

# Robin R Gutell

## List of Publications by Year in descending order

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116  
papers

12,776  
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23567

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g-index

128  
all docs

128  
docs citations

128  
times ranked

8510  
citing authors

#	ARTICLE	IF	CITATIONS
1	The universally conserved nucleotides of the small subunit ribosomal RNAs. <i>Rna</i> , 2022, 28, 623-644.	3.5	6
2	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	14.5	160
3	R2DT is a framework for predicting and visualising RNA secondary structure using templates. <i>Nature Communications</i> , 2021, 12, 3494.	12.8	58
4	Supersized Ribosomal RNA Expansion Segments in Asgard Archaea. <i>Genome Biology and Evolution</i> , 2020, 12, 1694-1710.	2.5	24
5	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	14.5	153
6	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	14.5	174
7	rRNA—the evolution of that magic molecule. <i>Rna</i> , 2015, 21, 627-629.	3.5	2
8	R3D-2-MSA: the RNA 3D structure-to-multiple sequence alignment server. <i>Nucleic Acids Research</i> , 2015, 43, W15-W23.	14.5	4
9	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D123-D129.	14.5	103
10	Helix Capping in RNA Structure. <i>PLoS ONE</i> , 2014, 9, e93664.	2.5	6
11	Ten lessons with Carl Woese about RNA and comparative analysis. <i>RNA Biology</i> , 2014, 11, 254-272.	3.1	12
12	Introduction to special Carl Woese issue in <i>RNA Biology</i> . <i>RNA Biology</i> , 2014, 11, 170-171.	3.1	0
13	Two accurate sequence, structure, and phylogenetic template-based RNA alignment systems. <i>BMC Systems Biology</i> , 2013, 7, S13.	3.0	9
14	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
15	Comparative Analysis of the Higher-Order Structure of RNA. , 2013, , 11-22.		4
16	An accurate scalable template-based alignment algorithm. , 2012, 2012, 1-7.		8
17	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
18	The Fragmented Mitochondrial Ribosomal RNAs of <i>Plasmodium falciparum</i> . <i>PLoS ONE</i> , 2012, 7, e38320.	2.5	109

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19	Structural Constraints Identified with Covariation Analysis in Ribosomal RNA. PLoS ONE, 2012, 7, e39383.	2.5	25
20	R-PASS: A Fast Structure-Based RNA Sequence Alignment Algorithm. , 2011, 2011, 618-622.		0
21	rCAD: A Novel Database Schema for the Comparative Analysis of RNA. , 2011, 2011, 15-22.		6
22	Statistical Potentials for Hairpin and Internal Loops Improve the Accuracy of the Predicted RNA Structure. Journal of Molecular Biology, 2011, 413, 473-483.	4.2	17
23	Tensor Decomposition Reveals Concurrent Evolutionary Convergences and Divergences and Correlations with Structural Motifs in Ribosomal RNA. PLoS ONE, 2011, 6, e18768.	2.5	5
24	RNA2DMap: A Visual Exploration Tool of the Information in RNA's Higher-Order Structure. , 2011, , 613-617.		5
25	Placement of attine ant-associated Pseudonocardia in a global Pseudonocardia phylogeny (Pseudonocardiaceae, Actinomycetales): a test of two symbiont-association models. Antonie Van Leeuwenhoek, 2010, 98, 195-212.	1.7	34
26	Fragmentation of the large subunit ribosomal RNA gene in oyster mitochondrial genomes. BMC Genomics, 2010, 11, 485.	2.8	16
27	Coarse-Grained Model for Simulation of RNA Three-Dimensional Structures. Journal of Physical Chemistry B, 2010, 114, 13497-13506.	2.6	83
28	The limits of nuclear-encoded SSU rDNA for resolving the diatom phylogeny. European Journal of Phycology, 2009, 44, 277-290.	2.0	79
29	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
30	Monophyly of terrestrial adephagan beetles as indicated by three nuclear genes (Coleoptera: Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 302	1.7	61
31	Correlation of RNA Secondary Structure Statistics with Thermodynamic Stability and Applications to Folding. Journal of Molecular Biology, 2009, 391, 769-783.	4.2	23
32	Covariant Evolutionary Event Analysis for Base Interaction Prediction Using a Relational Database Management System for RNA. Lecture Notes in Computer Science, 2009, 5566, 200-216.	1.3	8
33	Structure of the Mammalian 80S Ribosome at 8.7 Å.. Resolution. Structure, 2008, 16, 535-548.	3.3	135
34	The origin and evolution of the ribosome. Biology Direct, 2008, 3, 16.	4.6	71
35	Biclustering as a method for RNA local multiple sequence alignment. Bioinformatics, 2007, 23, 3289-3296.	4.1	17
36	Networks of interactions in the secondary and tertiary structure of ribosomal RNA. Physica A: Statistical Mechanics and Its Applications, 2007, 386, 564-572.	2.6	2

