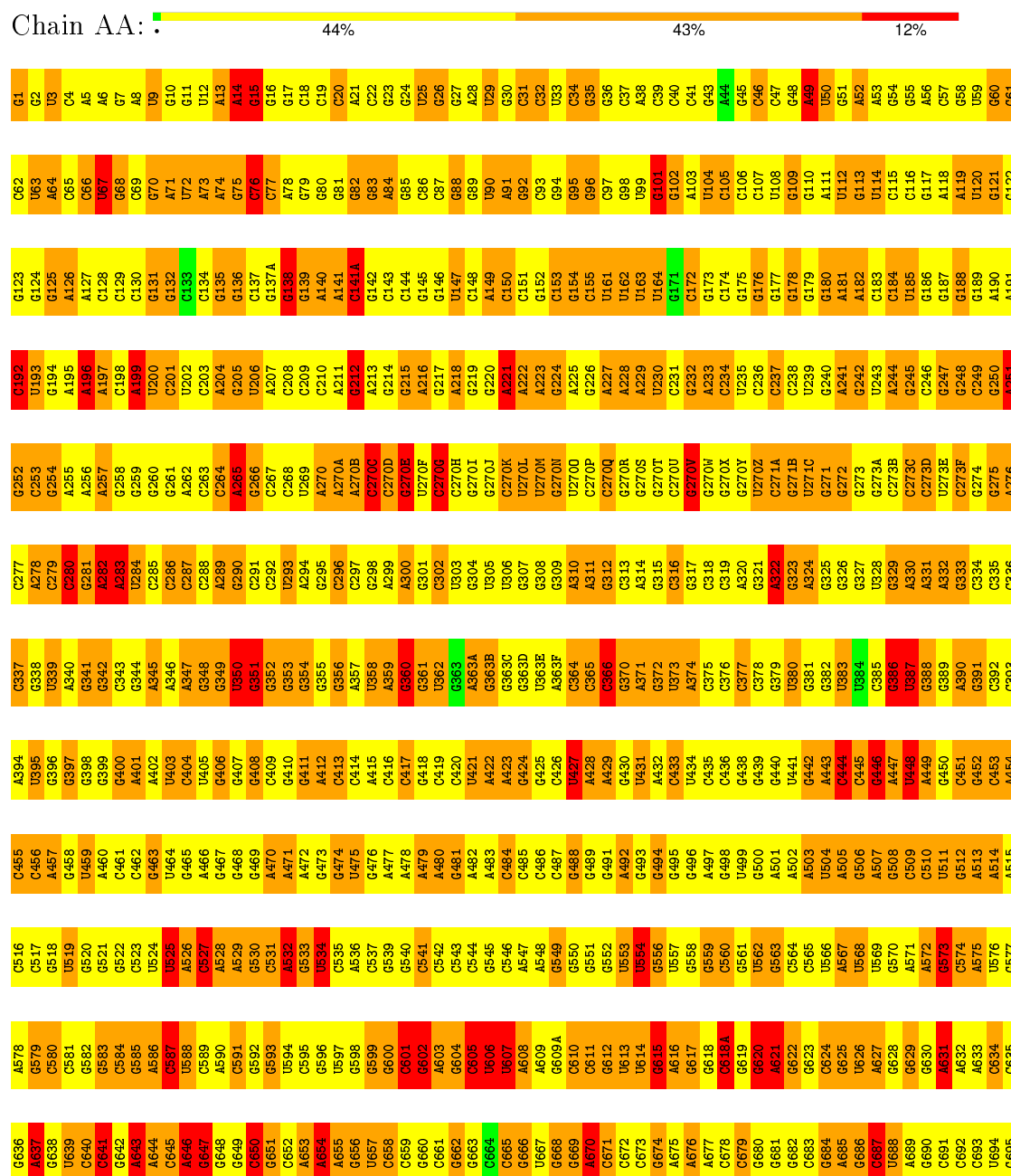


Mol	Chain	Residues	Atoms					AltConf
60	BZ	1	Total	C	N	O	P	0
			32	11	5	13	3	

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

• Molecule 1: 23S ribosomal RNA



C1598	C1538	A1477	G1448	G1368	C1298	G1238	A1177	G1117	A1057	G997	G938	C876	C816	C756	G696
C1599	G1539	G1478	A1419	A1369	G1299	G1239	C1178	C1118	G1058	C998	G939	U877	C817	U757	C697
C1600	G1479	G1480	A1420	G1360	U1300	U1240	C1179	C1119	G1059	U999	G940	A878	C818	U758	C698
C1601	U1541	G1481	G1421	G1361	A1301	A1241	G1120	G1120	U1060	A1000	A941	A879	A819	G759	A699
U1602	U1482	U1483	G1422	C1362	A1302	A1242	C1181	C1121	U1061	A1001	G942	G880	A820	G760	G701
C1603	A1543	G1483	G1423	C1363	G1303	G1243	C1182	G1122	G1062	G1002	U943	G881	A821	A761	G702
C1604	G1484	G1484	G1424	G1364	C1304	G1244	G1183	C1123	G1063	G1003	G844	G882	U822	U762	G703
C1605	G1485	G1425	G1426	A1365	C1305	G1245	G1184	C1124	U1065	C1004	A945	G883	A824	A764	G704
A1545A	A1486	G1426	G1427	A1366	C1306	A1246	G1185	G1125	U1066	C1006	G947	C885	C825	A765	A705
C1607	G1487	G1427	G1428	G1367	A1307	A1247	G1186	A1126	A1067	C1007	G948	C886	U826	C766	A706
C1608	G1488	G1428	G1429	G1368	A1308	G1248	G1187	A1127	G1068	U1008	C949	A887	U827	U767	G707
A1609	U1489	G1430	G1431	G1369	G1310	U1249	U1188	A1128	A1069	A1009	G950	C888	U828	C768	C708
A1610	A1490	C1430	G1310	C1370	G1310	G1250	A1189	A1129	A1070	C889	G951	C889	A829	G769	U709
C1611	G1491	U1431	G1311	G1371	G1311	G1251	G1190	U1130	G1071	A890	G952	A890	G830	G770	G710
C1612	G1492	U1432	U1433	U1372	U1312	G1252	G1191	G1131	G1072	A891	G953	A891	G831	G771	G711
C1613	C1493	U1433	A1434	A1373	G1313	A1253	G1192	A1132	G1073	A892	G954	C893	G832	U772	G712
A1614	A1494	A1434	G1435	G1374	C1314	U1254	G1193	U1133	A1074	C894	C955	C894	U833	U773	G713
A1615	A1495	A1435	G1436	C1375	C1315	U1255	A1194	G1134	G1075	U895	G956	U895	C834	A774	U714
A1616	A1496	G1436	G1437	C1376	U1316	G1256	G1195	C1135	C1076	A896	A857	C897	A835	G775	G715
C1617	U1497	C1437	U1438	A1377	A1317	C1257	C1196	G1136	A1077	U898	C958	C897	G836	G776	A716
A1618	U1498	U1438	A1439	G1378	G1318	G1258	G1197	G1137	U1078	A899	A959	C898	C837	A777	G717
G1619	G1499	G1440	G1380	A1379	G1319	G1259	U1198	G1138	C1079	A900	C961	A900	U839	A778	A718
G1620	G1500	G1441	G1381	G1380	G1320	G1260	U1199	G1139	C1080	A901	C962	A901	C840	U779	C719
U1621	C1501	G1442	G1382	G1382	A1321	C1261	C1200	U1141	U1081	G963	C963	C902	C841	G780	C720
G1622	C1502	G1443	G1444	C1383	U1323	U1263	C1202	U1142	U1082	G964	U863	C903	A842	A781	C721
C1623	U1503	G1444	G1445	A1384	G1324	G1264	G1203	A1142A	U1083	C965	C965	C904	G843	A782	C722
G1624	C1504	A1444A	G1446	A1385	G1325	A1265	A1204	A1143	A1084	C966	U905	C905	C844	A783	G723
C1625	G1505	C1446	G1447	C1386	U1326	G1266	U1205	G1144	A1085	C967	G906	C912	U851	A784	U724
G1626	C1506	A1507	G1448	C1387	G1327	U1267	G1206	C1145	A1086	C968	U907	C913	G852	G785	G725
A1627	A1508	G1449	G1450	G1388	G1328	A1268	C1207	C1146	G1087	C969	U908	C914	C853	G786	G726
G1628	C1509	G1451	G1452	G1389	U1329	A1269	C1208	G1147	A1088	U909	C970	C915	G854	U787	A727
U1629	U1510	A1453	G1454	U1390	C1330	C1270	A1210	G1148	G1089	A910	C971	C916	G855	A788	G728
G1630	A1511	G1455	G1456	U1391	A1331	G1271	A1211	G1149	U1090	A911	C972	A917	C856	A789	G729
C1630A	G1512	C1456	G1457	G1392	G1332	A1272	G1211	C1150	G1091	C973	C974	U913	G857	C790	C730
A1631	C1513	C1457	C1458	A1393	C1333	U1273	G1212	G1151	G1092	A973	G974	C914	G858	C791	C731
A1632	G1514	G1458	G1459	U1394	G1334	A1274	A1213	C1152	G1093	C975	C975	C915	G859	G792	C732
G1633	U1515	U1459	U1460	U1395	U1335	A1275	A1214	C1153	U1094	C976	C976	C916	G860	A793	G733
A1634	C1516	G1460	G1461	A1396	A1336	A1276	G1215	G1154	A1095	C977	C977	C917	G861	G794	A734
C1635	U1517	G1462	G1463	U1397	G1337	G1277	G1216	A1155	A1096	C978	C978	A918	C857	C795	A735
G1636	C1518	C1464	C1465	C1398	G1338	G1278	C1217	A1156	U1097	C979	C979	G919	U858	C796	C736
A1637	G1519	G1466	G1467	G1399	G1339	G1279	C1218	G1157	A1098	C980	C980	G920	G862	C797	C737
G1638	U1520	U1468	G1469	G1400	U1340	G1280	A1220	C1158	G1099	C981	C981	G921	G863	G798	G738
A1639	G1521	G1470	G1471	G1401	U1341	G1281	C1221	U1159	C1100	C982	C982	G922	U864	G799	G739
C1640	C1522	C1469	C1470	C1402	A1342	U1282	C1222	G1160	U1101	C983	C983	U923	A865	A800	U740
A1641	U1523	C1471	C1472	C1403	G1343	G1283	C1223	C1161	C1102	C984	C984	C924	A866	G801	G741
G1642	G1524	C1473	C1474	C1404	G1344	A1284	G1224	G1162	A1103	C985	C985	C925	A867	A802	G742
C1643	G1525	C1475	C1476	U1405	C1345	G1285	G1225	G1163	C1104	C986	C986	C926	A868	U803	G743
G1644	G1526	G1465	G1466	U1406	G1346	A1286	G1226	G1164	U1105	C987	C987	C927	A869	A804	G744
G1645	C1527	G1467	G1468	C1407	G1347	A1287	A1227	U1165	G1106	C988	C988	C928	A870	G805	G745
C1646	G1528	C1469	C1470	C1408	G1348	U1288	G1228	C1166	G1107	C989	C989	G929	A871	C806	A746
G1647	A1529	C1471	C1472	G1409	A1349	U1289	C1229	U1167	U1108	C990	C990	G930	U872	U807	U747
C1648	U1530	A1469	G1470	G1410	C1350	C1290	C1230	G1168	C1109	C991	C991	G931	U873	G808	G748
G1649	C1531	C1471	C1472	C1411	C1351	C1291	G1231	G1169	G1110	C992	C992	G932	U874	G809	C749
A1651	C1532	A1471	C1473	A1412	U1352	U1292	G1232	G1170	A1111	C993	C993	G933	U875	U810	A750
C1533	G1533	A1472	G1473	G1413	A1353	C1293	G1233	G1171	G1112	C994	C994	G934	U876	U811	A751
G1534	G1474	G1475	G1476	G1414	A1354	U1294	U1234	G1172	U1113	C995	C995	G935	A877	C812	A752
U1535	U1535	C1477	C1478	U1415	G1355	C1295	U1235	G1173	G1114	C996	C996	G936	A878	U813	A753
A1536	G1475	G1476	G1477	G1416	G1356	G1296	G1236	U1175	G1115	C997	C997	G937	A879	C814	C754
C1537	C1476	C1477	C1478	C1417	U1357	C1297	A1237	G1176	C1116	G1056	A996	U937	G875	C815	C755

