Rolf Backofen

List of Publications by Year
in descending order

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200

papers

15,249

citations

41627

51

h-index

25983

112

g-index

225

all docs

225

docs citations

225

times ranked

19889

citing authors

#	Article	IF	Citations
1	RiboReport - benchmarking tools for ribosome profiling-based identification of open reading frames in bacteria. Briefings in Bioinformatics, 2022, 23, .	3.2	15
2	Ten simple rules for making a software tool workflow-ready. PLoS Computational Biology, 2022, 18, e1009823.	1.5	7
3	Spacer prioritization in CRISPRâ€"Cas9 immunity is enabled by the leader RNA. Nature Microbiology, 2022, 7, 530-541.	5.9	9
4	Gut microbiota drives age-related oxidative stress and mitochondrial damage in microglia via the metabolite N6-carboxymethyllysine. Nature Neuroscience, 2022, 25, 295-305.	7.1	84
5	Galaxy workflows for fragment-based virtual screening: a case study on the SARS-CoV-2 main protease. Journal of Cheminformatics, 2022, 14, 22.	2.8	2
6	Spectrum of Genetic Variants in a Cohort of 37 Laterality Defect Cases. Frontiers in Genetics, 2022, 13, 861236.	1.1	2
7	Galaxy: A Decade of Realising CWFR Concepts. Data Intelligence, 2022, 4, 358-371.	0.8	3
8	Expanding the Galaxyâ€™s reference data. Bioinformatics Advances, 2022, 2, .	0.9	0
9	Anti-CRISPR prediction using deep learning reveals an inhibitor of Cas13b nucleases. Molecular Cell, 2022, 82, 2714-2726.e4.	4.5	17
10	Loop detection using Hi-C data with HiCExplorer. GigaScience, 2022, 11, .	3.3	17
11	HRIBO: high-throughput analysis of bacterial ribosome profiling data. Bioinformatics, 2021, 37, 2061-2063.	1.8	11
12	pyGenomeTracks: reproducible plots for multivariate genomic datasetsÂ. Bioinformatics, 2021, 37, 422-423.	1.8	237
13	CRISPRidentify: identification of CRISPR arrays using machine learning approach. Nucleic Acids Research, 2021, 49, e20-e20.	6.5	44
14	ChiRA: an integrated framework for chimeric read analysis from RNA-RNA interactome and RNA structurome data. GigaScience, 2021, 10, .	3.3	6
15	Tool recommender system in Galaxy using deep learning. GigaScience, 2021, 10, .	3.3	9
16	Robust and efficient single-cell Hi-C clustering with approximate k-nearest neighbor graphs. Bioinformatics, 2021, 37, 4006-4013.	1.8	9
17	An Integrated Database of Small RNAs and Their Interplay With Transcriptional Gene Regulatory Networks in Corynebacteria. Frontiers in Microbiology, 2021, 12, 656435.	1.5	2
18	StoatyDive: Evaluation and classification of peak profiles for sequencing data. GigaScience, 2021, 10, .	3.3	3

