



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 07:43 PM UTC

PDB ID : 5A9Z / pdb_00005a9z
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 : 2015-07-23
Resolution : 4.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

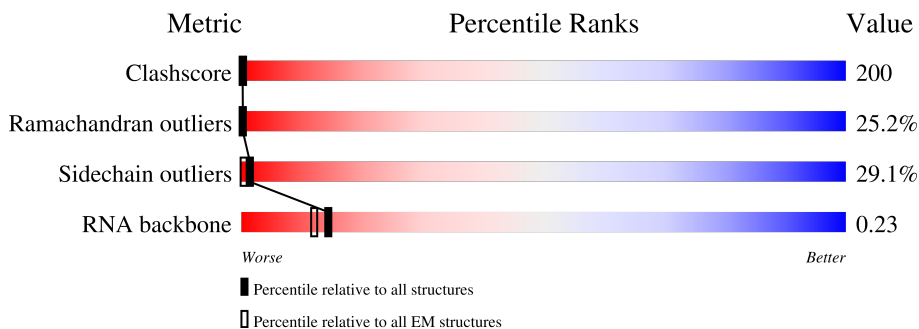
1 Overall quality at a glance ⓘ

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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	

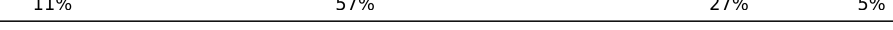
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Mol	Chain	Length	Quality of chain
8	AH	174	
9	AI	153	
10	AJ	134	
11	AK	139	
12	AL	122	
13	AM	145	
14	AN	136	
15	AO	117	
16	AP	110	
17	AQ	117	
18	AR	117	
19	AS	101	
20	AT	110	
21	AU	94	
22	AV	110	
23	AW	180	
24	AX	85	
25	AY	67	
26	AZ	59	
27	Aa	71	
28	Ab	57	
29	Ac	49	
30	Ad	49	
31	Ae	64	
32	Af	37	

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Mol	Chain	Length	Quality of chain
33	Ag	128	 52% 48%
34	BA	1515	 57% 33% 9%
35	BF	234	 43% 42% 14%
36	BG	206	 50% 39% 6%
37	BH	208	 48% 39% 11%
38	BI	150	 56% 35% 8%
39	BJ	101	 49% 41% 8%
40	BK	155	 50% 37% 9%
41	BL	138	 50% 39% 9%
42	BM	127	 56% 35% 6%
43	BN	98	 48% 44% 6%
44	BO	119	 54% 42% 4%
45	BP	124	 38% 49% 9%
46	BQ	114	 11% 57% 27% 5%
47	BR	60	 7% 48% 30% 15%
48	BS	88	 58% 34% 6%
49	BT	83	 49% 40% 11%
50	BU	104	 44% 43% 9%
51	BV	73	 56% 29% 14%
52	BW	80	 54% 39% 6%
53	BX	99	 5% 51% 38% 6%
54	BY	24	 63% 29% 8%
55	CA	593	 11% 56% 28% 5%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	GCP	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		
			877	553	175	149	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	AQ	117	Total	C	N	O	S	
			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	
			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	
			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	
			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		
			742	483	133	126	0	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	
			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	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		

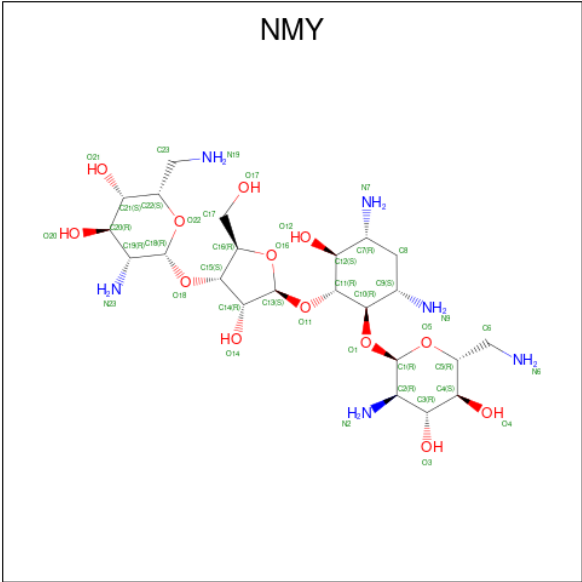
- Molecule 54 is a protein called 30S ribosomal protein Thx.

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.

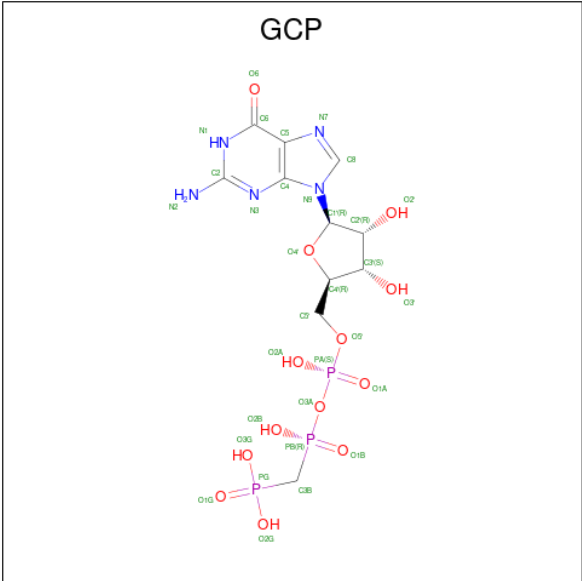
Mol	Chain	Residues	Atoms					AltConf	Trace
55	CA	593	Total	C	N	O	S	0	0
			4532	2856	791	868	17		

- Molecule 56 is NEOMYCIN (CCD ID: NMY) (formula: C₂₃H₄₆N₆O₁₃).



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

- Molecule 57 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

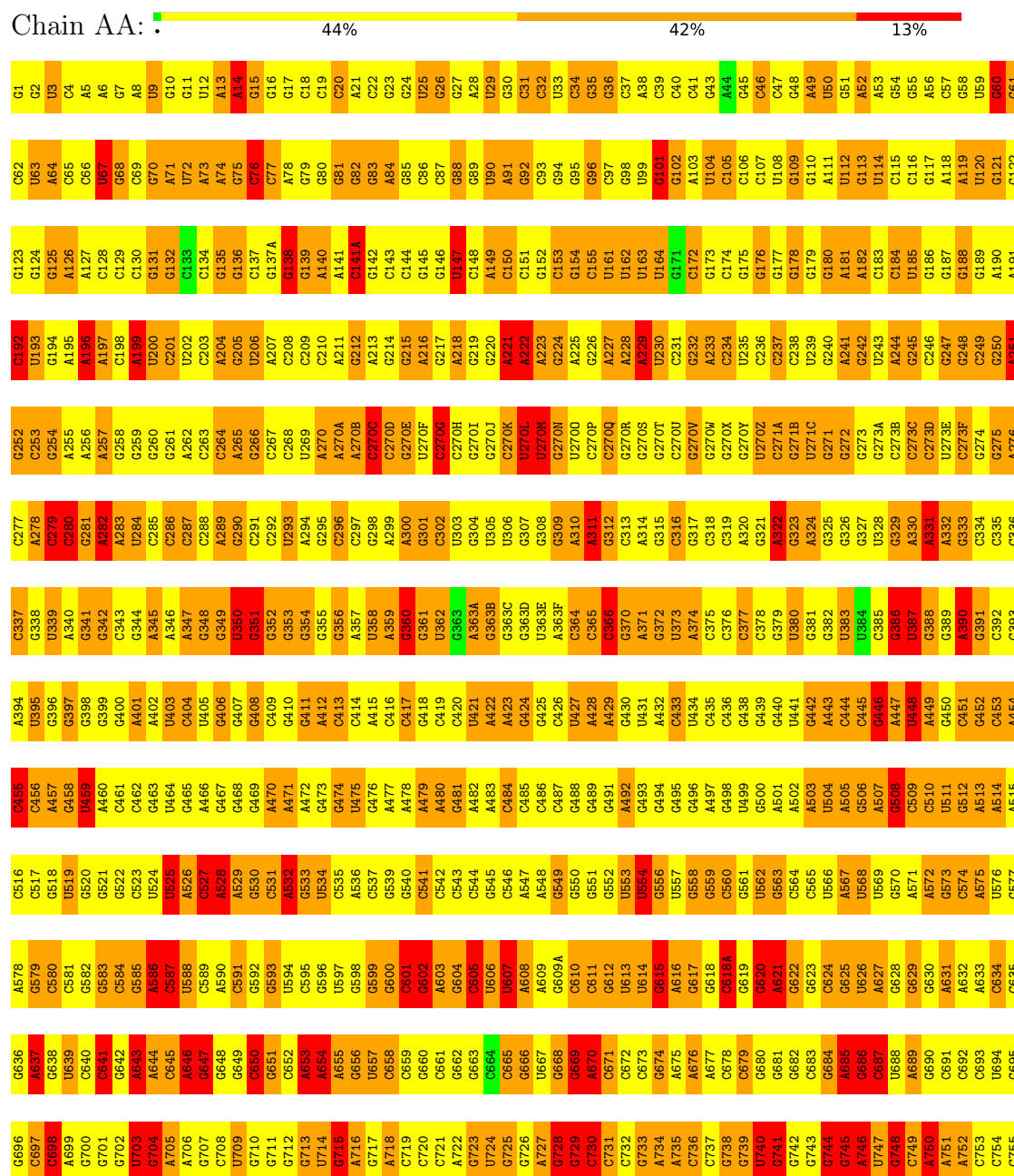


Mol	Chain	Residues	Atoms					AltConf
57	CA	1	Total	C	N	O	P	0
			32	11	5	13	3	

3 Residue-property plots

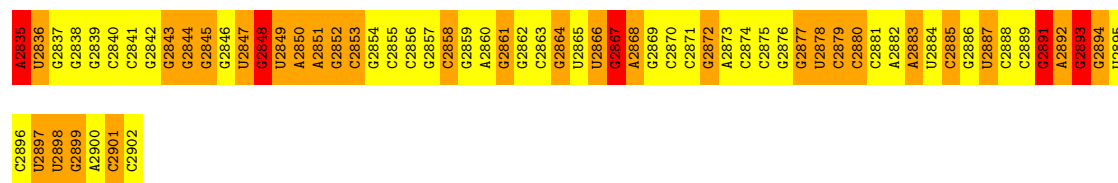
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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



