



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Aug 20, 2017 – 08:29 AM EDT

PDB ID : 5A9Z  
EMDB ID: : EMD-6396  
Title : Complex of Thermophilus thermophilus ribosome bound to BipA-GDPCP  
Authors : Kumar, V.; Chen, Y.; Ahmed, T.; Tan, J.; Ero, R.; Bhushan, S.; Gao, Y.-G.  
Deposited on : unknown  
Resolution : 4.70 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

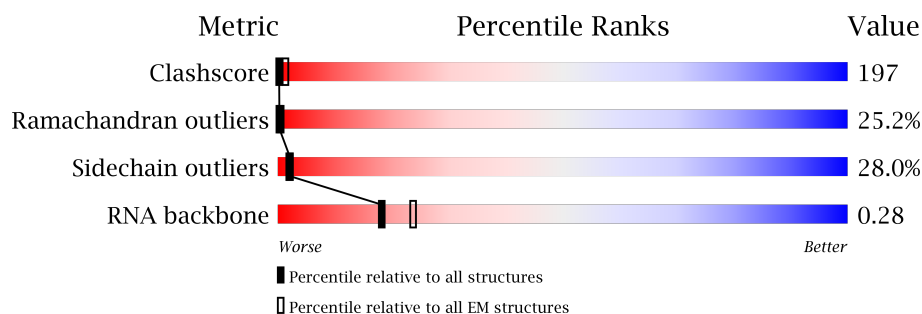
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.70 Å.

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









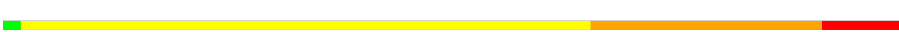





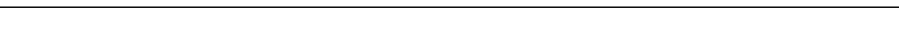

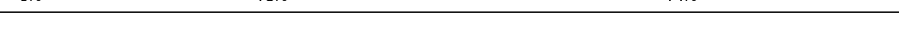

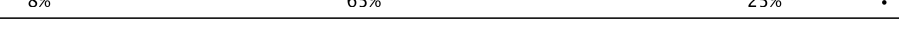




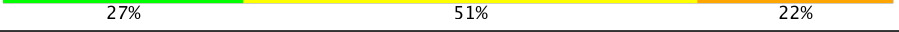



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	


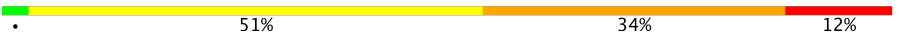
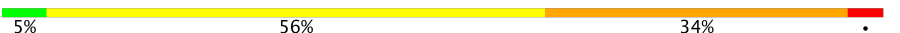


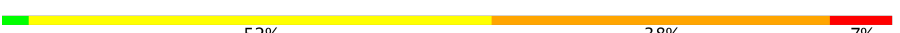
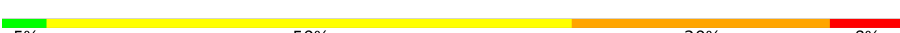




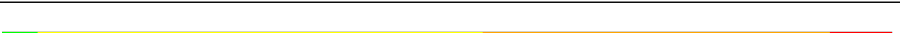







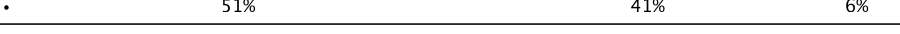


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Mol	Chain	Length	Quality of chain
9	AI	153	
10	AJ	134	
11	AK	139	
12	AL	122	
13	AM	145	
14	AN	136	
15	AO	117	
16	AP	110	
17	AQ	117	
18	AR	117	
19	AS	101	
20	AT	110	
21	AU	94	
22	AV	110	
23	AW	180	
24	AX	85	
25	AY	67	
26	AZ	59	
27	Aa	71	
28	Ab	57	
29	Ac	49	
30	Ad	49	
31	Ae	64	
32	Af	37	
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	CA	593	

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
56	NMY	AA	3001	-	-	X	-
57	GCP	CA	701	-	-	X	-

## 2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 150547 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 L10.

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

- Molecule 10 is a protein called 50S ribosomal protein L11.

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

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

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

- Molecule 13 is a protein called 50S ribosomal protein L15.

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

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

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

- Molecule 16 is a protein called 50S ribosomal protein L18.



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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

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

- Molecule 22 is a protein called 50S ribosomal protein L24.

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

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

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

- Molecule 25 is a protein called 50S ribosomal protein L29.

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

- Molecule 26 is a protein called 50S ribosomal protein L30.

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

- Molecule 27 is a protein called 50S ribosomal protein L31.

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

- Molecule 28 is a protein called 50S ribosomal protein L32.

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

- Molecule 29 is a protein called 50S ribosomal protein L33.

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

- Molecule 30 is a protein called 50S ribosomal protein L34.

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

- Molecule 31 is a protein called 50S ribosomal protein L35.

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

- Molecule 32 is a protein called 50S ribosomal protein L36.

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

- 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	S	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		

- 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		

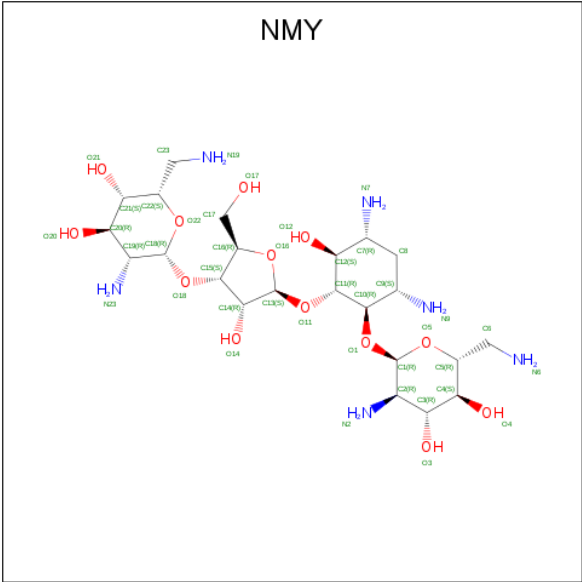
- Molecule 54 is a protein called 30S ribosomal protein Thx.

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

- Molecule 55 is a protein called BipA.

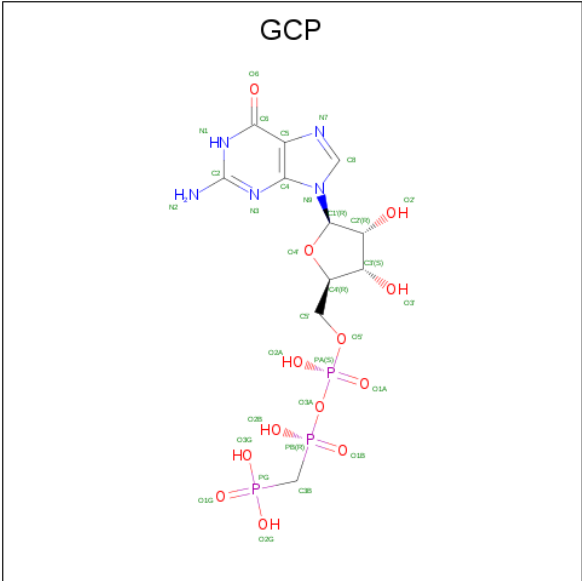
Mol	Chain	Residues	Atoms					AltConf	Trace
55	CA	593	Total	C	N	O	S	0	0
			4532	2856	791	868	17		

- Molecule 56 is NEOMYCIN (three-letter code: NMY) (formula: C<sub>23</sub>H<sub>46</sub>N<sub>6</sub>O<sub>13</sub>).



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

- Molecule 57 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).

