

Robin R Gutell

List of Publications by Year in descending order

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116
papers

12,776
citations

23567

58
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24258

110
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128
all docs

128
docs citations

128
times ranked

8510
citing authors

#	ARTICLE	IF	CITATIONS
1	The comparative RNA web (CRW) site: an online database of comparative sequence and structure information for ribosomal, intron, and other RNAs. <i>BMC Bioinformatics</i> , 2002, 3, 2.	2.6	1,278
2	Comparative Anatomy of 16-S-like Ribosomal RNA. <i>Progress in Molecular Biology and Translational Science</i> , 1985, 32, 155-216.	1.9	658
3	Construction and fine mapping of recombinant plasmids containing the <i>rrnB</i> ribosomal RNA operon of <i>E. coli</i> . <i>Plasmid</i> , 1981, 6, 112-118.	1.4	514
4	Architecture of ribosomal RNA: constraints on the sequence of "tetra-loops".. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 8467-8471.	7.1	508
5	Collection of small subunit (16S- and 16S-like) ribosomal RNA structures: 1994. <i>Nucleic Acids Research</i> , 1994, 22, 3502-3507.	14.5	451
6	A compilation of large subunit (23S and 23S-like) ribosomal RNA structures: 1993. <i>Nucleic Acids Research</i> , 1993, 21, 3055-3074.	14.5	442
7	RNAMotif, an RNA secondary structure definition and search algorithm. <i>Nucleic Acids Research</i> , 2001, 29, 4724-4735.	14.5	421
8	Secondary structure model for 23S ribosomal RNA. <i>Nucleic Acids Research</i> , 1981, 9, 6167-6189.	14.5	397
9	Secondary structure model for bacterial 16S ribosomal RNA: phylogenetic, enzymatic and chemical evidence. <i>Nucleic Acids Research</i> , 1980, 8, 2275-2294.	14.5	344
10	The accuracy of ribosomal RNA comparative structure models. <i>Current Opinion in Structural Biology</i> , 2002, 12, 301-310.	5.7	324
11	Representation of the secondary and tertiary structure of group I introns. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 273-280.	8.2	287
12	Identifying constraints on the higher-order structure of RNA: continued development and application of comparative sequence analysis methods. <i>Nucleic Acids Research</i> , 1992, 20, 5785-5795.	14.5	285
13	Characteristics of the nuclear (18S, 5.8S, 28S and 5S) and mitochondrial (12S and 16S) rRNA genes of <i>Apis mellifera</i> (Insecta: Hymenoptera): structure, organization, and retrotransposable elements. <i>Insect Molecular Biology</i> , 2006, 15, 657-686.	2.0	249
14	Collection of small subunit (16S- and 16S-like) ribosomal RNA structures. <i>Nucleic Acids Research</i> , 1993, 21, 3051-3054.	14.5	228
15	A molecular phylogeny of the marine red algae (Rhodophyta) based on the nuclear small-subunit rRNA gene.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 7276-7280.	7.1	195
16	Evaluation of the suitability of free-energy minimization using nearest-neighbor energy parameters for RNA secondary structure prediction. <i>BMC Bioinformatics</i> , 2004, 5, 105.	2.6	184
17	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	14.5	174
18	Comprehensive Comparison of Structural Characteristics in Eukaryotic Cytoplasmic Large Subunit (23S) Tj ETQq0 0 0 rgBT /Overlock 10 T	4.25	172

