

Timothy L Bailey

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

17
papers

3,352
citations

11
h-index

17
g-index

17
ext. papers

4,565
ext. citations

11.4
avg, IF

6.19
L-index

#	Paper	IF	Citations
17	STREME: Accurate and versatile sequence motif discovery. <i>Bioinformatics</i> , 2021 ,	7.2	43
16	T-Gene: improved target gene prediction. <i>Bioinformatics</i> , 2020 , 36, 3902-3904	7.2	4
15	MoMo: discovery of statistically significant post-translational modification motifs. <i>Bioinformatics</i> , 2019 , 35, 2774-2782	7.2	52
14	Homodimerization regulates an endothelial specific signature of the SOX18 transcription factor. <i>Nucleic Acids Research</i> , 2018 , 46, 11381-11395	20.1	13
13	Krüpel-like factors compete for promoters and enhancers to fine-tune transcription. <i>Nucleic Acids Research</i> , 2017 , 45, 6572-6588	20.1	26
12	Promiscuous DNA-binding of a mutant zinc finger protein corrupts the transcriptome and diminishes cell viability. <i>Nucleic Acids Research</i> , 2017 , 45, 1130-1143	20.1	23
11	CisMapper: predicting regulatory interactions from transcription factor ChIP-seq data. <i>Nucleic Acids Research</i> , 2017 , 45, e19	20.1	16
10	Differential motif enrichment analysis of paired ChIP-seq experiments. <i>BMC Genomics</i> , 2014 , 15, 752	4.5	17
9	DREME: motif discovery in transcription factor ChIP-seq data. <i>Bioinformatics</i> , 2011 , 27, 1653-9	7.2	716
8	MEME-ChIP: motif analysis of large DNA datasets. <i>Bioinformatics</i> , 2011 , 27, 1696-7	7.2	994
7	Motif Enrichment Analysis: a unified framework and an evaluation on ChIP data. <i>BMC Bioinformatics</i> , 2010 , 11, 165	3.6	358
6	Quantifying similarity between motifs. <i>Genome Biology</i> , 2007 , 8, R24	18.3	1065
5	MoMo: Discovery of statistically significant post-translational modification motifs		1
4	MoMo: Discovery of post-translational modification motifs		2
3	STREME: Accurate and versatile sequence motif discovery		5
2	SEA: Simple Enrichment Analysis of motifs		8
1	XSTREME: Comprehensive motif analysis of biological sequence datasets		9