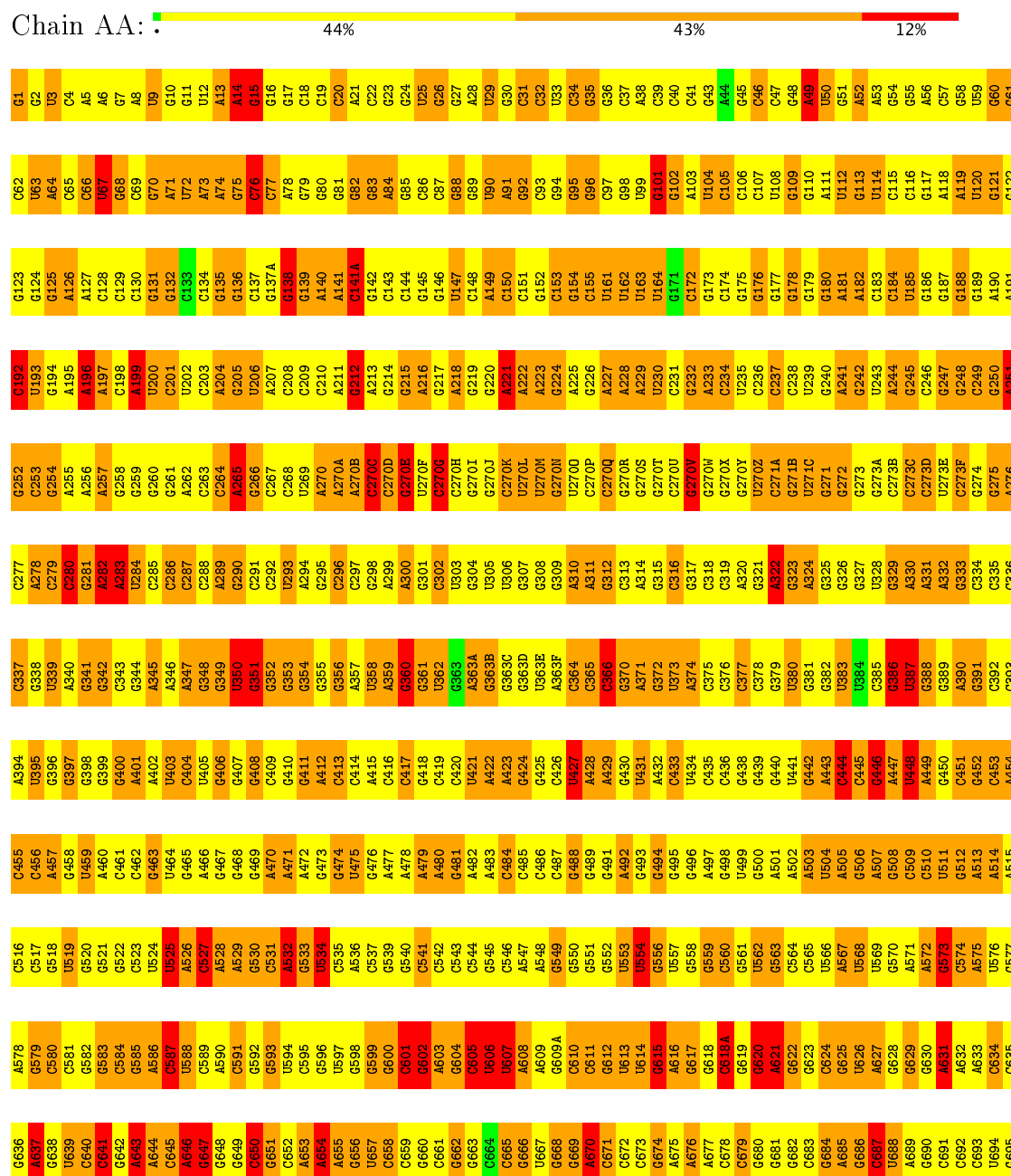


Mol	Chain	Residues	Atoms					AltConf
57	CA	1	Total	C	N	O	P	0
			32	11	5	13	3	

### 3 Residue-property plots

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

#### • Molecule 1: 23S ribosomal RNA





C1598	C1538	A1477	G1448	G1368	C1298	G1238	A1177	G1117	A1057	G997	G938	C876	C816	C756	G696
G1599	G1539	G1478	A1419	A1369	G1299	G1239	C1178	C1118	G1058	C998	G939	U877	C817	U757	C697
G1600	G1540	G1479	A1420	A1360	U1300	U1240	C1179	C1119	G1059	U999	G940	A878	C818	U758	C698
G1601	U1541	G1480	G1421	G1361	A1301	A1241	G1120	G1120	U1060	A1000	A941	G879	A819	G759	A699
U1602	U1482	U1483	G1422	C1362	A1302	A1242	C1121	C1121	U1061	A1001	G942	G880	A820	G760	G701
A1603	A1543	G1483	G1423	C1363	G1303	G1243	C1182	G1122	G1062	G1002	U943	G881	A821	A761	G702
C1604	C1544	G1484	G1424	G1364	C1304	G1244	G1183	C1123	G1063	G1003	G844	G882	U822	U762	G703
G1605	A1545	G1485	G1425	A1365	C1305	G1245	G1184	C1124	U1065	C1004	A945	G883	G823	G763	U704
G1606	A1546A	G1486	G1426	A1366	C1306	A1246	C1185	G1125	U1066	C1006	G946	G884	A824	A764	G704
C1607	C1546	G1487	A1427	A1367	A1307	A1247	G1186	A1126	G1067	C1007	G947	C885	C825	C766	A706
A1608	C1547	G1488	G1428	G1368	A1308	G1248	G1187	A1127	A1067	C1008	G948	C886	U826	G767	G707
A1609	C1548	U1489	G1429	G1369	U1309	U1249	U1188	A1128	G1068	A1009	C949	A887	U827	U768	C708
A1610	C1549	A1490	C1430	C1370	G1310	G1250	A1189	A1129	A1069	A1009	G950	C888	U828	G769	U709
C1611	C1550	G1491	U1431	G1371	G1311	C1251	G1190	U1130	A1070	A1010	C951	C889	A829	G770	G710
C1612	C1551	G1492	G1432	U1372	U1312	G1252	G1191	G1131	G1071	G1011	G952	A890	C830	G771	G711
C1613	U1552	C1493	U1433	A1373	C1313	A1253	G1192	A1132	C1072	U1012	A953	A891	C831	G772	G712
A1614	A1553	A1494	A1434	G1374	C1314	A1254	G1193	U1133	A1073	C1013	G954	C893	C832	U773	G713
C1615	A1554	A1495	G1435	C1375	C1315	U1255	A1194	G1134	G1074	U1014	C955	C894	U833	C774	U714
A1616	C1555	A1496	G1436	C1376	U1316	G1256	G1195	C1135	C1075	G1015	G956	U935	C834	A774	U715
C1617	C1556	U1497	C1437	G1377	A1317	C1257	C1196	G1136	C1076	G1016	A957	A896	A835	G775	G716
A1618	U1498	U1438	U1438	A1378	C1318	C1258	G1197	G1137	A1077	C1017	G958	C897	G836	G776	A716
G1619	A1558	A1439	A1439	G1379	G1319	G1259	U1198	G1138	U1078	C1018	A959	C898	C837	A777	G717
G1620	G1559	G1500	G1440	G1380	C1320	G1260	U1199	G1139	C1079	U1019	A960	A899	C838	G778	A718
U1621	G1560	C1501	G1441	G1381	A1321	C1261	C1200	G1140	C1080	A1020	C961	A900	U839	U779	C719
G1622	G1561	C1502	G1442	G1382	A1322	A1262	C1201	U1141	U1081	A1021	G962	A901	C840	G780	C720
C1623	A1562	U1503	G1443	C1383	U1323	U1263	C1202	U1142	U1082	G1022	U963	C902	A841	A781	C721
G1624	G1563	C1504	G1444	A1384	G1324	G1264	G1203	A1142A	U1083	U1023	C964	C903	G842	A782	C722
C1625	C1564	C1505	A1444A	A1385	G1325	A1265	A1204	A1143	A1084	G1024	C965	C904	G843	A783	G723
G1626	G1565	C1506	G1445	A1386	U1326	G1266	U1205	G1144	A1085	G1025	G966	U905	C844	A784	U724
G1627	A1566	A1507	G1446	C1387	C1327	U1267	G1206	C1145	A1086	U1026	C967	G906	G845	G785	G725
G1628	A1567	G1508	G1447	G1388	G1328	A1268	C1207	C1146	G1087	A1027	G968	U907	C846	G786	G726
U1629	G1568	C1509	G1448	G1389	U1329	A1269	C1208	C1147	A1088	A1028	U969	C908	U847	U787	A727
G1630	A1569	A1510	A1449	U1390	C1330	C1270	G1209	A1148	G1089	A1029	C970	A909	G848	A788	G728
C1630A	A1570	A1511	G1449A	U1391	A1331	G1271	A1210	G1149	U1090	G1030	C971	A910	A849	A789	G729
A1631	C1571	G1512	C1450	A1392	G1332	A1272	U1211	C1150	G1091	A1031	C972	A911	C850	C790	C730
A1632	A1572	C1513	C1451	A1393	C1333	U1273	G1212	G1151	G1092	A1032	A973	C912	U851	C791	C731
G1633	G1573	U1514	A1453	U1394	G1334	A1274	A1213	C1152	G1093	U1033	G974	U913	G852	G792	C732
A1634	C1574	C1515	U1454	A1395	U1335	A1275	A1214	C1153	U1094	G1034	C974A	C914	G853	A793	G733
C1635	U1575	U1396	G1455	A1396	A1336	A1276	G1215	G1154	A1095	U1035	G975	C915	G854	G794	A734
G1636	U1576	U1397	G1456	U1397	G1337	G1277	G1216	A1155	A1096	G1036	C976	G916	G855	C795	A735
A1637	C1577	C1398	A1457	G1398	G1338	A1278	C1217	A1156	U1097	G1037	G977	A917	C856	C796	C736
C1638	U1578	C1399	G1458	G1399	G1339	G1279	G1217	G1157	A1098	G1038	G978	A918	C857	C797	C737
A1639	A1579	U1520	G1459	G1401	U1340	G1280	A1220	C1158	G1099	C1039	G979	G919	U858	G798	G738
C1640	G1580	G1521	A1460	G1402	A1341	G1281	C1221	U1159	C1100	G1040	A980	G920	G859	G799	G739
A1641	G1581	G1522	G1461	C1403	A1342	U1282	C1222	G1160	U1101	C1041	A981	G921	U860	A800	U740
G1642	C1582	U1523	C1462	C1403	G1343	G1283	C1223	C1161	C1102	G1042	C982	U922	A861	G801	G741
C1643	A1583	G1524	C1463	C1404	G1344	A1284	G1224	G1162	A1103	C1043	A983	C923	G862	A802	G742
C1644	C1585	G1525	C1464	U1405	C1345	G1285	G1225	G1163	C1104	G1044	A984	C924	A863	U803	G743
G1645	G1586	G1526	G1465	U1406	G1346	A1286	G1226	G1164	U1105	A1045	C985	C925	G864	A804	G744
C1646	A1587	G1527	G1466	C1407	G1347	A1287	A1227	U1165	G1106	A1046	C986	A926	C865	G805	G745
G1647	C1588	A1528	C1467	C1408	G1348	U1288	G1228	C1166	G1107	G1047	C987	G928	A866	C806	A746
C1648	C1589	A1529	C1468	C1409	A1349	U1289	G1229	U1167	U1108	A1048	A988	G929	C867	U807	U747
G1649	U1590	A1469	G1470	C1410	C1350	C1290	C1230	G1168	C1109	C1049	G989	U930	U868	G808	G748
C1650	G1591	C1531	G1471	C1411	C1351	C1291	G1231	G1169	A1110	A1050	A990	G931	A869	G809	G749
G1651	C1592	C1532	A1471	A1412	U1352	U1292	G1232	G1170	A1111	G1051	C991	G932	A870	U810	A750
A1652	G1593	C1533	A1472	G1413	A1353	C1293	C1233	G1171	G1112	C1052	C992	A933	U871	U811	A751
C1653	G1594	G1473	G1473	G1414	A1354	U1294	U1234	G1173	U1113	C1053	G993	G934	A872	C812	A752
A1654	A1595	U1535	G1474	U1415	G1355	C1295	G1235	G1174	G1114	A1054	C994	C935	G873	U813	C753
C1655	C1596	G1475	G1475	G1416	G1356	G1296	G1236	U1175	G1115	G1055	C995	C936	G874	C814	C754
C1656	A1597	C1537	C1476	C1417	U1357	C1297	A1237	G1176	C1116	G1056	A996	U937	G875	C815	C755

