Andreas S Richter

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4390496/publications.pdf

Version: 2024-02-01

20 papers 7,766 citations

17 h-index

471061

752256 20 g-index

21 all docs

21 docs citations

times ranked

21

16359 citing authors

#	Article	IF	CITATIONS
1	deepTools2: a next generation web server for deep-sequencing data analysis. Nucleic Acids Research, 2016, 44, W160-W165.	6.5	5,157
2	IntaRNA: efficient prediction of bacterial sRNA targets incorporating target site accessibility and seed regions. Bioinformatics, 2008, 24, 2849-2856.	1.8	499
3	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
4	CopraRNA and IntaRNA: predicting small RNA targets, networks and interaction domains. Nucleic Acids Research, 2014, 42, W119-W123.	6.5	347
5	Freiburg RNA Tools: a web server integrating INTARNA, EXPARNA and LOCARNA. Nucleic Acids Research, 2010, 38, W373-W377.	6.5	212
6	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
7	Epigenomic Profiling of Human CD4+ T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. Immunity, 2016, 45, 1148-1161.	6.6	174
8	The small RNA PhrS stimulates synthesis of the <i>Pseudomonas aeruginosa</i> quinolone signal. Molecular Microbiology, 2011, 80, 868-885.	1.2	145
9	Freiburg RNA tools: a central online resource for RNA-focused research and teaching. Nucleic Acids Research, 2018, 46, W25-W29.	6.5	107
10	Standardizing chromatin research: a simple and universal method for ChIP-seq. Nucleic Acids Research, 2016, 44, e67-e67.	6.5	97
11	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
12	Epigenetic dynamics of monocyte-to-macrophage differentiation. Epigenetics and Chromatin, 2016, 9, 33.	1.8	73
13	An archaeal sRNA targeting cis - and trans -encoded mRNAs via two distinct domains. Nucleic Acids Research, 2012, 40, 10964-10979.	6.5	62
14	Accessibility and conservation: General features of bacterial small RNA–mRNA interactions?. RNA Biology, 2012, 9, 954-965.	1.5	56
15	PETcofold: predicting conserved interactions and structures of two multiple alignments of RNA sequences. Bioinformatics, 2011, 27, 211-219.	1.8	52
16	Forward Genetic Screens in Zebrafish Identify Pre-mRNA-Processing Pathways Regulating Early T Cell Development. Cell Reports, 2016, 17, 2259-2270.	2.9	24
17	Cell type specific gene expression analysis of prostate needle biopsies resolves tumor tissue heterogeneity. Oncotarget, 2015, 6, 1302-1314.	0.8	20
18	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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#	Article	IF	CITATIONS
19	The small RNA Aar in Acinetobacter baylyi: a putative regulator of amino acid metabolism. Archives of Microbiology, 2010, 192, 691-702.	1.0	12
20	Bioinformatics of prokaryotic RNAs. RNA Biology, 2014, 11, 470-483.	1.5	12