

# Marc Rehmsmeier

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11877192/publications.pdf>

Version: 2024-02-01

22  
papers

7,765  
citations

516710

16  
h-index

752698

20  
g-index

22  
all docs

22  
docs citations

22  
times ranked

12383  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	MOCCA: a flexible suite for modelling DNA sequence motif occurrence combinatorics. BMC Bioinformatics, 2021, 22, 234.	2.6	1
3	DNA sequence models of genome-wide DrosophilaÂmelanogaster Polycomb binding sites improve generalization to independent Polycomb Response Elements. Nucleic Acids Research, 2019, 47, 7781-7797.	14.5	15
4	Precrec: fast and accurate precisionâ€“recall and ROC curve calculations in R. Bioinformatics, 2017, 33, 145-147.	4.1	162
5	Computational Identification of Polycomb/Trithorax Response Elements. , 2017, , 7-24.		0
6	Comprehensive analysis of high-throughput screens with HiTSeekR. Nucleic Acids Research, 2016, 44, 6639-6648.	14.5	17
7	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
8	Comprehensive prediction of novel microRNA targets in Arabidopsis thaliana. Nucleic Acids Research, 2009, 37, 4010-4021.	14.5	99
9	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
10	Evolutionary Plasticity of Polycomb/Trithorax Response Elements in Drosophila Species. PLoS Biology, 2008, 6, e261.	5.6	39
11	The RNAhybrid approach to microRNA target prediction. , 2007, , 199-209.		0
12	Beyond Mfold: Recent advances in RNA bioinformatics. Journal of Biotechnology, 2006, 124, 41-55.	3.8	59
13	jPREDictor: a versatile tool for the prediction of cis-regulatory elements. Nucleic Acids Research, 2006, 34, W546-W550.	14.5	39
14	Complete probabilistic analysis of RNA shapes. BMC Biology, 2006, 4, 5.	3.8	66
15	RNAhybrid: microRNA target prediction easy, fast and flexible. Nucleic Acids Research, 2006, 34, W451-W454.	14.5	1,542
16	RNAshapes: an integrated RNA analysis package based on abstract shapes. Bioinformatics, 2006, 22, 500-503.	4.1	272
17	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
18	Abstract shapes of RNA. Nucleic Acids Research, 2004, 32, 4843-4851.	14.5	179

#	ARTICLE	IF	CITATIONS
19	Fast and effective prediction of microRNA/target duplexes. <i>Rna</i> , 2004, 10, 1507-1517.	3.5	2,157
20	Genome-Wide Prediction of Polycomb/Trithorax Response Elements in <i>Drosophila melanogaster</i> . <i>Developmental Cell</i> , 2003, 5, 759-771.	7.0	248
21	A Novel Approach to Remote Homology Detection: Jumping Alignments. <i>Journal of Computational Biology</i> , 2002, 9, 747-760.	1.6	33
22	Phylogenetic information improves homology detection. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 360-371.	2.6	19