A2533	U2593	G2413	U2233	C2163	U2102	A2042	C1982	G1922	A1853	G1793	G1726	C1657
A2534	C2594	G2414	G2234	C2164	C2103	C2043	C1983	U1923	A1854	U1794	U1727	C1658
G2535	G2595	G2415	G2235	G2165	C2104	C2044	G1984	G1924	G1855	G1795	G1728	U1659
U2536	G2476	G2416	G2236	G2166	C2105	C2045	G1985	C1925	G1856	U1796	G1729	C1660
G2537	G2477	G2417	G2237	U2167	G2106	G2046	A1986	U1926	G1857	G1797	G1730	G1661
A2538	G2478	G2418	G2238	G2168	C2107	U2047	G1987	A1927	G1858	U1798	G1731	G1662
G2539	G2479	U2419	G2239	A2169		G2048	C1988	A1928	A1859	G1799	U1732	C1663
C2540	C2480	A2420	G2300	A2170	G2110	G2049	C1989	G1929	G1860	C1800	G1733	A1664
A2541	G2481	G2421	C2301	A2171	C2111	C2050	G1990	G1930	G1861	G1801	G1734	A1665
A2542	G2482	G2422	G2302	U2172	G2112	A2051	G1991	U1931	G1862	A1802	C1735	G1666
G2543	C2483	U2423	G2303	A2173	U2113	G2052	G1992	A1932	G1863	A1803	C1741	G1667
G2544	G2484	G2424	G2304	A2174	G2114	G2053	G1993	G1933	G1864	A1804	G1742	A1668
G2545	G2485	A2425	A3305	C2175	G2115	A2054	G1994	U1934	G1865	U1805	G1743	A1669
U2546	G2486	A2426	G2306	A2176	G2116	C2055	U1995	G1935	C1870	C1806	G1746	C1670
G2547	G2487	G2427	G2307	C2177	A2117	G2056	C1996	A1936	A1871	G1807	U1747	U1671
G2548	A2488	G2428	G2308	C2178	U2118	A2057	G1997	A1937	A1872	U1808	G1748	C1672
G2549	G2489	G2429	A2309	C2179	A2119	A2058	G1998	A1938	G1878	A1809	U1749	U1673
G2550	G2490	G2430	G2310	U2180	G2120	A2059	C1999	U1939	C1879	A1810	G1750	G1674
C2551	U2491	U2431	G2311	G2181	G2121	A2060	G2000	U1940	C1880	G1811	C1751	C1675
U2552	U2492	A2432	G2312	G2182	U2122	G2061	A2001	C1941	C1881	A1812	C1752	A1676
G2553	C2493	G2433	G2313	G2183	G2123	A2062	G2002	C1942	C1882	G1813	G1753	A1677
A2554	G2494	A2434	C2314	G2184	G2124	C2063	G2003	U1943	G1883	A1814	C1754	G1678
U2555	G2495	A2435	G2315	C2185	G2125	G2064	G2004	U1944	G1884	A1815	G1755	U1679
G2556	G2496	G2436	G2316	G2186	A2126	C2065	A2005	G1945	A1885	G1816	G1756	U1680
G2557	A2497	U2437	C2317	G2187	G2127	C2066	C2006	U1946	C1886	G1817	U1757	G1681
C2558	G2498	U2438	G2318	C2188	C2128	G2067	C2007	C1947	C1887	U1818	G1758	G1682
G2559	G2499	G2379	G2319	U2189	C2129	U2068	C2008	G1948	G1888	A1819	A1759	C1683
C2560	U2500	C2440	A2320	G2190	U2130	G2069	G2009	G1949	A1889	U1820	A1760	C1684
A2561	C2501	G2441	G2321	G2191	G2131	G2070	G2010	G1950	A1890	A1821	C1761	C1685
G2562	G2502	C2442	U2622	G2192	U2132	A2071	U2011	U1951	G1891	G1822	A1762	C1686
G2563	A2503	C2443	G2323	G2193	G2133	G2072	G2012	A1952	C1892	G1823	G1763	G1687
A2564	U2504	G2444	C2324	G2194	A2134	C2073	A2013	A1953	C1893	G1824	G1764	U1688
G2565	G2505	G2445	G2325	C2195	A2135	U2074	A2014	G1954	C1894	A1825	C1765	A1689
A2566	G2506	G2446	A2326	C2196	C2136	U2075	A2015	U1955	G1895	G1826	U1766	C1690
G2567	U2507	G2447	A2327	U2197	C2137	U2076	U2016	G1956	G1896	C1827	C1767	C1691
G2568	A2448	A2449	A2328	A2198	C2138	A2077	U2017	C1957	G1897	G1828	U1768	U1692
G2569	G2509	U2449	G2329	A2199	C2139	C2078	G2018	G1958	U1898	A1829	G1769	U1693
C2570	C2510	U2450	G2330	C2205	C2140	U2079	A2019	G1959	G1899	C1830	G1770	C1694
G2571	U2511	A2451	G2331	C2206	G2141	G2080	A2020	A1960	A1900	G1831	C1771	G1695
A2572	C2512	C2452	U2332	C2207	C2142	C2081	C2021	C1961	A1901	C1832	C1772	G1696
G2573	G2513	A2453	A2333	U2208	C2143	A2082	U2022	C1962	C1902	U1833	A1773	G1697
G2574	U2514	G2454	G2334	C2209	U2144	G2083	G2023	U1963	G1903	U1834	C1774	A1698
G2575	C2515	G2455	A2335	G2210	C2145	C2084	G2024	G1964	G1904	G1835	U1775	G1699
G2576	G2516	G2456	A2336	G2211	C2146	C2085	G2025	G1965	C1905	C1836	G1776	A1700
U2577	G2517	U2457	G2337	A2212	G2147	U2086	C2026	A1966	G1906	C1837	U1777	A1701
G2578	U2518	G2458	G2338	U2213	G2148	G2087	G2027	C1967	G1907	C1838	U1778	G1702
A2579	G2519	A2459	G2339	G2215	G2149	G2088	U2028	G1968	C1908	G1839	U1779	G1703
G2580	C2520	G2460	G2340	G2216	U2150	U2089	G2029	A1969	C1909	G1840	G1780	G1704
G2581	C2521	C2461	G2341	G2217	G2151	G2090	A2030	A1970	G1910	U1841	G1781	G1705
G2582	U2522	U2462	C2342	G2218	G2152	U2091	A2031	A1971	U1911	G1842	C1782	U1706
G2583	G2523	C2463	C2343	G2219	G2153	U2092	G2032	A1972	A1912	C1843	A1783	G1707
U2584	C2524	C2464	U2344	G2224	G2154	G2093	A2033	G1973	A1913	C1844	A1784	C1708
G2585	G2525	C2465	G2345	A2225	G2155	G2094	U2034	C1974	G1914	G1845	U1785	U1709
C2586	U2526	A2466	A2346	G2226	G2156	C2095	G2035	G1975	U1915	A1846	A1786	C1710
U2587	G2527	G2467	C2347	A2227	U2096	U2096	G2036	U1976	A1916	A1847	C1711	G1711
G2588	U2528	U2468	U2348	G2228	G2157	C2097	G2037	U1977	U1917	A1848	C1712	C1712
U2589	G2529	A2469	G2349	C2229	G2158	U2098	G2038	A1978	A1918	G1849	A1788	U1716
A2590	U2530	G2470	C2350	G2230	G2160	U2099	C2039	C1979	A1919	G1850	C1790	G1717
C2591	A2531	C2471	G2351	G2231	C2161	C2040	C2040	G1980	U1851	A1791	A1791	G1718
G2592	G2532	G2472	A2352	U2232	G2162	G2101	U2041	A1981	G1921	C1852	G1792	G1725


U2653	A2712A	C2772	C2835	C2896
A2654	A2713	C2773	U2836	U2897
U2655	G2714	G2837	G2837	U2898
U2656	C2715	A2775	G2838	G2899
A2657	U2716	A2776	G2839	A2900
C2658	G2717	<b>G2777</b>	C2840	C2901
G2659	G2718	<b>A2778</b>	C2841	C2902
A2660	G2719	<b>G2779</b>	G2842	
C2661	U2720	<b>G2780</b>	G2843	
A2662	A2721	<b>A2781</b>	G2844	
C2663	G2722	G2782	G2845	
G2664	C2723	G2783	G2846	
A2665	<b>G2724</b>	G2784	U2847	
C2666	A2725	C2785	G2848	
C2667	<b>U2726</b>	<b>U2786</b>	U2849	
G2668	G2727	<b>C2787</b>	A2850	
C2669	U2728	C2788	A2851	
A2670	G2729	G2789	<b>C2852</b>	
A2671	C2730	A2790	C2853	
C2672	G2731	G2791	G2854	
G2673	G2732	G2792	C2855	
A2674	A2733	C2793	C2856	
C2675	G2734	G2794	G2857	
G2676	G2735	G2795	C2858	
C2677	G2736	U2797	G2859	
C2678	<b>G2737</b>	C2798	A2860	
A2679	A2738	A2799	<b>G2861</b>	
C2680	U2739	A2801	C2862	
C2681	A2740	C2802	C2863	
U2682	A2741	C2803	G2864	
C2683	C2742	C2804	U2865	
U2684	C2743	G2805	U2866	
G2685	C2744	G2807	<b>G2867</b>	
C2686	<b>U2745</b>	U2808	A2868	
U2687	C2746	C2809	G2869	
U2688	<b>G2747</b>	C2810	C2870	
U2689	A2748	A2811	C2871	
C2690	A2749	G2812	G2872	
C2691	A2750	A2813	A2873	
A2692	G2751	G2814	C2874	
C2693	C2752	C2815	C2875	
G2694	A2753	C2816	G2876	
C2695	U2754	G2817	G2877	
U2696	<b>U2755</b>	G2818	U2878	
G2697	<b>U2756</b>	G2819	C2879	
U2698	A2757	A2820	C2880	
C2699	A2758	<b>A2821</b>	C2881	
C2700	G2759	G2822	A2882	
C2701	G2760	A2823	A2883	
U2702	G2761	C2824	U2884	
C2703	G2762	C2825	<b>C2885</b>	
C2704	G2763	A2826	G2886	
<b>A2705</b>	A2764	C2827	U2887	
<b>G2706</b>	A2765	C2828	C2888	
G2707	G2766	C2829	C2889	
G2708	C2767	G2830	<b>C2891</b>	
G2709	C2768	G2831	A2892	
C2710	G2769	U2832	G2893	
A2711	G2770	G2833	G2894	
U2712	C2771	U2834	U2895	

• 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	
<b>G7</b>	G67	
U8	C68	
G9	G69	
C10	C70	
C11	C71	
C12	G72	
A13	A73	
U14	<b>U74</b>	
C15	G75	
<b>G16</b>	G76	
C17	U77	
G18	A78	
C19	C79	
C20	U80	
G21	G81	
U22	G82	
G23	G83	
G24	C84	
A25	G85	
A26	G86	
C27	C87	
C28	C88	
A29	<b>G89</b>	
C30	A89A	
C31	<b>C89A</b>	
C32	C91	
G33	G92	
U34	C93	
U35	C94	
C36	U95	
C37	G96	
C38	G97	
A39	G98	
U40	A99	
U41	G100	
C42	<b>A101</b>	
C43	G102	
G44	U103	
A45	A104	
A46	G105	
C47	G106	
U48	U107	
A49	C108	
G50	<b>G109</b>	
G51	G110	
A52	U111	
A53	G112	
G54	C113	
U55	G114	
<b>G56</b>	G115	
A57	G116	
A58	G117	

• Molecule 3: 50S ribosomal protein L1

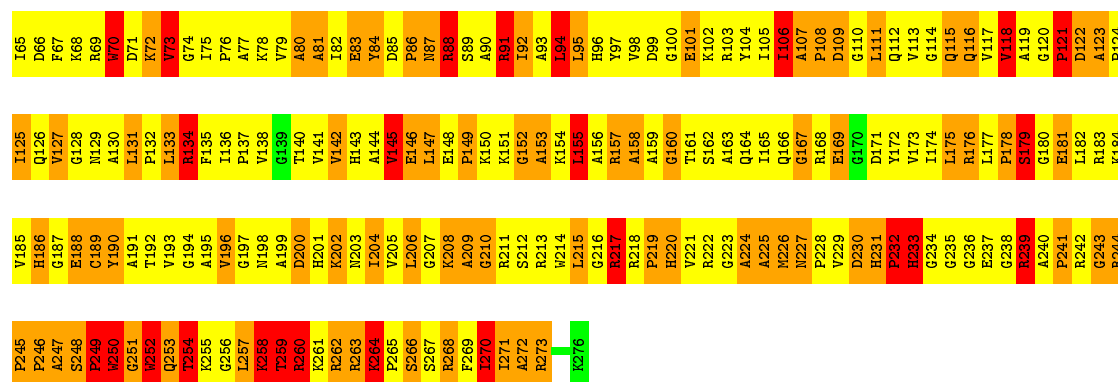
Chain AC:  7% 71% 19%

<b>P1</b>	V62	A122	P182
G4	S63	V123	E183
K5	L64	V124	K184
R6	P65	S125	L185
Y7	H66	S126	A186
R8	G67	L127	D187
<b>A9</b>	L68	G128	N188
G69	A69	A129	I189
L10	K70	I130	<b>H190</b>
L11	Q71	L131	A191
V12	W72	G132	F192
K13	R73	<b>P133</b>	I193
V14	V74	R134	K194
D15	L75	<b>G135</b>	A195
A76	A76	L136	L196
<b>M17</b>	I77	L137	E197
K18	A78	P138	<b>A198</b>
I19	K79	<b>H139</b>	H199
<b>Y20</b>	G80	P140	K200
T21	E81	K141	P201
L22	K82	A142	E202
D23	I83	G143	G203
E24	R84	T144	A204
G85	<b>E85</b>	V145	K205
A25	A86	G146	G206
G83	E87	F147	T207
L28	<b>E88</b>	M148	F208
V29	A89	L149	L209
K30	G90	G150	R210
E31	A91	E151	S211
L32	D92	V152	V212
A33	Y93	I153	Y213
T34	V94	A154	V214
A35	G95	E155	T215
K36	G96	L156	T216
F37	E97	K157	<b>M218</b>
D38	<b>E98</b>	<b>A158</b>	<b>G219</b>
E39	I99	G159	P220
T40	I100	R160	S221
V41	Q101	<b>I161</b>	N221
E42	K102	E162	V222
V43	I103	F163	R223
H44	L104	R164	I224
A45	D105	<b>N165</b>	N225
<b>A101</b>	<b>G106</b>	D166	P226
K46	W107	K167	H227
L47	M108	T168	S228
<b>G148</b>	D109	G169	
I49	F110	A170	
D50	D111	I171	
P51	A112	H172	
R52	V113	A173	
R53	V114	P174	
S54	A115	V175	
D55	G116	G176	
<b>G56</b>	<b>P117</b>	K177	
N57	<b>P117</b>	L178	
V58	D118	S179	
<b>R59</b>	V119	M120	
G60	<b>P181</b>	F180	
T61	G121		

