

Bartek Wilczynski

List of Publications by Citations

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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	Biopython: freely available Python tools for computational molecular biology and bioinformatics. <i>Bioinformatics</i> , 2009 , 25, 1422-3	7.2	2308
38	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
37	Applying dynamic Bayesian networks to perturbed gene expression data. <i>BMC Bioinformatics</i> , 2006 , 7, 249	3.6	105
36	BNFinder: exact and efficient method for learning Bayesian networks. <i>Bioinformatics</i> , 2009 , 25, 286-7	7.2	75
35	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
34	Challenges for modeling global gene regulatory networks during development: insights from Drosophila. <i>Developmental Biology</i> , 2010 , 340, 161-9	3.1	44
33	Dynamic CRM occupancy reflects a temporal map of developmental progression. <i>Molecular Systems Biology</i> , 2010 , 6, 383	12.2	37
32	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
31	Discovering regulatory binding-site modules using rule-based learning. <i>Genome Research</i> , 2005 , 15, 856-66	6.7	34
30	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
29	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
28	Finding evolutionarily conserved cis-regulatory modules with a universal set of motifs. <i>BMC Bioinformatics</i> , 2009 , 10, 82	3.6	20
27	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. <i>Development (Cambridge)</i> , 2014 , 141, 2633-43	6.6	18
26	BNFinder2: Faster Bayesian network learning and Bayesian classification. <i>Bioinformatics</i> , 2013 , 29, 2068-70	7.0	18
25	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
24	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, 1503-15	3.2	10
23	Optimally choosing PWM motif databases and sequence scanning approaches based on ChIP-seq data. <i>BMC Bioinformatics</i> , 2015 , 16, 140	3.6	9

22	Using local gene expression similarities to discover regulatory binding site modules. <i>BMC Bioinformatics</i> , 2006 , 7, 505	3.6	8
21	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
20	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
19	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
18	Supervised learning method for predicting chromatin boundary associated insulator elements. <i>Journal of Bioinformatics and Computational Biology</i> , 2014 , 12, 1442006	1	6
17	Distributed Bayesian networks reconstruction on the whole genome scale. <i>PeerJ</i> , 2018 , 6, e5692	3.1	5
16	BPscore: An Effective Metric for Meaningful Comparisons of Structural Chromosome Segmentations. <i>Journal of Computational Biology</i> , 2019 , 26, 305-314	1.7	4
15	WeBIAS: a web server for publishing bioinformatics applications. <i>BMC Research Notes</i> , 2015 , 8, 628	2.3	2
14	RECORD: Reference-Assisted Genome Assembly for Closely Related Genomes. <i>International Journal of Genomics</i> , 2015 , 2015, 563482	2.5	2
13	A Computer Scientist's Guide to the Regulatory Genome. <i>Fundamenta Informaticae</i> , 2010 , 103, 323-332	1	2
12	MEMOFinder: combining de novo motif prediction methods with a database of known motifs. <i>Nature Precedings</i> , 2008 ,		2
11	Regulatory Network Reconstruction Using Stochastic Logical Networks. <i>Lecture Notes in Computer Science</i> , 2006 , 142-154	0.9	2
10	Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. <i>Nature Communications</i> , 2021 , 12, 3621	17.4	2
9	FastBill: An Improved Tool for Prediction of Cis-Regulatory Modules. <i>Journal of Computational Biology</i> , 2017 , 24, 193-199	1.7	1
8	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
7	Automated inference of gene regulatory networks using explicit regulatory modules. <i>Journal of Theoretical Biology</i> , 2020 , 486, 110091	2.3	1
6	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
5	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

4 Machine learning and deep learning for the advancement of epigenomics **2020**, 217-237

3 Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. *Journal of Cell Science*, **2014**, 127, e1-e1

5.3

2 HiCEnterprise: identifying long range chromosomal contacts in Hi-C data. *PeerJ*, **2021**, 9, e10558

3.1

1 QChromosomeVisualizer: A new tool for 3D visualization of long simulations of polymer-like chromosome models. *Methods*, **2020**, 181-182, 80-85

4.6