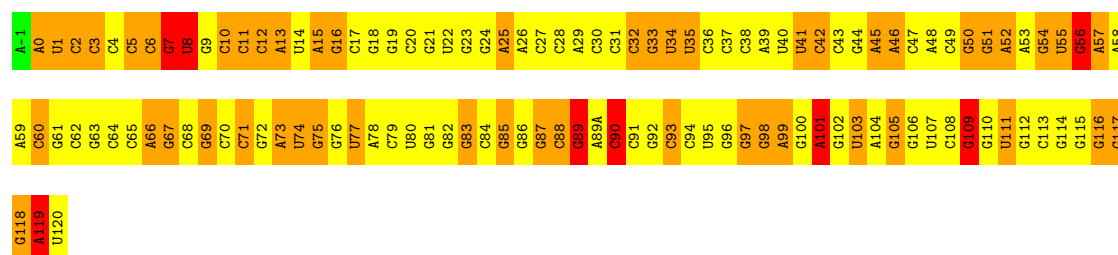
G1726	C1657	C1598	G1538	A1477	G1418	G1358	G1298	G1288	A1177	G1117	A1057	G997	G938	G876	C816	C756
U1727	C1658	C1599	G1539	G1478	A1419	A1389	G1299	G1289	C1178	C1118	G1058	C998	G939	U877	C817	U757
G1728	C1659	C1600	G1540	G1479	U1420	A1360	U1300	U1240	C1179	C1119	G1059	U999	G940	A878	G818	C758
A1729	C1660	G1601	U1541	G1480	G1421	G1361	A1301	A1241	A1180	G1120	U1060	A1000	A941	G879	A819	G759
G1730	G1661	U1602	G1542	U1482	G1423	C1362	A1302	G1242	C1181	G1121	U1061	A1001	G942	G880	A820	G760
U1731	C1662	A1603	A1543	G1483	G1424	C1363	G1303	G1243	A1182	G1122	G1062	G1002	U943	G881	A821	A761
A1732	C1663	G1604	G1544	G1484	G1424	G1364	C1304	G1244	G1183	G1123	G1063	G1003	G944	G882	U822	U762
G1733	A1664	C1605	A1545	G1485	G1425	A1365	C1305	G1245	G1184	G1124	C1064	C1004	A945	G883	G823	G763
C1734	G1666	G1606	U1546	A1486	G1426	A1366	C1306	G1246	C1185	G1125	U1065	C1005	G946	G884	A824	A764
G1741	G1667	C1607	G1547	G1487	A1427	A1367	A1307	A1247	G1186	A1127	U1066	C1006	G947	C885	U826	C766
C1742	A1668	A1609	C1548	G1488	C1428	G1368	G1308	G1248	G1187	A1128	G1067	G1007	G948	C886	U827	G767
G1743	U1669	G1610	C1549	U1489	G1429	G1369	G1309	U1249	U1188	A1129	G1068	C1008	C949	A887	U828	G768
C1744	C1670	C1611	C1550	G1490	C1430	C1370	G1310	G1250	U1189	U1130	A1069	A1009	G950	C888	U829	G769
G1747	U1671	C1612	C1551	G1491	U1431	G1371	G1311	C1251	G1190	U1131	A1070	A1010	C951	C889	G830	G770
G1748	C1672	G1613	G1552	C1492	C1432	A1372	U1312	G1252	G1191	G1132	G1071	G1011	G952	A890	G831	G771
A1749	A1673	A1614	C1553	C1493	A1433	A1373	C1313	A1253	G1192	U1012	A953	U1012	G953	G892	G832	G772
G1750	G1674	A1615	A1554	A1495	G1434	C1374	C1314	A1254	G1193	U1013	A954	C1013	G954	C893	U773	C773
C1751	C1675	A1616	G1555	A1496	G1435	C1375	C1315	U1255	A1194	G1134	G1074	U1014	G955	C894	U833	A774
G1752	A1676	C1617	C1556	U1497	G1437	G1377	A1317	C1257	G1196	G1136	C1076	G1016	A957	A896	C834	A775
G1753	U1677	A1618	C1557	U1498	U1438	A1378	C1318	G1258	G1197	G1137	U1077	G1017	U958	C897	G836	G776
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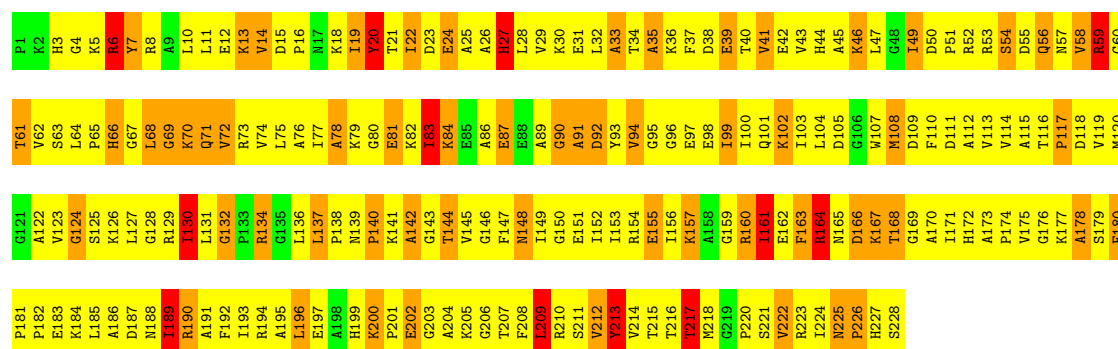
- Molecule 2: 5S ribosomal RNA