• Molecule 4: 50S ribosomal protein L2

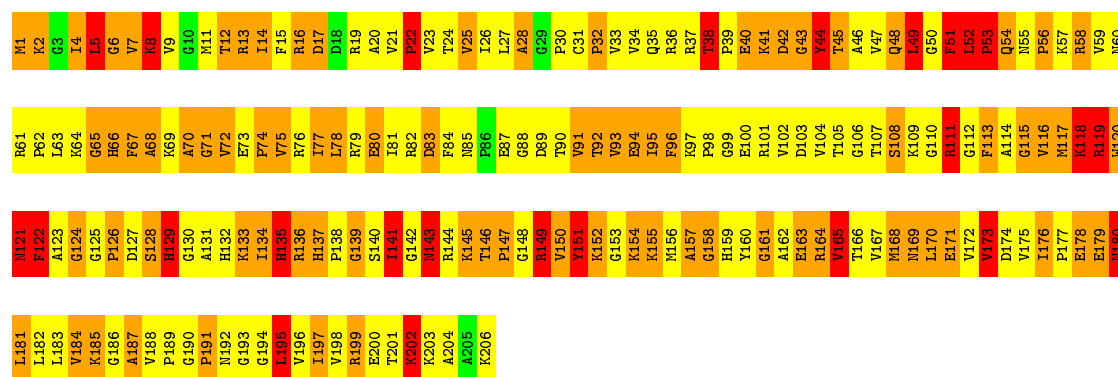
Chain AD:  52% 35% 11%

K5	F6	K7	P8	Y9	T10	P11	S12	R13	F15	M16	T17	V18	A19	D20	F21	S22	E23	I24	T25	K26	T27	E28	P29	E30	K31	S32	L33	V34	K35	P36	L37	K38	K39	T40	G41	G42	R43	N44	N45	Q46	G47	R48	I49	T50	V51	R52	F53	R54	G55	G56	G57	H58	K59	R60	L61	Y62	R63	I64
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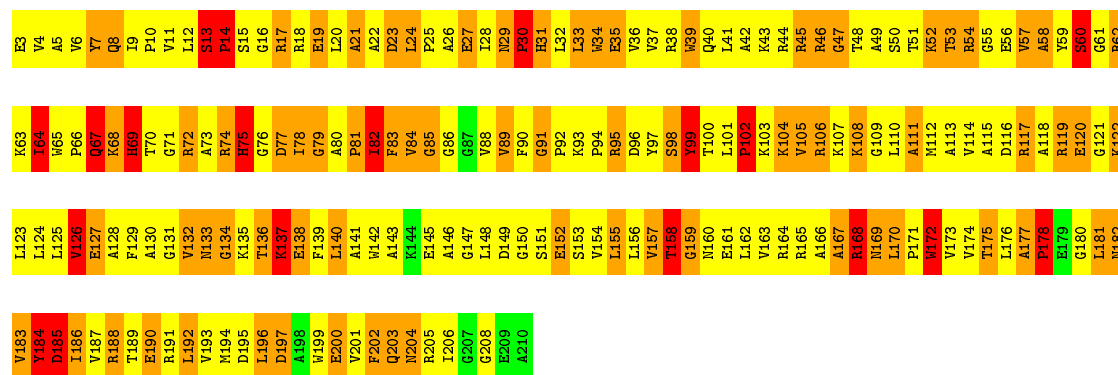
### • Molecule 5: 50S ribosomal protein L3

Chain AE: . 46% 39% 12%



### • Molecule 6: 50S ribosomal protein L4

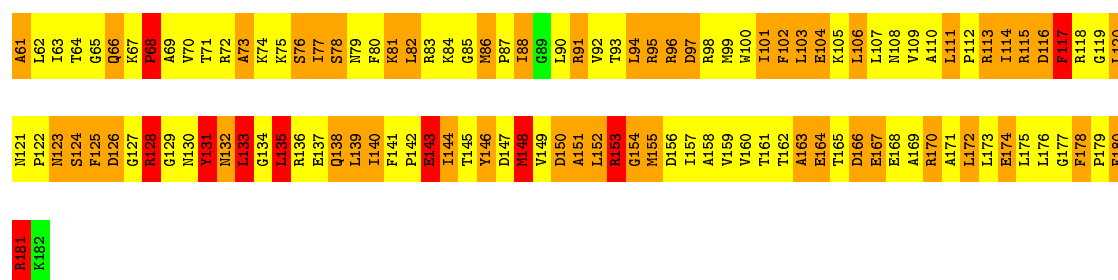
Chain AF: . 51% 36% 9%



### • Molecule 7: 50S ribosomal protein L5

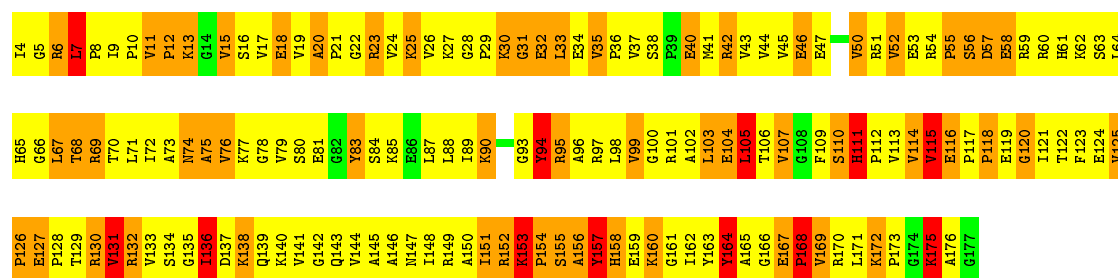
Chain AG: . 54% 36% 9%





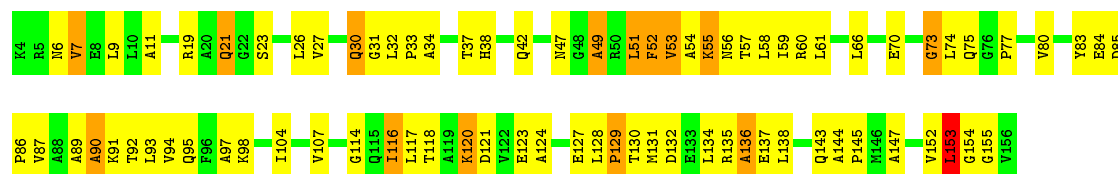
• Molecule 8: 50S ribosomal protein L6

Chain AH: 6% 54% 33% 7%



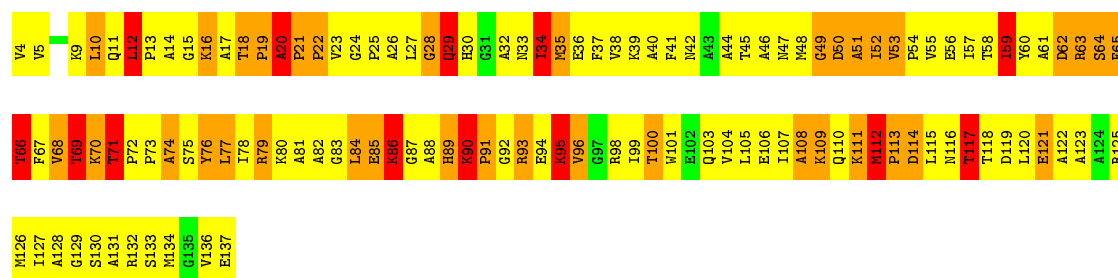
• Molecule 9: 50S ribosomal protein L10

Chain AI: 48% 42% 9%



• Molecule 10: 50S ribosomal protein L11

Chain AJ: 7% 57% 27% 10%



• Molecule 11: 50S ribosomal protein L13

Chain AK: 40% 50% 9%



V62 T63 T64 T65 T66 T67 T68 T69 T70 T71 T72 T73 T74 T75 T76 T77 T78 T79 T80 T81 T82 T83 T84 T85 T86 T87 T88 T89 T90 T91 T92 T93 T94 T95 T96 T97 T98 T99 E100 E101 E102 E103 E104 E105 E106 E107 E108 E109 E110 E111 E112 E113 E114 E115 E116 E117 E118 E119 E120 E121

V122 V123 V124 V125 V126 V127 V128 V129 V130 V131 V132 V133 V134 V135 E136 E137 E138 E139 V140

- Molecule 12: 50S ribosomal protein L14

Chain AL:  46% 43% 11%

K1 K2 K3 K4 K5 K6 K7 K8 K9 K10 K11 K12 K13 K14 K15 K16 K17 K18 K19 K20 K21 K22 K23 K24 K25 K26 K27 K28 K29 K30 K31 K32 K33 K34 K35 K36 K37 K38 K39 K40 K41 K42 K43 K44 K45 K46 K47 K48 K49 K50 K51 K52 K53 K54 K55 K56 K57 K58 K59 K60

V61 V62 V63 V64 V65 V66 V67 V68 V69 V70 V71 V72 V73 V74 V75 V76 V77 V78 V79 V80 V81 V82 V83 V84 V85 V86 V87 V88 V89 V90 V91 V92 V93 V94 V95 V96 V97 V98 V99 G100 G101 G102 G103 G104 G105 E106 E107 E108 E109 E110 E111 E112 E113 E114 E115 E116 E117 E118 E119 E120

V121 L122

- Molecule 13: 50S ribosomal protein L15

Chain AM:  6% 39% 46% 9%

L6 L7 L8 L9 L10 L11 L12 L13 L14 L15 L16 L17 L18 L19 L20 L21 L22 L23 L24 L25 L26 L27 L28 L29 L30 L31 L32 L33 L34 L35 L36 L37 L38 L39 L40 L41 L42 L43 L44 L45 L46 L47 L48 L49 L50 L51 L52 L53 L54 L55 L56 L57 L58 L59 L60

G66 G67 G68 G69 G70 G71 G72 G73 G74 G75 G76 G77 G78 G79 G80 G81 G82 G83 G84 G85 G86 G87 G88 G89 G90 G91 G92 G93 G94 G95 G96 G97 G98 G99 L100 L101 L102 L103 L104 L105 L106 L107 L108 L109 L110 L111 L112 L113 L114 L115 L116 L117 L118 L119 L120 L121 L122 L123 L124 L125

V126 V127 V128 V129 V130 V131 V132 V133 V134 V135 V136 V137 V138 V139 V140 V141 V142 V143 V144 V145 V146 V147 V148 V149 V150

- Molecule 14: 50S ribosomal protein L16


Chain AN:  36% 50% 12%

R6 R7 R8 R9 R10 R11 R12 R13 R14 R15 R16 R17 R18 R19 R20 R21 R22 R23 R24 R25 R26 R27 R28 R29 R30 R31 R32 R33 R34 R35 R36 R37 R38 R39 R40 R41 R42 R43 R44 R45 R46 R47 R48 R49 R50 R51 R52 R53 R54 R55 R56 R57 R58 R59 R60 R61 R62 R63 R64 R65

I66 I67 I68 I69 I70 I71 I72 I73 I74 I75 I76 I77 I78 I79 I80 I81 I82 I83 I84 I85 I86 I87 I88 I89 I90 I91 I92 I93 I94 I95 I96 I97 I98 I99 F100 F101 F102 F103 F104 F105 F106 F107 F108 F109 F110 F111 F112 F113 F114 F115 F116 F117 F118 F119 F120 F121 F122 F123 F124 F125

P126 P127 P128 P129 P130 P131 P132 P133 P134 P135 P136 P137 P138 P139 P140 P141

- Molecule 15: 50S ribosomal protein L17

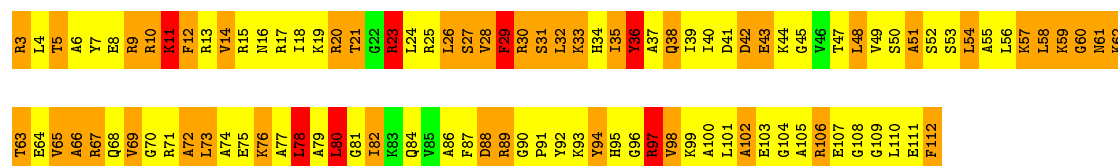
Chain AO:  64% 26% 9%

R2 R3 R4 R5 R6 R7 R8 R9 R10 R11 R12 R13 R14 R15 R16 R17 R18 R19 R20 R21 R22 R23 R24 R25 R26 R27 R28 R29 R30 R31 R32 R33 R34 R35 R36 R37 R38 R39 R40 R41 R42 R43 R44 R45 R46 R47 R48 R49 R50 R51 R52 R53 R54 R55 R56 R57 R58 R59 R60 R61