G2592	G2593	G2594	G2595	G2596	G2597	G2598	G2599	G2600	G2601	G2602	G2603	G2604	G2605	G2606	G2607	G2608	G2609	G2610	G2611	G2612	G2613	G2614	G2615	G2616	G2617	G2618	G2619	G2620	G2621	G2622	G2623	G2624	G2625	G2626	G2627	G2628	G2629	G2630	G2631	G2632	G2633	G2634	G2635	G2636	G2637	G2638	G2639	G2640	G2641	G2642	G2643	G2644	G2645	G2646	G2647	G2648	G2649	G2650	G2651										
A2412	A2413	A2414	A2415	A2416	A2417	A2418	A2419	A2420	A2421	A2422	A2423	A2424	A2425	A2426	A2427	A2428	A2429	A2430	A2431	A2432	A2433	A2434	A2435	A2436	A2437	A2438	A2439	A2440	A2441	A2442	A2443	A2444	A2445	A2446	A2447	A2448	A2449	A2450	A2451	A2452	A2453	A2454	A2455	A2456	A2457	A2458	A2459	A2460	A2461	A2462	A2463	A2464	A2465	A2466	A2467	A2468	A2469	A2470	A2471										
A2352	A2353	A2354	A2355	A2356	A2357	A2358	A2359	A2360	A2361	A2362	A2363	A2364	A2365	A2366	A2367	A2368	A2369	A2370	A2371	A2372	A2373	A2374	A2375	A2376	A2377	A2378	A2379	A2380	A2381	A2382	A2383	A2384	A2385	A2386	A2387	A2388	A2389	A2390	A2391	A2392	A2393	A2394	A2395	A2396	A2397	A2398	A2399	A2400	A2401	A2402	A2403	A2404	A2405	A2406	A2407	A2408	A2409	A2410	A2411										
C2292	C2293	C2294	C2295	C2296	C2297	C2298	C2299	C2300	C2301	C2302	C2303	C2304	C2305	C2306	C2307	C2308	C2309	C2310	C2311	C2312	C2313	C2314	C2315	C2316	C2317	C2318	C2319	C2320	C2321	C2322	C2323	C2324	C2325	C2326	C2327	C2328	C2329	C2330	C2331	C2332	C2333	C2334	C2335	C2336	C2337	C2338	C2339	C2340	C2341	C2342	C2343	C2344	C2345	C2346	C2347	C2348	C2349	C2350	C2351										
U2232	U2233	U2234	U2235	U2236	U2237	U2238	U2239	U2240	U2241	U2242	U2243	U2244	U2245	U2246	U2247	U2248	U2249	U2250	U2251	U2252	U2253	U2254	U2255	U2256	U2257	U2258	U2259	U2260	U2261	U2262	U2263	U2264	U2265	U2266	U2267	U2268	U2269	U2270	U2271	U2272	U2273	U2274	U2275	U2276	U2277	U2278	U2279	U2280	U2281	U2282	U2283	U2284	U2285	U2286	U2287	U2288	U2289	U2290	U2291										
G2162	G2163	G2164	G2165	G2166	G2167	G2168	G2169	G2170	G2171	G2172	G2173	G2174	G2175	G2176	G2177	G2178	G2179	G2180	G2181	G2182	G2183	G2184	G2185	G2186	G2187	G2188	G2189	G2190	G2191	G2192	G2193	G2194	G2195	G2196	G2197	G2198	G2199	G2200	G2201	G2202	G2203	G2204	G2205	G2206	G2207	G2208	G2209	G2210	G2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	G2219	G2220	G2221	G2222	G2223	G2224	G2225	G2226	G2227	G2228	G2229	G2230	G2231
U2102	U2103	G2104	G2105	G2106	G2107	U2108	U2109	G2110	G2111	G2112	G2113	G2114	G2115	G2116	G2117	U2118	U2119	G2120	G2121	G2122	G2123	G2124	G2125	G2126	G2127	G2128	G2129	U2130	G2131	G2132	G2133	G2134	G2135	G2136	G2137	G2138	G2139	G2140	G2141	G2142	G2143	G2144	G2145	G2146	G2147	G2148	G2149	U2150	G2151	G2152	G2153	G2154	G2155	G2156	G2157	G2158	G2159	G2160	G2161	G2162									
A2042	C2043	C2044	C2045	C2046	C2047	C2048	C2049	C2050	C2051	C2052	C2053	C2054	C2055	C2056	C2057	C2058	C2059	C2060	C2061	C2062	C2063	C2064	C2065	C2066	C2067	C2068	C2069	C2070	C2071	C2072	C2073	C2074	C2075	C2076	C2077	C2078	C2079	C2080	C2081	C2082	C2083	C2084	C2085	C2086	C2087	C2088	C2089	C2090	C2091	C2092	C2093	C2094	C2095	C2096	C2097	C2098	C2099	C2100	C2101										
C1982	C1983	C1984	C1985	C1986	C1987	C1988	C1989	C1990	C1991	C1992	C1993	C1994	C1995	C1996	C1997	C1998	C1999	C2000	C2001	C2002	C2003	C2004	C2005	C2006	C2007	C2008	C2009	C2010	C2011	C2012	C2013	C2014	C2015	C2016	C2017	C2018	C2019	C2020	C2021	C2022	C2023	C2024	C2025	C2026	C2027	C2028	C2029	C2030	C2031	C2032	C2033	C2034	C2035	C2036	C2037	C2038	C2039	C2040	C2041										
G1922	G1923	C1924	C1925	C1926	C1927	C1928	C1929	G1930	G1931	C1932	G1933	C1934	C1935	C1936	C1937	C1938	C1939	C1940	C1941	C1942	C1943	C1944	C1945	C1946	C1947	C1948	C1949	C1950	C1951	C1952	C1953	C1954	C1955	C1956	C1957	C1958	C1959	C1960	C1961	C1962	C1963	C1964	C1965	C1966	C1967	C1968	C1969	C1970	C1971	C1972	C1973	C1974	C1975	C1976	C1977	C1978	C1979	C1980	C1981										
A1853	A1854	C1855	C1856	C1857	C1858	C1859	C1860	C1861	C1862	C1863	C1864	C1865	C1866	C1867	C1868	C1869	C1870	C1871	C1872	C1873	C1874	C1875	C1876	C1877	C1878	C1879	C1880	C1881	C1882	C1883	C1884	C1885	C1886	C1887	C1888	C1889	C1890	C1891	C1892	C1893	C1894	C1895	C1896	C1897	C1898	C1899	C1900	C1901	C1902	C1903	C1904	C1905	C1906	C1907	C1908	C1909	C1910	C1911	C1912	C1913	C1914	C1915	C1916	C1917	C1918	C1919	C1920	C1921	
G1726	U1727	C1728	C1729	C1730	C1731	C1732	C1733	C1734	C1735	C1736	C1737	C1738	C1739	C1740	C1741	C1742	C1743	C1744	C1745	C1746	C1747	C1748	C1749	C1750	C1751	C1752	C1753	C1754	C1755	C1756	C1757	C1758	C1759	C1760	C1761	C1762	C1763	C1764	C1765	C1766	C1767	C1768	C1769	C1770	C1771	C1772	C1773	C1774	C1775	C1776	C1777	C1778	C1779	C1780	C1781	C1782	C1783	C1784	C1785	C1786	C1787	C1788	C1789	C1790	C1791	C1792			
C1657	C1658	C1659	C1660	C1661	C1662	C1663	C1664	C1665	C1666	C1667	C1668	C1669	C1670	C1671	C1672	C1673	C1674	C1675	C1676	C1677	C1678	C1679	C1680	C1681	C1682	C1683	C1684	C1685	C1686	C1687	C1688	C1689	C1690	C1691	C1692	C1693	C1694	C1695	C1696	C1697	C1698	C1699	C1700	C1701	C1702	C1703	C1704	C1705	C1706	C1707	C1708	C1709	C1710	C1711	C1712	C1713	C1714	C1715	C1716	C1717	C1718	C1719	C1720						


C2652	U2712	C2771	G2834	U2895
U2653	A2712A	C2772	A2835	C2896
A2654	G2713	C2773	G2836	U2897
G2655	G2714	C2774	G2837	U2898
U2656	G2715	A2775	G2838	G2899
A2657	U2716	A2776	G2839	A2900
C2658	C2717	C2777	C2840	C2901
A2659	G2718	A2778	C2841	C2902
G2660	G2719	A2779	G2842	
A2661	U2720	C2780	G2843	
A2662	A2721	A2781	G2844	
G2663	G2722	G2782	G2845	
G2664	C2723	G2783	U2847	
A2665	C2724	C2784	G2848	
C2666	A2725	C2785	U2849	
C2667	U2726	U2786	A2850	
G2668	G2727	C2787	A2851	
C2669	U2728	C2788	G2852	
A2670	G2729	C2789	C2853	
A2671	C2730	A2790	G2854	
A2672	G2731	C2791	C2855	
G2673	G2732	G2792	C2856	
G2674	A2733	G2793	G2857	
A2675	G2734	C2794	C2858	
C2676	A2735	G2795	G2859	
C2677	G2736	U2797	A2860	
C2678	G2737	C2798	C2861	
A2679	A2738	A2799	G2862	
C2680	U2739	A2801	C2863	
C2681	A2740	C2802	C2864	
U2682	C2741	C2803	U2865	
C2683	C2742	C2804	U2866	
U2684	C2743	G2805	C2867	
G2685	G2744	U2807	A2868	
G2686	C2745	C2746	G2869	
U2687	U2746	A2809	C2870	
U2688	G2747	A2810	C2871	
U2689	A2748	G2811	G2872	
C2690	A2749	G2812	A2873	
C2691	A2750	A2813	C2874	
C2692	C2751	C2814	C2875	
A2693	C2752	C2815	G2876	
G2694	A2753	C2816	G2877	
C2695	U2754	G2817	U2878	
U2696	C2755	G2818	C2879	
G2697	U2756	A2820	C2880	
U2698	A2757	G2821	C2881	
C2699	A2758	G2822	A2882	
C2700	G2759	A2823	U2883	
C2701	C2760	C2824	U2884	
U2702	G2761	C2825	C2885	
C2703	G2762	A2826	G2886	
C2704	G2763	A2827	U2887	
A2705	A2764	A2765	C2888	
G2706	A2765	C2828	C2889	
G2707	G2766	C2829	G2891	
G2708	C2767	G2830	A2892	
G2709	C2768	U2831	G2893	
C2710	C2769	U2832	G2894	
A2711	G2770	G2833		

• Molecule 2: 5S ribosomal RNA

Chain AB:  52% 39% 9%

A-1	A59	G118
A0	C60	A119
U1	G61	U120
C2	C62	
C3	G63	
C4	C64	
C5	C65	
C6	A66	
G7	C68	
U8	C69	
C10	C70	
C11	C71	
C12	G72	
A13	U74	
U14	G75	
G15	G76	
A16	U77	
C17	A78	
G18	C79	
C19	U80	
C20	C81	
G21	C82	
U22	G83	
G23	C84	
C24	G85	
A25	G86	
C26	C87	
C27	C88	
C28	G89	
A29	C90	
C30	C91	
C31	G92	
C32	C93	
G33	C94	
U34	U95	
U35	G96	
C36	G97	
C37	A98	
C38	A99	
A40	G100	
U41	A101	
C42	G102	
C43	U103	
G44	A104	
A45	G105	
A46	U106	
C47	U107	
A48	C108	
C49	G109	
G50	G110	
G51	U111	
A52	G112	
A53	C113	
G54	G114	
U55	G115	
G56	G116	
A57	G117	
A58		