Chain AB: 52% 41% 7%



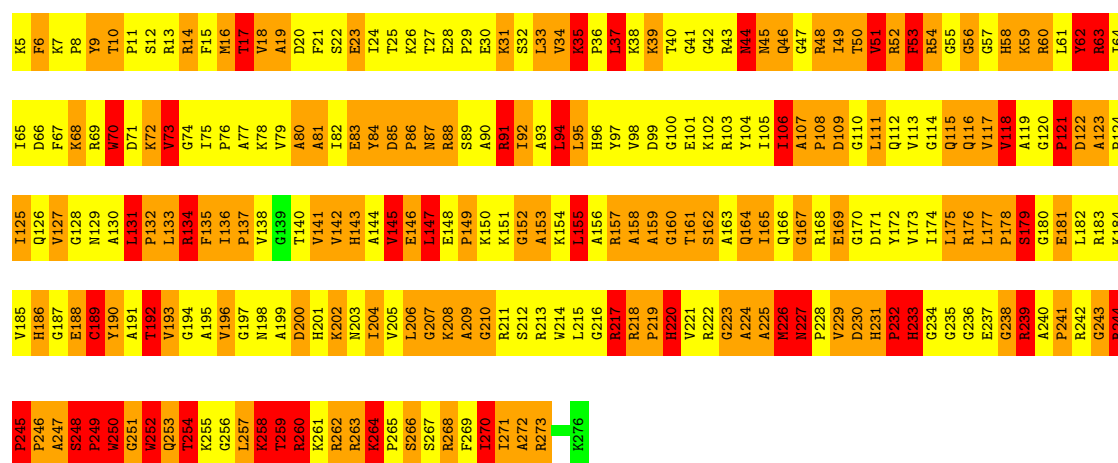
- Molecule 3: 50S ribosomal protein L1

Chain AC: 6% 63% 26% 5%

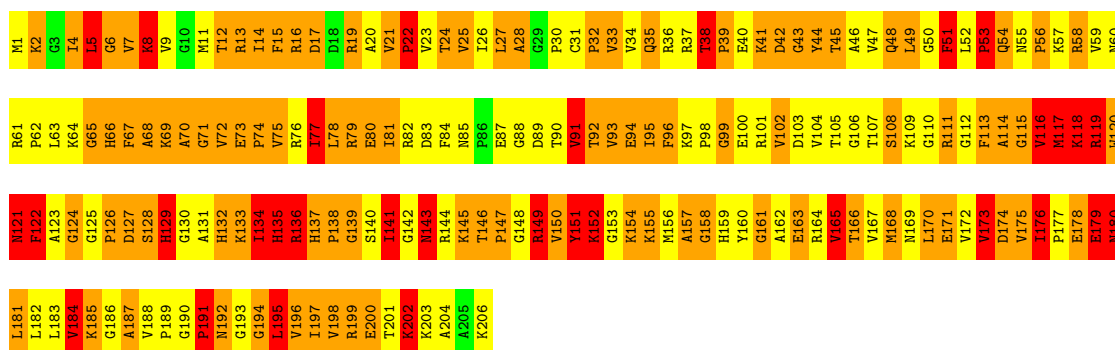


- Molecule 4: 50S ribosomal protein L2

Chain AD: 43% 40% 15%

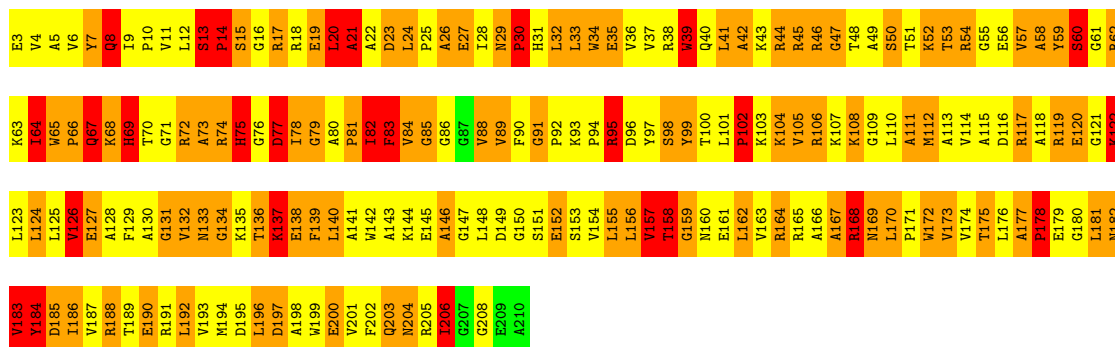


Chain AE:  36% 46% 16%



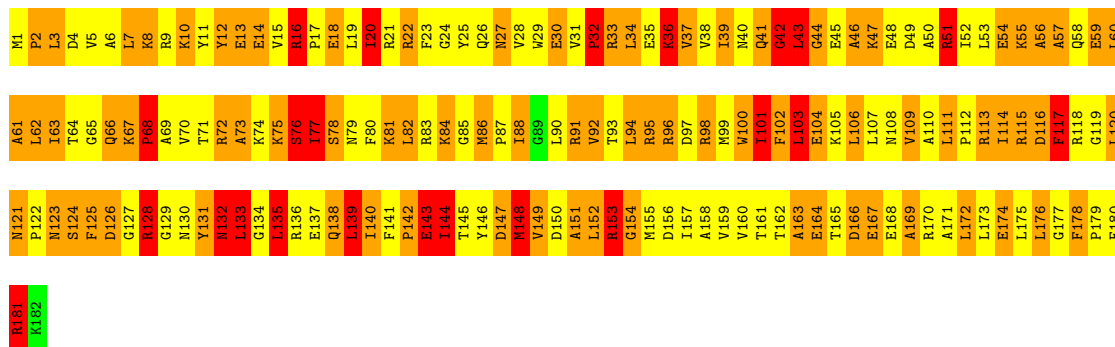
• Molecule 6: 50S ribosomal protein L4

Chain AF:  43% 42% 13%

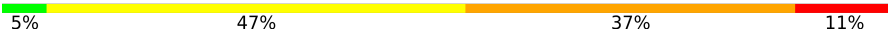


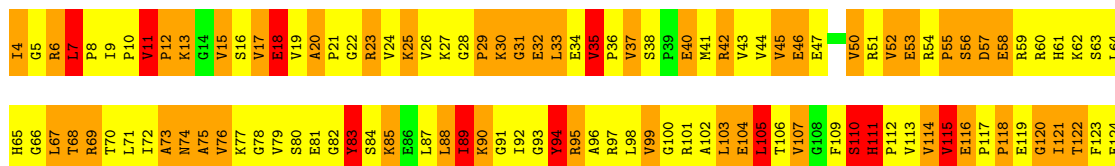
• Molecule 7: 50S ribosomal protein L5

Chain AG:  42% 44% 13%



• Molecule 8: 50S ribosomal protein L6

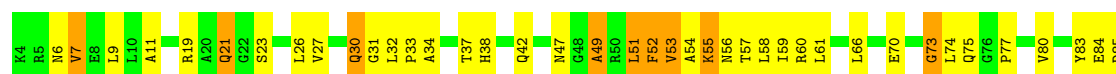
Chain AH:  5% 47% 37% 11%





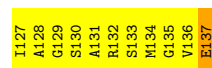
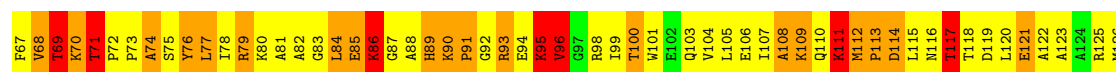
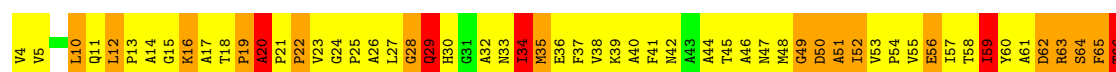
• Molecule 9: 50S ribosomal protein L10

Chain AI: 44% 44% 11%



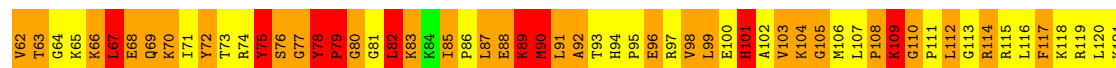
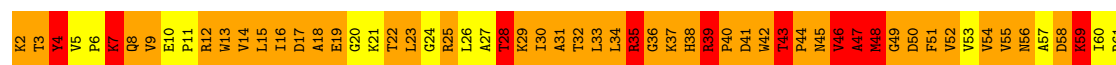
• Molecule 10: 50S ribosomal protein L11

Chain AJ: 7% 57% 27% 9%



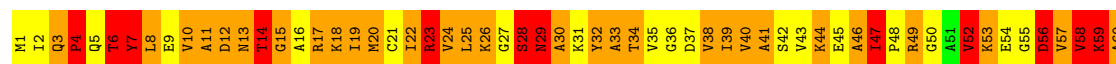
• Molecule 11: 50S ribosomal protein L13

Chain AK: 32% 51% 17%



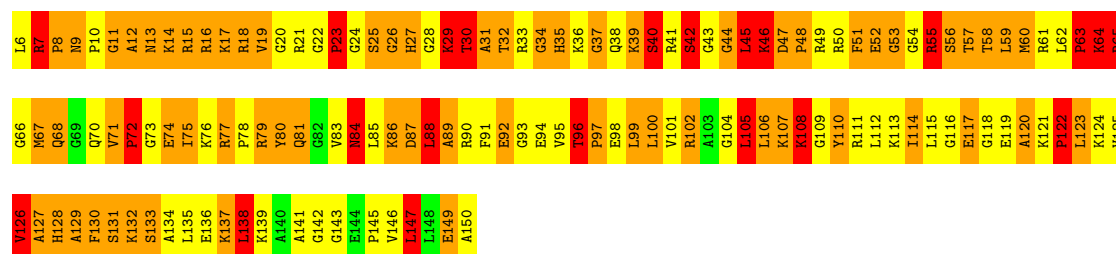
• Molecule 12: 50S ribosomal protein L14

Chain AL: 28% 51% 20%



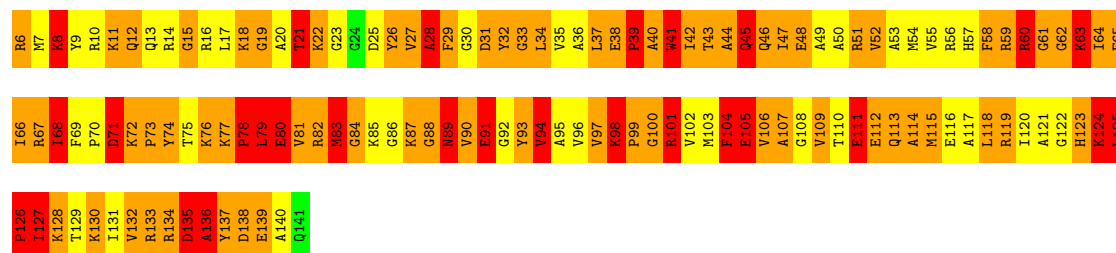
• Molecule 13: 50S ribosomal protein L15

Chain AM: 

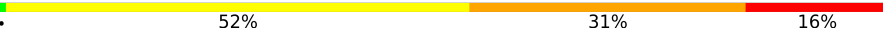


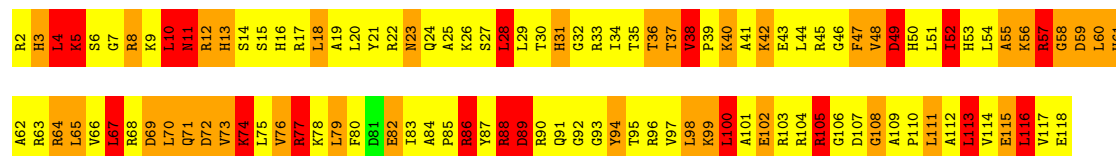
- Molecule 14: 50S ribosomal protein L16