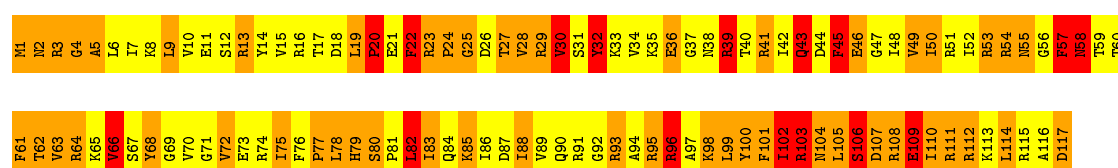
• Molecule 16: 50S ribosomal protein L18

Chain AP: . 50% 40% 6%



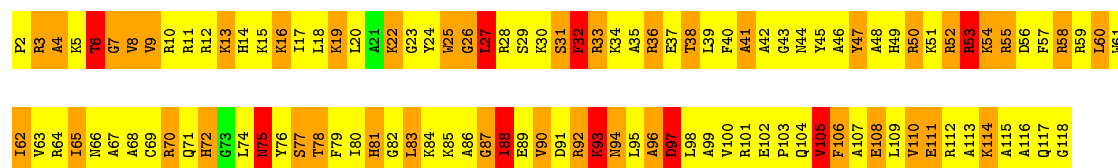
• Molecule 17: 50S ribosomal protein L19

Chain AQ: 43% 44% 14%



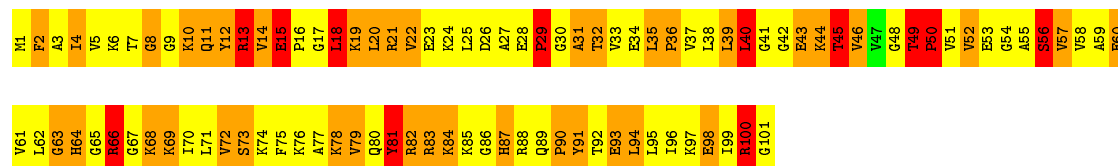
• Molecule 18: 50S ribosomal protein L20

Chain AR: . 56% 35% 8%



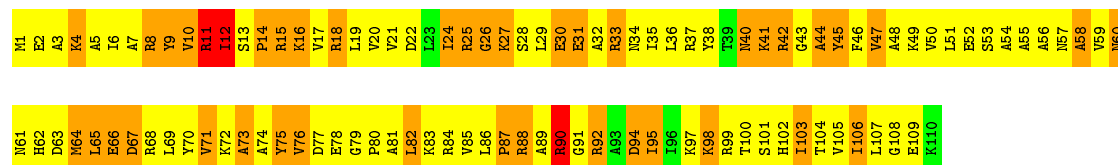
• Molecule 19: 50S ribosomal protein L21

Chain AS: . 49% 39% 12%



• Molecule 20: 50S ribosomal protein L22

Chain AT: 5% 56% 36%



- Molecule 21: 50S ribosomal protein L23

Chain AU: 



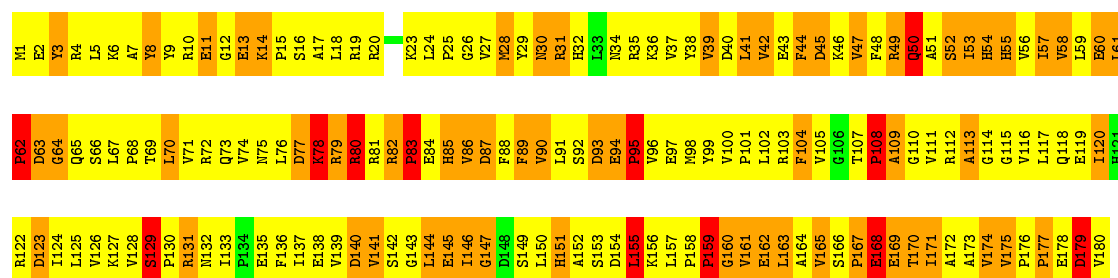
- Molecule 22: 50S ribosomal protein L24

Chain AV: 




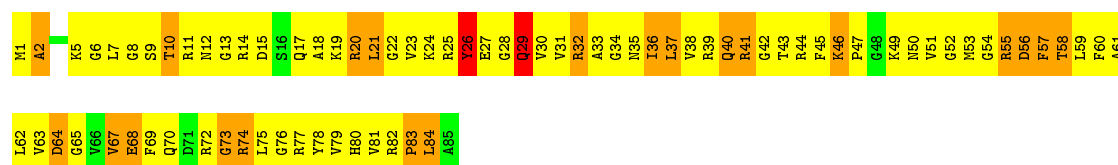
- Molecule 23: 50S ribosomal protein L25

Chain AW: 



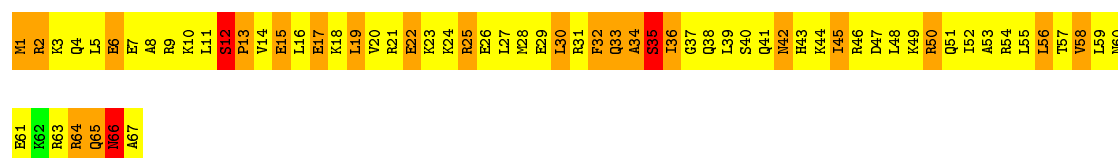
- Molecule 24: 50S ribosomal protein L27

Chain AX: 



- Molecule 25: 50S ribosomal protein L29

Chain AY: 





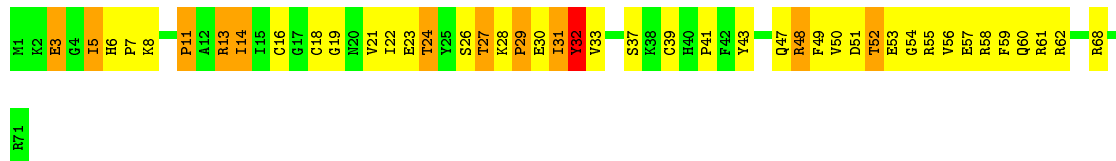
- Molecule 26: 50S ribosomal protein L30

Chain AZ:  5% 46% 44% 5%



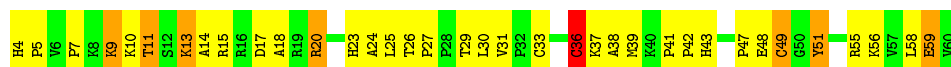
- Molecule 27: 50S ribosomal protein L31

Chain Aa:  38% 45% 15%



- Molecule 28: 50S ribosomal protein L32

Chain Ab:  37% 49% 12%



- Molecule 29: 50S ribosomal protein L33

Chain Ac:  27% 51% 22%



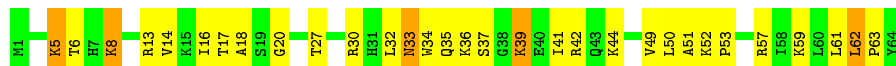
- Molecule 30: 50S ribosomal protein L34

Chain Ad:  53% 37% 10%



- Molecule 31: 50S ribosomal protein L35

Chain Ae:  52% 41% 8%



- Molecule 32: 50S ribosomal protein L36

Chain Af:  62% 32% 5%



- 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%

U5	U6	U65	C131	C186E	G251	C311	G371	A431	G503	C563	G623	G683	U743	G803
G6	G66	G66	C132	C186F	U252	C312	C372	A432	G504	C564	G624	A684	C744	U804
A8	G68	G67	U133	C187	U253	A313	A373	A433	G505	C565	G625	G685	C745	C805
G9	G69	G68	A134	U188	G254	A314	A374	U434	G506	C566	G626	U686	C746	C806
A10	G73	G69	C135	U189	G255	A315	U375	C435	G508	C568	G628	G688	C748	C808
G11	G74	G73	C136	G190	G256	G316	G376	C436	G509	C569	G629	C689	C749	G809
U12	G75	G75	C137	G191A	G257	G317	G377	U437	A510	C570	G630	G690	C750	C810
U13	G76	G76	G138	G191B	G258	G318	G378	G438	A511	C571	G631	G691	C751	C811
U14	G77	G77	A140	G191C	G259	G319	C379	A439	U512	C572	G632	U692	C752	C812
G15	G78	G78	U141	U191D	G260	C320	G380	A440	U513	C573	A632	G693	C753	C813
A16	G79	G79	G142	G191E	U261	A321	C381	C442	C514	A574	G634	A694	C754	A814
U17	G81	G80	G143	U191F	A262	C322	A382	C443	G515	G575	G635	A695	C755	A815
C18	G81	G81	G144	U192	U264	U323	A383	G444	U516	G576	U636	A696	C756	A816
C19	U82	U82	G145	C193	G265	A325	C385	G445	G517	C577	G637	U697	C757	C817
U20	U84	U84	G146	C194	G266	G326	C386	G447	C518	C578	G638	G698	C758	C818
G21	U85	U85	G147	A195	C267	A327	U387	A448	C519	G579	G639	U699	C759	A819
G22	U86	U86	G148	A196	G268	C328	U388	C449	U520	U580	A640	G700	C760	U820
C23	A87	A87	A149	A197	C269	A329	A389	G450	G521	G581	U641	C701	C761	G821
U24	C88	C88	C150	G198	A270	C330	C390	A451	G522	U582	A642	A702	C762	C822
C25	U89	U89	C151	G199	C271	G331	G391	A452	A523	C583	G643	G703	C763	G823
U26	C90	C90	A152	G200	C272	G332	G392	A453	G524	C584	G644	A704	C764	C824
G27	C91	C91	C153	C201	A273	G333	A393	C454	C525	G585	G645	U705	C765	G825
G28	G92	G92	C154	U208	A274	C334	G394	C455	C526	C586	U646	A706	C766	C826
C29	U93	U93	C155	U209	G275	G335	C395	C456	G527	G587	C647	C707	C767	U827
U30	G95	G95	G156	U210	G276	C336	G396	C457	C528	G588	A648	C708	C768	A828
G31	G96	G96	G157	G216	C277	C337	A397	C458	G529	C589	G649	G709	C769	G829
A32	U97	U97	G158	C217	G278	A338	C398	G459	G530	C590	G650	C710	C770	G830
A33	C99	C99	A159	C218	A279	C339	G399	C460	U531	U591	C651	A711	C771	C831
C34	A101	A101	G160	C219	C280	U340	C400	C461	G532	U592	G652	A712	C772	C832
G35	G102	G102	A161	C220	G281	C341	C401	G467	A533	G593	A653	G713	C773	C833
C36	C103	C103	A162	C221	A282	C342	C402	A468	U534	G594	G654	C714	C774	C834
U37	G104	G104	C163	C222	C283	U343	C403	G474	A535	G595	A655	A715	C775	U835
G38	C105	C105	U164	U223	G284	A344	U404	G475	C536	C596	G656	C716	C776	G836
C39	C106	C106	C165	C224	G285	C345	U405	G476	G537	C597	G657	A717	C777	G837
G40	G107	G107	G166	C225	U286	G346	G406	G477	G538	U598	G658	C718	C778	G838
C41	U108	U108	G167	G226	U287	G347	G407	A478	A539	C599	U659	C719	C779	U841
G42	A109	A109	G168	G227	A288	C348	A408	C479	G540	C600	G660	C720	C780	C842
C43	C110	C110	C169	U228	G289	A349	G409	U480	G541	C601	G661	G721	C781	U843
G44	G111	G111	U170	U229	C290	G350	G410	U481	G542	A602	G662	A722	C782	C848
U45	G112	G112	A171	G230	C291	G351	A411	A482	C543	U603	A663	G723	C783	C849
G46	G113	G113	G172	G231	G292	C352	A412	C483	C544	G604	G664	G724	C784	U850
C47	U114	U114	U173	G232	G293	A353	G413	G484	C545	U605	A665	G725	C785	G851
C48	G115	G115	C174	C233	U294	G354	A414	G485	G546	G606	G666	C726	C786	G852
U49	A116	A116	C175	C234	C295	C355	A415	U486	A547	A607	G667	G727	C787	G853
A50	U118	U118	C176	C235	U296	A356	G416	A487	C548	U608	G668	A728	C788	G854
G51	G119	G119	C177	G236	G297	G357	C417	C488	C549	A609	U669	A729	C789	G855
G52	A120	A120	C178	G237	A298	U358	C418	G489	G550	G610	G670	G730	C790	C856
A53	C54	C54	A179	G238	G299	U359	C419	G490	U551	A611	G671	G731	C791	C857
C54	C121	C121	U180	A300	A300	A360	U420	G491	U552	C612	U672	C732	C792	G858
A55	G122	G122	G181	C241	G301	G361	U421	G492	A553	C613	G673	A733	C793	A859
U56	C123	C123	U182	C242	G302	G362	C422	G493	C554	A614	G674	G734	C794	A860
G57	G124	G124	A183	A243	A303	A363	G423	U494	C555	C615	A675	C735	C795	G861
C58	U125	U125	G184	U244	U304	A364	G424	A495	C556	G616	A676	C736	C796	C862
A59	G126	G126	A185	C245	G305	U365	G425	A496	C557	G617	U677	A737	C797	U863
G60	G127	G127	C186	A246	G306	C366	G426	U497	G558	C618	U678	C738	C798	A864
G61	G128	G128	C186A	G247	C307	U367	U427	A498	A559	U619	C679	C739	C799	A865
U62	U129	U129	C186B	C248	C308	U368	G428	G500	U560	C620	C680	U740	C800	C866
C63	G129A	G129A	G186C	U249	C309	C369	U429	C501	U561	A621	C681	C741	C801	G867
G64	C186D	C186D		A250	G310	C370	A430	G502	C562	A622	G682	C742	C802	C868

