

Marc Rehmsmeier

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

7,765
citations

516710

16
h-index

752698

20
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22
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docs citations

22
times ranked

12383
citing authors

#	ARTICLE	IF	CITATIONS
1	The Precision-Recall Plot Is More Informative than the ROC Plot When Evaluating Binary Classifiers on Imbalanced Datasets. PLoS ONE, 2015, 10, e0118432.	2.5	2,354
2	Fast and effective prediction of microRNA/target duplexes. Rna, 2004, 10, 1507-1517.	3.5	2,157
3	RNAhybrid: microRNA target prediction easy, fast and flexible. Nucleic Acids Research, 2006, 34, W451-W454.	14.5	1,542
4	A functional screen implicates microRNA-138-dependent regulation of the depalmitoylation enzyme APT1 in dendritic spine morphogenesis. Nature Cell Biology, 2009, 11, 705-716.	10.3	437
5	RNAshapes: an integrated RNA analysis package based on abstract shapes. Bioinformatics, 2006, 22, 500-503.	4.1	272
6	Genome-Wide Prediction of Polycomb/Trithorax Response Elements in Drosophila melanogaster. Developmental Cell, 2003, 5, 759-771.	7.0	248
7	Abstract shapes of RNA. Nucleic Acids Research, 2004, 32, 4843-4851.	14.5	179
8	Precrec: fast and accurate precision-recall and ROC curve calculations in R. Bioinformatics, 2017, 33, 145-147.	4.1	162
9	Comprehensive prediction of novel microRNA targets in Arabidopsis thaliana. Nucleic Acids Research, 2009, 37, 4010-4021.	14.5	99
10	Complete probabilistic analysis of RNA shapes. BMC Biology, 2006, 4, 5.	3.8	66
11	Beyond Mfold: Recent advances in RNA bioinformatics. Journal of Biotechnology, 2006, 124, 41-55.	3.8	59
12	jPREdictor: a versatile tool for the prediction of cis-regulatory elements. Nucleic Acids Research, 2006, 34, W546-W550.	14.5	39
13	Evolutionary Plasticity of Polycomb/Trithorax Response Elements in Drosophila Species. PLoS Biology, 2008, 6, e261.	5.6	39
14	A Novel Approach to Remote Homology Detection: Jumping Alignments. Journal of Computational Biology, 2002, 9, 747-760.	1.6	33
15	Comparative homology agreement search: An effective combination of homology-search methods. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13814-13819.	7.1	21
16	Phylogenetic information improves homology detection. Proteins: Structure, Function and Bioinformatics, 2001, 45, 360-371.	2.6	19
17	Comprehensive analysis of high-throughput screens with HiTSeekR. Nucleic Acids Research, 2016, 44, 6639-6648.	14.5	17
18	DNA sequence models of genome-wide Drosophila melanogaster Polycomb binding sites improve generalization to independent Polycomb Response Elements. Nucleic Acids Research, 2019, 47, 7781-7797.	14.5	15

#	ARTICLE	IF	CITATIONS
19	MGcount: a total RNA-seq quantification tool to address multi-mapping and multi-overlapping alignments ambiguity in non-coding transcripts. BMC Bioinformatics, 2022, 23, 39.	2.6	6
20	MOCCA: a flexible suite for modelling DNA sequence motif occurrence combinatorics. BMC Bioinformatics, 2021, 22, 234.	2.6	1
21	The RNAhybrid approach to microRNA target prediction. , 2007, , 199-209.		0
22	Computational Identification of Polycomb/Trithorax Response Elements. , 2017, , 7-24.		0