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19	A novel clade of protistan parasites near the animal-fungal divergence.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 11907-11912.	7.1	162
20	Phylogenetic Analyses of Basal Angiosperms Based on Nine Plastid, Mitochondrial, and Nuclear Genes. International Journal of Plant Sciences, 2005, 166, 815-842.	1.3	162
21	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. Nucleic Acids Research, 2021, 49, D212-D220.	14.5	160
22	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	14.5	153
23	Higher order structural elements in ribosomal RNAs: pseudo-knots and the use of noncanonical pairs.. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 663-667.	7.1	148
24	ITS secondary structure derived from comparative analysis: implications for sequence alignment and phylogeny of the Asteraceae. Molecular Phylogenetics and Evolution, 2003, 29, 216-234.	2.7	141
25	Modeling a Minimal Ribosome Based on Comparative Sequence Analysis. Journal of Molecular Biology, 2002, 321, 215-234.	4.2	139
26	Morphological, Molecular, and Phylogenetic Characterization of <i>Nosema ceranae</i> , a Microsporidian Parasite Isolated from the European Honey Bee, <i>Apis mellifera</i> . Journal of Eukaryotic Microbiology, 2009, 56, 142-147.	1.7	139
27	A comparative database of group I intron structures. Nucleic Acids Research, 1994, 22, 3508-3510.	14.5	138
28	Structure of the Mammalian 80S Ribosome at 8.7 Å... Resolution. Structure, 2008, 16, 535-548.	3.3	135
29	A major family of motifs involving G ? A mismatches in ribosomal RNA. Journal of Molecular Biology, 1994, 242, 1-8.	4.2	126
30	Folding of circularly permuted transfer RNAs. Science, 1991, 254, 1361-1364.	12.6	124
31	Phylogenetic Analysis of Molluscan Mitochondrial LSU rDNA Sequences and Secondary Structures. Molecular Phylogenetics and Evolution, 2000, 15, 83-102.	2.7	110
32	A story: unpaired adenosine bases in ribosomal RNAs. Journal of Molecular Biology, 2000, 304, 335-354.	4.2	109
33	The Fragmented Mitochondrial Ribosomal RNAs of Plasmodium falciparum. PLoS ONE, 2012, 7, e38320.	2.5	109
34	Evidence for several higher order structural elements in ribosomal RNA.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 3119-3122.	7.1	108
35	Assessing the reliability of RNA folding using statistical mechanics. Journal of Molecular Biology, 1997, 267, 1104-1112.	4.2	104
36	Regulation and trafficking of three distinct 18 S ribosomal RNAs during development of the malaria parasite. Journal of Molecular Biology, 1997, 269, 203-213.	4.2	103

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37	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D123-D129.	14.5	103
38	Analysis of the Chloroplast Large Subunit Ribosomal RNA Gene from 17 <i>Chlamydomonas</i> Taxa. <i>Journal of Molecular Biology</i> , 1993, 232, 446-467.	4.2	95
39	The chemical basis of adenosine conservation throughout the <i>Tetrahymena</i> ribozyme. <i>Rna</i> , 1998, 4, 498-519.	3.5	95
40	Further characterization of the extremely small mitochondrial ribosomal RNAs from trypanosomes: a detailed comparison of the 9S and 12S RNAs from <i>Crithidia fasciculata</i> and <i>Trypanosoma brucei</i> with rRNAs from other organisms. <i>Nucleic Acids Research</i> , 1985, 13, 4171-4190.	14.5	92
41	A compilation of large subunit (23S-like) ribosomal RNA sequences presented in a secondary structure format. <i>Nucleic Acids Research</i> , 1990, 18, 2319-2330.	14.5	92
42	A preliminary investigation of the order Bangiales (Bangioophycidae, Rhodophyta) based on sequences of nuclear small-subunit ribosomal RNA genes. <i>Phycological Research</i> , 1995, 43, 71-79.	1.6	86
43	Phylogeny of the Chlamydomonadales (Chlorophyceae): A Comparison of Ribosomal RNA Gene Sequences from the Nucleus and the Chloroplast. <i>Molecular Phylogenetics and Evolution</i> , 1996, 5, 391-402.	2.7	86
44	Predicting U-turns in Ribosomal RNA with Comparative Sequence Analysis. <i>Journal of Molecular Biology</i> , 2000, 300, 791-803.	4.2	85
45	A Structural Model for the Large Subunit of the Mammalian Mitochondrial Ribosome. <i>Journal of Molecular Biology</i> , 2006, 358, 193-212.	4.2	85
46	Coarse-Grained Model for Simulation of RNA Three-Dimensional Structures. <i>Journal of Physical Chemistry B</i> , 2010, 114, 13497-13506.	2.6	83
47	Diversity of Base-pair Conformations and their Occurrence in rRNA Structure and RNA Structural Motifs. <i>Journal of Molecular Biology</i> , 2004, 344, 1225-1249.	4.2	80
48	The limits of nuclear-encoded SSU rDNA for resolving the diatom phylogeny. <i>European Journal of Phycology</i> , 2009, 44, 277-290.	2.0	79
49	Comparative studies of RNA: inferring higher-order structure from patterns of sequence variation. <i>Current Opinion in Structural Biology</i> , 1993, 3, 313-322.	5.7	76
50	Identification of Base-triples in RNA using Comparative Sequence Analysis. <i>Journal of Molecular Biology</i> , 1995, 248, 27-43.	4.2	76
51	The Lonepair Triloop: A New Motif in RNA Structure. <i>Journal of Molecular Biology</i> , 2003, 325, 65-83.	4.2	75
52	Specificity between Lactobacilli and Hymenopteran Hosts Is the Exception Rather than the Rule. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1803-1812.	3.1	75
53	The origin and evolution of the ribosome. <i>Biology Direct</i> , 2008, 3, 16.	4.6	71
54	Unique phylogenetic position of Diplomonadida based on the complete small subunit ribosomal RNA sequence of <i>Giardia ardeae</i> , <i>G. muris</i> , <i>G. duodenalis</i> and <i>Hexamita</i> sp.. <i>FASEB Journal</i> , 1993, 7, 223-231.	0.5	68