• Molecule 3: 50S ribosomal protein L1

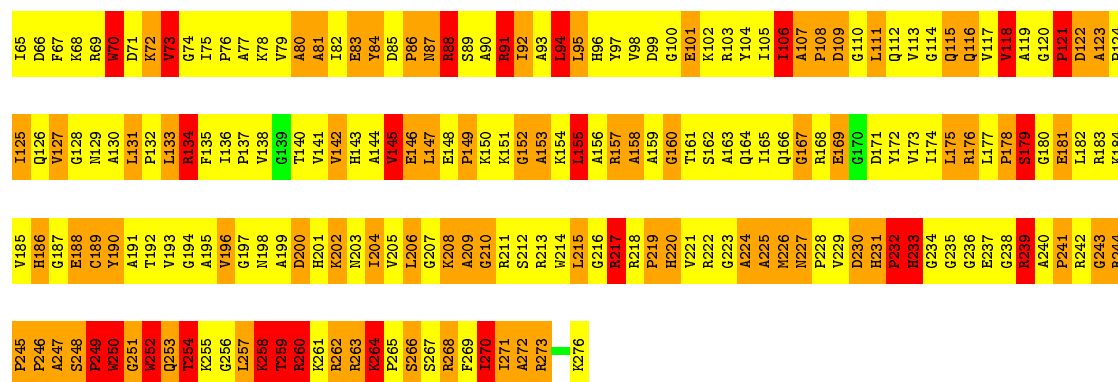
Chain AC:  6% 74% 18%

P1	T61	G121	P181
K2	V62	A122	P182
H3	S63	V123	E183
G4	L64	G124	K184
K5	P65	S125	L185
R6	H66	K126	A186
Y7	G67	L127	D187
L8	L68	G128	N188
A9	G69	R129	I189
L10	K70	L130	A190
L11	Q71	L131	A191
E12	V72	G132	F192
K13	R73	P133	I193
V14	V74	R134	A194
D15	L75	G135	A195
P16	A76	L136	L196
K17	I77	L137	E197
A18	A78	P138	A198
K19	K79	N139	H199
G80	G80	P140	K200
E81	E81	K141	T201
K82	K82	A142	E202
I83	I83	G143	G203
K84	K84	T144	A204
E85	E85	V145	
A86	A86	G146	T207
E87	E87	N147	F208
E88	E88	N148	L209
A89	A89	I149	R210
G90	G90	G150	S211
A91	A91	E151	V212
D92	D92	I152	Y213
Y93	Y93	L153	V214
K94	K94	R154	T215
G95	G95	E155	T216
E96	E96	I156	T217
E97	E97	K157	M218
E98	E98	A158	G219
E99	E99	G159	F220
I100	I100	R160	S221
Q101	Q101	V161	V222
E102	E102	F162	R223
V103	V103	F163	I224
L104	L104	R164	I225
D105	D105	N165	F226
G106	G106	D166	E227
W107	W107	K167	S228
M108	M108	T168	
G109	G109	G169	
D110	D110	A170	
D111	D111	I171	
A112	A112	H172	
V113	V113	A173	
S114	S114	P174	
D115	D115	V175	
O116	O116	G176	
P117	P117	K177	
D118	D118	A178	
V119	V119	S179	
R120	R120	R180	

• Molecule 4: 50S ribosomal protein L2

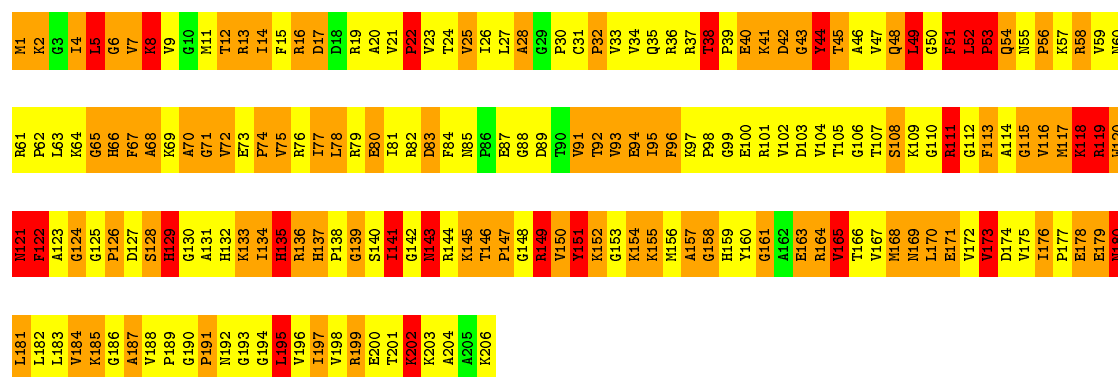
Chain AD:  53% 34% 11%

K5	F6	K7	T10	P11	S12	K13	R14	F15	M16	T17	V18	A19	D20	F21	S22	E23	T24	T25	K26	T27	E28	P29	E30	R31	S32	L33	V34	K35	P36	L37	K38	K39	T40	G41	G42	R43	I44	N45	O46	G47	R48	I49	V50	V51	R52	F53	R54	G55	G56	G57	H58	X59	R60	L61	V62	R63	I64
----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



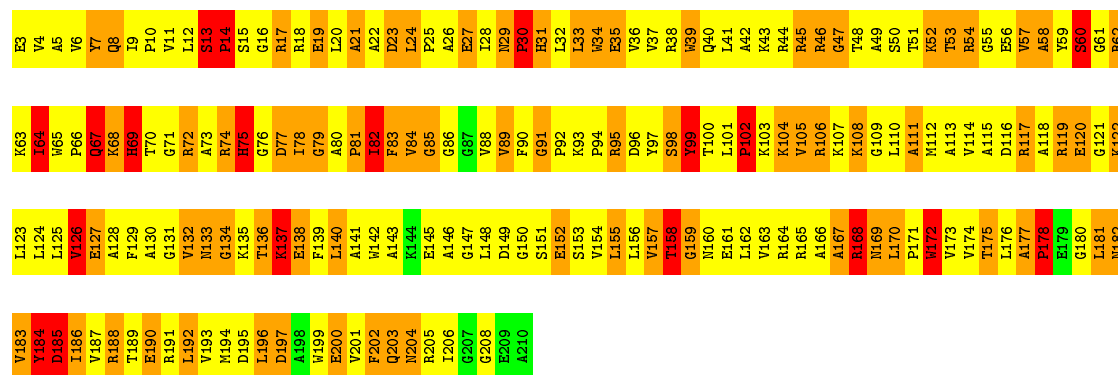
• Molecule 5: 50S ribosomal protein L3

Chain AE: 45% 39% 12%



• Molecule 6: 50S ribosomal protein L4

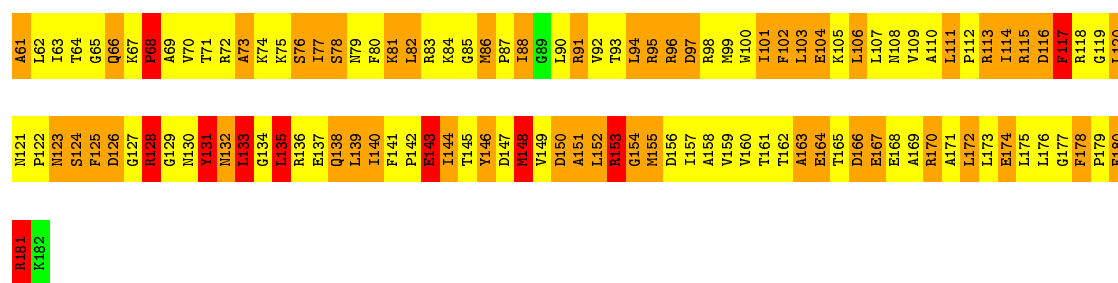
Chain AF: 51% 36% 9%



• Molecule 7: 50S ribosomal protein L5

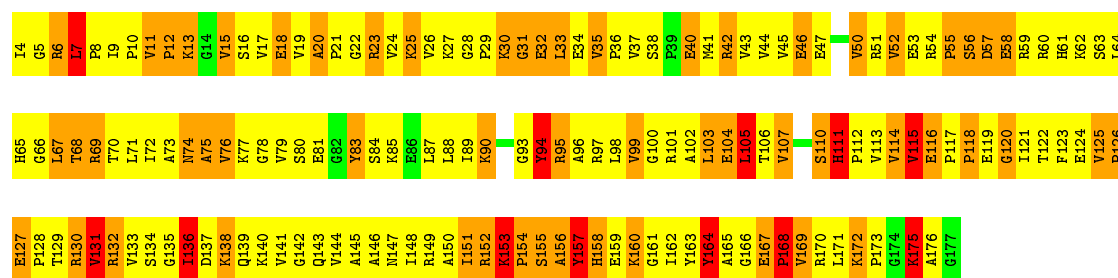
Chain AG: 54% 36% 9%





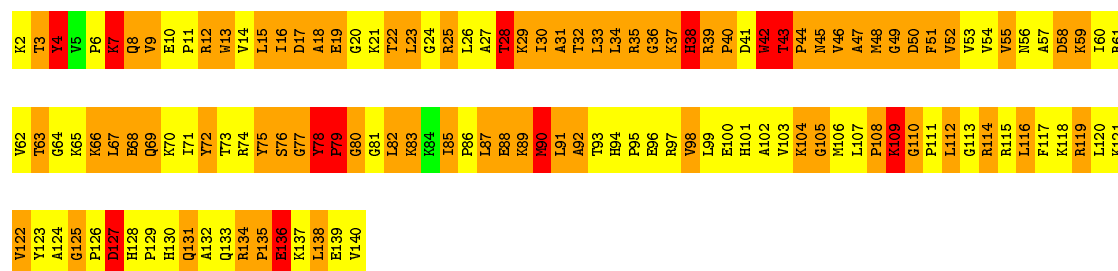
• Molecule 8: 50S ribosomal protein L6

Chain AH: 7% 53% 33% 7%



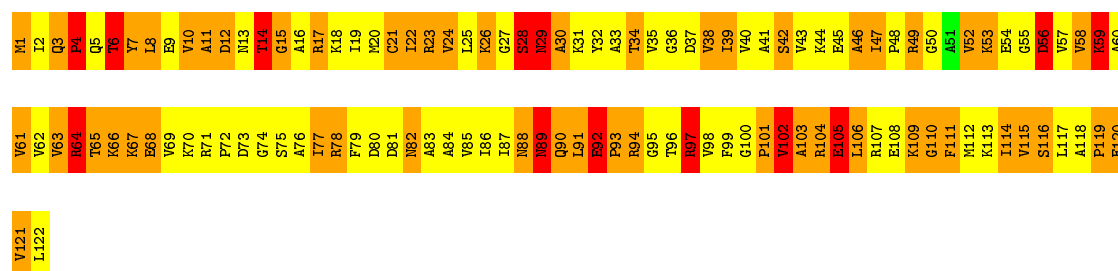
• Molecule 9: 50S ribosomal protein L13

Chain AK: 40% 50% 9%



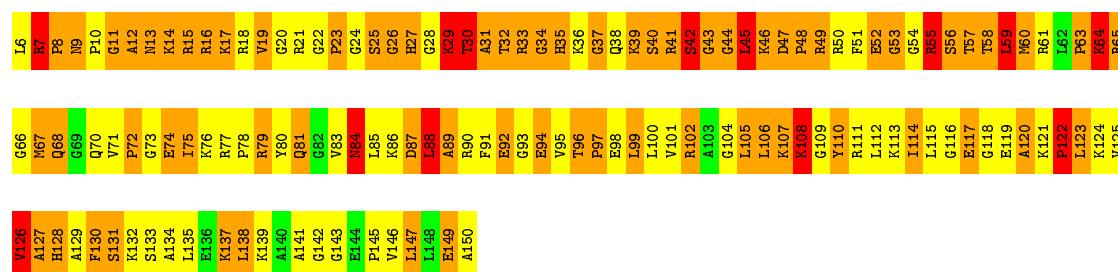
• Molecule 10: 50S ribosomal protein L14