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37	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
38	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
39	THE EVOLUTION OF ELONGATE SHAPE IN DIATOMS1. <i>Journal of Phycology</i> , 2006, 42, 655-668.	2.3	58
40	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
41	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
42	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
43	Phylogenetic Analyses of Basal Angiosperms Based on Nine Plastid, Mitochondrial, and Nuclear Genes. <i>International Journal of Plant Sciences</i> , 2005, 166, 815-842.	1.3	162
44	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
45	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
46	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
47	The exon context and distribution of Euascomycetes rRNA spliceosomal introns. <i>BMC Evolutionary Biology</i> , 2003, 3, 7.	3.2	11
48	ITS secondary structure derived from comparative analysis: implications for sequence alignment and phylogeny of the Asteraceae. <i>Molecular Phylogenetics and Evolution</i> , 2003, 29, 216-234.	2.7	141
49	Phylogenetic relationships among 28 spirotrichous ciliates documented by rDNA. <i>Molecular Phylogenetics and Evolution</i> , 2003, 29, 258-267.	2.7	67
50	The Lonepair Triloop: A New Motif in RNA Structure. <i>Journal of Molecular Biology</i> , 2003, 325, 65-83.	4.2	75
51	Modeling a Minimal Ribosome Based on Comparative Sequence Analysis. <i>Journal of Molecular Biology</i> , 2002, 321, 215-234.	4.2	139
52	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
53	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
54	The accuracy of ribosomal RNA comparative structure models. <i>Current Opinion in Structural Biology</i> , 2002, 12, 301-310.	5.7	324

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55	A PROPOSAL FOR A NEW RED ALGAL ORDER, THE THOREALES 1. <i>Journal of Phycology</i> , 2002, 38, 807-820.	2.3	49
56	: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
57	RNA Motif, an RNA secondary structure definition and search algorithm. <i>Nucleic Acids Research</i> , 2001, 29, 4724-4735.	14.5	421
58	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
59	Group I intron lateral transfer between red and brown algal ribosomal RNA. <i>Current Genetics</i> , 2001, 40, 82-90.	1.7	39
60	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
61	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
62	Phylogenetic Analysis of Molluscan Mitochondrial LSU rDNA Sequences and Secondary Structures. <i>Molecular Phylogenetics and Evolution</i> , 2000, 15, 83-102.	2.7	110
63	Predicting U-turns in Ribosomal RNA with Comparative Sequence Analysis. <i>Journal of Molecular Biology</i> , 2000, 300, 791-803.	4.2	85
64	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
65	A story: unpaired adenosine bases in ribosomal RNAs. <i>Journal of Molecular Biology</i> , 2000, 304, 335-354.	4.2	109
66	<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
67	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
68	A Functional Ribosomal RNA Tertiary Structure Involves a Base Triple Interaction. <i>Biochemistry</i> , 1998, 37, 11980-11988.	2.5	43
69	The chemical basis of adenosine conservation throughout the <i>Tetrahymena</i> ribozyme. <i>Rna</i> , 1998, 4, 498-519.	3.5	95
70	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
71	Assessing the reliability of RNA folding using statistical mechanics. <i>Journal of Molecular Biology</i> , 1997, 267, 1104-1112.	4.2	104
72	Regulation and trafficking of three distinct 18 S ribosomal RNAs during development of the malaria parasite. <i>Journal of Molecular Biology</i> , 1997, 269, 203-213.	4.2	103

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73	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
74	Comprehensive Comparison of Structural Characteristics in Eukaryotic Cytoplasmic Large Subunit (23) Tj ETQq0 0 0 rgBT /Overlock 10 T	4.25	172
75	A novel clade of protistan parasites near the animal-fungal divergence.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 11907-11912.	7.1	162
76	An analysis of large rRNA sequences folded by a thermodynamic method. <i>Folding &amp; Design</i> , 1996, 1, 419-430.	4.5	38
77	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
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	Are red algae plants?. <i>Botanical Journal of the Linnean Society</i> , 1995, 118, 81-105.	1.6	56
80	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
81	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
82	Identification of Base-triples in RNA using Comparative Sequence Analysis. <i>Journal of Molecular Biology</i> , 1995, 248, 27-43.	4.2	76
83	Are red algae plants?. <i>Botanical Journal of the Linnean Society</i> , 1995, 118, 81-105.	1.6	12
84	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
85	Collection of small subunit (16S- and 16S-like) ribosomal RNA structures: 1994. <i>Nucleic Acids Research</i> , 1994, 22, 3502-3507.	14.5	451
86	A comparative database of group I intron structures. <i>Nucleic Acids Research</i> , 1994, 22, 3508-3510.	14.5	138
87	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
88	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
89	A major family of motifs involving G ? A mismatches in ribosomal RNA. <i>Journal of Molecular Biology</i> , 1994, 242, 1-8.	4.2	126
90	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