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55	Phylogenetic and molecular characterization of a 23S rRNA gene positions the genus <i>Campylobacter</i> in the epsilon subdivision of the Proteobacteria and shows that the presence of transcribed spacers is common in <i>Campylobacter</i> spp. <i>Journal of Bacteriology</i> , 1994, 176, 4597-4609.	2.2	68
56	Phylogenetic relationships among 28 spirotrichous ciliates documented by rDNA. <i>Molecular Phylogenetics and Evolution</i> , 2003, 29, 258-267.	2.7	67
57	:A:A and A:G base-pairs at the ends of 16 s and 23 s rRNA helices. <i>Journal of Molecular Biology</i> , 2001, 310, 735-753.	4.2	63
58	Monophyly of terrestrial adephagan beetles as indicated by three nuclear genes (Coleoptera: Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 622	1.7	61
59	A secondary structural model of the 28S rRNA expansion segments D2 and D3 from rootworms and related leaf beetles (Coleoptera: Chrysomelidae; Galerucinae). <i>Insect Molecular Biology</i> , 2004, 13, 495-518.	2.0	60
60	Distribution of rRNA Introns in the Three-dimensional Structure of the Ribosome. <i>Journal of Molecular Biology</i> , 2002, 323, 35-52.	4.2	58
61	THE EVOLUTION OF ELONGATE SHAPE IN DIATOMS1. <i>Journal of Phycology</i> , 2006, 42, 655-668.	2.3	58
62	R2DT is a framework for predicting and visualising RNA secondary structure using templates. <i>Nature Communications</i> , 2021, 12, 3494.	12.8	58
63	Are red algae plants?. <i>Botanical Journal of the Linnean Society</i> , 1995, 118, 81-105.	1.6	56
64	Molecular relationships among the Gracilariaceae (Rhodophyta): further observations on some undetermined species. <i>European Journal of Phycology</i> , 1994, 29, 195-202.	2.0	55
65	A Structural and Phylogenetic Analysis of the Group IC1 Introns in the Order Bangiales (Rhodophyta). <i>Molecular Biology and Evolution</i> , 2001, 18, 1654-1667.	8.9	54
66	A PROPOSAL FOR A NEW RED ALGAL ORDER, THE THOREALES 1. <i>Journal of Phycology</i> , 2002, 38, 807-820.	2.3	49
67	Assessing the odd secondary structural properties of nuclear small subunit ribosomal RNA sequences (18S) of the twisted-wing parasites (Insecta: Strepsiptera). <i>Insect Molecular Biology</i> , 2005, 14, 625-643.	2.0	46
68	Protistan parasite QPX of hard-shell clam <i>Mercenaria mercenaria</i> is a member of Labyrinthulomycota. <i>Diseases of Aquatic Organisms</i> , 2000, 42, 185-190.	1.0	45
69	Characterization of the rDNA unit and sequence analysis of the small subunit rRNA and 5.8S rRNA genes from <i>Tritrichomonas foetus</i> . <i>Molecular and Biochemical Parasitology</i> , 1992, 52, 75-83.	1.1	43
70	A Functional Ribosomal RNA Tertiary Structure Involves a Base Triple Interaction. <i>Biochemistry</i> , 1998, 37, 11980-11988.	2.5	43
71	Transcriptional mapping of plasmid pKK3535. <i>Journal of Molecular Biology</i> , 1981, 146, 433-449.	4.2	41
72	Probing the conformation of 18S rRNA in yeast 40S ribosomal subunits with kethoxal. <i>Biochemistry</i> , 1984, 23, 3322-3330.	2.5	39