Chain AL: 46% 43% 11%

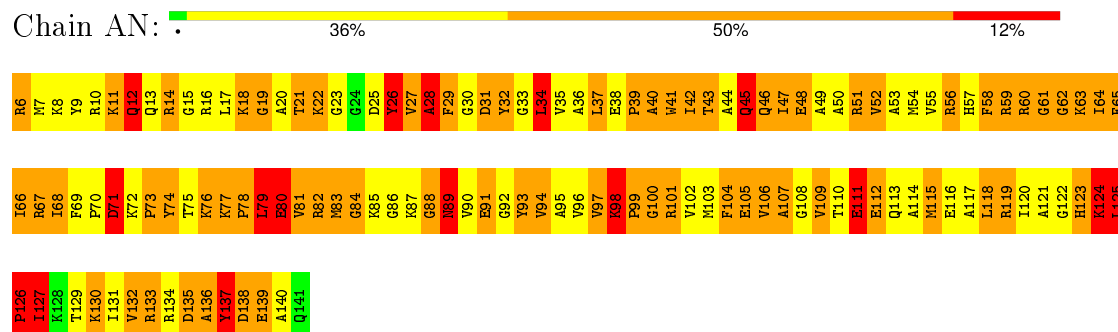


• Molecule 11: 50S ribosomal protein L15

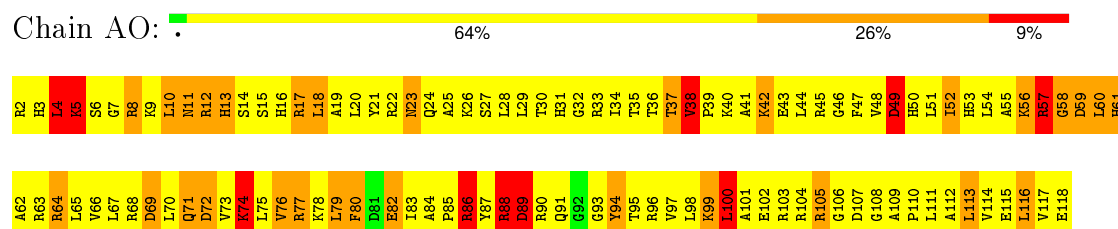
Chain AM: 6% 39% 47% 9%



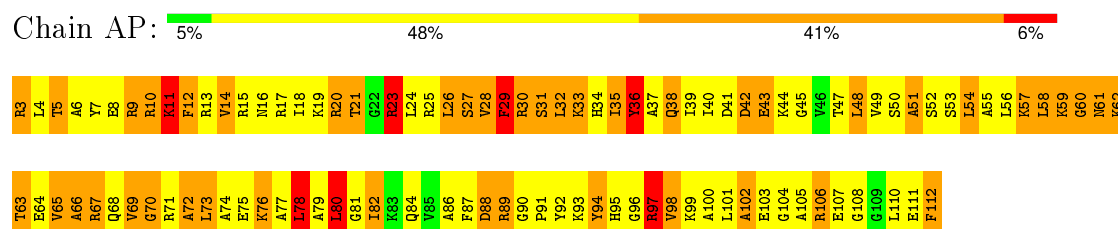
- Molecule 12: 50S ribosomal protein L16



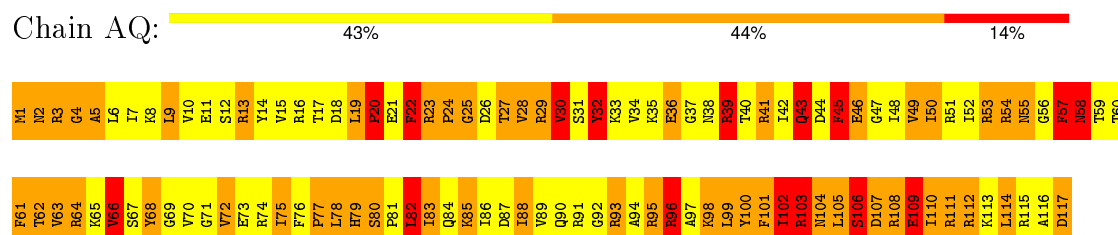
- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18

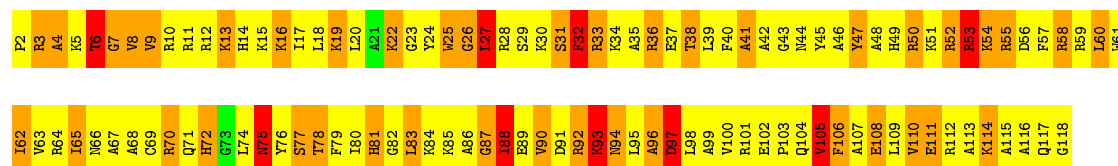


- Molecule 15: 50S ribosomal protein L19



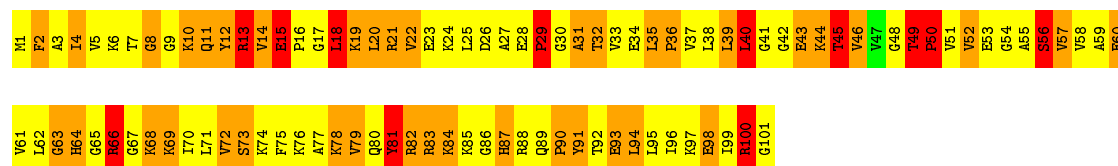
- Molecule 16: 50S ribosomal protein L20

Chain AR: 

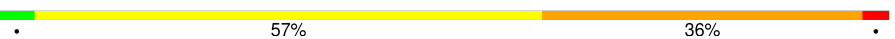


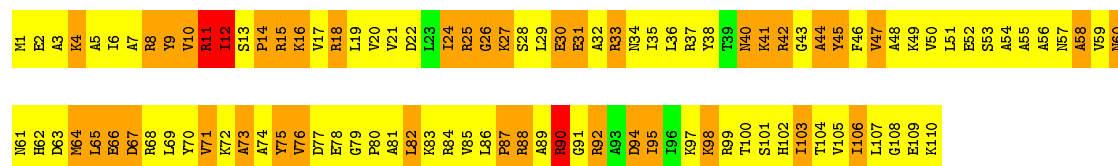
- Molecule 17: 50S ribosomal protein L21

Chain AS: 

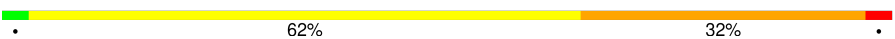


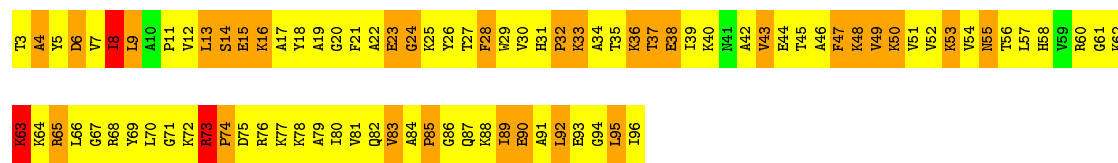
- Molecule 18: 50S ribosomal protein L22

Chain AT: 



- Molecule 19: 50S ribosomal protein L23

Chain AU: 



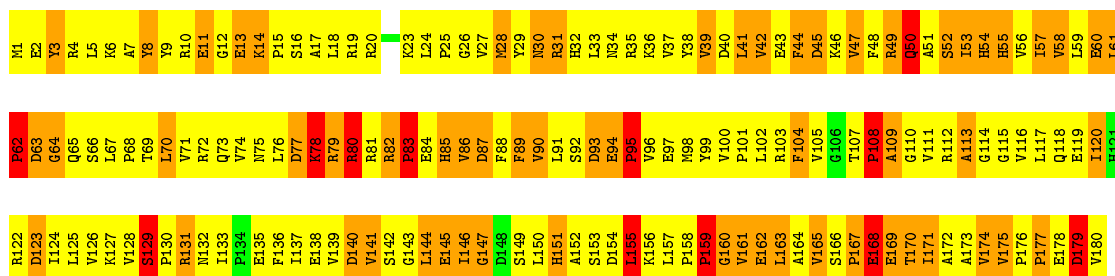
- Molecule 20: 50S ribosomal protein L24

Chain AV: 



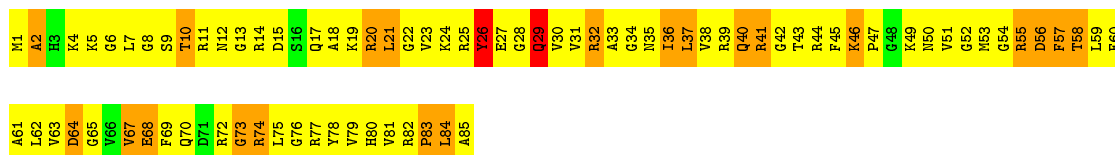
- Molecule 21: 50S ribosomal protein L25

Chain AW: 



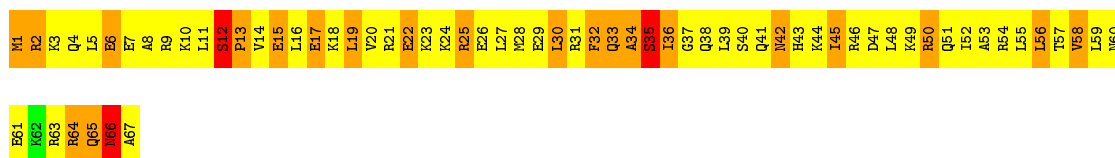
- Molecule 22: 50S ribosomal protein L27

Chain AX: 6% 67% 25%



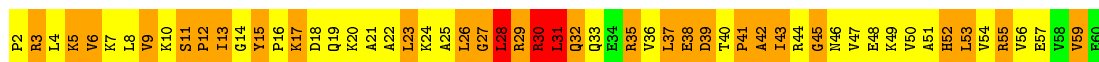
- Molecule 23: 50S ribosomal protein L29

Chain AY: 63% 31%

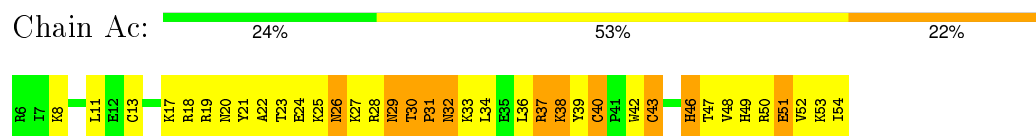


- Molecule 24: 50S ribosomal protein L30

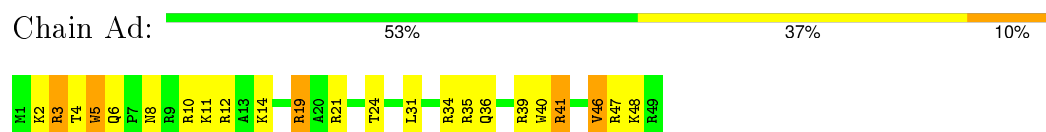
Chain AZ: 5% 46% 44% 5%



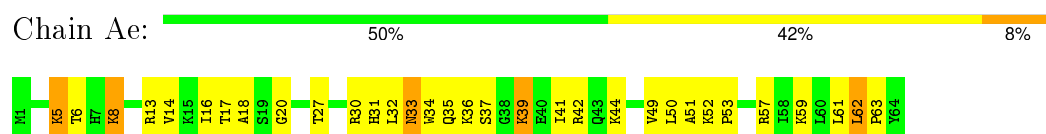
- Molecule 27: 50S ribosomal protein L33



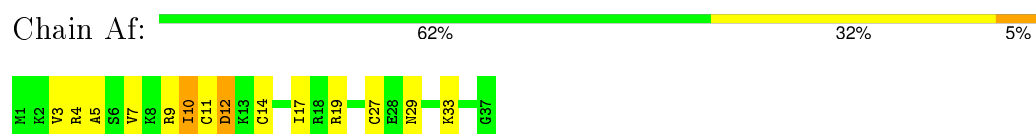
- Molecule 28: 50S ribosomal protein L34



