

Rfam 11.0: 10 years of RNA families

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Citation Report

#	ARTICLE	IF	CITATIONS
3	The 2013 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2012, 41, D1-D7.	6.5	94
4	LocARNAscan: Incorporating thermodynamic stability in sequence and structure-based RNA homology search. <i>Algorithms for Molecular Biology</i> , 2013, 8, 14.	0.3	14
5	Genome-wide annotation of genes and noncoding RNAs of foxtail millet in response to simulated drought stress by deep sequencing. <i>Plant Molecular Biology</i> , 2013, 83, 459-473.	2.0	157
6	Long Noncoding RNA: a New Player of Heart Failure?. <i>Journal of Cardiovascular Translational Research</i> , 2013, 6, 876-883.	1.1	101
7	Analysis of the canine brain transcriptome with an emphasis on the hypothalamus and cerebral cortex. <i>Mammalian Genome</i> , 2013, 24, 484-499.	1.0	26
8	Analysis of base-pairing probabilities of RNA molecules involved in protein-RNA interactions. <i>Bioinformatics</i> , 2013, 29, 2524-2528.	1.8	10
9	Insights into snoRNA biogenesis and processing from PAR-CLIP of snoRNA core proteins and small RNA sequencing. <i>Genome Biology</i> , 2013, 14, R45.	13.9	129
10	Comparative genomics of metabolic capacities of regulons controlled by cis-regulatory RNA motifs in bacteria. <i>BMC Genomics</i> , 2013, 14, 597.	1.2	39
11	Fast online and index-based algorithms for approximate search of RNA sequence-structure patterns. <i>BMC Bioinformatics</i> , 2013, 14, 226.	1.2	6
12	Identification and characterisation of non-coding small RNAs in the pathogenic filamentous fungus <i>Trichophyton rubrum</i> . <i>BMC Genomics</i> , 2013, 14, 931.	1.2	6
13	iMir: An integrated pipeline for high-throughput analysis of small non-coding RNA data obtained by smallRNA-Seq. <i>BMC Bioinformatics</i> , 2013, 14, 362.	1.2	62
14	Transcriptome analysis of the filamentous fungus <i>Aspergillus nidulans</i> directed to the global identification of promoters. <i>BMC Genomics</i> , 2013, 14, 847.	1.2	56
15	2D Meets 4G: G-Quadruplexes in RNA Secondary Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 832-844.	1.9	37
16	Detection of non-coding RNA in bacteria and archaea using the DETR TM PROK Galaxy pipeline. <i>Methods</i> , 2013, 63, 60-65.	1.9	21
17	Evidence for the widespread distribution of CRISPR-Cas system in the Phylum <i>Cyanobacteria</i> . <i>RNA Biology</i> , 2013, 10, 687-693.	1.5	86
18	RNA structures regulating ribosomal protein biosynthesis in bacilli. <i>RNA Biology</i> , 2013, 10, 1180-1184.	1.5	36
19	MicroRNAs: Essential players in the regulation of inflammation. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 132, 15-26.	1.5	180
20	Transcriptome-wide identification and characterization of the <i>Procambarus clarkii</i> microRNAs potentially related to immunity against <i>Spiroplasma eriocheiris</i> infection. <i>Fish and Shellfish Immunology</i> , 2013, 35, 607-617.	1.6	45