Chain AN: 



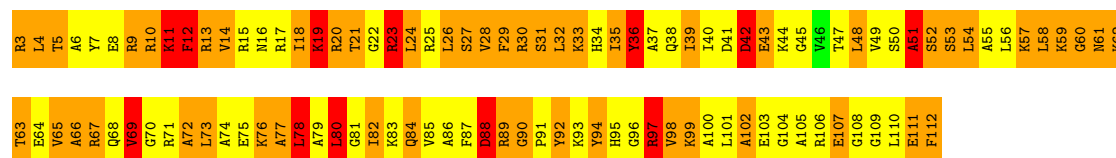
- Molecule 15: 50S ribosomal protein L17

Chain AO: 



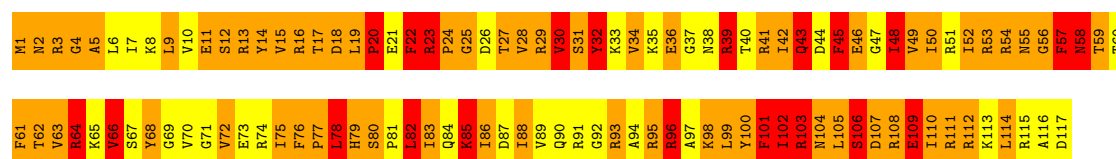
- Molecule 16: 50S ribosomal protein L18

Chain AP: 



- Molecule 17: 50S ribosomal protein L19

Chain AQ: 



- Molecule 18: 50S ribosomal protein L20

P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	P14	P15	P16	P17	P18	P19	P20	P21	P22	P23	P24	P25	P26	P27	P28	P29	P30	P31	P32	P33	P34	P35	P36	P37	P38	P39	P40	P41	P42	P43	P44	P45	P46	P47	P48	P49	P50	P51	P52	P53	P54	P55	P56	P57	P58	P59	P60	P61																																																																																																																																																																																																																																																																																																																																																																																																																
162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	62

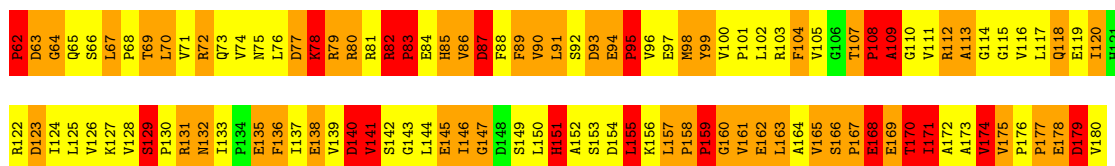
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V61	L62	G63	H64	G65	R66	G67	K68	G69	I70	L71	V72	S73	K74	F75	K76	A77	K78	V79	Q80	R81	R82	R83	K84	K85	G86	H87	R88	R89	P90	Y91	T92	E93	L94	L95	I96	K97	K98	E99	I99	R100	G101																		

M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	M18	M19	M20	M21	M22	M23	M24	M25	M26	M27	M28	M29	M30	M31	M32	M33	M34	M35	M36	M37	M38	M39	M40	M41	M42	M43	M44	M45	M46	M47	M48	M49	M50	M51	M52	M53	M54	M55	M56	M57	M58	M59	M60
M61	M62	M63	M64	M65	M66	M67	M68	M69	M70	M71	M72	M73	M74	M75	M76	M77	M78	M79	M80	M81	M82	M83	M84	M85	M86	M87	M88	M89	M90	M91	M92	M93	M94	M95	M96	M97	M98	M99	M100	M101	M102	M103	M104	M105	M106	M107	M108	M109	M110										

[illegible]

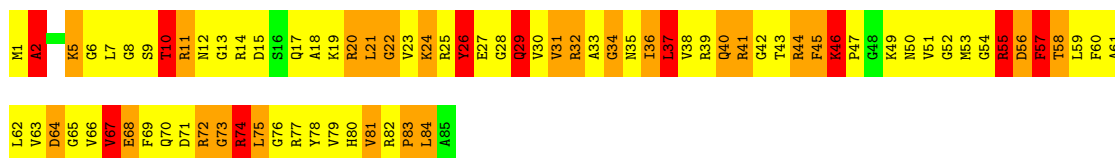
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I61	E62	K63	E64	A65	P66	L67	H68	A69	S70	K71	V72	R73	P74	I75	C76	P77	A78	I79	K80	R81	T82	T83	R84	V85	R86	K87	K88	F89	L90	E91	N92	G93	K94	K95	I96	R97	V98	C99	A100	K101	G102	G103	A104	A105	L106	D107	T108	E109	E110										

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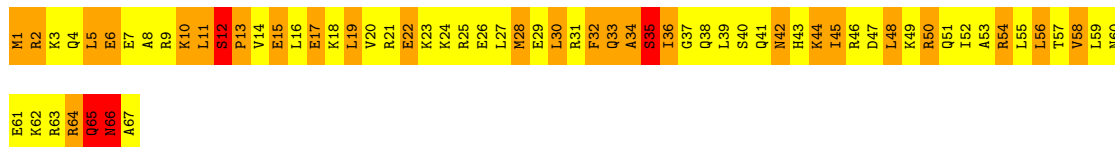
- Molecule 24: 50S ribosomal protein L27

Chain AX: 6% 54% 28% 12%



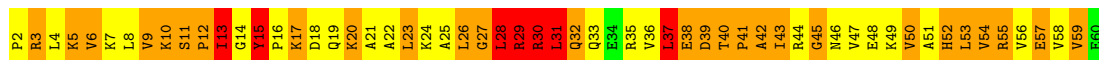
- Molecule 25: 50S ribosomal protein L29

Chain AY: 55% 39% 6%



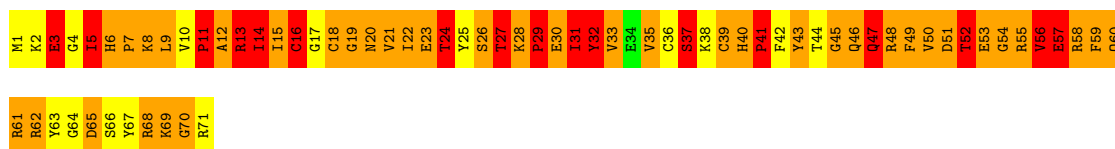
- Molecule 26: 50S ribosomal protein L30

Chain AZ: 39% 46% 12%



- Molecule 27: 50S ribosomal protein L31

Chain Aa: 21% 54% 24%



- Molecule 28: 50S ribosomal protein L32

Chain Ab: 28% 51% 19%



- Molecule 29: 50S ribosomal protein L33

Chain Ac: 16% 55% 27%



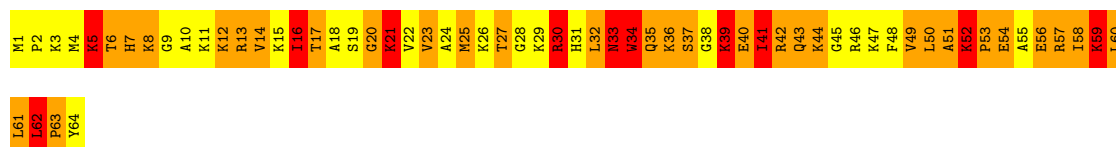
• Molecule 30: 50S ribosomal protein L34