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19	<tt>CRISPRloci:</tt>Âcomprehensive and accurate annotation of CRISPRâ€“Cas systems. Nucleic Acids Research, 2021, 49, W125-W130.	6.5	16
20	A SARS-CoV-2 sequence submission tool for the European Nucleotide Archive. Bioinformatics, 2021, 37, 3983-3985.	1.8	3
21	Structure-aware machine learning identifies microRNAs operating as Toll-like receptor 7/8 ligands. RNA Biology, 2021, 18, 268-277.	1.5	6
22	Chemotherapy-induced transposable elements activate MDA5 to enhance haematopoietic regeneration. Nature Cell Biology, 2021, 23, 704-717.	4.6	40
23	CdrS Is a Global Transcriptional Regulator Influencing Cell Division in Haloferax volcanii. MBio, 2021, 12, e0141621.	1.8	14
24	RNAProt: an efficient and feature-rich RNA binding protein binding site predictor. GigaScience, 2021, 10, .	3.3	11
25	The temperature-regulated DEAD-box RNA helicase CrhR interactome: autoregulation and photosynthesis-related transcripts. Journal of Experimental Botany, 2021, , .	2.4	7
26	A distinct CD38+CD45RA+ population of CD4+, CD8+, and double-negative T cells is controlled by FAS. Journal of Experimental Medicine, 2021, 218, .	4.2	25
27	Scool: a new data storage format for single-cell Hi-C data. Bioinformatics, 2021, 37, 2053-2054.	1.8	3
28	Casboundary: automated definition of integral Cas cassettes. Bioinformatics, 2021, 37, 1352-1359.	1.8	8
29	Peakhood: individual site context extraction for CLIP-seq peak regions. Bioinformatics, 2021, , .	1.8	0
30	Transcriptome-wide <i>in vivo</i> mapping of cleavage sites for the compact cyanobacterial ribonuclease E reveals insights into its function and substrate recognition. Nucleic Acids Research, 2021, 49, 13075-13091.	6.5	17
31	CRISPR-Cas bioinformatics. Methods, 2020, 172, 3-11.	1.9	45
32	Evolutionary classification of CRISPRâ€“Cas systems: a burst of class 2 and derived variants. Nature Reviews Microbiology, 2020, 18, 67-83.	13.6	1,427
33	FLASH: ultra-fast protocol to identify RNAâ€“protein interactions in cells. Nucleic Acids Research, 2020, 48, e15-e15.	6.5	21
34	NanoGalaxy: Nanopore long-read sequencing data analysis in Galaxy. GigaScience, 2020, 9, .	3.3	23
35	Generation of pure monocultures of human microglia-like cells from induced pluripotent stem cells. Stem Cell Research, 2020, 49, 102046.	0.3	29
36	Nephronophthisis gene products display RNA-binding properties and are recruited to stress granules. Scientific Reports, 2020, 10, 15954.	1.6	13

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37	The locality dilemma of Sankoff-like RNA alignments. Bioinformatics, 2020, 36, i242-i250.	1.8	0
38	Precursor Intensity-Based Label-Free Quantification Software Tools for Proteomic and Multi-Omic Analysis within the Galaxy Platform. Proteomes, 2020, 8, 15.	1.7	9
39	Galaxy CLIP-Explorer: a web server for CLIP-Seq data analysis. GigaScience, 2020, 9, .	3.3	8
40	Fast and accurate structure probability estimation for simultaneous alignment and folding of RNAs with Markov chains. Algorithms for Molecular Biology, 2020, 15, 19.	0.3	2
41	Adaptation induced by self-targeting in a type I-B CRISPR-Cas system. Journal of Biological Chemistry, 2020, 295, 13502-13515.	1.6	6
42	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. GigaScience, 2020, 9, .	3.3	14
43	A global data-driven census of<i>Salmonella</i>small proteins and their potential functions in bacterial virulence. MicroLife, 2020, 1, .	1.0	34
44	Improving CLIP-seq data analysis by incorporating transcript information. BMC Genomics, 2020, 21, 894.	1.2	8
45	Galaxy HiCExplorer 3: a web server for reproducible Hi-C, capture Hi-C and single-cell Hi-C data analysis, quality control and visualization. Nucleic Acids Research, 2020, 48, W177-W184.	6.5	188
46	MutaRNA: analysis and visualization of mutation-induced changes in RNA structure. Nucleic Acids Research, 2020, 48, W287-W291.	6.5	15
47	CRISPRcasIdentifier: Machine learning for accurate identification and classification of CRISPR-Cas systems. GigaScience, 2020, 9, .	3.3	31
48	The democratization of bioinformatics: A software engineering perspective. GigaScience, 2020, 9, .	3.3	3
49	CopomuSâ€”Ranking Compensatory Mutations to Guide RNA-RNA Interaction Verification Experiments. International Journal of Molecular Sciences, 2020, 21, 3852.	1.8	0
50	The impact of various seed, accessibility and interaction constraints on sRNA target prediction- a systematic assessment. BMC Bioinformatics, 2020, 21, 15.	1.2	5
51	Heterogeneous networks integration for diseaseâ€“gene prioritization with node kernels. Bioinformatics, 2020, 36, 2649-2656.	1.8	15
52	Comprehensive search for accessory proteins encoded with archaeal and bacterial type III CRISPR-<i>cas</i> gene cassettes reveals 39 new <i>cas</i> gene families. RNA Biology, 2019, 16, 530-542.	1.5	97
53	CRISPR-Cas systems in multicellular cyanobacteria. RNA Biology, 2019, 16, 518-529.	1.5	31
54	ShaKer: RNA SHAPE prediction using graph kernel. Bioinformatics, 2019, 35, i354-i359.	1.8	9