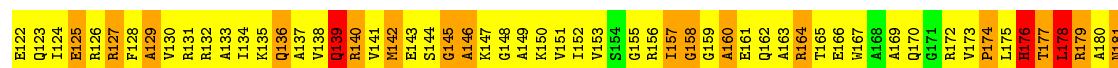
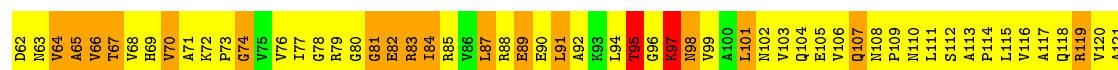
- Molecule 35: 30S ribosomal protein S2

Chain BF: 



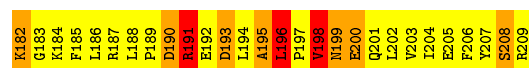
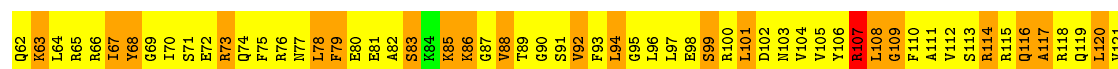
• Molecule 36: 30S ribosomal protein S3

Chain BG: 5% 56% 34%



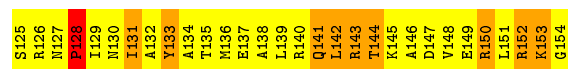
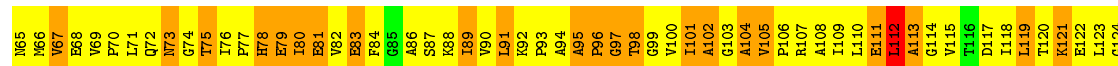
• Molecule 37: 30S ribosomal protein S4

Chain BH: 53% 38% 7%



• Molecule 38: 30S ribosomal protein S5

Chain BI: 63% 33%



• Molecule 39: 30S ribosomal protein S6

Chain BJ: 52% 38% 7%

M1 R2 R3 R4 R5 R6 R7 R8 R9 R10 R11 R12 R13 R14 R15 R16 R17 R18 R19 R20 R21 R22 R23 R24 R25 R26 R27 R28 R29 R30 R31 R32 R33 R34 R35 R36 R37 R38 R39 R40 R41 R42 R43 R44 R45 R46 R47 R48 R49 R50 R51 R52 R53 R54 R55 R56 R57 R58 R59 R60

L61 M62 Y63 Q64 V65 V66 V67 V68 V69 V70 V71 V72 V73 V74 V75 V76 V77 V78 V79 V80 V81 V82 V83 V84 V85 V86 V87 V88 V89 V90 V91 V92 V93 V94 V95 V96 V97 V98 V99 V100 V101

• Molecule 40: 30S ribosomal protein S7

Chain BK: 5% 59% 29% 8%

A2 R3 R4 R5 R6 R7 R8 R9 R10 R11 R12 R13 R14 R15 R16 R17 R18 R19 R20 R21 R22 R23 R24 R25 R26 R27 R28 R29 R30 R31 R32 R33 R34 R35 R36 R37 R38 R39 R40 R41 R42 R43 R44 R45 R46 R47 R48 R49 R50 R51 R52 R53 R54 R55 R56 R57 R58 R59 R60

Q64 A65 A66 A67 A68 A69 A70 A71 A72 A73 A74 A75 A76 A77 A78 A79 A80 A81 A82 A83 A84 A85 A86 A87 A88 A89 A90 A91 A92 A93 A94 A95 A96 A97 A98 A99 A100 A101

L124 M125 D126 A127 A128 A129 G130 G131 G132 G133 G134 G135 G136 G137 G138 G139 G140 G141 G142 G143 G144 G145 G146 G147 G148 G149 G150 G151 G152 G153 G154 G155 G156

• Molecule 41: 30S ribosomal protein S8

Chain BL: 56% 34% 8%

M1 L2 L3 L4 L5 L6 L7 L8 L9 L10 L11 L12 L13 L14 L15 L16 L17 L18 L19 L20 L21 L22 L23 L24 L25 L26 L27 L28 L29 L30 L31 L32 L33 L34 L35 L36 L37 L38 L39 L40 L41 L42 L43 L44 L45 L46 L47 L48 L49 L50 L51 L52 L53 L54 L55 L56 L57 L58 L59 L60

V61 V62 V63 V64 V65 V66 V67 V68 V69 V70 V71 V72 V73 V74 V75 V76 V77 V78 V79 V80 V81 V82 V83 V84 V85 V86 V87 V88 V89 V90 V91 V92 V93 V94 V95 V96 V97 V98 V99 V100 V101 V102 V103 V104 V105 V106 V107 V108 V109 V110 V111 V112 V113 V114 V115 V116 V117 V118 V119 V120

D121 R122 E123 A124 A125 K126 K127 L128 G129 G130 G131 G132 E133 E134 E135 E136 E137 E138

• Molecule 42: 30S ribosomal protein S9

Chain BM: 61% 31% 6%

E2 Q3 Q4 Y5 Y6 Y7 Y8 Y9 Y10 Y11 Y12 Y13 Y14 Y15 Y16 Y17 Y18 Y19 Y20 Y21 Y22 Y23 Y24 Y25 Y26 Y27 Y28 Y29 Y30 Y31 Y32 Y33 Y34 Y35 Y36 Y37 Y38 Y39 Y40 Y41 Y42 Y43 Y44 Y45 Y46 Y47 Y48 Y49 Y50 Y51 Y52 Y53 Y54 Y55 Y56 Y57 Y58 Y59 Y60 A61

Y62 I63 T64 V65 V66 V67 V68 V69 V70 V71 V72 V73 V74 V75 V76 V77 V78 V79 V80 V81 V82 V83 V84 V85 V86 V87 V88 V89 V90 V91 V92 V93 V94 V95 V96 V97 V98 V99 V100 V101 V102 V103 V104 V105 V106 V107 V108 V109 V110 V111 V112 V113 V114 V115 V116 V117 V118 V119 V120 R121

A122 F123 Q124 Y125 S126 K127 R128

• Molecule 43: 30S ribosomal protein S10

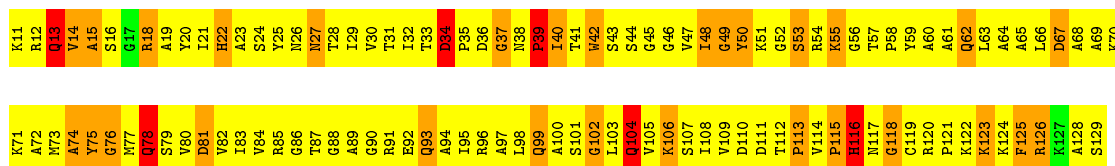
Chain BN: 55% 39%

K3 L4 L5 L6 L7 L8 L9 L10 L11 L12 L13 L14 L15 L16 L17 L18 L19 L20 L21 L22 L23 L24 L25 L26 L27 L28 L29 L30 L31 L32 L33 L34 L35 L36 L37 L38 L39 L40 L41 L42 L43 L44 L45 L46 L47 L48 L49 L50 L51 L52 L53 L54 L55 L56 L57 L58 L59 R60 E61 E62



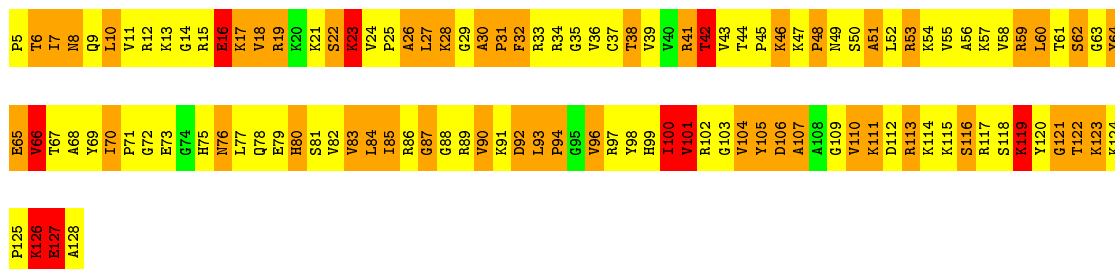
• Molecule 44: 30S ribosomal protein S11

Chain BO: . 69% 24% 5%



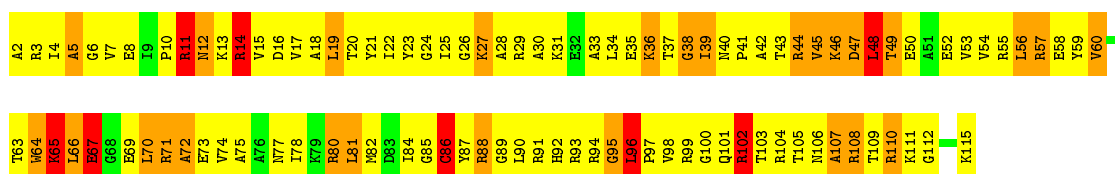
• Molecule 45: 30S ribosomal protein S12

Chain BP: . 50% 39% 7%



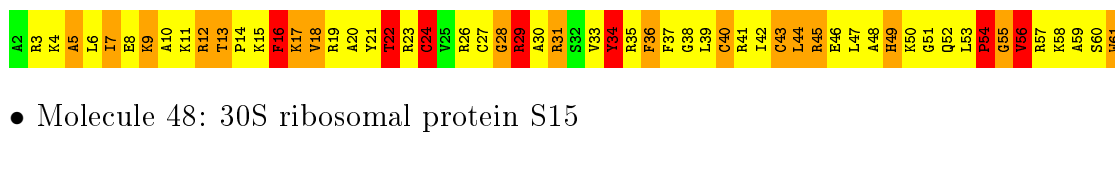
• Molecule 46: 30S ribosomal protein S13

Chain BQ: 10% 60% 24% 7%



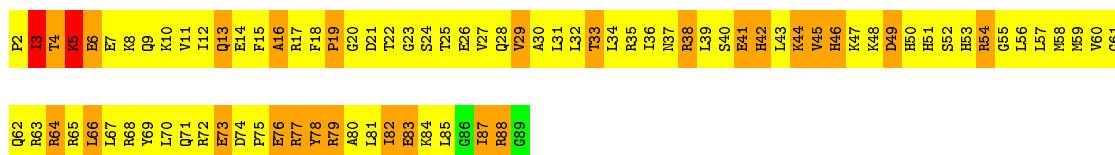
• Molecule 47: 30S ribosomal protein S14 type Z

