

Bartek Wilczyński

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

5,394
citations

567144

15
h-index

345118

36
g-index

56
all docs

56
docs citations

56
times ranked

10279
citing authors

#	ARTICLE	IF	CITATIONS
1	Biopython: freely available Python tools for computational molecular biology and bioinformatics. <i>Bioinformatics</i> , 2009, 25, 1422-1423.	1.8	4,097
2	Tissue-specific analysis of chromatin state identifies temporal signatures of enhancer activity during embryonic development. <i>Nature Genetics</i> , 2012, 44, 148-156.	9.4	453
3	Applying dynamic Bayesian networks to perturbed gene expression data. <i>BMC Bioinformatics</i> , 2006, 7, 249.	1.2	133
4	A specialized histone H1 variant is required for adaptive responses to complex abiotic stress and related DNA methylation in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2015, 169, pp.00493.2015.	2.3	101
5	BNFinder: exact and efficient method for learning Bayesian networks. <i>Bioinformatics</i> , 2009, 25, 286-287.	1.8	89
6	<i>Arabidopsis</i> SWI/SNF chromatin remodeling complex binds both promoters and terminators to regulate gene expression. <i>Nucleic Acids Research</i> , 2017, 45, gkw1273.	6.5	58
7	Challenges for modeling global gene regulatory networks during development: Insights from <i>Drosophila</i> . <i>Developmental Biology</i> , 2010, 340, 161-169.	0.9	57
8	Endothelial cell differentiation is encompassed by changes in long range interactions between inactive chromatin regions. <i>Nucleic Acids Research</i> , 2018, 46, 1724-1740.	6.5	48
9	Dynamic CRM occupancy reflects a temporal map of developmental progression. <i>Molecular Systems Biology</i> , 2010, 6, 383.	3.2	44
10	Discovering regulatory binding-site modules using rule-based learning. <i>Genome Research</i> , 2005, 15, 856-866.	2.4	41
11	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.	1.5	38
12	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. <i>Development (Cambridge)</i> , 2014, 141, 2633-2643.	1.2	25
13	Finding evolutionarily conserved cis-regulatory modules with a universal set of motifs. <i>BMC Bioinformatics</i> , 2009, 10, 82.	1.2	24
14	BNFinder2: Faster Bayesian network learning and Bayesian classification. <i>Bioinformatics</i> , 2013, 29, 2068-2070.	1.8	24
15	Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. <i>Nature Communications</i> , 2021, 12, 3621.	5.8	22
16	Active enhancer positions can be accurately predicted from chromatin marks and collective sequence motif data. <i>BMC Systems Biology</i> , 2013, 7, S16.	3.0	15
17	Genome-Wide Analysis of <i>Drosophila</i> 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, 1503-1515.	0.8	15
18	Using local gene expression similarities to discover regulatory binding site modules. <i>BMC Bioinformatics</i> , 2006, 7, 505.	1.2	12

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19	Optimally choosing PWM motif databases and sequence scanning approaches based on ChIP-seq data. <i>BMC Bioinformatics</i> , 2015, 16, 140.	1.2	12
20	Potential protective role of Grainyhead-like genes in the development of clear cell renal cell carcinoma. <i>Molecular Carcinogenesis</i> , 2017, 56, 2414-2423.	1.3	11
21	Coordinated expression and genetic polymorphisms in Grainyhead-like genes in human non-melanoma skin cancers. <i>BMC Cancer</i> , 2018, 18, 23.	1.1	10
22	Supervised learning method for predicting chromatin boundary associated insulator elements. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1442006.	0.3	8
23	Taking promoters out of enhancers in sequence based predictions of tissue-specific mammalian enhancers. <i>BMC Medical Genomics</i> , 2017, 10, 34.	0.7	8
24	Distributed Bayesian networks reconstruction on the whole genome scale. <i>PeerJ</i> , 2018, 6, e5692.	0.9	8
25	BPscore: An Effective Metric for Meaningful Comparisons of Structural Chromosome Segmentations. <i>Journal of Computational Biology</i> , 2019, 26, 305-314.	0.8	6
26	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.	1.5	6
27	MEMOFinder: combining de novo motif prediction methods with a database of known motifs. <i>Nature Precedings</i> , 2008, , .	0.1	3
28	WeBIAS: a web server for publishing bioinformatics applications. <i>BMC Research Notes</i> , 2015, 8, 628.	0.6	3
29	FastBill: An Improved Tool for Prediction of Cis-Regulatory Modules. <i>Journal of Computational Biology</i> , 2017, 24, 193-199.	0.8	3
30	Regulatory Network Reconstruction Using Stochastic Logical Networks. <i>Lecture Notes in Computer Science</i> , 2006, , 142-154.	1.0	3
31	A Computer Scientist's Guide to the Regulatory Genome. <i>Fundamenta Informaticae</i> , 2010, 103, 323-332.	0.3	2
32	RECORD: Reference-Assisted Genome Assembly for Closely Related Genomes. <i>International Journal of Genomics</i> , 2015, 2015, 1-10.	0.8	2
33	Automated inference of gene regulatory networks using explicit regulatory modules. <i>Journal of Theoretical Biology</i> , 2020, 486, 110091.	0.8	2
34	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.	1.6	2
35	Reconstruction of Mammalian Cell Cycle Regulatory Network from Microarray Data Using Stochastic Logical Networks. <i>Lecture Notes in Computer Science</i> , 2007, , 121-135.	1.0	2
36	HiCEnterprise: identifying long range chromosomal contacts in Hi-C data. <i>PeerJ</i> , 2021, 9, e10558.	0.9	1

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37	Overweight Mice Show Coordinated Homeostatic and Hedonic Transcriptional Response across Brain. ENeuro, 2018, 5, ENEURO.0287-18.2018.	0.9	1
38	QChromosomeVisualizer: A new tool for 3D visualization of long simulations of polymer-like chromosome models. Methods, 2020, 181-182, 80-85.	1.9	0
39	Machine learning and deep learning for the advancement of epigenomics. , 2020, , 217-237.		0
40	HERON: A Novel Tool Enables Identification of Long, Weakly Enriched Genomic Domains in ChIP-seq Data. International Journal of Molecular Sciences, 2021, 22, 8123.	1.8	0
41	K-mer Content Changes with Node Degree in Promoter-Enhancer Network of Mouse ES Cells. International Journal of Molecular Sciences, 2021, 22, 8067.	1.8	0
42	A stochastic extension of R. Thomas regulatory network modelling. , 0, , .		0
43	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. Journal of Cell Science, 2014, 127, e1-e1.	1.2	0