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55	uORF-Toolsâ€"Workflow for the determination of translation-regulatory upstream open reading frames. PLoS ONE, 2019, 14, e0222459.	1.1	7
56	A pan-cancer analysis of synonymous mutations. Nature Communications, 2019, 10, 2569.	5.8	147
57	The RNA workbench 2.0: next generation RNA data analysis. Nucleic Acids Research, 2019, 47, W511-W515.	6.5	13
58	GraphClust2: Annotation and discovery of structured RNAs with scalable and accessible integrative clustering. GigaScience, 2019, 8, .	3.3	12
59	IntaRNAhelix-composing RNAâ€"RNA interactions from stable inter-molecular helices boosts bacterial sRNA target prediction. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940009.	0.3	5
60	Cross-cleavage activity of Cas6b in crRNA processing of two different CRISPR-Cas systems in Methanosarcina mazei GÃ¶1. RNA Biology, 2019, 16, 492-503.	1.5	11
61	Integration of accessibility data from structure probing into RNAâ€"RNA interaction prediction. Bioinformatics, 2019, 35, 2862-2864.	1.8	12
62	The nuts and bolts of the <i>Haloferax</i> CRISPR-Cas system I-B. RNA Biology, 2019, 16, 469-480.	1.5	29
63	hnRNP R and its main interactor, the noncoding RNA 7SK, coregulate the axonal transcriptome of motoneurons. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2859-E2868.	3.3	37
64	Structure and Interaction Prediction in Prokaryotic RNA Biology. Microbiology Spectrum, 2018, 6, .	1.2	9
65	MechRNA: prediction of lncRNA mechanisms from RNAâ€"RNA and RNAâ€"protein interactions. Bioinformatics, 2018, 34, 3101-3110.	1.8	48
66	In vitro iCLIP-based modeling uncovers how the splicing factor U2AF2 relies on regulation by cofactors. Genome Research, 2018, 28, 699-713.	2.4	62
67	Distinct epigenetic programs regulate cardiac myocyte development and disease in the human heart in vivo. Nature Communications, 2018, 9, 391.	5.8	181
68	Comparative RNA Genomics. Methods in Molecular Biology, 2018, 1704, 363-400.	0.4	8
69	Combinatorial Omics Analysis Reveals Perturbed Lysosomal Homeostasis in Collagen VII-deficient Keratinocytes. Molecular and Cellular Proteomics, 2018, 17, 565-579.	2.5	25
70	The RNA-binding protein ARPP21 controls dendritic branching by functionally opposing the miRNA it hosts. Nature Communications, 2018, 9, 1235.	5.8	55
71	uvCLAP is a fast and non-radioactive method to identify in vivo targets of RNA-binding proteins. Nature Communications, 2018, 9, 1142.	5.8	22
72	CMV: visualization for RNA and protein family models and their comparisons. Bioinformatics, 2018, 34, 2676-2678.	1.8	5