Chain Ad: 45% 47% 8%



• Molecule 31: 50S ribosomal protein L35

Chain Ae: 36% 47% 17%



• Molecule 32: 50S ribosomal protein L36

Chain Af: 5% 54% 32% 8%



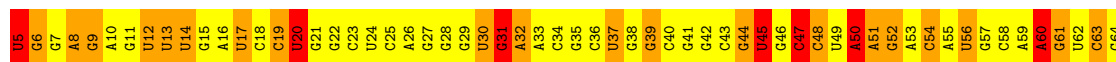
• Molecule 33: Unknown peptide

Chain Ag: 52% 48%

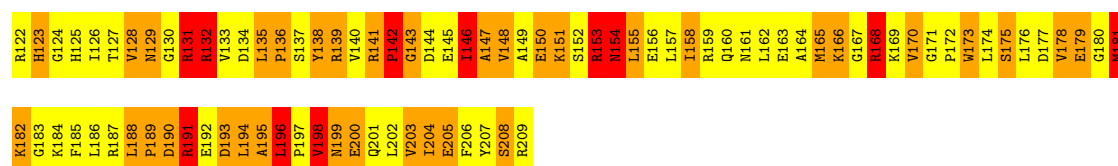


• Molecule 34: 16S ribosomal RNA

Chain BA: 57% 33% 9%

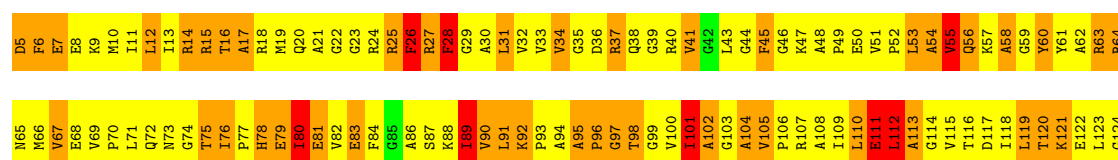


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C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
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G1104	A1105	G1106	G1107	G1108	G1109	A1110	A1111	A1112	A1113	C1114	C1115	C1116	G1117	G1118	C1119	G1120	G1121	U1122	U1123	U1124	U1125	U1126	U1127	U1128	U1129	U1130	U1131	U1132	U1133	U1134	U1135	U1136	U1137	U1138	U1139	U1140	U1141	U1142	U1143	U1144	U1145	U1146	U1147	U1148	U1149	U1150	U1151	U1152	U1153	U1154	U1155	U1156	U1157	U1158	U1159	U1160	U1161	U1162	U1163	U1164	U1165	U1166	U1167	U1168	U1169	U1170	U1171	U1172	U1173	U1174	U1175	U1176	U1177	U1178	U1179	U1180	U1181	U1182	U1183	U1184	U1185	U1186	U1187	U1188	U1189	U1190	U1191	U1192	U1193	U1194	U1195	U1196	U1197	U1198	U1199	U1200	U1201	U1202	U1203	U1204	U1205	U1206	U1207	U1208	U1209	U1210	U1211	U1212	U1213	U1214	U1215	U1216	U1217	U1218	U1219	U1220	U1221	U1222	U1223	U1224	U1225	U1226	U1227	U1228	U1229	U1230	U1231	U1232	U1233	U1234	U1235	U1236	U1237	U1238	U1239	U1240	U1241	U1242	U1243	U1244	U1245	U1246	U1247	U1248	U1249	U1250	U1251	U1252	U1253	U1254	U1255	U1256	U1257	U1258	U1259	U1260	U1261	U1262	U1263	U1264	U1265	U1266	U1267	U1268	U1269	U1270	U1271	U1272	U1273	U1274	U1275	U1276	U1277	U1278	U1279	U1280	U1281	U1282	U1283	U1284	U1285	U1286	U1287	U1288	U1289	U1290	U1291	U1292	U1293	U1294	U1295	U1296	U1297	U1298	U1299	U1300	U1301	U1302	U1303	U1304	U1305	U1306	U1307	U1308	U1309	U1310																																																																																																																																																																																																																																																																																																																																																																																																																						
A1044	C1045	A1046	G1047	G1048	G1049	G1050	C1051	U1052	G1053	C1054	A1055	U1056	G1057	G1058	C1059	C1060	G1061	U1062	C1063	G1064	U1065	C1066	U1067	G1068	C1069	U1070	C1071	G1072	C1073	G1074	C1075	C1076	G1077	U1078	G1079	A1080	G1081	G1082	U1083	G1084	U1085	U1086	G1087	G1088	G1089	U1090	U1091	A1092	G1093	G1094	U1095	C1096	C1097	G1098	C1099	C1100	A1101	A1102	C1103	C1104	C1105	C1106	C1107	C1108	C1109	C1110	C1111	C1112	C1113	C1114	C1115	C1116	C1117	C1118	C1119	C1120	C1121	C1122	C1123	C1124	C1125	C1126	C1127	C1128	C1129	C1130	C1131	C1132	C1133	C1134	C1135	C1136	C1137	C1138	C1139	C1140	C1141	C1142	C1143	C1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155	C1156	C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201	C1202	C1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310																																																																																																																																																																																																																																																																																																																																																										
U743	C744	C685	C686	C687	C688	C689	C690	C691	C692	C693	C694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	C712	C713	C714	C715	C716	C717	C718	C719	C720	C721	C722	C723	C724	C725	C726	C727	C728	C729	C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835	C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	G1000	G1001	G1002	G1003	G1004	G1005	G1006	G1007	G1008	G1009	G1010	G1011	G1012	G1013	G1014	G1015	G1016	G1017	G1018	G1019	G1020	G1021	G1022	G1023	G1024	G1025	G1026	G1027	G1028	G1029	G1030	G1031	G1032	G1033	G1034	G1035	G1036	G1037	G1038	G1039	G1040	G1041	G1042	G1043	G1044	G1045	G1046	G1047	G1048	G1049	G1050	G1051	G1052	G1053	G1054	G1055	G1056	G1057	G1058	G1059	G1060	G1061	G1062	G1063	G1064	G1065	G1066	G1067	G1068	G1069	G1070	G1071	G1072	G1073	G1074	G1075	G1076	G1077	G1078	G1079	G1080	G1081	G1082	G1083	G1084	G1085	G1086	G1087	G1088	G1089	G1090	G1091	G1092	G1093	G1094	G1095	G1096	G1097	G1098	G1099	G1100	G1101	G1102	G1103	G1104	G1105	G1106	G1107	G1108	G1109	G1110	G1111	G1112	G1113	G1114	G1115	G1116	G1117	G1118	G1119	G1120	G1121	G1122	G1123	G1124	G1125	G1126	G1127	G1128	G1129	G1130	G1131	G1132	G1133	G1134	G1135	G1136	G1137	G1138	G1139	G1140	G1141	G1142	G1143	G1144	G1145	G1146	G1147	G1148	G1149	G1150	G1151	G1152	G1153	G1154	G1155	G1156	G1157	G1158	G1159	G1160	G1161	G1162	G1163	G1164	G1165	G1166	G1167	G1168	G1169	G1170	G1171	G1172	G1173	G1174	G1175	G1176	G1177	G1178	G1179	G1180	G1181	G1182	G1183	G1184	G1185	G1186	G1187	G1188	G1189	G1190	G1191	G1192	G1193	G1194	G1195	G1196	G1197	G1198	G1199	G1200	G1201	G1202	G1203	G1204	G1205	G1206	G1207	G1208	G1209	G1210	G1211	G1212	G1213	G1214	G1215	G1216	G1217	G1218	G1219	G1220	G1221	G1222	G1223	G1224</



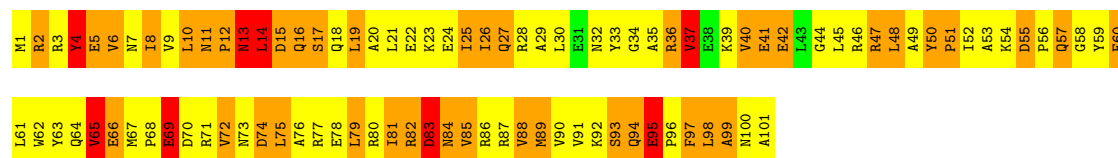
• Molecule 38: 30S ribosomal protein S5

Chain BI: . 56% 35% 8%



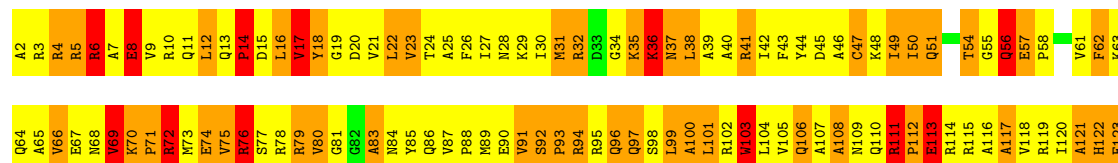
• Molecule 39: 30S ribosomal protein S6

Chain BJ: . 49% 41% 8%



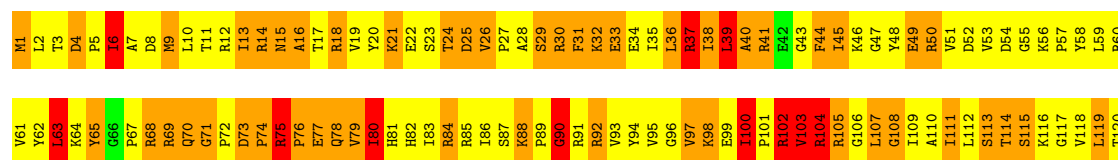
• Molecule 40: 30S ribosomal protein S7

Chain BK: . 50% 37% 9%



• Molecule 41: 30S ribosomal protein S8

Chain BL: . 50% 39% 9%





- Molecule 47: 30S ribosomal protein S14 type Z

Chain BR: 7% 48% 30% 15%



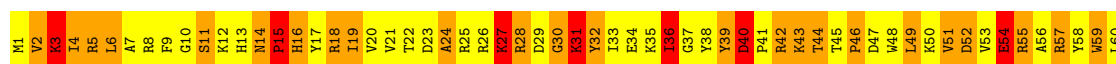
- Molecule 48: 30S ribosomal protein S15

Chain BS: 58% 34% 6%



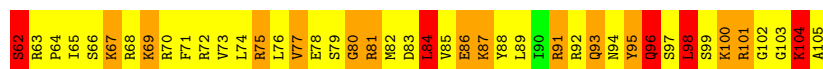
- Molecule 49: 30S ribosomal protein S16

Chain BT: 49% 40% 11%



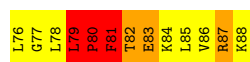
- Molecule 50: 30S ribosomal protein S17

Chain BU: 44% 43% 9%



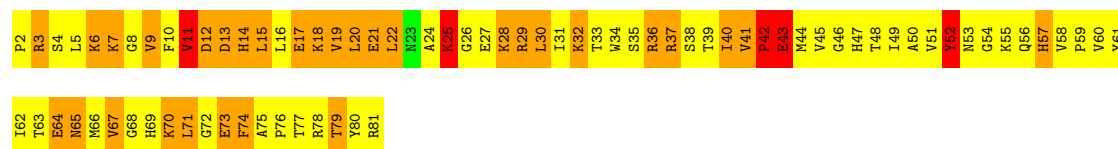
- Molecule 51: 30S ribosomal protein S18