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21	Comprehensive discovery and characterization of small RNAs in <i>Corynebacterium glutamicum</i> ATCC 13032. <i>BMC Genomics</i> , 2013, 14, 714.	1.2	61
22	The <i>agr</i> Locus Regulates Virulence and Colonization Genes in <i>Clostridium difficile</i> 027. <i>Journal of Bacteriology</i> , 2013, 195, 3672-3681.	1.0	99
23	Complete Genome Sequence of Encapsulated <i>Haemophilus influenzae</i> Type f KR494, an Invasive Isolate That Caused Necrotizing Myositis. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
24	Complete Genome Sequence of the <i>Escherichia coli</i> PMV-1 Strain, a Model Extraintestinal Pathogenic <i>E. coli</i> Strain Used for Host-Pathogen Interaction Studies. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
25	Small, Smaller, Smallest: The Origins and Evolution of Ancient Dual Symbioses in a Phloem-Feeding Insect. <i>Genome Biology and Evolution</i> , 2013, 5, 1675-1688.	1.1	276
26	<i>glu</i> -RNA. , 2013, , .		1
27	The RNA Newton polytope and learnability of energy parameters. <i>Bioinformatics</i> , 2013, 29, i300-i307.	1.8	3
28	Continuing analysis of microRNA origins. <i>Mobile Genetic Elements</i> , 2013, 3, e27755.	1.8	35
29	A second eukaryotic group with mitochondrion-encoded tmRNA. <i>RNA Biology</i> , 2013, 10, 1117-1124.	1.5	18
30	High-resolution definition of the <i>Vibrio cholerae</i> essential gene set with hidden Markov model-based analyses of transposon-insertion sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, 9033-9048.	6.5	115
31	CMCompare webserver: comparing RNA families via covariance models. <i>Nucleic Acids Research</i> , 2013, 41, W499-W503.	6.5	10
32	Infernal 1.1: 100-fold faster RNA homology searches. <i>Bioinformatics</i> , 2013, 29, 2933-2935.	1.8	2,281
33	A comparison of dense transposon insertion libraries in the <i>Salmonella</i> serovars Typhi and Typhimurium. <i>Nucleic Acids Research</i> , 2013, 41, 4549-4564.	6.5	108
34	Morphology, Physiological Characteristics, and Complete Sequence of Marine Bacteriophage Φ RIO-1 Infecting <i>Pseudoalteromonas marina</i> . <i>Journal of Virology</i> , 2013, 87, 9189-9198.	1.5	26
35	Identification of Cassava MicroRNAs under Abiotic Stress. <i>International Journal of Genomics</i> , 2013, 2013, 1-10.	0.8	57
36	Conserved miRNAs Are Candidate Post-Transcriptional Regulators of Developmental Arrest in Free-Living and Parasitic Nematodes. <i>Genome Biology and Evolution</i> , 2013, 5, 1246-1260.	1.1	31
37	Approaches to querying bacterial genomes with transposon-insertion sequencing. <i>RNA Biology</i> , 2013, 10, 1161-1169.	1.5	132
38	Using RNA inverse folding to identify IRES-like structural subdomains. <i>RNA Biology</i> , 2013, 10, 1842-1852.	1.5	20