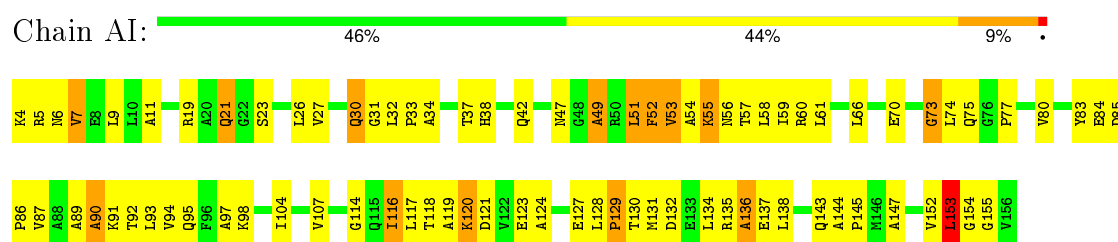
- Molecule 29: 50S ribosomal protein L35



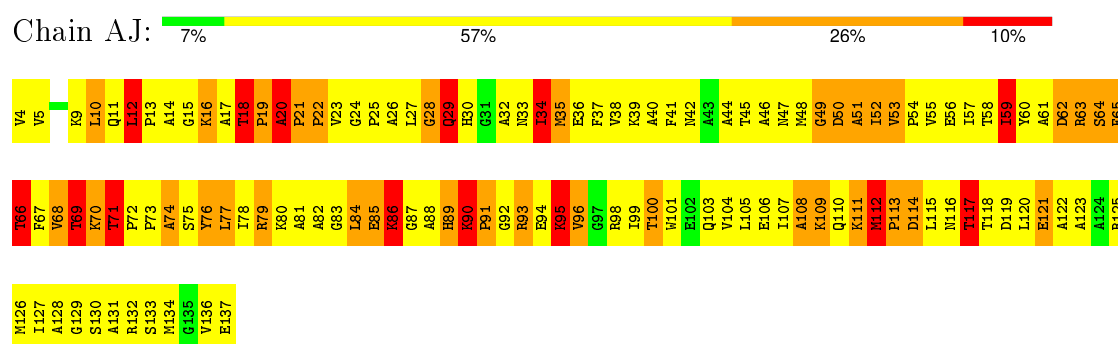
- Molecule 30: 50S ribosomal protein L36



- Molecule 31: 50S ribosomal protein L10



- Molecule 32: 50S ribosomal protein L11



- Molecule 33: Unknown peptide

Chain Ag:

100%

There are no outlier residues recorded for this chain.

● Molecule 34: 16S ribosomal RNA

Chain BA:

56%

36%

7%

6803	U743	6683	C623	A563	C503	A493	G371	C311	G251	C186E	C131	U65	U5
U804	C744	A684	C624	A564	C504	A494	C372	C312	U252	C186F	C132	G66	G6
C805	C745	G685	G625	U565	C505	A495	A373	A303	U253	C187	U133	C67	G7
A806	A746	U686	U626	G566	G506	U494	A374	C314	G254	U188	A134	G68	A8
C747	C747	A687	G627	G567	C507	A496	U375	A315	G255	U189	C135	G69	G9
C808	C748	G688	G628	G568	C508	A497	G376	G316	U256	G190	C136	G73	G10
C809	C749	C689	G629	C569	A509	U497	C377	G317	G257	G191A	C137	C74	G11
C810	C750	G690	C630	C570	A510	A498	C378	G318	G258	G191B	C138	C75	U12
C811	U751	G691	G631	U571	C511	A499	C379	G319	G259	G191C	C139	G76	U13
C812	C752	U692	A632	A572	U512	A440	G380	C320	G260	U191D	A140	C77	U14
A813	A753	G693	G633	A573	C513	A441	C381	A321	U261	G191E	A141	G78	G15
A814	C754	A694	C634	A574	C514	A442	A382	C322	A262	U191F	A142	G79	G16
A815	C755	A695	G635	G575	G515	A443	A383	U323	A263	G191	A143	G80	U17
A816	C756	A696	U636	G576	U516	A444	A384	G324	U264	U192	C18	G81	C18
C817	U757	U697	G637	G577	A517	A445	C385	A325	G265	C193	G145	U82	C19
G818	C758	G698	G638	C578	C518	A446	C386	G326	G266	C194	G146	U84	U20
A819	A759	C699	G639	G579	C519	A447	U387	A327	G267	A195	G147	U85	G21
U820	C760	U700	A640	U580	A520	A448	G388	C328	C268	A196	G148	U86	G22
G821	C761	C701	U641	G581	G521	A449	A389	A329	C269	A197	A149	A87	C23
C822	C762	A642	A642	U582	C522	A451	C390	C330	A270	G198	C150	C88	U24
G823	C763	A643	C643	A583	A523	A452	C391	G331	C271	G199	A151	U89	C25
C824	C764	A704	G644	G584	G524	A453	G392	G332	C272	G200	A152	C90	A26
G825	C765	U705	C645	G585	C525	A454	A393	G333	C273	C201	C153	C91	G27
C826	A766	A706	U646	G586	C526	A455	G394	C334	A274	U208	C154	G92	G28
C767	A767	C707	C947	G587	G527	A456	C395	C335	G275	G209	C155	U93	G29
A828	A768	C708	G648	G588	C528	A457	C396	C336	G276	U210	G156	G95	G31
C829	C769	G709	A649	C589	G529	A458	A397	C337	C277	G216	G157	G96	C31
G830	C770	G710	G650	C590	G530	A459	C398	A338	G278	C217	G158	U97	A32
C771	C771	C651	U651	U591	U531	A460	C399	C339	A279	C218	G159	C99	A33
C772	U772	A712	U652	G592	A532	A461	C400	U340	C280	C219	A160	A101	C34
C833	C773	G713	A653	G593	C533	A462	C401	C341	G281	G220	A161	G102	G35
C834	C774	A654	U654	U594	U534	A463	A402	C342	A282	C221	A162	C103	C36
U835	C775	A715	A655	G595	A535	A464	C403	U343	C283	U222	C163	G104	U37
G776	C776	A716	C656	C596	C536	A465	U404	A344	G284	U223	G164	G105	G38
C837	A777	C717	G657	G597	G537	A466	A405	C345	G285	C224	C165	G106	G39
C778	C778	G718	G658	U598	G538	A467	A406	G346	G286	C225	G166	G107	C40
U841	C779	C719	C659	U599	A539	A468	G407	C347	U287	G226	G167	G108	C41
C842	A780	C720	G660	C600	G540	A469	A408	G348	A288	G227	G168	A109	G42
U843	C781	G721	G661	C601	G541	A470	A409	A349	G289	A228	C169	C110	C43
C848	A782	A722	G662	A602	G542	A481	A410	G350	C290	U229	G170	G111	G44
C849	C783	U723	A663	U603	C543	A482	A411	C351	C291	G230	A171	G112	U45
U850	C784	G724	G664	C604	G544	A483	A412	C352	G292	C231	A172	G113	G46
G851	C785	G725	A665	U605	C545	A484	G413	A353	G293	G232	U173	G114	G47
G852	C786	G666	G666	G606	G546	A485	A414	G354	U294	C233	C174	G115	C48
G853	C787	A727	G667	A607	G547	A486	A415	C355	C295	C234	C175	U49	C49
U854	A788	C728	G668	A608	G548	A487	A416	A356	U296	C235	C176	G117	A50
G855	U789	U669	U669	A609	C549	C488	C417	G357	G297	G236	C177	U118	A51
C856	A790	C730	G670	G610	G550	A489	C418	U358	A298	C237	C178	A119	G52
C857	C791	G731	G671	A611	U551	A490	C419	U359	G299	G238	A179	A120	A53
C858	A792	C732	U672	C612	U552	A491	U420	A360	C300	G239	C180	C54	C50
A859	C793	A733	G673	C613	A553	A492	U421	G361	G301	G240	G181	G122	A55
U860	A794	G734	G674	A614	C554	A493	C422	A362	G302	C242	U182	C123	U56
C795	C795	C735	A675	C615	C555	U494	A423	G363	A303	A243	G183	G124	C57
C862	C796	C736	A676	G616	C556	A495	G424	A364	U304	U244	G184	U125	C58
U863	C797	A737	U677	G617	G557	A496	G425	U365	G305	C245	A185	G126	A59
A864	C798	C738	U678	C618	G558	U497	G426	C366	G306	A246	C186	G127	C60
C865	C799	C739	C679	U619	A559	A498	U427	G367	C307	G247	C187	G128	C61
C866	G800	U740	C680	U560	C560	A500	G428	U368	C308	C248	C188	U129	G62
C867	U801	G741	C681	A621	U561	C501	U429	C369	G309	U249	G189	C129A	C63
C868	C802	C742	C682	A622	C562	C502	A429	C370	C210	G250	C190	A130	C64

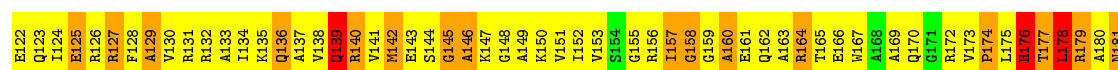
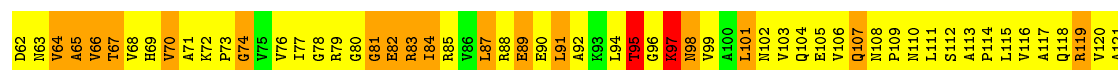
- Molecule 35: 30S ribosomal protein S2

Chain BF: 



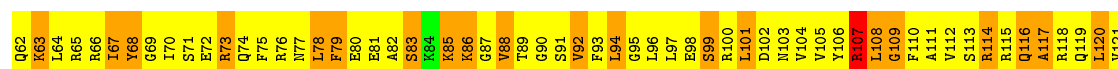
- Molecule 36: 30S ribosomal protein S3

Chain BG: 5% 56% 34%



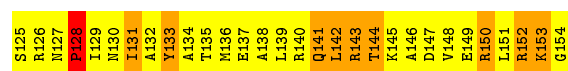
- Molecule 37: 30S ribosomal protein S4

Chain BH: 54% 37% 7%



- Molecule 38: 30S ribosomal protein S5

Chain BI: 63% 33%



- Molecule 39: 30S ribosomal protein S6

Chain BJ: 53% 37% 7%

M1 R2 R3 Y4 E5 V6 W7 I8 V9 L10 L11 L12 M13 M14 L15 D16 Q16 S17 Q18 Q19 L20 A20 L21 L22 E23 K23 E24 I25 I26 Q27 R28 A29 L30 L31 E31 N32 Y33 G34 A35 A36 V37 E38 K39 V40 E41 E42 L43 G44 L45 R46 R47 L48 A49 Y50 Y51 I52 A53 K54 D55 P56 Q57 G58 Y59 F60

L61 M62 Y63 Q64 V65 E66 W67 P68 E69 D70 R71 L72 V73 W74 D75 L76 A77 R78 R79 E80 L81 L82 R83 D83 N84 E85 E86 R87 R88 E89 V90 V91 V92 R93 R94 R95 E96 P96 F97 E98 A99 N100 A101

• Molecule 40: 30S ribosomal protein S7

Chain BK: 5% 59% 29% 8%

A2 R3 R4 R5 R6 E6 A7 E8 E9 R10 R11 Q12 L13 Q14 E15 D16 L17 V18 Y19 R20 G21 D22 V21 L22 L23 Y24 Q25 R26 A27 E28 E29 R30 R31 R32 R33 R34 Q35 Q36 K37 L38 A39 R40 R41 L42 L43 V44 Q45 A46 A47 N48 Q49 R50 Q51 E52 T53 G55 E56 E57 V58 R59 Q60 V61 F62 E63