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91	A molecular phylogeny of the marine red algae (Rhodophyta) based on the nuclear small-subunit rRNA gene.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 7276-7280.	7.1	195
92	Analysis of the Chloroplast Large Subunit Ribosomal RNA Gene from 17 Chlamydomonas Taxa. Journal of Molecular Biology, 1993, 232, 446-467.	4.2	95
93	The Primary and Secondary Structures of the 23S Ribosomal RNA from Thermoplasma acidophilum Define an Ancient Archaeal Divergence. Systematic and Applied Microbiology, 1993, 16, 333-341.	2.8	1
94	Comparative studies of RNA: inferring higher-order structure from patterns of sequence variation. Current Opinion in Structural Biology, 1993, 3, 313-322.	5.7	76
95	Collection of small subunit (16S- and 16S-like) ribosomal RNA structures. Nucleic Acids Research, 1993, 21, 3051-3054.	14.5	228
96	A compilation of large subunit (23S and 23S-like) ribosomal RNA structures: 1993. Nucleic Acids Research, 1993, 21, 3055-3074.	14.5	442
97	Unique phylogenetic position of Diplomonadida based on the complete small subunit ribosomal RNA sequence of Giardia ardeae, G. muris, G. duodenalis and Hexamita sp.. FASEB Journal, 1993, 7, 223-231.	0.5	68
98	Identifying constraints on the higher-order structure of RNA: continued development and application of comparative sequence analysis methods. Nucleic Acids Research, 1992, 20, 5785-5795.	14.5	285
99	The nucleotide sequence of the entire ribosomal DNA operon and the structure of the large subunit rRNA of Giardia muris. Journal of Molecular Evolution, 1992, 35, 318-328.	1.8	20
100	Characterization of the rDNA unit and sequence analysis of the small subunit rRNA and 5.8S rRNA genes from Tritrichomonas foetus. Molecular and Biochemical Parasitology, 1992, 52, 75-83.	1.1	43
101	Folding of circularly permuted transfer RNAs. Science, 1991, 254, 1361-1364.	12.6	124
102	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
103	Architecture of ribosomal RNA: constraints on the sequence of "tetra-loops" .. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 8467-8471.	7.1	508
104	A compilation of large subunit (23S-like) ribosomal RNA sequences presented in a secondary structure format. Nucleic Acids Research, 1990, 18, 2319-2330.	14.5	92
105	Additional Watson-Crick Interactions Suggest a Structural Core in Large Subunit Ribosomal RNA. Journal of Biomolecular Structure and Dynamics, 1989, 7, 181-186.	3.5	22
106	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
107	Studies on the structure and function of 16S ribosomal RNA using structure-specific chemical probes. Journal of Biosciences, 1985, 8, 747-755.	1.1	1
108	Further characterization of the extremely small mitochondrial ribosomal RNAs from trypanosomes: a detailed comparison of the 9S and 12S RNAs from Crithidia fasciculata and Trypanosoma brucei with rRNAs from other organisms. Nucleic Acids Research, 1985, 13, 4171-4190.	14.5	92

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109	Comparative Anatomy of 16-S-like Ribosomal RNA. Progress in Molecular Biology and Translational Science, 1985, 32, 155-216.	1.9	658
110	Probing the conformation of 18S rRNA in yeast 40S ribosomal subunits with kethoxal. Biochemistry, 1984, 23, 3322-3330.	2.5	39
111	Probing the conformation of 26S rRNA in yeast 60S ribosomal subunits with kethoxal. Biochemistry, 1984, 23, 3330-3335.	2.5	17
112	A consensus model of the Escherichia coli ribosome. Trends in Biochemical Sciences, 1983, 8, 359-363.	7.5	21
113	Transcriptional mapping of plasmid pKK3535. Journal of Molecular Biology, 1981, 146, 433-449.	4.2	41
114	Construction and fine mapping of recombinant plasmids containing the rrnB ribosomal RNA operon of E. coli. Plasmid, 1981, 6, 112-118.	1.4	514
115	Secondary structure model for 23S ribosomal RNA. Nucleic Acids Research, 1981, 9, 6167-6189.	14.5	397
116	Secondary structure model for bacterial 16S ribosomal RNA: phylogenetic, enzymatic and chemical evidence. Nucleic Acids Research, 1980, 8, 2275-2294.	14.5	344