Chain BV: 56% 29% 14%



- Molecule 52: 30S ribosomal protein S19

Chain BW: 54% 39% 6%



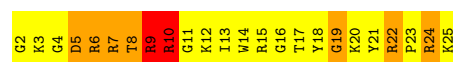
- Molecule 53: 30S ribosomal protein S20

Chain BX: 5% 51% 38% 6%



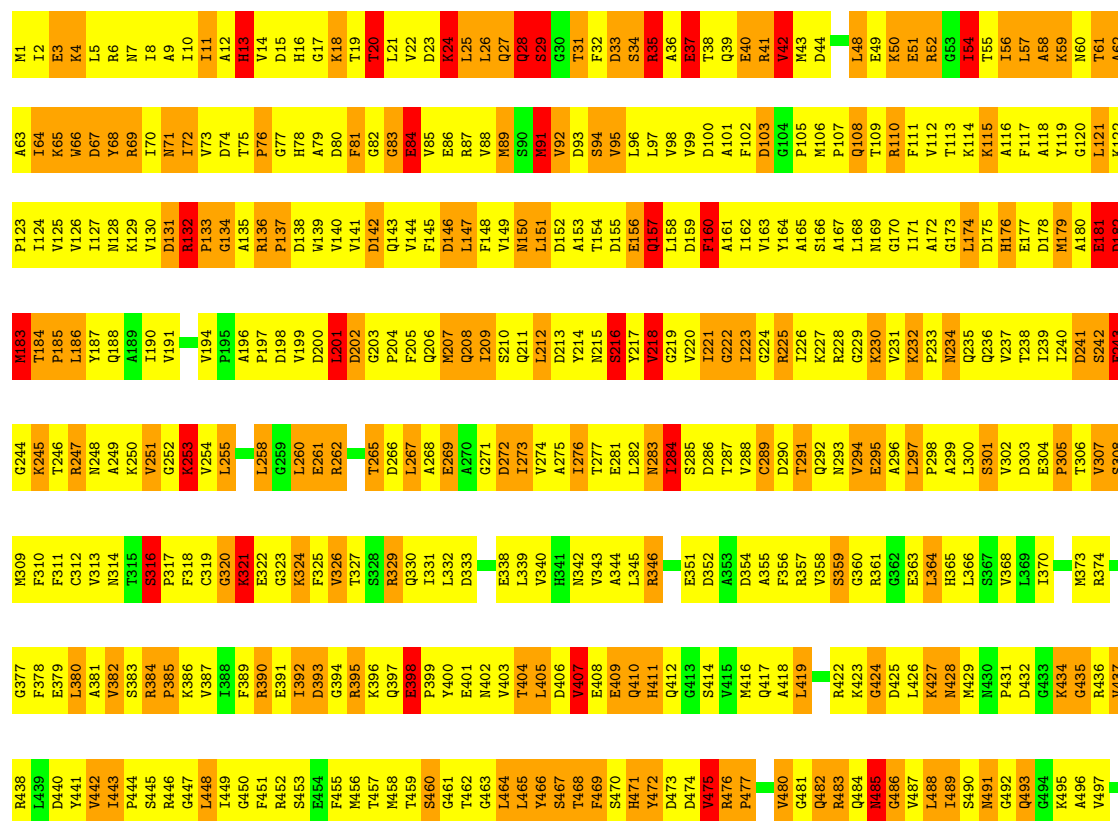
- Molecule 54: 30S ribosomal protein Thx

Chain BY: 63% 29% 8%



- Molecule 55: BipA

Chain CA: 11% 56% 28% 5%



A500	I572	A501	D573	F502	D574	G503	D575	L504	E576	Q505	L577	D506	V578	E579	V580	T581	P582	T583	S584	I585	R586	I587	R588	K589	L592	T593	D596	R597	R598	R599	A600	N601	A602	A603	P604	K605	V507	G508	K509	L510	F511	L512	G513	H514	G515	A516	E517	V518	Y519	E520	G521	Q522	I523	I524	G525	I526	H527	S528	R529	S530	N531	D532	L533	T534	V535	N536	G537	L538	T539	G540	K541	K542	D552	E553	A554	V555	V558	I561	T564	L565	E566	Q567	A568	L569	E570	F571
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	61165	Depositor
Resolution determination method	Not provided	
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: NMY, GCP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.69	17/69677 (0.0%)	1.05	366/108754 (0.3%)
2	AB	0.56	0/2954	0.95	5/4606 (0.1%)
3	AC	0.79	0/1775	1.36	32/2393 (1.3%)
4	AD	0.97	1/2174 (0.0%)	1.76	56/2927 (1.9%)
5	AE	1.06	5/1611 (0.3%)	1.65	45/2171 (2.1%)
6	AF	0.83	0/1660	1.50	35/2247 (1.6%)
7	AG	0.83	1/1507 (0.1%)	1.53	34/2027 (1.7%)
8	AH	0.82	2/1354 (0.1%)	1.48	28/1831 (1.5%)
9	AI	0.67	1/751 (0.1%)	1.20	6/1042 (0.6%)
10	AJ	0.56	0/1012	0.91	4/1373 (0.3%)
11	AK	1.02	1/1140 (0.1%)	1.64	30/1537 (2.0%)
12	AL	1.24	3/942 (0.3%)	1.96	48/1268 (3.8%)
13	AM	1.00	2/1123 (0.2%)	1.63	33/1493 (2.2%)
14	AN	0.99	0/1100	1.76	35/1470 (2.4%)
15	AO	0.98	1/974 (0.1%)	1.60	28/1302 (2.2%)
16	AP	1.00	0/887	1.65	28/1180 (2.4%)
17	AQ	1.14	2/990 (0.2%)	1.85	34/1325 (2.6%)
18	AR	1.02	1/982 (0.1%)	1.50	21/1306 (1.6%)
19	AS	1.16	2/790 (0.3%)	1.93	32/1057 (3.0%)
20	AT	0.89	1/886 (0.1%)	1.51	17/1189 (1.4%)
21	AU	0.77	0/756	1.38	15/1015 (1.5%)
22	AV	0.75	0/857	1.57	22/1142 (1.9%)
23	AW	0.92	1/1467 (0.1%)	1.78	55/1992 (2.8%)
24	AX	0.86	0/679	1.59	21/902 (2.3%)
25	AY	0.83	0/569	1.32	8/751 (1.1%)
26	AZ	0.86	1/474 (0.2%)	1.62	13/635 (2.0%)
27	Aa	1.10	0/594	1.85	26/795 (3.3%)
28	Ab	1.03	2/459 (0.4%)	1.76	20/621 (3.2%)
29	Ac	1.10	0/433	1.88	15/576 (2.6%)
30	Ad	0.98	0/438	1.34	4/575 (0.7%)
31	Ae	0.83	0/523	1.62	18/690 (2.6%)
32	Af	0.82	0/310	1.56	6/407 (1.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	BA	0.65	3/36437 (0.0%)	0.99	133/56865 (0.2%)
35	BF	0.87	1/1935 (0.1%)	1.50	38/2609 (1.5%)
36	BG	0.70	0/1636	1.33	21/2205 (1.0%)
37	BH	0.89	3/1733 (0.2%)	1.42	26/2318 (1.1%)
38	BI	0.86	0/1162	1.47	22/1564 (1.4%)
39	BJ	0.85	0/856	1.28	7/1154 (0.6%)
40	BK	0.77	0/1276	1.37	21/1709 (1.2%)
41	BL	0.85	0/1136	1.35	13/1527 (0.9%)
42	BM	0.75	0/1029	1.16	9/1379 (0.7%)
43	BN	0.70	0/807	1.33	10/1085 (0.9%)
44	BO	0.85	0/900	1.58	23/1213 (1.9%)
45	BP	0.78	0/986	1.49	21/1320 (1.6%)
46	BQ	0.35	0/924	0.68	0/1238
47	BR	0.72	0/501	1.34	8/664 (1.2%)
48	BS	0.83	0/745	1.33	9/992 (0.9%)
49	BT	0.87	0/716	1.35	12/963 (1.2%)
50	BU	0.99	1/870 (0.1%)	1.51	20/1159 (1.7%)
51	BV	0.79	0/603	1.61	13/799 (1.6%)
52	BW	0.63	1/661 (0.2%)	1.31	4/890 (0.4%)
53	BX	0.94	0/765	1.28	8/1007 (0.8%)
54	BY	0.57	0/212	1.26	3/277 (1.1%)
55	CA	0.40	2/4598 (0.0%)	0.74	4/6200 (0.1%)
All	All	0.74	55/162336 (0.0%)	1.17	1565/241736 (0.6%)

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
2	AB	0	17
3	AC	0	1
5	AE	0	1
6	AF	0	1
9	AI	0	2
11	AK	0	1
14	AN	0	1
17	AQ	0	1
19	AS	0	1
27	Aa	0	1
28	Ab	0	1

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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
55	CA	0	1
All	All	0	633

The worst 5 of 55 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	1060	U	O3'-P	-64.22	0.64	1.61
34	BA	1317	C	O3'-P	-56.08	0.77	1.61
1	AA	1203	G	O3'-P	-27.75	1.19	1.61
34	BA	1167	A	O3'-P	16.69	1.86	1.61
9	AI	153	LEU	C-N	-15.26	1.11	1.33