Q64 A65 E66 E67 V68 W69 R70 R71 R72 R73 R74 E75 V76 R77 S78 R79 R80 G81 G82 A83 N84 E85 Y86 Q86 R87 A88 E89 E90 V91 R92 R93 R94 R95 R96 Q97 Q98 S98 L99 L100 A101 R102 R103 V104 V105 Q106 A107 A108 N109 Q110 Q111 R112 P112 E113 R114 R115 G116 A117 Q118 V119 I120 A121 E122 E123

L124 M125 D126 A127 A128 E129 G130 K131 G132 G133 G134 A135 V136 K137 K138 E139 D140 V141 E142 E143 M144 A145 E146 A147 N148 R149 R150 Y151 A152 H153 H154 R155 W156

• Molecule 41: 30S ribosomal protein S8

Chain BL: 56% 34% 8%

M1 L2 T3 D4 P5 I6 A7 D8 M9 L10 T11 L12 R13 I14 A15 N16 A17 T18 R19 V20 Y21 R22 K23 E24 T25 D26 V27 P28 R29 S30 R31 R32 E33 E34 I35 I36 L37 R38 L39 A40 R41 E42 G43 G44 I45 K46 G47 Y48 E49 R50 V51 D52 D53 D54 G55 G56 K57 Y58 L59 R60

V61 V62 L63 M64 V65 G66 P67 R68 R69 Q70 G71 G72 P73 D74 F75 R76 R77 Q78 Q79 R80 R81 H82 R83 R84 R85 V86 S87 R88 R89 P90 R91 R92 R93 Y94 Y95 Y96 G97 Y98 R99 E100 P101 R102 V103 V104 R105 G106 L107 G108 T109 A110 T111 L112 S113 T114 S115 K116 G117 V118 L119 T120

D121 R122 E123 A124 R125 K126 L127 G128 V129 G130 G131 G132 E133 L134 C135 E136 V137 W138

• Molecule 42: 30S ribosomal protein S9

Chain BM: 61% 31% 6%

E2 Q3 Y4 Y5 G6 T7 G8 R9 R10 K11 E12 E13 A14 V15 A16 R17 V18 F19 L20 R21 F22 H23 G24 G25 K26 V26 T27 V28 N29 R30 G31 Q32 D33 F34 N35 E36 Y37 F38 Q39 L40 L41 V42 R43 A44 A45 A46 L47 E48 E49 P49 L50 R51 R52 A53 K54 Y55 G56 K57 E58 F59 D60 A61

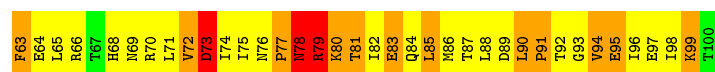
Y62 I63 T64 V65 R66 G67 G68 G69 R70 S71 L72 G73 Q74 V75 A76 R77 A78 R79 G80 G81 I82 A83 R84 A85 K86 V86 Q87 Y88 N89 R90 P91 D92 R93 R94 A95 G96 L96 Y97 K98 L99 G100 F101 L102 T103 R104 A105 A106 A107 V108 V109 E110 R111 K112 K113 Y114 G115 K116 H117 K118 A119 R120 R121

A122 F123 Q124 Y125 S126 K127 R128

• Molecule 43: 30S ribosomal protein S10

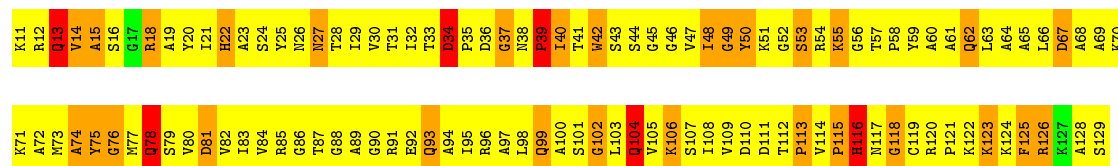
Chain BN: 55% 39%

K3 L4 I6 K7 L8 R9 G10 F11 D12 H13 H14 K15 L16 D17 A18 S19 A20 A21 Q22 K23 V24 E25 A26 A27 R28 R29 S30 G31 A32 A33 Y34 S35 G36 P37 P38 I38 P39 L40 P41 T42 R43 V44 R45 R46 F47 T48 V49 I50 R51 G52 P53 F54 K55 H56 K57 D58 S59 R60 E61 H62



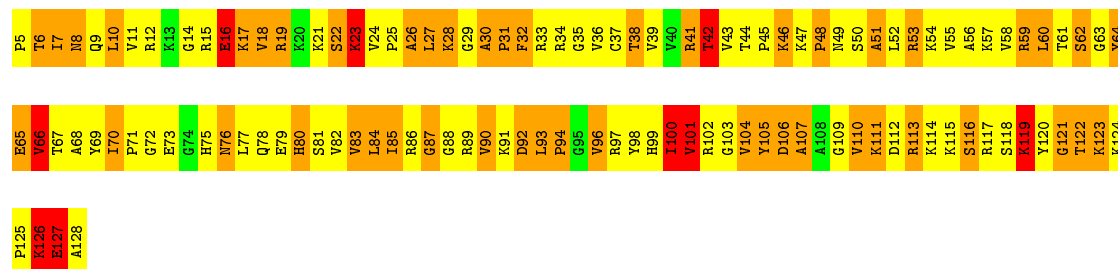
• Molecule 44: 30S ribosomal protein S11

Chain BO: . 69% 24% 5%



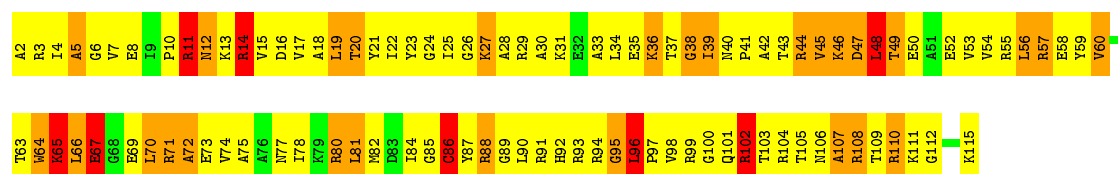
• Molecule 45: 30S ribosomal protein S12

Chain BP: 5% 49% 39% 7%



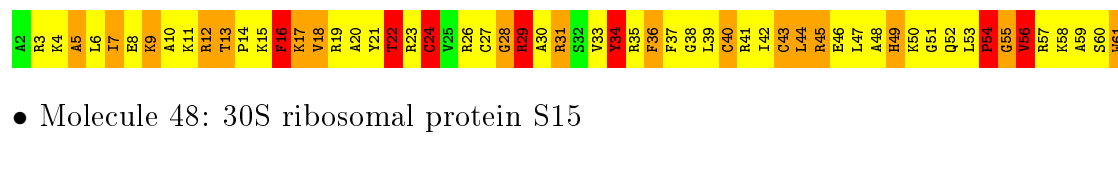
• Molecule 46: 30S ribosomal protein S13

Chain BQ: 10% 59% 25% 7%



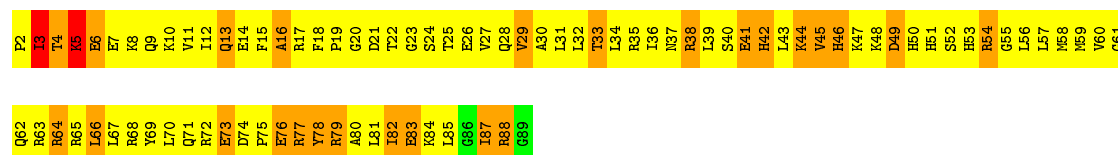
• Molecule 47: 30S ribosomal protein S14 type Z

Chain BR: 5% 55% 28% 12%

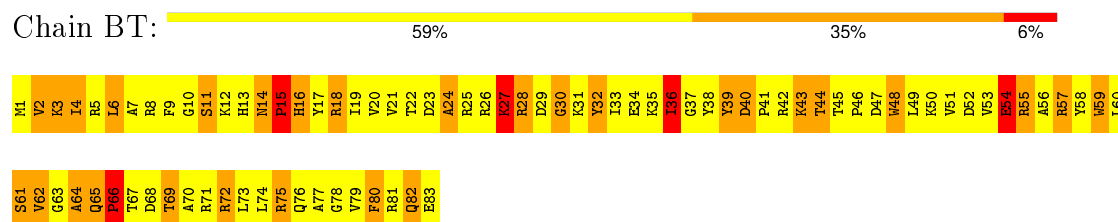


• Molecule 48: 30S ribosomal protein S15

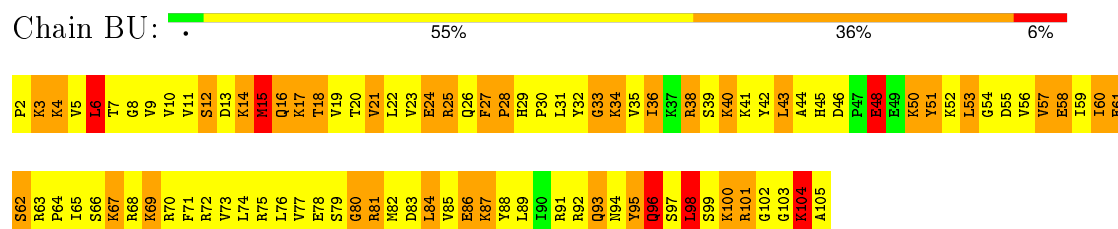
Chain BS: . 67% 28%



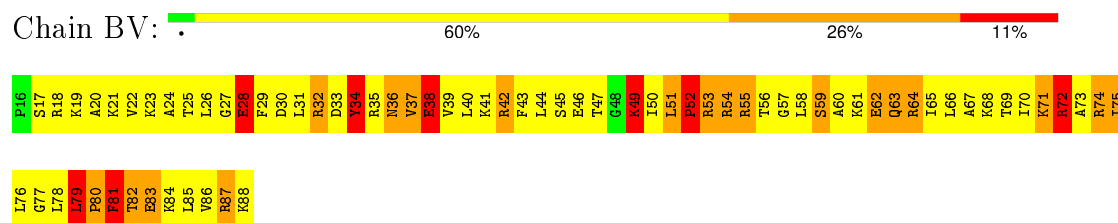
- Molecule 49: 30S ribosomal protein S16



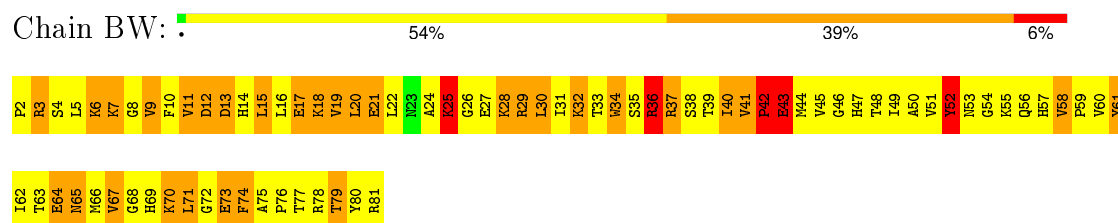
- Molecule 50: 30S ribosomal protein S17



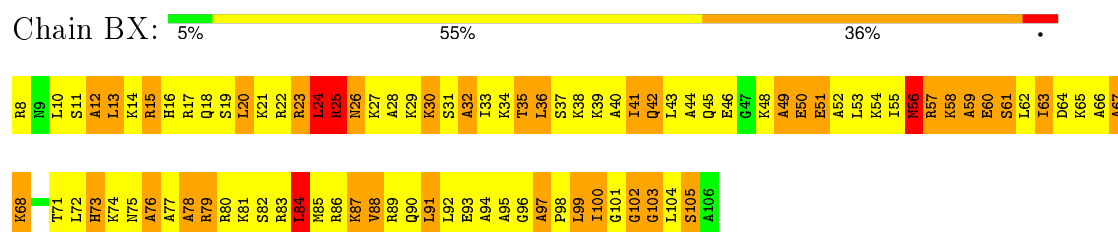
- Molecule 51: 30S ribosomal protein S18