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73	Interactive implementations of thermodynamics-based RNA structure and RNAâ€“RNA interaction prediction approaches for example-driven teaching. PLoS Computational Biology, 2018, 14, e1006341.	1.5	9
74	GraphDDP: a graph-embedding approach to detect differentiation pathways in single-cell-data using prior class knowledge. Nature Communications, 2018, 9, 3685.	5.8	9
75	Structure and Interaction Prediction in Prokaryotic RNA Biology. , 2018, , 563-579.		0
76	Analysis of the androgen receptorâ€“regulated lncRNA landscape identifies a role for ARLNC1 in prostate cancer progression. Nature Genetics, 2018, 50, 814-824.	9.4	196
77	AptaSUITE: A Full-Featured Bioinformatics Framework for the Comprehensive Analysis of Aptamers from HT-SELEX Experiments. Molecular Therapy - Nucleic Acids, 2018, 11, 515-517.	2.3	54
78	Freiburg RNA tools: a central online resource for RNA-focused research and teaching. Nucleic Acids Research, 2018, 46, W25-W29.	6.5	107
79	Community-Driven Data Analysis Training for Biology. Cell Systems, 2018, 6, 752-758.e1.	2.9	141
80	Practical Computational Reproducibility in the Life Sciences. Cell Systems, 2018, 6, 631-635.	2.9	100
81	Galaxy HiCExplorer: a web server for reproducible Hi-C data analysis, quality control and visualization. Nucleic Acids Research, 2018, 46, W11-W16.	6.5	168
82	GLASSgo â€“ Automated and Reliable Detection of sRNA Homologs From a Single Input Sequence. Frontiers in Genetics, 2018, 9, 124.	1.1	53
83	An Efficient Semi-supervised Learning Approach to Predict SH2 Domain Mediated Interactions. Methods in Molecular Biology, 2017, 1555, 83-97.	0.4	0
84	<i>GRIN3B</i> missense mutation as an inherited risk factor for schizophrenia: whole-exome sequencing in a family with a familiar history of psychotic disorders. Genetical Research, 2017, 99, e1.	0.3	15
85	Computational analysis of CLIP-seq data. Methods, 2017, 118-119, 60-72.	1.9	36
86	Mechanism of Î²-actin mRNA Recognition by ZBP1. Cell Reports, 2017, 18, 1187-1199.	2.9	43
87	Differentiation of ncRNAs from small mRNAs in Escherichia coli O157:H7 EDL933 (EHEC) by combined RNAseq and RIBOseq â€“ ryhB encodes the regulatory RNA RyhB and a peptide, RyhP. BMC Genomics, 2017, 18, 216.	1.2	43
88	IntaRNA 2.0: enhanced and customizable prediction of RNAâ€“RNA interactions. Nucleic Acids Research, 2017, 45, W435-W439.	6.5	472
89	The RNA workbench: best practices for RNA and high-throughput sequencing bioinformatics in Galaxy. Nucleic Acids Research, 2017, 45, W560-W566.	6.5	38
90	 <tt>RNAscClust</tt>: clustering RNA sequences using structure conservation and graph based motifs. Bioinformatics, 2017, 33, 2089-2096.	1.8	26

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91	RNA-bioinformatics: Tools, services and databases for the analysis of RNA-based regulation. Journal of Biotechnology, 2017, 261, 76-84.	1.9	21
92	DHX9 suppresses RNA processing defects originating from the Alu invasion of the human genome. Nature, 2017, 544, 115-119.	13.7	415
93	sRNA₁₅₄ a newly identified regulator of nitrogen fixation in <i>Methanosarcina mazei</i> strain GÃ¶1. RNA Biology, 2017, 14, 1544-1558.	1.5	53
94	A mutually exclusive stemâ€“loop arrangement in roX2 RNA is essential for X-chromosome regulation in <i>Drosophila</i>. Genes and Development, 2017, 31, 1973-1987.	2.7	24
95	Methanosarcina Spherical Virus, a Novel Archaeal Lytic Virus Targeting Methanosarcina Strains. Journal of Virology, 2017, 91, .	1.5	35
96	RIP-Seq Suggests Translational Regulation by L7Ae in <i>Archaea</i>. MBio, 2017, 8, .	1.8	23
97	Recent advances in RNA folding. Journal of Biotechnology, 2017, 261, 97-104.	1.9	66
98	Plasticity of archaeal C/D box sRNA biogenesis. Molecular Microbiology, 2017, 103, 151-164.	1.2	10
99	Structural constraints and enzymatic promiscuity in the Cas6-dependent generation of crRNAs. Nucleic Acids Research, 2017, 45, 915-925.	6.5	53
100	<i>Photorhabdus</i>â€nematode symbiosis is dependent on <i>hfq</i>â€mediated regulation of secondary metabolites. Environmental Microbiology, 2017, 19, 119-129.	1.8	60
101	EBF1 binds to EBNA2 and promotes the assembly of EBNA2 chromatin complexes in B cells. PLoS Pathogens, 2017, 13, e1006664.	2.1	25
102	CRISPR and Salty: CRISPR-Cas Systems in Haloarchaea. Nucleic Acids and Molecular Biology, 2017, , 243-269.	0.2	4
103	GenToS: Use of Orthologous Gene Information to Prioritize Signals from Human GWAS. PLoS ONE, 2016, 11, e0162466.	1.1	2
104	5'-Hydroxymethylcytosine Precedes Loss of CpG Methylation in Enhancers and Genes Undergoing Activation in Cardiomyocyte Maturation. PLoS ONE, 2016, 11, e0166575.	1.1	13
105	MicroRNA Profiling in Aqueous Humor of Individual Human Eyes by Next-Generation Sequencing. , 2016, 57, 1706.		47
106	Global <scp>RNA</scp> recognition patterns of postâ€transcriptional regulators Hfq and CsrA revealed by <scp>UV</scp> crosslinking <i>inÂvivo</i>. EMBO Journal, 2016, 35, 991-1011.	3.5	296
107	Characterizing leader sequences of CRISPR loci. Bioinformatics, 2016, 32, i576-i585.	1.8	81
108	AptaTRACE Elucidates RNA Sequence-Structure Motifs from Selection Trends in HT-SELEX Experiments. Cell Systems, 2016, 3, 62-70.	2.9	55