The worst 5 of 1565 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	BA	1317	C	P-O3'-C3'	-39.34	61.18	120.20
34	BA	1317	C	O3'-P-O5'	38.74	162.12	104.00
1	AA	1060	U	O3'-P-O5'	36.31	158.46	104.00
1	AA	2448	A	C5'-C4'-O4'	-21.83	76.36	109.10
1	AA	1203	G	P-O3'-C3'	21.78	152.87	120.20

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	16235	0
2	AB	2641	0	1337	609	0
3	AC	1742	0	1796	724	0
4	AD	2124	0	2207	1530	0
5	AE	1578	0	1647	1107	0
6	AF	1625	0	1666	836	0
7	AG	1482	0	1546	898	0
8	AH	1328	0	1407	742	0
9	AI	752	0	363	210	0
10	AJ	993	0	1019	749	0
11	AK	1113	0	1183	802	0
12	AL	932	0	994	778	0
13	AM	1106	0	1183	821	0
14	AN	1080	0	1127	752	0
15	AO	960	0	1021	616	0
16	AP	877	0	938	533	0
17	AQ	976	0	1030	693	0
18	AR	964	0	1022	744	0
19	AS	779	0	852	585	0
20	AT	876	0	941	476	0
21	AU	742	0	800	368	0
22	AV	844	0	930	434	0
23	AW	1435	0	1463	753	0
24	AX	670	0	700	359	0
25	AY	567	0	621	324	0
26	AZ	469	0	518	329	0
27	Aa	581	0	577	398	0
28	Ab	445	0	459	284	0
29	Ac	426	0	452	283	0
30	Ad	430	0	480	277	0
31	Ae	515	0	587	410	0
32	Af	307	0	335	156	0
33	Ag	620	0	136	155	0
34	BA	32554	0	16389	7535	0
35	BF	1900	0	1951	1092	0
36	BG	1612	0	1677	741	0
37	BH	1703	0	1763	889	0
38	BI	1146	0	1207	605	0
39	BJ	843	0	857	410	0
40	BK	1257	0	1296	582	0
41	BL	1116	0	1177	739	0
42	BM	1010	0	1035	499	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	BN	794	0	840	375	0
44	BO	885	0	904	470	0
45	BP	970	0	1057	534	0
46	BQ	914	0	954	658	0
47	BR	492	0	529	284	0
48	BS	734	0	771	377	0
49	BT	700	0	720	365	0
50	BU	857	0	930	476	0
51	BV	597	0	668	388	0
52	BW	647	0	653	538	0
53	BX	763	0	857	418	0
54	BY	208	0	221	92	0
55	CA	4532	0	4424	2490	0
56	AA	42	0	46	19	0
56	BA	42	0	46	15	0
57	CA	32	0	14	39	0
All	All	150547	0	103595	50553	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 200.

The worst 5 of 50553 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	3
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	AI	151/153 (99%)	89 (59%)	33 (22%)	29 (19%)	0	2
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	3
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	2
21	AU	92/94 (98%)	57 (62%)	16 (17%)	19 (21%)	0	1
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	1
24	AX	83/85 (98%)	52 (63%)	21 (25%)	10 (12%)	0	5
25	AY	65/67 (97%)	36 (55%)	20 (31%)	9 (14%)	0	3
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	5
39	BJ	99/101 (98%)	58 (59%)	19 (19%)	22 (22%)	0	1
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	2
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	2
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	2
49	BT	81/83 (98%)	42 (52%)	24 (30%)	15 (18%)	0	2
50	BU	102/104 (98%)	62 (61%)	23 (22%)	17 (17%)	0	3
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
55	CA	587/593 (99%)	313 (53%)	170 (29%)	104 (18%)	0	2
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%)	147 (82%)	33 (18%)	2	10
4	AD	215/215 (100%)	150 (70%)	65 (30%)	0	3
5	AE	166/166 (100%)	102 (61%)	64 (39%)	0	1
6	AF	164/164 (100%)	103 (63%)	61 (37%)	0	1
7	AG	156/156 (100%)	111 (71%)	45 (29%)	0	3
8	AH	143/143 (100%)	101 (71%)	42 (29%)	0	3
10	AJ	101/101 (100%)	68 (67%)	33 (33%)	0	2
11	AK	118/118 (100%)	73 (62%)	45 (38%)	0	1
12	AL	100/100 (100%)	62 (62%)	38 (38%)	0	1
13	AM	111/111 (100%)	74 (67%)	37 (33%)	0	2
14	AN	106/106 (100%)	65 (61%)	41 (39%)	0	1
15	AO	100/100 (100%)	70 (70%)	30 (30%)	0	3
16	AP	87/87 (100%)	63 (72%)	24 (28%)	0	3
17	AQ	105/105 (100%)	67 (64%)	38 (36%)	0	1
18	AR	93/93 (100%)	64 (69%)	29 (31%)	0	2
19	AS	82/82 (100%)	58 (71%)	24 (29%)	0	3
20	AT	90/90 (100%)	62 (69%)	28 (31%)	0	2
21	AU	76/76 (100%)	54 (71%)	22 (29%)	0	3
22	AV	91/91 (100%)	72 (79%)	19 (21%)	1	7
23	AW	159/159 (100%)	116 (73%)	43 (27%)	0	3
24	AX	67/67 (100%)	49 (73%)	18 (27%)	0	3
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%)	43 (68%)	20 (32%)	0	2
28	Ab	50/50 (100%)	33 (66%)	17 (34%)	0	2
29	Ac	48/48 (100%)	31 (65%)	17 (35%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Ad	42/42 (100%)	30 (71%)	12 (29%)	0	3
31	Ae	54/54 (100%)	39 (72%)	15 (28%)	0	3
32	Af	34/34 (100%)	29 (85%)	5 (15%)	3	14
35	BF	202/202 (100%)	133 (66%)	69 (34%)	0	2
36	BG	160/160 (100%)	121 (76%)	39 (24%)	1	5
37	BH	180/180 (100%)	129 (72%)	51 (28%)	0	3
38	BI	115/115 (100%)	76 (66%)	39 (34%)	0	2
39	BJ	90/90 (100%)	62 (69%)	28 (31%)	0	2
40	BK	126/126 (100%)	93 (74%)	33 (26%)	0	4
41	BL	119/119 (100%)	85 (71%)	34 (29%)	0	3
42	BM	98/98 (100%)	74 (76%)	24 (24%)	1	4
43	BN	88/88 (100%)	67 (76%)	21 (24%)	1	5
44	BO	90/90 (100%)	75 (83%)	15 (17%)	2	11
45	BP	104/104 (100%)	79 (76%)	25 (24%)	1	5
46	BQ	92/92 (100%)	66 (72%)	26 (28%)	0	3
47	BR	49/49 (100%)	37 (76%)	12 (24%)	1	4
48	BS	79/79 (100%)	62 (78%)	17 (22%)	1	6
49	BT	72/72 (100%)	47 (65%)	25 (35%)	0	2
50	BU	96/96 (100%)	69 (72%)	27 (28%)	0	3
51	BV	64/64 (100%)	51 (80%)	13 (20%)	1	8
52	BW	71/71 (100%)	53 (75%)	18 (25%)	0	4
53	BX	76/76 (100%)	59 (78%)	17 (22%)	1	6
54	BY	19/19 (100%)	17 (90%)	2 (10%)	6	22
55	CA	479/507 (94%)	343 (72%)	136 (28%)	0	3
All	All	5383/5411 (100%)	3814 (71%)	1569 (29%)	1	3

5 of 1569 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	BF	91	PRO
40	BK	113	GLU
35	BF	185	ILE
35	BF	84	GLU
37	BH	141	ARG

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

Mol	Chain	Res	Type
37	BH	201	GLN
43	BN	68	HIS
39	BJ	13	ASN
40	BK	109	ASN
44	BO	117	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	2884/2889 (99%)	1267 (43%)	253 (8%)
2	AB	122/123 (99%)	46 (37%)	3 (2%)
34	BA	1514/1515 (99%)	484 (31%)	140 (9%)
All	All	4520/4527 (99%)	1797 (39%)	396 (8%)

5 of 1797 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	2610	C
34	BA	327	A
1	AA	2690	C
34	BA	47	C
34	BA	495	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	-	43,45,45	0.49	0	62,67,67	1.22	7 (11%)
56	NMY	BA	1601	-	43,45,45	0.48	0	62,67,67	1.07	6 (9%)
57	GCP	CA	701	-	32,34,34	1.46	7 (21%)	49,54,54	1.82	8 (16%)

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	-	-	4/18/94/94	1/4/4/4
56	NMY	BA	1601	-	-	5/18/94/94	0/4/4/4
57	GCP	CA	701	-	-	6/19/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	CA	701	GCP	C5-C4	3.21	1.47	1.38
57	CA	701	GCP	PG-O2G	2.90	1.61	1.55
57	CA	701	GCP	PG-O3G	2.89	1.61	1.55
57	CA	701	GCP	PB-O3A	2.72	1.61	1.58
57	CA	701	GCP	C6-N1	-2.39	1.34	1.38

