## Timothy L Bailey

## List of Publications by Citations

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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<br/>papers3,352<br/>citations11<br/>h-index17<br/>g-index17<br/>ext. papers4,565<br/>ext. citations11.4<br/>avg, IF6.19<br/>L-index

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