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109	The lncRNA landscape of breast cancer reveals a role for DSCAM-AS1 in breast cancer progression. Nature Communications, 2016, 7, 12791.	5.8	196
110	The role of Cas8Âin typeÂI CRISPR interference. Bioscience Reports, 2015, 35, .	1.1	37
111	antaRNA â€“ Multi-objective inverse folding of pseudoknot RNA using ant-colony optimization. BMC Bioinformatics, 2015, 16, 389.	1.2	19
112	SPARSE: quadratic time simultaneous alignment and folding of RNAs without sequence-based heuristics. Bioinformatics, 2015, 31, 2489-2496.	1.8	37
113	antaRNA: ant colony-based RNA sequence design. Bioinformatics, 2015, 31, 3114-3121.	1.8	35
114	Deciphering the Epigenetic Code of Cardiac Myocyte Transcription. Circulation Research, 2015, 117, 413-423.	2.0	71
115	An Active Immune Defense with a Minimal CRISPR (Clustered Regularly Interspaced Short Palindromic) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	26
116	An updated evolutionary classification of CRISPRâ€“Cas systems. Nature Reviews Microbiology, 2015, 13, 722-736.	13.6	2,081
117	SimiRa: A tool to identify coregulation between microRNAs and RNA-binding proteins. RNA Biology, 2015, 12, 998-1009.	1.5	14
118	RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF-ÎºB pathway. Nature Communications, 2015, 6, 7367.	5.8	99
119	Cell type specific gene expression analysis of prostate needle biopsies resolves tumor tissue heterogeneity. Oncotarget, 2015, 6, 1302-1314.	0.8	20
120	A Complex of Cas Proteins 5, 6, and 7 Is Required for the Biogenesis and Stability of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-derived RNAs (crRNAs) in Haloferax volcanii. Journal of Biological Chemistry, 2014, 289, 7164-7177.	1.6	65
121	Atom mapping with constraint programming. Algorithms for Molecular Biology, 2014, 9, 23.	0.3	14
122	Bioinformatics of prokaryotic RNAs. RNA Biology, 2014, 11, 470-483.	1.5	12
123	Dynamic DNA methylation orchestrates cardiomyocyte development, maturation and disease. Nature Communications, 2014, 5, 5288.	5.8	272
124	MoDPepInt: an interactive web server for prediction of modular domainâ€“peptide interactions. Bioinformatics, 2014, 30, 2668-2669.	1.8	37
125	Graph-distance distribution of the Boltzmann ensemble of RNA secondary structures. Algorithms for Molecular Biology, 2014, 9, 19.	0.3	0
126	ExpaRNA-P: simultaneous exact pattern matching and folding of RNAs. BMC Bioinformatics, 2014, 15, 404.	1.2	12