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73	Group I intron lateral transfer between red and brown algal ribosomal RNA. <i>Current Genetics</i> , 2001, 40, 82-90.	1.7	39
74	The UAA/GAN Internal Loop Motif: A New RNA Structural Element that Forms a Cross-strand AAA Stack and Long-range Tertiary Interactions. <i>Journal of Molecular Biology</i> , 2006, 360, 978-988.	4.2	39
75	An analysis of large rRNA sequences folded by a thermodynamic method. <i>Folding & Design</i> , 1996, 1, 419-430.	4.5	38
76	Placement of attine ant-associated Pseudonocardia in a global Pseudonocardia phylogeny (Pseudonocardiaceae, Actinomycetales): a test of two symbiont-association models. <i>Antonie Van Leeuwenhoek</i> , 2010, 98, 195-212.	1.7	34
77	Inferring the Conformation of RNA Base Pairs and Triples from Patterns of Sequence Variation. <i>Nucleic Acids Research</i> , 1997, 25, 1559-1564.	14.5	32
78	Genetic and comparative analyses reveal an alternative secondary structure in the region of nt 912 of <i>Escherichia coli</i> 16S rRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 10555-10559.	7.1	29
79	A Comparison of the Crystal Structures of Eukaryotic and Bacterial SSU Ribosomal RNAs Reveals Common Structural Features in the Hypervariable Regions. <i>PLoS ONE</i> , 2012, 7, e38203.	2.5	27
80	Structural Constraints Identified with Covariation Analysis in Ribosomal RNA. <i>PLoS ONE</i> , 2012, 7, e39383.	2.5	25
81	Function of tyrosyl-tRNA synthetase in splicing group I introns: an induced-fit model for binding to the P4-P6 domain based on analysis of mutations at the junction of the P4-P6 stacked helices 1. Edited by D. Draper. <i>Journal of Molecular Biology</i> , 2000, 301, 265-283.	4.2	24
82	Supersized Ribosomal RNA Expansion Segments in Asgard Archaea. <i>Genome Biology and Evolution</i> , 2020, 12, 1694-1710.	2.5	24
83	Correlation of RNA Secondary Structure Statistics with Thermodynamic Stability and Applications to Folding. <i>Journal of Molecular Biology</i> , 2009, 391, 769-783.	4.2	23
84	Additional Watson-Crick Interactions Suggest a Structural Core in Large Subunit Ribosomal RNA. <i>Journal of Biomolecular Structure and Dynamics</i> , 1989, 7, 181-186.	3.5	22
85	Accelerated Evolution of Functional Plastid rRNA and Elongation Factor Genes Due to Reduced Protein Synthetic Load After the Loss of Photosynthesis in the Chlorophyte Alga <i>Polytoma</i> . <i>Molecular Biology and Evolution</i> , 2001, 18, 1810-1822.	8.9	22
86	A consensus model of the <i>Escherichia coli</i> ribosome. <i>Trends in Biochemical Sciences</i> , 1983, 8, 359-363.	7.5	21
87	<i>Ichthyophonus irregularis</i> sp. nov. from the yellowtail flounder <i>Limanda ferruginea</i> from the Nova Scotia shelf. <i>Diseases of Aquatic Organisms</i> , 2000, 41, 31-36.	1.0	21
88	The nucleotide sequence of the entire ribosomal DNA operon and the structure of the large subunit rRNA of <i>Giardia muris</i> . <i>Journal of Molecular Evolution</i> , 1992, 35, 318-328.	1.8	20
89	Probing the conformation of 26S rRNA in yeast 60S ribosomal subunits with kethoxal. <i>Biochemistry</i> , 1984, 23, 3330-3335.	2.5	17
90	Biclustering as a method for RNA local multiple sequence alignment. <i>Bioinformatics</i> , 2007, 23, 3289-3296.	4.1	17