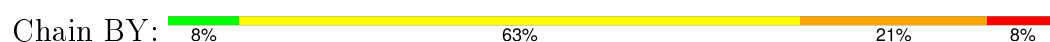
- Molecule 52: 30S ribosomal protein S19



- Molecule 53: 30S ribosomal protein S20



- Molecule 54: 30S ribosomal protein Thx



P305	E371	D432	Q493	B553
T306	N372	G433	G494	A554
S307	M373	K434	K495	V555
S308	R374	G435	A496	V556
V309	R375	R436	V497	L557
F310	E376	V437	A498	V558
F311	G377	R438	F499	P559
C312	F378	L439	A500	P560
V313	E379	D440	L501	L561
N314	L380	Y441	F502	N562
T315	A381	Y442	G503	N563
S316	V382	I443	L504	T564
P317	S383	P444	Q505	L565
F318	R384	S445	D506	B566
C319	P385	R446	R507	Q567
G320	K386	G447	G508	A568
K321	V387	L448	K509	B570
E322	I388	T449	L510	P571
G323	F389	G450	F511	L572
K324	R390	F451	L512	D573
F325	E391	R452	G513	D574
V326	I392	S453	H514	D575
T327	D393	E454	G515	D576
S328	G394	F455	A516	B577
R329	R395	M456	E517	L577
Q330	K396	T457	V518	V578
I331	Q397	M458	Y519	B579
L332	E398	T459	B520	V580
D333	P399	S460	G521	T581
E338	Y400	G461	Q522	P582
L339	E401	T462	I523	T583
V340	N402	G463	I524	S584
H341	V403	L464	G525	L585
D352	T404	L465	I526	B586
A353	L405	Y466	H527	L587
D354	D406	S467	S528	B588
A355	V407	T468	R529	K589
F356	E408	F469	S530	B590
R357	E409	S470	N531	B591
V358	Q410	H471	D532	L592
S359	H411	Y472	L533	T593
G360	Q412	D473	T534	D596
R361	G413	D474	V535	B597
G362	S414	V475	N536	R598
E363	V415	R476	C537	B599
L364	M416	P477	L538	A600
R365	Q417	V480	T539	N601
L366	A418	G481	G540	B602
S367	L419	Q482	K541	A603
V368	E422	R483	L542	P604
L369	K423	Q484	T544	R605
P431	G424	N485	N545	
	D425	G486	M546	
	L426	V487	R547	
	K427	L488	A548	
	N428	I489	S549	
	M429	G550	A551	
	N430	N491	D552	

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTFFIND3	Depositor
Microscope	OTHER	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1.5	Depositor
Maximum defocus (nm)	4.0	Depositor
Magnification	Not provided	Depositor
Image detector	FALCON II DIRECT ELECTRON	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, 8AN, NMY

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 2$	RMSZ	$\# Z > 2$
1	AA	1.00	107/69678 (0.2%)	1.08	348/108758 (0.3%)
10	AL	0.92	1/942 (0.1%)	1.31	10/1268 (0.8%)
11	AM	0.71	0/1123	1.12	5/1493 (0.3%)
12	AN	0.72	0/1100	1.19	8/1470 (0.5%)
13	AO	0.70	0/974	1.06	2/1302 (0.2%)
14	AP	0.72	0/887	1.06	4/1180 (0.3%)
15	AQ	0.85	0/990	1.31	9/1325 (0.7%)
16	AR	0.76	0/982	1.08	0/1306
17	AS	0.87	1/790 (0.1%)	1.28	9/1057 (0.9%)
18	AT	0.66	0/886	1.04	1/1189 (0.1%)
19	AU	0.57	0/756	0.93	0/1015
2	AB	0.83	4/2954 (0.1%)	0.99	7/4606 (0.2%)
20	AV	0.54	0/857	1.05	2/1142 (0.2%)
21	AW	0.66	0/1467	1.11	7/1992 (0.4%)
22	AX	0.65	0/679	1.04	1/902 (0.1%)
23	AY	0.59	0/569	0.88	0/751
24	AZ	0.59	0/474	1.10	2/635 (0.3%)
25	Aa	0.84	1/594 (0.2%)	1.31	8/795 (1.0%)
26	Ab	0.72	0/459	1.16	3/621 (0.5%)
27	Ac	0.85	1/433 (0.2%)	1.36	5/576 (0.9%)
28	Ad	0.73	0/438	1.01	0/575
29	Ae	0.59	0/523	1.14	5/690 (0.7%)
3	AC	0.54	0/1772	0.87	0/2383
30	Af	0.59	0/310	1.08	1/407 (0.2%)
31	AI	0.50	1/751 (0.1%)	0.82	4/1042 (0.4%)
32	AJ	0.52	0/1012	0.64	8/1373 (0.6%)
34	BA	0.92	26/36437 (0.1%)	1.10	139/56865 (0.2%)
35	BF	0.65	0/1935	1.00	4/2609 (0.2%)
36	BG	0.55	0/1636	0.92	4/2205 (0.2%)
37	BH	0.64	1/1733 (0.1%)	0.98	3/2318 (0.1%)
38	BI	0.63	0/1162	1.01	3/1564 (0.2%)
39	BJ	0.60	0/856	0.95	0/1154

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
4	AD	0.72	2/2174 (0.1%)	1.19	13/2927 (0.4%)
40	BK	0.57	0/1276	0.90	3/1709 (0.2%)
41	BL	0.62	0/1136	1.01	3/1527 (0.2%)
42	BM	0.54	0/1029	0.83	0/1379
43	BN	0.48	0/807	0.89	1/1085 (0.1%)
44	BO	0.62	0/900	0.98	0/1213
45	BP	0.60	0/986	1.00	3/1320 (0.2%)
46	BQ	0.33	0/924	0.45	2/1238 (0.2%)
47	BR	0.55	0/501	0.97	1/664 (0.2%)
48	BS	0.62	0/745	0.95	0/992
49	BT	0.62	0/716	0.95	1/963 (0.1%)
5	AE	0.75	0/1611	1.16	13/2171 (0.6%)
50	BU	0.68	1/870 (0.1%)	0.99	2/1159 (0.2%)
51	BV	0.59	0/603	1.01	1/799 (0.1%)
52	BW	0.53	1/661 (0.2%)	1.34	5/890 (0.6%)
53	BX	0.65	0/765	1.00	2/1007 (0.2%)
54	BY	0.45	0/212	0.80	0/277
55	BC	0.36	0/1809	0.67	0/2819
56	BD	0.37	0/1784	0.68	0/2780
56	BE	0.35	0/1784	0.70	0/2780
57	BZ	0.37	0/4678	0.50	16/6310 (0.3%)
6	AF	0.64	0/1660	1.03	4/2247 (0.2%)
7	AG	0.62	0/1507	1.06	4/2027 (0.2%)
8	AH	0.59	0/1354	0.98	4/1831 (0.2%)
9	AK	0.78	1/1140 (0.1%)	1.16	8/1537 (0.5%)
All	All	0.86	148/167791 (0.1%)	1.05	688/250219 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	432
12	AN	0	1
15	AQ	0	1
17	AS	0	1
2	AB	0	17
25	Aa	0	1
26	Ab	0	1
3	AC	0	1
31	AI	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	BA	0	170
37	BH	0	1
39	BJ	0	1
44	BO	0	1
47	BR	0	1
5	AE	0	1
6	AF	0	1
9	AK	0	1
All	All	0	634

The worst 5 of 148 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	1060	U	O3'-P	-80.27	0.64	1.61
34	BA	1317	C	O3'-P	-70.10	0.77	1.61
1	AA	1203	G	O3'-P	-34.75	1.19	1.61
34	BA	1167	A	O3'-P	20.86	1.86	1.61
1	AA	2500	U	C4-O4	18.56	1.38	1.23

The worst 5 of 688 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	BA	1064	G	N1-C2-N2	-71.66	51.71	116.20
34	BA	1064	G	N3-C2-N2	57.63	160.24	119.90
34	BA	1317	C	P-O3'-C3'	-48.78	61.17	119.70
34	BA	1317	C	O3'-P-O5'	30.58	162.11	104.00
1	AA	1060	U	O3'-P-O5'	28.68	158.49	104.00

There are no chirality outliers.

5 of 634 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	14	A	Sidechain
1	AA	25	U	Sidechain
1	AA	3	U	Sidechain
1	AA	31	C	Sidechain
1	AA	9	U	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	62218	0	31250	16189	0
2	AB	2641	0	1337	612	0
3	AC	1742	0	1779	1073	0
4	AD	2124	0	2207	1489	0
5	AE	1578	0	1647	1111	0
6	AF	1625	0	1666	824	0
7	AG	1482	0	1546	878	0
8	AH	1328	0	1407	716	0
9	AK	1113	0	1183	775	0
10	AL	932	0	992	735	0
11	AM	1106	0	1183	771	0
12	AN	1080	0	1127	743	0
13	AO	960	0	1021	592	0
14	AP	877	0	938	509	0
15	AQ	976	0	1031	647	0
16	AR	964	0	1022	730	0
17	AS	779	0	852	567	0
18	AT	876	0	941	442	0
19	AU	742	0	800	355	0
20	AV	844	0	930	431	0
21	AW	1435	0	1463	733	0
22	AX	670	0	700	380	0
23	AY	567	0	621	306	0
24	AZ	469	0	518	322	0
25	Aa	581	0	577	0	0
26	Ab	445	0	459	0	0
27	Ac	426	0	452	0	0
28	Ad	430	0	480	0	0
29	Ae	515	0	587	0	0
30	Af	307	0	335	0	0
31	AI	752	0	363	165	0
32	AJ	993	0	1019	739	0
33	Ag	620	0	132	0	0
34	BA	32554	0	16390	7456	0
35	BF	1900	0	1951	1054	0
36	BG	1612	0	1677	720	0
37	BH	1703	0	1763	850	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	BI	1146	0	1207	586	0
39	BJ	843	0	857	393	0
40	BK	1257	0	1296	564	0
41	BL	1116	0	1177	722	0
42	BM	1010	0	1035	505	0
43	BN	794	0	840	371	0
44	BO	885	0	904	471	0
45	BP	970	0	1057	519	0
46	BQ	914	0	954	640	0
47	BR	492	0	529	283	0
48	BS	734	0	771	348	0
49	BT	700	0	720	351	0
50	BU	857	0	930	454	0
51	BV	597	0	666	373	0
52	BW	647	0	653	536	0
53	BX	763	0	857	410	0
54	BY	208	0	221	88	0
55	BC	1619	0	819	220	0
56	BD	1597	0	802	300	0
56	BE	1597	0	799	357	0
57	BZ	4610	0	4492	2673	0
58	AA	42	0	46	25	0
58	BA	42	0	46	15	0
59	AA	44	0	18	80	0
60	BZ	32	0	14	38	0
All	All	155482	0	106056	49352	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 197.