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	CA	701	GCP	C5-C4-N3	-6.17	118.57	128.39
57	CA	701	GCP	C2-N3-C4	5.07	121.03	112.30
57	CA	701	GCP	N9-C4-N3	4.58	135.12	125.95
57	CA	701	GCP	PB-O3A-PA	-3.63	120.51	132.37
56	BA	1601	NMY	C13-C14-C15	3.49	106.30	102.10

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	AA	3001	NMY	C19-C18-O18-C15
56	BA	1601	NMY	O5-C5-C6-N6
56	BA	1601	NMY	C14-C13-O11-C11
57	CA	701	GCP	PG-C3B-PB-O1B
57	CA	701	GCP	PG-C3B-PB-O2B

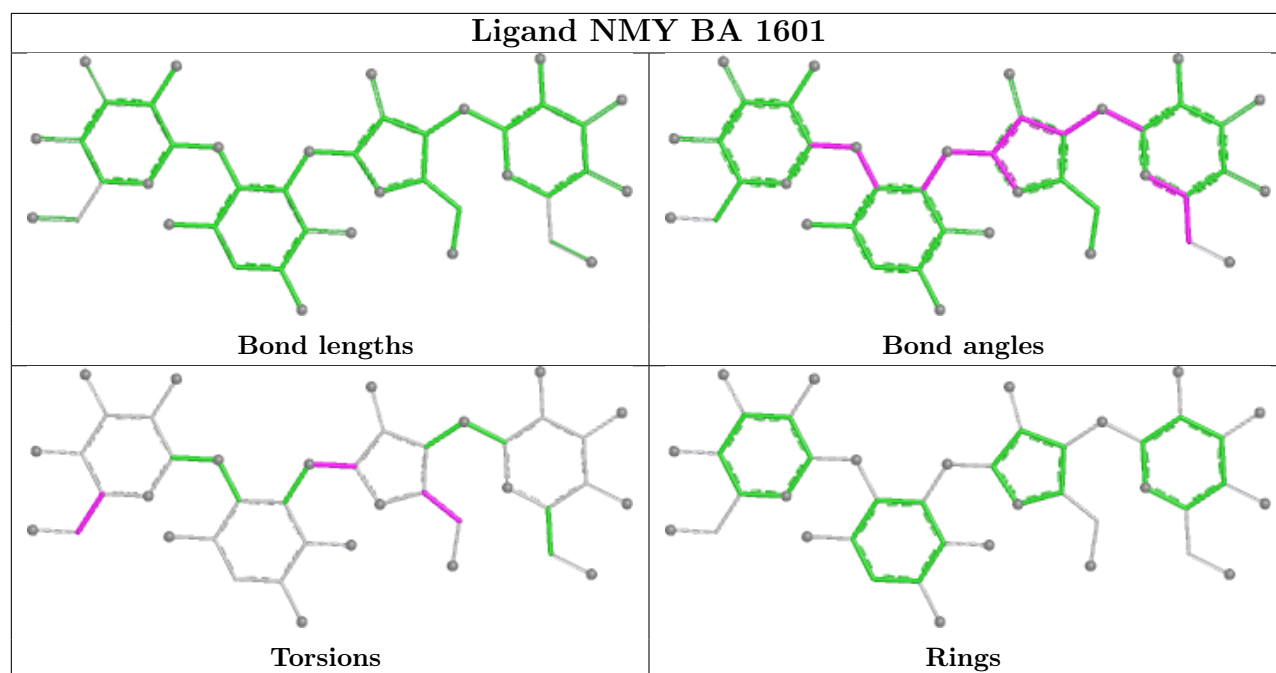
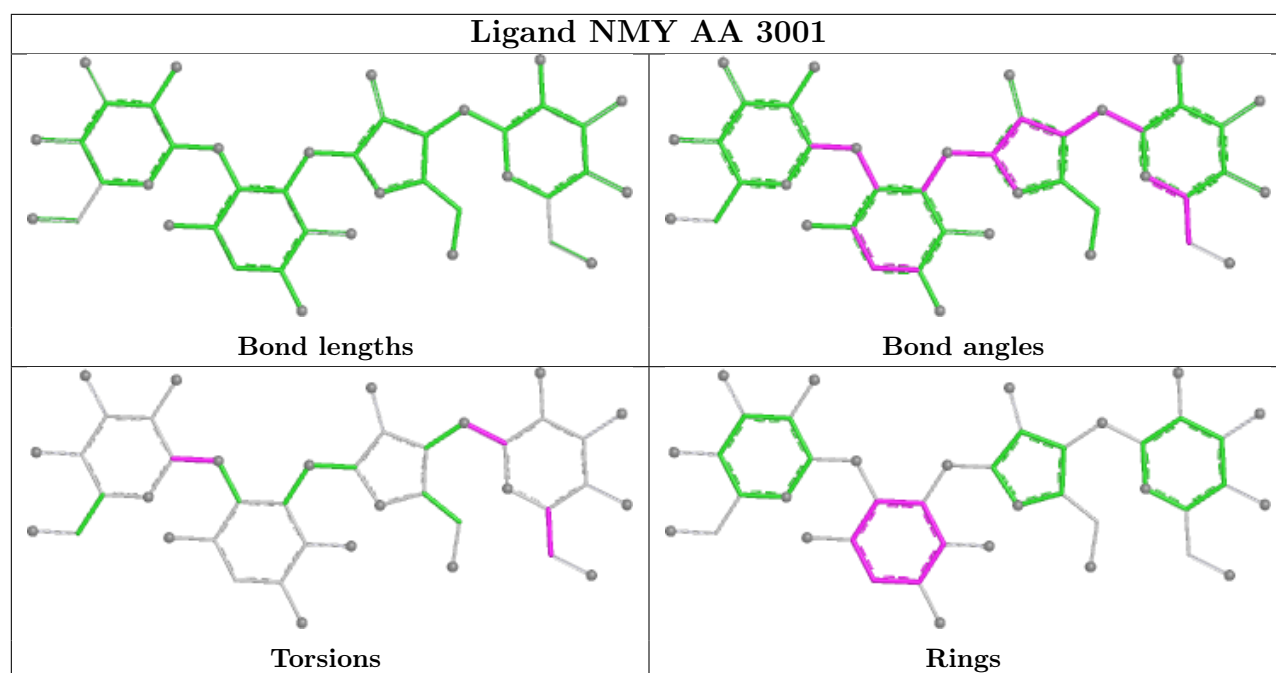
All (1) ring outliers are listed below:

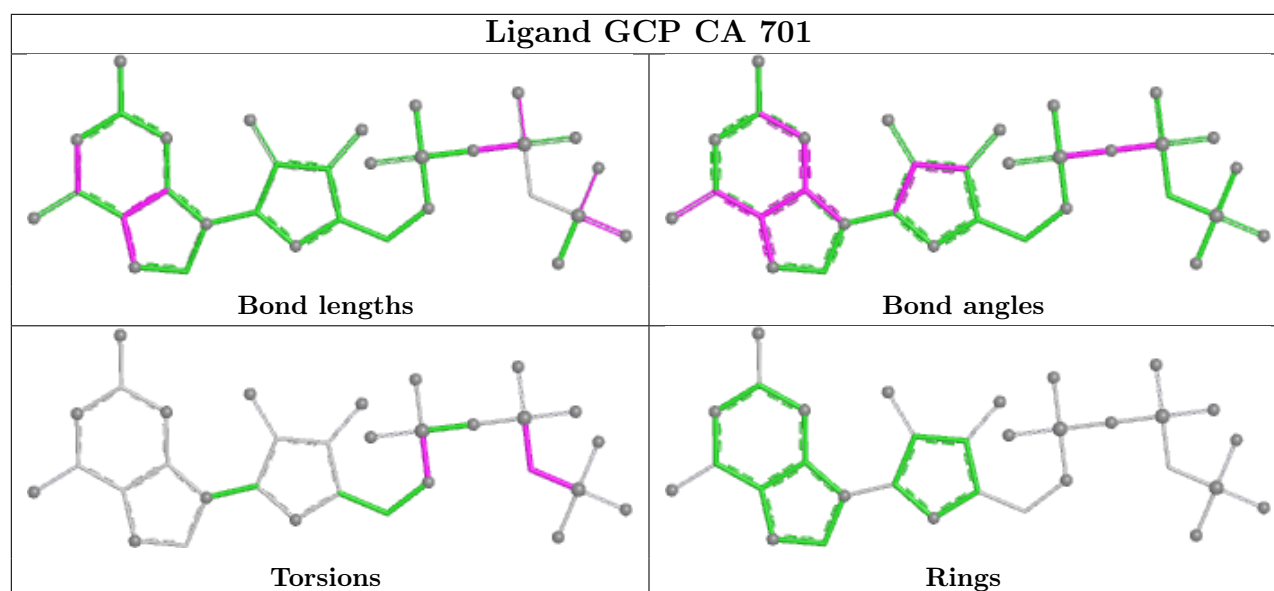
Mol	Chain	Res	Type	Atoms
56	AA	3001	NMY	C10-C11-C12-C7-C8-C9

3 monomers are involved in 73 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	AA	3001	NMY	19	0
56	BA	1601	NMY	15	0
57	CA	701	GCP	39	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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
1	AA	2893:G	O3'	2894:G	P	5.34
1	CA	277:THR	C	281:GLU	N	5.08

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6396. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.