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91	Statistical Potentials for Hairpin and Internal Loops Improve the Accuracy of the Predicted RNA Structure. <i>Journal of Molecular Biology</i> , 2011, 413, 473-483.	4.2	17
92	Fragmentation of the large subunit ribosomal RNA gene in oyster mitochondrial genomes. <i>BMC Genomics</i> , 2010, 11, 485.	2.8	16
93	Complete sequences and organization of the rRNA operon from <i>Campylobacter jejuni</i> TGH9011 (ATCC43431). <i>Gene</i> , 1995, 164, 101-106.	2.2	15
94	Partial nucleotide sequence of a single ribosomal RNA coding region and secondary structure of the large subunit 25 s rRNA of <i>Candida albicans</i> . <i>Current Genetics</i> , 1994, 26, 321-328.	1.7	12
95	Are red algae plants?. <i>Botanical Journal of the Linnean Society</i> , 1995, 118, 81-105.	1.6	12
96	Ten lessons with Carl Woese about RNA and comparative analysis. <i>RNA Biology</i> , 2014, 11, 254-272.	3.1	12
97	Characterization of a flatworm ribosomal RNA-encoding gene: promoter sequence and small subunit rRNA secondary structure. <i>Gene</i> , 1996, 171, 215-220.	2.2	11
98	The exon context and distribution of Euarcomycetes rRNA spliceosomal introns. <i>BMC Evolutionary Biology</i> , 2003, 3, 7.	3.2	11
99	Two accurate sequence, structure, and phylogenetic template-based RNA alignment systems. <i>BMC Systems Biology</i> , 2013, 7, S13.	3.0	9
100	An accurate scalable template-based alignment algorithm. , 2012, 2012, 1-7.		8
101	Covariant Evolutionary Event Analysis for Base Interaction Prediction Using a Relational Database Management System for RNA. <i>Lecture Notes in Computer Science</i> , 2009, 5566, 200-216.	1.3	8
102	Identity and geometry of a base triple in 16S rRNA determined by comparative sequence analysis and molecular modeling. <i>Rna</i> , 1999, 5, 1430-1439.	3.5	7
103	rCAD: A Novel Database Schema for the Comparative Analysis of RNA. , 2011, 2011, 15-22.		6
104	Helix Capping in RNA Structure. <i>PLoS ONE</i> , 2014, 9, e93664.	2.5	6
105	The universally conserved nucleotides of the small subunit ribosomal RNAs. <i>Rna</i> , 2022, 28, 623-644.	3.5	6
106	EVIDENCE FOR LATERAL TRANSFER OF AN IE INTRON BETWEEN FUNGAL AND RED ALGAL SMALL SUBUNIT RRNA GENES1. <i>Journal of Phycology</i> , 2005, 41, 380-390.	2.3	5
107	Tensor Decomposition Reveals Concurrent Evolutionary Convergences and Divergences and Correlations with Structural Motifs in Ribosomal RNA. <i>PLoS ONE</i> , 2011, 6, e18768.	2.5	5
108	RNA2DMap: A Visual Exploration Tool of the Information in RNA's Higher-Order Structure. , 2011, , 613-617.		5

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109	R3D-2-MSA: the RNA 3D structure-to-multiple sequence alignment server. <i>Nucleic Acids Research</i> , 2015, 43, W15-W23.	14.5	4
110	Comparative Analysis of the Higher-Order Structure of RNA. , 2013, , 11-22.		4
111	Networks of interactions in the secondary and tertiary structure of ribosomal RNA. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 386, 564-572.	2.6	2
112	rRNA—the evolution of that magic molecule. <i>Rna</i> , 2015, 21, 627-629.	3.5	2
113	Studies on the structure and function of 16S ribosomal RNA using structure-specific chemical probes. <i>Journal of Biosciences</i> , 1985, 8, 747-755.	1.1	1
114	The Primary and Secondary Structures of the 23S Ribosomal RNA from <i>Thermoplasma acidophilum</i> Define an Ancient Archaeal Divergence. <i>Systematic and Applied Microbiology</i> , 1993, 16, 333-341.	2.8	1
115	R-PASS: A Fast Structure-Based RNA Sequence Alignment Algorithm. , 2011, 2011, 618-622.		0
116	Introduction to special Carl Woese issue in <i>RNA Biology</i> . <i>RNA Biology</i> , 2014, 11, 170-171.	3.1	0