The worst 5 of 49352 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)
32:AJ:112:MET:SD	32:AJ:122:ALA:HB2	1.28	1.70
3:AC:171:ILE:CD1	3:AC:192:PHE:CZ	1.75	1.70
34:BA:1226:C:C4	46:BQ:104:ARG:HG3	1.16	1.69
1:AA:716:A:C2	48:BS:44:LYS:HG3	1.30	1.67
32:AJ:75:SER:HB3	32:AJ:130:SER:CB	1.24	1.66

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	
3	AC	220/228 (96%)	153 (70%)	39 (18%)	28 (13%)	0	8
4	AD	270/272 (99%)	125 (46%)	59 (22%)	86 (32%)	0	0
5	AE	204/206 (99%)	117 (57%)	31 (15%)	56 (28%)	0	0
6	AF	206/208 (99%)	109 (53%)	46 (22%)	51 (25%)	0	1
7	AG	180/182 (99%)	79 (44%)	47 (26%)	54 (30%)	0	0
8	AH	172/174 (99%)	80 (46%)	46 (27%)	46 (27%)	0	0
9	AK	137/139 (99%)	64 (47%)	28 (20%)	45 (33%)	0	0
10	AL	120/122 (98%)	59 (49%)	23 (19%)	38 (32%)	0	0
11	AM	143/145 (99%)	57 (40%)	36 (25%)	50 (35%)	0	0
12	AN	134/136 (98%)	49 (37%)	33 (25%)	52 (39%)	0	0
13	AO	115/117 (98%)	57 (50%)	39 (34%)	19 (16%)	0	5
14	AP	108/110 (98%)	48 (44%)	28 (26%)	32 (30%)	0	0
15	AQ	115/117 (98%)	52 (45%)	26 (23%)	37 (32%)	0	0
16	AR	115/117 (98%)	35 (30%)	50 (44%)	30 (26%)	0	1
17	AS	99/101 (98%)	52 (52%)	19 (19%)	28 (28%)	0	0
18	AT	108/110 (98%)	63 (58%)	24 (22%)	21 (19%)	0	3
19	AU	92/94 (98%)	57 (62%)	16 (17%)	19 (21%)	0	3
20	AV	108/110 (98%)	43 (40%)	32 (30%)	33 (31%)	0	0
21	AW	178/180 (99%)	96 (54%)	43 (24%)	39 (22%)	0	2
22	AX	83/85 (98%)	52 (63%)	21 (25%)	10 (12%)	0	9
23	AY	65/67 (97%)	36 (55%)	20 (31%)	9 (14%)	0	6
24	AZ	57/59 (97%)	34 (60%)	8 (14%)	15 (26%)	0	1
25	Aa	69/71 (97%)	23 (33%)	15 (22%)	31 (45%)	0	0
26	Ab	55/57 (96%)	14 (26%)	19 (34%)	22 (40%)	0	0
27	Ac	47/49 (96%)	14 (30%)	7 (15%)	26 (55%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Ad	47/49 (96%)	20 (43%)	12 (26%)	15 (32%)	0	0
29	Ae	62/64 (97%)	23 (37%)	17 (27%)	22 (36%)	0	0
30	Af	35/37 (95%)	20 (57%)	5 (14%)	10 (29%)	0	0
31	AI	151/153 (99%)	89 (59%)	33 (22%)	29 (19%)	0	3
32	AJ	132/134 (98%)	56 (42%)	44 (33%)	32 (24%)	0	1
35	BF	232/234 (99%)	114 (49%)	41 (18%)	77 (33%)	0	0
36	BG	204/206 (99%)	107 (52%)	46 (22%)	51 (25%)	0	1
37	BH	206/208 (99%)	95 (46%)	58 (28%)	53 (26%)	0	1
38	BI	148/150 (99%)	93 (63%)	38 (26%)	17 (12%)	0	9
39	BJ	99/101 (98%)	58 (59%)	19 (19%)	22 (22%)	0	2
40	BK	153/155 (99%)	73 (48%)	45 (29%)	35 (23%)	0	1
41	BL	136/138 (99%)	68 (50%)	35 (26%)	33 (24%)	0	1
42	BM	125/127 (98%)	62 (50%)	33 (26%)	30 (24%)	0	1
43	BN	96/98 (98%)	52 (54%)	20 (21%)	24 (25%)	0	1
44	BO	117/119 (98%)	65 (56%)	29 (25%)	23 (20%)	0	3
45	BP	122/124 (98%)	50 (41%)	30 (25%)	42 (34%)	0	0
46	BQ	112/114 (98%)	64 (57%)	28 (25%)	20 (18%)	0	4
47	BR	58/60 (97%)	24 (41%)	16 (28%)	18 (31%)	0	0
48	BS	86/88 (98%)	36 (42%)	35 (41%)	15 (17%)	0	4
49	BT	81/83 (98%)	42 (52%)	24 (30%)	15 (18%)	0	3
50	BU	102/104 (98%)	62 (61%)	23 (22%)	17 (17%)	0	5
51	BV	71/73 (97%)	26 (37%)	26 (37%)	19 (27%)	0	0
52	BW	78/80 (98%)	30 (38%)	25 (32%)	23 (30%)	0	0
53	BX	97/99 (98%)	38 (39%)	32 (33%)	27 (28%)	0	0
54	BY	22/24 (92%)	9 (41%)	6 (27%)	7 (32%)	0	0
57	BZ	603/605 (100%)	280 (46%)	200 (33%)	123 (20%)	0	3
All	All	6575/6683 (98%)	3224 (49%)	1675 (26%)	1676 (26%)	0	1

5 of 1676 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	35	ALA
3	AC	39	GLU

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Mol	Chain	Res	Type
3	AC	54	SER
3	AC	61	THR
3	AC	72	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AC	180/180 (100%)	151 (84%)	29 (16%)	3	21
4	AD	215/215 (100%)	153 (71%)	62 (29%)	0	4
5	AE	166/166 (100%)	102 (61%)	64 (39%)	0	0
6	AF	164/164 (100%)	105 (64%)	59 (36%)	0	1
7	AG	156/156 (100%)	112 (72%)	44 (28%)	0	4
8	AH	143/143 (100%)	108 (76%)	35 (24%)	1	7
9	AK	118/118 (100%)	79 (67%)	39 (33%)	0	2
10	AL	100/100 (100%)	69 (69%)	31 (31%)	0	3
11	AM	111/111 (100%)	71 (64%)	40 (36%)	0	1
12	AN	106/106 (100%)	65 (61%)	41 (39%)	0	0
13	AO	100/100 (100%)	71 (71%)	29 (29%)	0	3
14	AP	87/87 (100%)	63 (72%)	24 (28%)	0	4
15	AQ	105/105 (100%)	68 (65%)	37 (35%)	0	1
16	AR	93/93 (100%)	64 (69%)	29 (31%)	0	3
17	AS	82/82 (100%)	57 (70%)	25 (30%)	0	3
18	AT	90/90 (100%)	64 (71%)	26 (29%)	0	4
19	AU	76/76 (100%)	57 (75%)	19 (25%)	1	6
20	AV	91/91 (100%)	72 (79%)	19 (21%)	1	11
21	AW	159/159 (100%)	120 (76%)	39 (24%)	1	7
22	AX	67/67 (100%)	51 (76%)	16 (24%)	1	7
23	AY	62/62 (100%)	44 (71%)	18 (29%)	0	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	AZ	51/51 (100%)	36 (71%)	15 (29%)	0	3
25	Aa	63/63 (100%)	45 (71%)	18 (29%)	0	4
26	Ab	50/50 (100%)	31 (62%)	19 (38%)	0	0
27	Ac	48/48 (100%)	32 (67%)	16 (33%)	0	2
28	Ad	42/42 (100%)	29 (69%)	13 (31%)	0	3
29	Ae	54/54 (100%)	44 (82%)	10 (18%)	2	15
30	Af	34/34 (100%)	29 (85%)	5 (15%)	4	25
32	AJ	101/101 (100%)	71 (70%)	30 (30%)	0	3
35	BF	202/202 (100%)	138 (68%)	64 (32%)	0	3
36	BG	160/160 (100%)	123 (77%)	37 (23%)	1	8
37	BH	180/180 (100%)	131 (73%)	49 (27%)	0	5
38	BI	115/115 (100%)	78 (68%)	37 (32%)	0	3
39	BJ	90/90 (100%)	61 (68%)	29 (32%)	0	3
40	BK	126/126 (100%)	93 (74%)	33 (26%)	0	6
41	BL	119/119 (100%)	86 (72%)	33 (28%)	0	4
42	BM	98/98 (100%)	73 (74%)	25 (26%)	1	6
43	BN	88/88 (100%)	67 (76%)	21 (24%)	1	7
44	BO	90/90 (100%)	73 (81%)	17 (19%)	2	14
45	BP	104/104 (100%)	81 (78%)	23 (22%)	1	10
46	BQ	92/92 (100%)	67 (73%)	25 (27%)	0	5
47	BR	49/49 (100%)	36 (74%)	13 (26%)	0	5
48	BS	79/79 (100%)	64 (81%)	15 (19%)	2	14
49	BT	72/72 (100%)	49 (68%)	23 (32%)	0	3
50	BU	96/96 (100%)	67 (70%)	29 (30%)	0	3
51	BV	64/64 (100%)	48 (75%)	16 (25%)	1	6
52	BW	71/71 (100%)	52 (73%)	19 (27%)	0	5
53	BX	76/76 (100%)	59 (78%)	17 (22%)	1	10
54	BY	19/19 (100%)	17 (90%)	2 (10%)	8	39
57	BZ	486/514 (95%)	338 (70%)	148 (30%)	0	3
All	All	5390/5418 (100%)	3864 (72%)	1526 (28%)	2	4

5 of 1526 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	AW	179	ASP
35	BF	20	GLU
57	BZ	115	LYS
23	AY	12	SER
26	Ab	51	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 192 such sidechains are listed below:

Mol	Chain	Res	Type
29	Ae	35	GLN
36	BG	170	GLN
57	BZ	150	ASN
30	Af	36	GLN
35	BF	204	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	2881/2889 (99%)	1265 (43%)	253 (8%)
2	AB	122/123 (99%)	46 (37%)	3 (2%)
34	BA	1514/1515 (99%)	484 (31%)	140 (9%)
55	BC	75/76 (98%)	26 (34%)	0
56	BD	74/75 (98%)	31 (41%)	2 (2%)
56	BE	74/75 (98%)	23 (31%)	1 (1%)
All	All	4740/4753 (99%)	1875 (39%)	399 (8%)

5 of 1875 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	13	A
1	AA	14	A
1	AA	15	G
1	AA	20	C
1	AA	26	G

5 of 399 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	2021	C
1	AA	2503	A
34	BA	1239	A

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Mol	Chain	Res	Type
1	AA	2047	U
1	AA	2240	C

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](#)

5 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	NMY	AA	3001	-	45,45,45	0.51	0	59,67,67	1.15	7 (11%)
59	8AN	AA	3002	1,56	18,24,25	1.13	1 (5%)	10,35,38	2.37	2 (20%)
59	8AN	AA	3003	1,56,22	18,24,25	1.13	1 (5%)	10,35,38	2.38	1 (10%)
58	NMY	BA	1601	-	45,45,45	0.50	0	59,67,67	1.03	6 (10%)
60	GCP	BZ	701	-	29,34,34	1.73	7 (24%)	32,54,54	1.72	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
58	NMY	AA	3001	-	-	0/18/94/94	1/4/4/4
59	8AN	AA	3002	1,56	-	0/3/25/26	0/3/3/3
59	8AN	AA	3003	1,56,22	-	0/3/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	NMY	BA	1601	-	-	0/18/94/94	0/4/4/4
60	GCP	BZ	701	-	-	0/15/38/38	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	BZ	701	GCP	PG-O2G	-2.64	1.48	1.54
60	BZ	701	GCP	PB-O2B	2.13	1.61	1.56
60	BZ	701	GCP	PB-O3A	2.63	1.61	1.58
60	BZ	701	GCP	PG-O3G	2.66	1.61	1.54
59	AA	3002	8AN	C5-C4	3.07	1.47	1.40

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AA	3003	8AN	N3-C2-N1	-6.59	123.69	128.87
59	AA	3002	8AN	N3-C2-N1	-6.55	123.73	128.87
60	BZ	701	GCP	C5-C6-N1	-4.18	118.06	123.52
60	BZ	701	GCP	N3-C2-N1	-3.47	122.84	127.56
60	BZ	701	GCP	C6-C5-C4	-3.18	117.22	120.86

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	AA	3001	NMY	C10-C11-C12-C7-C8-C9

5 monomers are involved in 158 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	AA	3001	NMY	25	0
59	AA	3002	8AN	45	0
59	AA	3003	8AN	35	0
58	BA	1601	NMY	15	0
60	BZ	701	GCP	38	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	10
34	BA	3
3	AC	3
33	Ag	2
31	AI	1

The worst 5 of 19 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Ag	30:UNK	C	123:UNK	N	31.39
1	AA	164:U	O3'	171:G	P	7.68
1	AA	2893:G	O3'	2894:G	P	5.34
1	AA	2107:C	O3'	2108:C	P	4.97
1	AC	180:PHE	C	181:PRO	N	4.62