Chain BR: 5% 55% 28% 12%

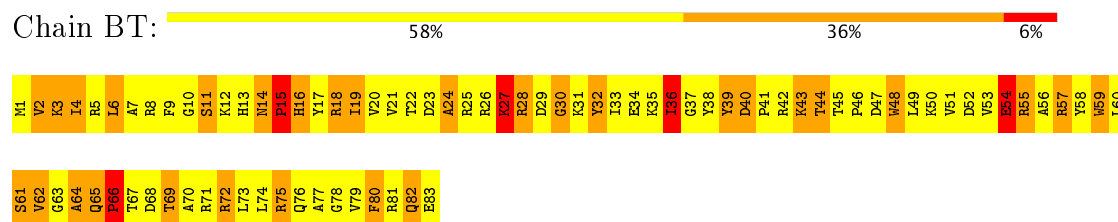


• Molecule 48: 30S ribosomal protein S15

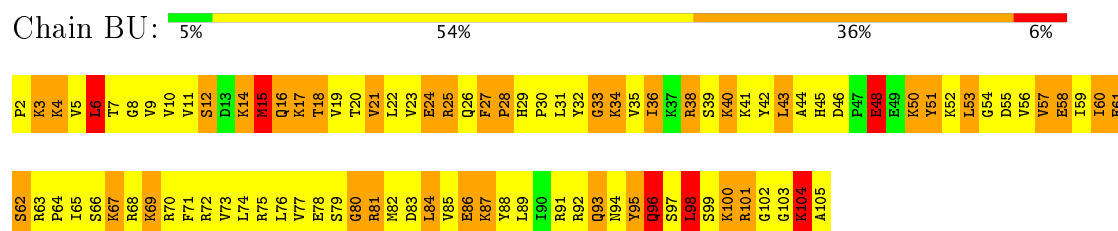
Chain BS: . 66% 30%



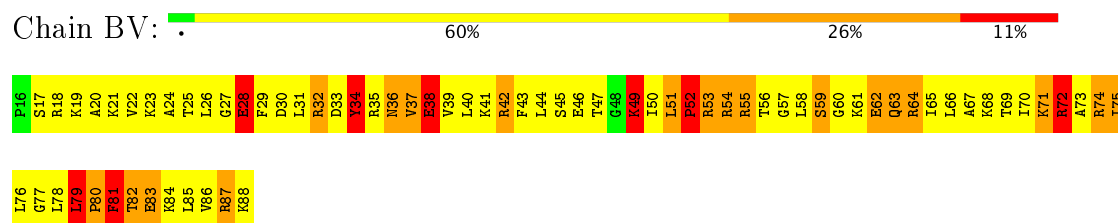
- Molecule 49: 30S ribosomal protein S16



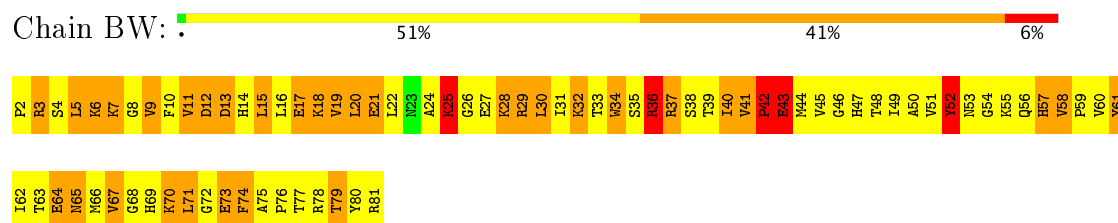
- Molecule 50: 30S ribosomal protein S17



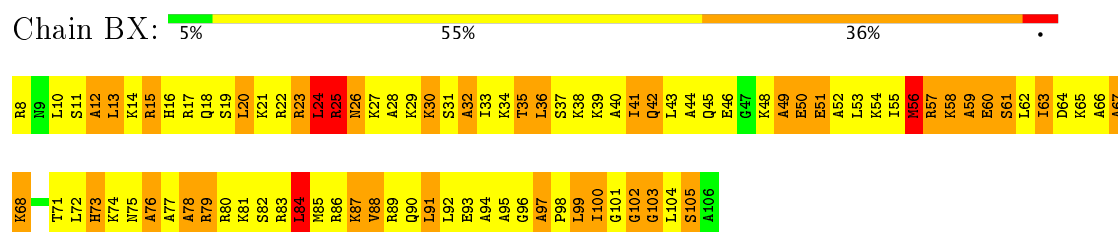
- Molecule 51: 30S ribosomal protein S18



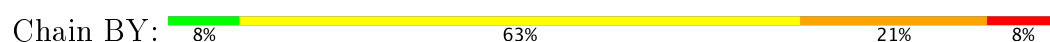
- Molecule 52: 30S ribosomal protein S19

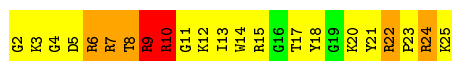


- Molecule 53: 30S ribosomal protein S20

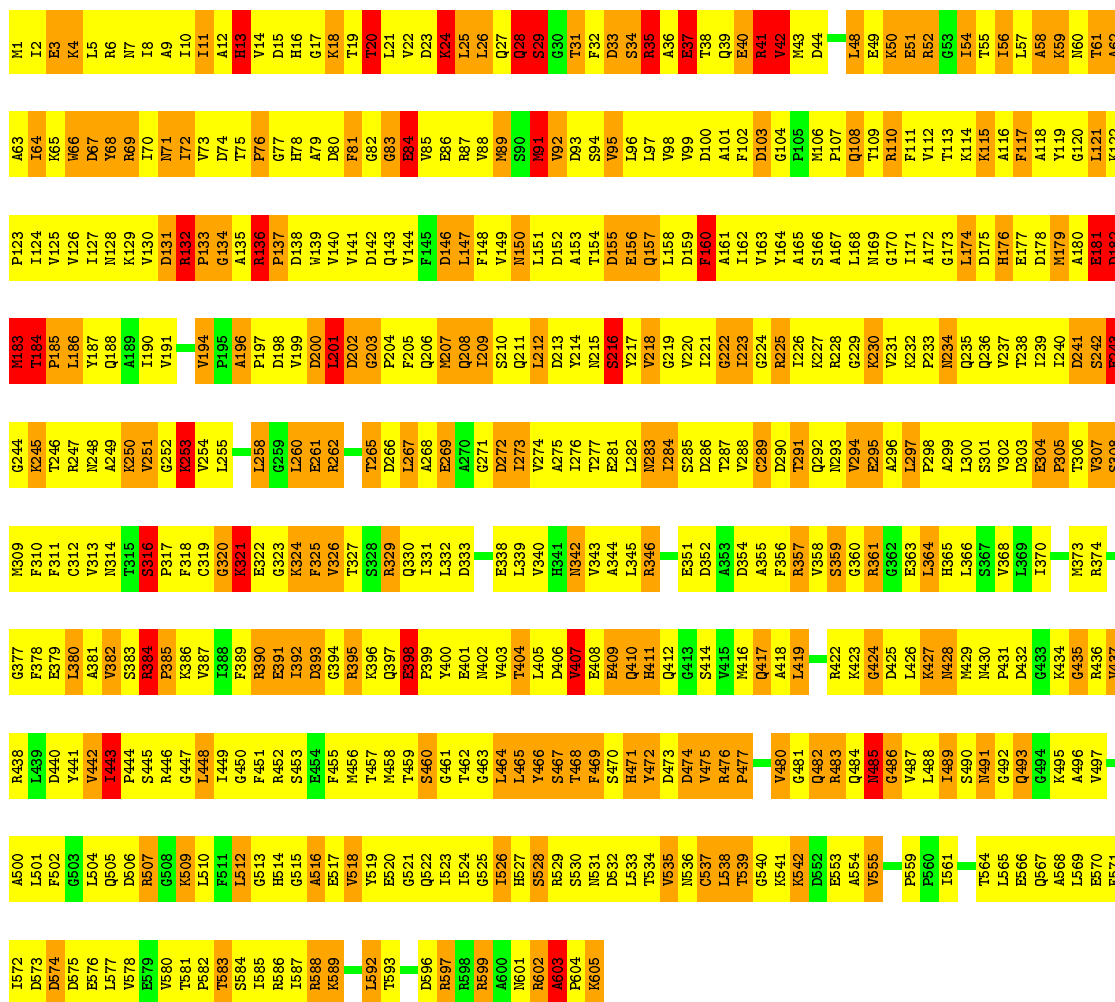
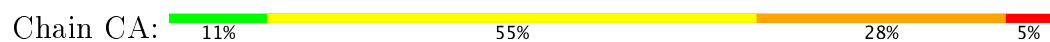


- Molecule 54: 30S ribosomal protein Thx





- Molecule 55: BipA





## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	61165	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTFFIND3	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	53000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GCP, 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	106/69677 (0.2%)	1.08	349/108754 (0.3%)
10	AJ	0.52	0/1012	0.64	8/1373 (0.6%)
11	AK	0.78	1/1140 (0.1%)	1.16	8/1537 (0.5%)
12	AL	0.92	1/942 (0.1%)	1.31	10/1268 (0.8%)
13	AM	0.71	0/1123	1.12	5/1493 (0.3%)
14	AN	0.72	0/1100	1.19	8/1470 (0.5%)
15	AO	0.70	0/974	1.06	2/1302 (0.2%)
16	AP	0.72	0/887	1.06	4/1180 (0.3%)
17	AQ	0.85	0/990	1.31	9/1325 (0.7%)
18	AR	0.76	0/982	1.08	0/1306
19	AS	0.87	1/790 (0.1%)	1.28	9/1057 (0.9%)
2	AB	0.83	4/2954 (0.1%)	0.99	7/4606 (0.2%)
20	AT	0.66	0/886	1.04	1/1189 (0.1%)
21	AU	0.57	0/756	0.93	0/1015
22	AV	0.54	0/857	1.04	2/1142 (0.2%)
23	AW	0.66	0/1467	1.11	7/1992 (0.4%)
24	AX	0.65	0/679	1.04	1/902 (0.1%)
25	AY	0.59	0/569	0.88	0/751
26	AZ	0.59	0/474	1.09	2/635 (0.3%)
27	Aa	0.84	1/594 (0.2%)	1.31	8/795 (1.0%)
28	Ab	0.72	0/459	1.16	3/621 (0.5%)
29	Ac	0.85	1/433 (0.2%)	1.36	5/576 (0.9%)
3	AC	0.54	0/1775	0.86	0/2393
30	Ad	0.73	0/438	1.01	0/575
31	Ae	0.60	0/523	1.14	5/690 (0.7%)
32	Af	0.59	0/310	1.08	1/407 (0.2%)
34	BA	0.92	25/36437 (0.1%)	1.09	139/56865 (0.2%)
35	BF	0.64	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	0.63	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	2/963 (0.2%)
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	CA	0.36	0/4598	0.49	15/6200 (0.2%)
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	AI	0.50	1/751 (0.1%)	0.82	4/1042 (0.4%)
All	All	0.87	146/162336 (0.1%)	1.06	689/241736 (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	430
11	AK	0	1
14	AN	0	1
17	AQ	0	1
19	AS	0	1
2	AB	0	17
27	Aa	0	1
28	Ab	0	1
3	AC	0	1
34	BA	0	170
37	BH	0	1
39	BJ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
44	BO	0	1
47	BR	0	1
5	AE	0	1
55	CA	0	1
6	AF	0	1
9	AI	0	2
All	All	0	633

The worst 5 of 146 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	-70.09	0.77	1.61
1	AA	1203	G	O3'-P	-34.69	1.19	1.61
34	BA	1167	A	O3'-P	20.86	1.86	1.61
1	AA	2500	U	C4-O4	18.53	1.38	1.23

The worst 5 of 689 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	57.69	160.28	119.90
34	BA	1317	C	P-O3'-C3'	-48.76	61.18	119.70
34	BA	1317	C	O3'-P-O5'	30.59	162.12	104.00
1	AA	1060	U	O3'-P-O5'	28.66	158.46	104.00

There are no chirality outliers.