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127	BlockClust: efficient clustering and classification of non-coding RNAs from short read RNA-seq profiles. Bioinformatics, 2014, 30, i274-i282.	1.8	17
128	CopraRNA and IntaRNA: predicting small RNA targets, networks and interaction domains. Nucleic Acids Research, 2014, 42, W119-W123.	6.5	347
129	CRISPRstrand: predicting repeat orientations to determine the crRNA-encoding strand at CRISPR loci. Bioinformatics, 2014, 30, i489-i496.	1.8	57
130	GraphProt: modeling binding preferences of RNA-binding proteins. Genome Biology, 2014, 15, R17.	13.9	247
131	Cluster based prediction of PDZ-peptide interactions. BMC Genomics, 2014, 15, S5.	1.2	16
132	Biological and bioinformatical approaches to study crosstalk of long-non-coding RNAs and chromatin-modifying proteins. Cell and Tissue Research, 2014, 356, 507-526.	1.5	16
133	Simultaneous Alignment and Folding of Protein Sequences. Journal of Computational Biology, 2014, 21, 477-491.	0.8	0
134	Autosomal dominant immune dysregulation syndrome in humans with CTLA4 mutations. Nature Medicine, 2014, 20, 1410-1416.	15.2	723
135	Lineage-specific splicing of a brain-enriched alternative exon promotes glioblastoma progression. Journal of Clinical Investigation, 2014, 124, 2861-2876.	3.9	83
136	MOF-associated complexes ensure stem cell identity and Xist repression. ELife, 2014, 3, e02024.	2.8	76
137	LocARNAscan: Incorporating thermodynamic stability in sequence and structure-based RNA homology search. Algorithms for Molecular Biology, 2013, 8, 14.	0.3	14
138	Tandem Stem-Loops in roX RNAs Act Together to Mediate X Chromosome Dosage Compensation in Drosophila. Molecular Cell, 2013, 51, 156-173.	4.5	152
139	Comparative genomics boosts target prediction for bacterial small RNAs. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3487-96.	3.3	208
140	Essential requirements for the detection and degradation of invaders by the<i>Haloferax volcanii</i>CRISPR/Cas system I-B. RNA Biology, 2013, 10, 865-874.	1.5	59
141	Two CRISPR-Cas systems in<i><i>Methanosarcina mazei</i></i>strain GÃ¶1 display common processing features despite belonging to different types I and III. RNA Biology, 2013, 10, 779-791.	1.5	50
142	Comparative analysis of Cas6b processing and CRISPR RNA stability. RNA Biology, 2013, 10, 700-707.	1.5	22
143	CRISPRmap: an automated classification of repeat conservation in prokaryotic adaptive immune systems. Nucleic Acids Research, 2013, 41, 8034-8044.	6.5	152
144	CRISPR-Cas Systems in the Cyanobacterium Synechocystis sp. PCC6803 Exhibit Distinct Processing Pathways Involving at Least Two Cas6 and a Cmr2 Protein. PLoS ONE, 2013, 8, e56470.	1.1	144

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145	SPARSE: Quadratic Time Simultaneous Alignment and Folding of RNAs without Sequence-Based Heuristics. Lecture Notes in Computer Science, 2013, , 289-290.	1.0	1
146	Navigating the unexplored seascape of pre-miRNA candidates in single-genome approaches. Bioinformatics, 2012, 28, 3034-3041.	1.8	6
147	CARNA--alignment of RNA structure ensembles. Nucleic Acids Research, 2012, 40, W49-W53.	6.5	23
148	Global or local? Predicting secondary structure and accessibility in mRNAs. Nucleic Acids Research, 2012, 40, 5215-5226.	6.5	139
149	LocARNA-P: Accurate boundary prediction and improved detection of structural RNAs. Rna, 2012, 18, 900-914.	1.6	326
150	Accessibility and conservation: General features of bacterial small RNAâ€“mRNA interactions?. RNA Biology, 2012, 9, 954-965.	1.5	56
151	An archaeal sRNA targeting cis - and trans -encoded mRNAs via two distinct domains. Nucleic Acids Research, 2012, 40, 10964-10979.	6.5	62
152	GraphClust: alignment-free structural clustering of local RNA secondary structures. Bioinformatics, 2012, 28, i224-i232.	1.8	69
153	Bioinformatics of Bacterial sRNAs and Their Targets. , 2012, , 221-239.		1
154	Exact Pattern Matching for RNA Structure Ensembles. Lecture Notes in Computer Science, 2012, , 245-260.	1.0	2
155	Structator: fast index-based search for RNA sequence-structure patterns. BMC Bioinformatics, 2011, 12, 214.	1.2	23
156	Fast RNA structure alignment for crossing input structures. Journal of Discrete Algorithms, 2011, 9, 2-11.	0.7	0
157	Sparse RNA folding: Time and space efficient algorithms. Journal of Discrete Algorithms, 2011, 9, 12-31.	0.7	45
158	The PETfold and PETcofold web servers for intra- and intermolecular structures of multiple RNA sequences. Nucleic Acids Research, 2011, 39, W107-W111.	6.5	29
159	PETcofold: predicting conserved interactions and structures of two multiple alignments of RNA sequences. Bioinformatics, 2011, 27, 211-219.	1.8	52
160	TassDB2 - A comprehensive database of subtle alternative splicing events. BMC Bioinformatics, 2010, 11, 216.	1.2	20
161	Identification and characterization of NAGNAG alternative splicing in the moss Physcomitrella patens. BMC Plant Biology, 2010, 10, 76.	1.6	13
162	Hierarchical folding of multiple sequence alignments for the prediction of structures and RNA-RNA interactions. Algorithms for Molecular Biology, 2010, 5, 22.	0.3	13