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39	Genome Sequence of <i>Thalassolituus oleivorans</i> MIL-1 (DSM 14913 ^T). <i>Genome Announcements</i> , 2013, 1, e0014113.	0.8	20
40	Computational identification of functional RNA homologs in metagenomic data. <i>RNA Biology</i> , 2013, 10, 1170-1179.	1.5	56
41	Open-Phylo: a customizable crowd-computing platform for multiple sequence alignment. <i>Genome Biology</i> , 2013, 14, R116.	13.9	20
42	The Complete Genome Sequence of <i>Methanobrevibacter</i> sp. AbM4. <i>Standards in Genomic Sciences</i> , 2013, 8, 215-227.	1.5	42
43	Transcriptome Analysis in Sheepgrass (<i>Leymus chinensis</i>): A Dominant Perennial Grass of the Eurasian Steppe. <i>PLoS ONE</i> , 2013, 8, e67974.	1.1	68
44	Identification and Characterization of MicroRNAs in the Leaf of Ma Bamboo (<i>Dendrocalamus</i> Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.1	19
45	Comprehensive Analysis of Long Non-Coding RNAs in Ovarian Cancer Reveals Global Patterns and Targeted DNA Amplification. <i>PLoS ONE</i> , 2013, 8, e80306.	1.1	90
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47	pY RNA1-s2: A Highly Retina-Enriched Small RNA That Selectively Binds to Matr3 (Matr3). <i>PLoS ONE</i> , 2014, 9, e88217.	1.1	16
48	Natural Antisense Transcripts and Long Non-Coding RNA in <i>Neurospora crassa</i> . <i>PLoS ONE</i> , 2014, 9, e91353.	1.1	42
49	Resistance Determinants and Mobile Genetic Elements of an NDM-1-Encoding <i>Klebsiella pneumoniae</i> Strain. <i>PLoS ONE</i> , 2014, 9, e99209.	1.1	123
50	Discovery and Comparative Profiling of microRNAs in Representative Monopodial Bamboo (<i>Phyllostachys edulis</i>) and Sympodial Bamboo (<i>Dendrocalamus latiflorus</i>). <i>PLoS ONE</i> , 2014, 9, e102375.	1.1	11
51	Exploring MicroRNA-Like Small RNAs in the Filamentous Fungus <i>Fusarium oxysporum</i> . <i>PLoS ONE</i> , 2014, 9, e104956.	1.1	100
52	Transcriptomic Analysis of Tail Regeneration in the Lizard <i>Anolis carolinensis</i> Reveals Activation of Conserved Vertebrate Developmental and Repair Mechanisms. <i>PLoS ONE</i> , 2014, 9, e105004.	1.1	112
53	Patterns of MiRNA Expression in Arctic Charr Development. <i>PLoS ONE</i> , 2014, 9, e106084.	1.1	22
54	Genome-Scale Transcriptome Analysis of the Alpine "Glasshouse" Plant <i>Rheum nobile</i> (Polygonaceae) with Special Translucent Bracts. <i>PLoS ONE</i> , 2014, 9, e110712.	1.1	8
55	Comparative Genomics of Transcriptional Regulation of Methionine Metabolism in Proteobacteria. <i>PLoS ONE</i> , 2014, 9, e113714.	1.1	20
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58	<i>De novo</i> Assembly and Analysis of the Northern Leopard Frog <i>Rana pipiens</i> Transcriptome. Journal of Genomics, 2014, 2, 141-149.	0.6	13
59	The k-junction motif in RNA structure. Nucleic Acids Research, 2014, 42, 5322-5331.	6.5	21
60	The draft genome of the large yellow croaker reveals well-developed innate immunity. Nature Communications, 2014, 5, 5227.	5.8	163
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63	Integrated analysis of miRNA and mRNA expression profiles in response to Cd exposure in rice seedlings. BMC Genomics, 2014, 15, 835.	1.2	75
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76	RNase P RNA from the Recently Evolved Plastid of <i>Paulinella</i> and from Algae. <i>International Journal of Molecular Sciences</i> , 2014, 15, 20859-20875.	1.8	3
77	Robust Identification of Noncoding RNA from Transcriptomes Requires Phylogenetically-Informed Sampling. <i>PLoS Computational Biology</i> , 2014, 10, e1003907.	1.5	49
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82	miRNEST 2.0: a database of plant and animal microRNAs. <i>Nucleic Acids Research</i> , 2014, 42, D74-D77.	6.5	68
83	In vitro Transcriptome Analysis of Two Chinese Isolates of <i>Streptococcus suis</i> Serotype 2. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 266-275.	3.0	4
84	Transcriptional landscape and essential genes of <i>Neisseria gonorrhoeae</i> . <i>Nucleic Acids Research</i> , 2014, 42, 10579-10595.	6.5	74
85	Primary transcriptome map of the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> . <i>BMC Genomics</i> , 2014, 15, 684.	1.2	99
86	RNA-sequencing analysis of <i>Trichophyton rubrum</i> transcriptome in response to sublethal doses of acriflavine. <i>BMC Genomics</i> , 2014, 15, S1.	1.2	36
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94	Settling Down: The Genome of <i>Serratia symbiotica</i> from the Aphid <i>Cinara tujafilina</i> Zooms in on the Process of Accommodation to a Cooperative Intracellular Life. <i>Genome Biology and Evolution</i> , 2014, 6, 1683-1698.	1.1	88
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110	Systematic characterization of small RNAome during zebrafish early developmental stages. <i>BMC Genomics</i> , 2014, 15, 117.	1.2	27

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127	A Coverage Criterion for Spaced Seeds and Its Applications to Support Vector Machine String Kernels and k -Mer Distances. <i>Journal of Computational Biology</i> , 2014, 21, 947-963.	0.8	22
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#	ARTICLE	IF	CITATIONS
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