

Bartek Wilczynski

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.

39
papers

3,285
citations

14
h-index

56
g-index

56
ext. papers

4,564
ext. citations

6
avg, IF

4.57
L-index

#	Paper	IF	Citations
39	HiCEnterprise: identifying long range chromosomal contacts in Hi-C data. <i>PeerJ</i> , 2021 , 9, e10558	3.1	
38	Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. <i>Nature Communications</i> , 2021 , 12, 3621	17.4	2
37	Careful feature selection is key in classification of Alzheimer's disease patients based on whole-genome sequencing data. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab069	3.7	0
36	The role of epigenetic modifications, long-range contacts, enhancers and topologically associating domains in the regulation of glioma grade-specific genes. <i>Scientific Reports</i> , 2021 , 11, 15668	4.9	1
35	Machine learning and deep learning for the advancement of epigenomics 2020 , 217-237		
34	Automated inference of gene regulatory networks using explicit regulatory modules. <i>Journal of Theoretical Biology</i> , 2020 , 486, 110091	2.3	1
33	QChromosomeVisualizer: A new tool for 3D visualization of long simulations of polymer-like chromosome models. <i>Methods</i> , 2020 , 181-182, 80-85	4.6	
32	BPscore: An Effective Metric for Meaningful Comparisons of Structural Chromosome Segmentations. <i>Journal of Computational Biology</i> , 2019 , 26, 305-314	1.7	4
31	Endothelial cell differentiation is encompassed by changes in long range interactions between inactive chromatin regions. <i>Nucleic Acids Research</i> , 2018 , 46, 1724-1740	20.1	26
30	Coordinated expression and genetic polymorphisms in Grainyhead-like genes in human non-melanoma skin cancers. <i>BMC Cancer</i> , 2018 , 18, 23	4.8	6
29	Distributed Bayesian networks reconstruction on the whole genome scale. <i>PeerJ</i> , 2018 , 6, e5692	3.1	5
28	Potential protective role of Grainyhead-like genes in the development of clear cell renal cell carcinoma. <i>Molecular Carcinogenesis</i> , 2017 , 56, 2414-2423	5	6
27	Taking promoters out of enhancers in sequence based predictions of tissue-specific mammalian enhancers. <i>BMC Medical Genomics</i> , 2017 , 10, 34	3.7	6
26	FastBill: An Improved Tool for Prediction of Cis-Regulatory Modules. <i>Journal of Computational Biology</i> , 2017 , 24, 193-199	1.7	1
25	Arabidopsis SWI/SNF chromatin remodeling complex binds both promoters and terminators to regulate gene expression. <i>Nucleic Acids Research</i> , 2017 , 45, 3116-3129	20.1	37
24	Optimally choosing PWM motif databases and sequence scanning approaches based on ChIP-seq data. <i>BMC Bioinformatics</i> , 2015 , 16, 140	3.6	9
23	WeBIAS: a web server for publishing bioinformatics applications. <i>BMC Research Notes</i> , 2015 , 8, 628	2.3	2

22	RECORD: Reference-Assisted Genome Assembly for Closely Related Genomes. <i>International Journal of Genomics</i> , 2015 , 2015, 563482	2.5	2
21	Genome-Wide Analysis of Drosophila RBF2 Protein Highlights the Diversity of RB Family Targets and Possible Role in Regulation of Ribosome Biosynthesis. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1503-1522	3.2	10
20	A Specialized Histone H1 Variant Is Required for Adaptive Responses to Complex Abiotic Stress and Related DNA Methylation in Arabidopsis. <i>Plant Physiology</i> , 2015 , 169, 2080-101	6.6	72
19	Supervised learning method for predicting chromatin boundary associated insulator elements. <i>Journal of Bioinformatics and Computational Biology</i> , 2014 , 12, 1442006	1	6
18	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. <i>Development (Cambridge)</i> , 2014 , 141, 2633-43	6.6	18
17	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. <i>Journal of Cell Science</i> , 2014 , 127, e1-e1	5.3	
16	Active enhancer positions can be accurately predicted from chromatin marks and collective sequence motif data. <i>BMC Systems Biology</i> , 2013 , 7 Suppl 6, S16	3.5	12
15	BNFinder2: Faster Bayesian network learning and Bayesian classification. <i>Bioinformatics</i> , 2013 , 29, 2068-70	7.0	18
14	Tissue-specific analysis of chromatin state identifies temporal signatures of enhancer activity during embryonic development. <i>Nature Genetics</i> , 2012 , 44, 148-56	36.3	370
13	Predicting spatial and temporal gene expression using an integrative model of transcription factor occupancy and chromatin state. <i>PLoS Computational Biology</i> , 2012 , 8, e1002798	5	32
12	A Computer Scientist's Guide to the Regulatory Genome. <i>Fundamenta Informaticae</i> , 2010 , 103, 323-332	1	2
11	Challenges for modeling global gene regulatory networks during development: insights from Drosophila. <i>Developmental Biology</i> , 2010 , 340, 161-9	3.1	44
10	Dynamic CRM occupancy reflects a temporal map of developmental progression. <i>Molecular Systems Biology</i> , 2010 , 6, 383	12.2	37
9	Finding evolutionarily conserved cis-regulatory modules with a universal set of motifs. <i>BMC Bioinformatics</i> , 2009 , 10, 82	3.6	20
8	Biopython: freely available Python tools for computational molecular biology and bioinformatics. <i>Bioinformatics</i> , 2009 , 25, 1422-3	7.2	2308
7	BNFinder: exact and efficient method for learning Bayesian networks. <i>Bioinformatics</i> , 2009 , 25, 286-7	7.2	75
6	MEMOFinder: combining de novo motif prediction methods with a database of known motifs. <i>Nature Precedings</i> , 2008 ,		2
5	Reconstruction of Mammalian Cell Cycle Regulatory Network from Microarray Data Using Stochastic Logical Networks. <i>Lecture Notes in Computer Science</i> , 2007 , 121-135	0.9	1

4	Applying dynamic Bayesian networks to perturbed gene expression data. <i>BMC Bioinformatics</i> , 2006 , 7, 249	3.6	105
3	Using local gene expression similarities to discover regulatory binding site modules. <i>BMC Bioinformatics</i> , 2006 , 7, 505	3.6	8
2	Regulatory Network Reconstruction Using Stochastic Logical Networks. <i>Lecture Notes in Computer Science</i> , 2006 , 142-154	0.9	2
1	Discovering regulatory binding-site modules using rule-based learning. <i>Genome Research</i> , 2005 , 15, 856-667	3.6	34