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163	Computational prediction of sRNAs and their targets in bacteria. RNA Biology, 2010, 7, 33-42.	1.5	97
164	Sparsification of RNA structure prediction including pseudoknots. Algorithms for Molecular Biology, 2010, 5, 39.	0.3	17
165	Lifting Prediction to Alignment of RNA Pseudoknots. Journal of Computational Biology, 2010, 17, 429-442.	0.8	18
166	Seed-based I<scp>nta</scp>RNA prediction combined with GFP-reporter system identifies mRNA targets of the small RNA Yfr1. Bioinformatics, 2010, 26, 1-5.	1.8	90
167	Freiburg RNA Tools: a web server integrating INTARNA, EXPARNA and LOCARNA. Nucleic Acids Research, 2010, 38, W373-W377.	6.5	212
168	Accurate prediction of NAGNAG alternative splicing. Nucleic Acids Research, 2009, 37, 3569-3579.	6.5	25
169	Lightweight comparison of RNAs based on exact sequenceâ€"structure matches. Bioinformatics, 2009, 25, 2095-2102.	1.8	31
170	Simultaneous Alignment and Folding of Protein Sequences. Lecture Notes in Computer Science, 2009, , 339-355.	1.0	2
171	Fast RNA Structure Alignment for Crossing Input Structures. Lecture Notes in Computer Science, 2009, , 236-248.	1.0	6
172	Sparse RNA Folding: Time and Space Efficient Algorithms. Lecture Notes in Computer Science, 2009, , 249-262.	1.0	17
173	Lifting Prediction to Alignment of RNA Pseudoknots. Lecture Notes in Computer Science, 2009, , 285-301.	1.0	3
174	Efficient Sequence Alignment with Side-Constraints by Cluster Tree Elimination. Constraints, 2008, 13, 110-129.	0.4	3
175	Improved identification of conserved cassette exons using Bayesian networks. BMC Bioinformatics, 2008, 9, 477.	1.2	6
176	Selection against tandem splice sites affecting structured protein regions. BMC Evolutionary Biology, 2008, 8, 89.	3.2	12
177	Alternative splicing at NAGNAG acceptors in Arabidopsis thaliana SR and SR-related protein-coding genes. BMC Genomics, 2008, 9, 159.	1.2	49
178	IntaRNA: efficient prediction of bacterial sRNA targets incorporating target site accessibility and seed regions. Bioinformatics, 2008, 24, 2849-2856.	1.8	499
179	Unifying evolutionary and thermodynamic information for RNA folding of multiple alignments. Nucleic Acids Research, 2008, 36, 6355-6362.	6.5	79
180	Assessing the fraction of short-distance tandem splice sites under purifying selection. Rna, 2008, 14, 616-629.	1.6	17

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181	Fixed Parameter Tractable Alignment of RNA Structures Including Arbitrary Pseudoknots. , 2008, , 69-81.		12
182	Pre-mRNA Secondary Structures Influence Exon Recognition. PLoS Genetics, 2007, 3, e204.	1.5	166
183	Inferring Noncoding RNA Families and Classes by Means of Genome-Scale Structure-Based Clustering. PLoS Computational Biology, 2007, 3, e65.	1.5	424
184	TassDB: a database of alternative tandem splice sites. Nucleic Acids Research, 2007, 35, D188-D192.	6.5	27
185	Locality and Gaps in RNA Comparison. Journal of Computational Biology, 2007, 14, 1074-1087.	0.8	8
186	BioBayesNet: a web server for feature extraction and Bayesian network modeling of biological sequence data. Nucleic Acids Research, 2007, 35, W688-W693.	6.5	17
187	Violating the splicing rules: TG dinucleotides function as alternative 3' splice sites in U2-dependent introns. Genome Biology, 2007, 8, R154.	13.9	35
188	RNAs everywhere: genome-wide annotation of structured RNAs. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 1-25.	0.6	46
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