5 of 633 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	31272	15887	0
2	AB	2641	0	1337	608	0
3	AC	1742	0	1796	714	0
4	AD	2124	0	2207	1503	0
5	AE	1578	0	1647	1110	0
6	AF	1625	0	1666	824	0
7	AG	1482	0	1546	871	0
8	AH	1328	0	1407	721	0
9	AI	752	0	363	162	0
10	AJ	993	0	1019	732	0
11	AK	1113	0	1183	776	0
12	AL	932	0	994	755	0
13	AM	1106	0	1183	780	0
14	AN	1080	0	1127	737	0
15	AO	960	0	1021	587	0
16	AP	877	0	938	513	0
17	AQ	976	0	1030	671	0
18	AR	964	0	1022	727	0
19	AS	779	0	852	574	0
20	AT	876	0	941	443	0
21	AU	742	0	800	354	0
22	AV	844	0	930	427	0
23	AW	1435	0	1463	729	0
24	AX	670	0	700	350	0
25	AY	567	0	621	306	0
26	AZ	469	0	518	318	0
27	Aa	581	0	577	0	0
28	Ab	445	0	459	0	0
29	Ac	426	0	452	0	0
30	Ad	430	0	480	0	0
31	Ae	515	0	587	0	0
32	Af	307	0	335	0	0
33	Ag	620	0	136	0	0
34	BA	32554	0	16389	7527	0
35	BF	1900	0	1951	1054	0
36	BG	1612	0	1677	714	0
37	BH	1703	0	1763	853	0
38	BI	1146	0	1207	582	0
39	BJ	843	0	857	391	0
40	BK	1257	0	1296	558	0
41	BL	1116	0	1177	720	0
42	BM	1010	0	1035	483	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	BN	794	0	840	367	0
44	BO	885	0	904	464	0
45	BP	970	0	1057	521	0
46	BQ	914	0	954	646	0
47	BR	492	0	529	278	0
48	BS	734	0	771	368	0
49	BT	700	0	720	362	0
50	BU	857	0	930	461	0
51	BV	597	0	668	367	0
52	BW	647	0	653	524	0
53	BX	763	0	857	409	0
54	BY	208	0	221	89	0
55	CA	4532	0	4424	2444	0
56	AA	42	0	46	23	0
56	BB	42	0	46	15	0
57	CA	32	0	14	39	0
All	All	150547	0	103595	47924	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 47924 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)
10:AJ:112:MET:SD	10:AJ:122:ALA:HB2	1.28	1.69
34:BA:1318:A:H2'	52:BW:37:ARG:CB	1.23	1.68
34:BA:1226:C:C4	46:BQ:104:ARG:HG3	1.16	1.67
34:BA:1311:G:C6	34:BA:1327:C:C5	1.80	1.66
55:CA:13:HIS:CD2	55:CA:106:MET:HB2	1.30	1.66

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	226/228 (99%)	155 (69%)	41 (18%)	30 (13%)	0	6
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	1
9	AI	151/153 (99%)	89 (59%)	33 (22%)	29 (19%)	0	3
10	AJ	132/134 (98%)	56 (42%)	44 (33%)	32 (24%)	0	1
11	AK	137/139 (99%)	64 (47%)	28 (20%)	45 (33%)	0	0
12	AL	120/122 (98%)	59 (49%)	23 (19%)	38 (32%)	0	0
13	AM	143/145 (99%)	57 (40%)	36 (25%)	50 (35%)	0	0
14	AN	134/136 (98%)	49 (37%)	33 (25%)	52 (39%)	0	0
15	AO	115/117 (98%)	57 (50%)	39 (34%)	19 (16%)	0	4
16	AP	108/110 (98%)	48 (44%)	29 (27%)	31 (29%)	0	0
17	AQ	115/117 (98%)	52 (45%)	26 (23%)	37 (32%)	0	0
18	AR	115/117 (98%)	35 (30%)	50 (44%)	30 (26%)	0	1
19	AS	99/101 (98%)	52 (52%)	19 (19%)	28 (28%)	0	0
20	AT	108/110 (98%)	63 (58%)	24 (22%)	21 (19%)	0	3
21	AU	92/94 (98%)	57 (62%)	16 (17%)	19 (21%)	0	2
22	AV	108/110 (98%)	43 (40%)	32 (30%)	33 (31%)	0	0
23	AW	178/180 (99%)	96 (54%)	43 (24%)	39 (22%)	0	2
24	AX	83/85 (98%)	52 (63%)	21 (25%)	10 (12%)	0	7
25	AY	65/67 (97%)	36 (55%)	20 (31%)	9 (14%)	0	6
26	AZ	57/59 (97%)	34 (60%)	8 (14%)	15 (26%)	0	1
27	Aa	69/71 (97%)	23 (33%)	16 (23%)	30 (44%)	0	0
28	Ab	55/57 (96%)	14 (26%)	19 (34%)	22 (40%)	0	0
29	Ac	47/49 (96%)	14 (30%)	7 (15%)	26 (55%)	0	0
30	Ad	47/49 (96%)	20 (43%)	12 (26%)	15 (32%)	0	0
31	Ae	62/64 (97%)	23 (37%)	18 (29%)	21 (34%)	0	0
32	Af	35/37 (95%)	20 (57%)	5 (14%)	10 (29%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	57 (28%)	54 (26%)	0	1
38	BI	148/150 (99%)	93 (63%)	38 (26%)	17 (12%)	0	8
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%)	29 (26%)	19 (17%)	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	3
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	4
51	BV	71/73 (97%)	26 (37%)	26 (37%)	19 (27%)	0	1
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
55	CA	587/593 (99%)	313 (53%)	170 (29%)	104 (18%)	0	3
All	All	6565/6671 (98%)	3259 (50%)	1650 (25%)	1656 (25%)	0	1

5 of 1656 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	35	ALA
3	AC	39	GLU
3	AC	54	SER
3	AC	61	THR
3	AC	66	HIS



### 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	19
4	AD	215/215 (100%)	153 (71%)	62 (29%)	0	3
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	3
8	AH	143/143 (100%)	108 (76%)	35 (24%)	1	6
10	AJ	101/101 (100%)	71 (70%)	30 (30%)	0	3
11	AK	118/118 (100%)	79 (67%)	39 (33%)	0	2
12	AL	100/100 (100%)	69 (69%)	31 (31%)	0	2
13	AM	111/111 (100%)	71 (64%)	40 (36%)	0	1
14	AN	106/106 (100%)	65 (61%)	41 (39%)	0	0
15	AO	100/100 (100%)	71 (71%)	29 (29%)	0	3
16	AP	87/87 (100%)	63 (72%)	24 (28%)	0	4
17	AQ	105/105 (100%)	68 (65%)	37 (35%)	0	1
18	AR	93/93 (100%)	64 (69%)	29 (31%)	0	2
19	AS	82/82 (100%)	57 (70%)	25 (30%)	0	3
20	AT	90/90 (100%)	64 (71%)	26 (29%)	0	3
21	AU	76/76 (100%)	57 (75%)	19 (25%)	1	6
22	AV	91/91 (100%)	72 (79%)	19 (21%)	1	9
23	AW	159/159 (100%)	120 (76%)	39 (24%)	1	6
24	AX	67/67 (100%)	51 (76%)	16 (24%)	1	6
25	AY	62/62 (100%)	44 (71%)	18 (29%)	0	3
26	AZ	51/51 (100%)	36 (71%)	15 (29%)	0	3
27	Aa	63/63 (100%)	45 (71%)	18 (29%)	0	3
28	Ab	50/50 (100%)	31 (62%)	19 (38%)	0	1
29	Ac	48/48 (100%)	33 (69%)	15 (31%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Ad	42/42 (100%)	29 (69%)	13 (31%)	0	2
31	Ae	54/54 (100%)	44 (82%)	10 (18%)	2	13
32	Af	34/34 (100%)	29 (85%)	5 (15%)	3	22
35	BF	202/202 (100%)	138 (68%)	64 (32%)	0	2
36	BG	160/160 (100%)	123 (77%)	37 (23%)	1	7
37	BH	180/180 (100%)	131 (73%)	49 (27%)	0	4
38	BI	115/115 (100%)	78 (68%)	37 (32%)	0	2
39	BJ	90/90 (100%)	61 (68%)	29 (32%)	0	2
40	BK	126/126 (100%)	93 (74%)	33 (26%)	0	5
41	BL	119/119 (100%)	86 (72%)	33 (28%)	0	4
42	BM	98/98 (100%)	73 (74%)	25 (26%)	0	6
43	BN	88/88 (100%)	67 (76%)	21 (24%)	1	6
44	BO	90/90 (100%)	73 (81%)	17 (19%)	2	12
45	BP	104/104 (100%)	81 (78%)	23 (22%)	1	8
46	BQ	92/92 (100%)	67 (73%)	25 (27%)	0	4
47	BR	49/49 (100%)	36 (74%)	13 (26%)	0	5
48	BS	79/79 (100%)	64 (81%)	15 (19%)	2	12
49	BT	72/72 (100%)	49 (68%)	23 (32%)	0	2
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%)	51 (72%)	20 (28%)	0	3
53	BX	76/76 (100%)	59 (78%)	17 (22%)	1	8
54	BY	19/19 (100%)	17 (90%)	2 (10%)	8	34
55	CA	481/507 (95%)	350 (73%)	131 (27%)	0	4
All	All	5385/5411 (100%)	3876 (72%)	1509 (28%)	2	4

5 of 1509 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	AW	3	TYR
31	Ae	62	LEU
55	CA	48	LEU
23	AW	86	VAL
26	AZ	37	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 186 such sidechains are listed below:

Mol	Chain	Res	Type
30	Ad	36	GLN
36	BG	139	GLN
53	BX	73	HIS
31	Ae	33	ASN
35	BF	135	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	2880/2889 (99%)	1261 (43%)	253 (8%)
2	AB	122/123 (99%)	46 (37%)	3 (2%)
34	BA	1514/1515 (99%)	484 (31%)	140 (9%)
All	All	4516/4527 (99%)	1791 (39%)	396 (8%)

5 of 1791 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 396 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	2017	U
1	AA	2500	U
34	BA	1214	C
1	AA	2033	A
1	AA	2225	A

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

3 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	$\# Z  > 2$
56	NMY	AA	3001	-	45,45,45	0.52	0	59,67,67	1.20	7 (11%)
56	NMY	BB	1601	-	45,45,45	0.51	0	59,67,67	1.11	6 (10%)
57	GCP	CA	701	-	25,34,34	2.58	8 (32%)	28,54,54	1.22	2 (7%)

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
56	NMY	AA	3001	-	-	0/18/94/94	1/4/4/4
56	NMY	BB	1601	-	-	0/18/94/94	0/4/4/4
57	GCP	CA	701	-	-	0/18/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	CA	701	GCP	C4-N9	-10.34	1.34	1.47
57	CA	701	GCP	C8-N9	-3.85	1.35	1.46
57	CA	701	GCP	C5-C6	-2.42	1.48	1.53
57	CA	701	GCP	C2-N1	-2.19	1.35	1.44
57	CA	701	GCP	PB-O2B	2.11	1.61	1.56

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	CA	701	GCP	PA-O3A-PB	-3.69	120.51	132.39
56	AA	3001	NMY	C18-O18-C15	-2.55	111.77	118.00
56	BB	1601	NMY	C1-O1-C10	-2.55	111.78	118.00
56	AA	3001	NMY	C13-O11-C11	-2.55	111.78	118.00
56	AA	3001	NMY	C1-O1-C10	-2.55	111.79	118.00

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

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

3 monomers are involved in 77 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	AA	3001	NMY	23	0
56	BB	1601	NMY	15	0
57	CA	701	GCP	39	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	11
33	Ag	3
34	BA	3
55	CA	2
9	AI	1

The worst 5 of 20 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	CA	542:LYS	C	552:ASP	N	16.28
1	AA	164:U	O3'	171:G	P	7.69

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	2893:G	O3'	2894:G	P	5.34
1	CA	277:THR	C	281:GLU	N	5.08