

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	HiCEnterprise: identifying long range chromosomal contacts in Hi-C data. PeerJ, 2021, 9, e10558.	0.9	1
2	Mapping chromatin accessibility and active regulatory elements reveals pathological mechanisms in human gliomas. Nature Communications, 2021, 12, 3621.	5.8	22
3	Careful feature selection is key in classification of Alzheimer's disease patients based on whole-genome sequencing data. NAR Genomics and Bioinformatics, 2021, 3, lqab069.	1.5	6
4	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
5	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
6	The role of epigenetic modifications, long-range contacts, enhancers and topologically associating domains in the regulation of glioma grade-specific genes. Scientific Reports, 2021, 11, 15668.	1.6	2
7	QChromosomeVisualizer: A new tool for 3D visualization of long simulations of polymer-like chromosome models. Methods, 2020, 181-182, 80-85.	1.9	0
8	Automated inference of gene regulatory networks using explicit regulatory modules. Journal of Theoretical Biology, 2020, 486, 110091.	0.8	2
9	Machine learning and deep learning for the advancement of epigenomics. , 2020, , 217-237.		0
10	BPscore: An Effective Metric for Meaningful Comparisons of Structural Chromosome Segmentations. Journal of Computational Biology, 2019, 26, 305-314.	0.8	6
11	Endothelial cell differentiation is encompassed by changes in long range interactions between inactive chromatin regions. Nucleic Acids Research, 2018, 46, 1724-1740.	6.5	48
12	Coordinated expression and genetic polymorphisms in Grainyhead-like genes in human non-melanoma skin cancers. BMC Cancer, 2018, 18, 23.	1.1	10
13	Distributed Bayesian networks reconstruction on the whole genome scale. PeerJ, 2018, 6, e5692.	0.9	8
14	Overweight Mice Show Coordinated Homeostatic and Hedonic Transcriptional Response across Brain. ENeuro, 2018, 5, ENEURO.0287-18.2018.	0.9	1
15	Arabidopsis SWI/SNF chromatin remodeling complex binds both promoters and terminators to regulate gene expression. Nucleic Acids Research, 2017, 45, gkw1273.	6.5	58
16	Potential protective role of Grainyhead-like genes in the development of clear cell renal cell carcinoma. Molecular Carcinogenesis, 2017, 56, 2414-2423.	1.3	11
17	Taking promoters out of enhancers in sequence based predictions of tissue-specific mammalian enhancers. BMC Medical Genomics, 2017, 10, 34.	0.7	8
18	FastBill: An Improved Tool for Prediction of Cis-Regulatory Modules. Journal of Computational Biology, 2017, 24, 193-199.	0.8	3

#	ARTICLE	IF	CITATIONS
19	WeBIAS: a web server for publishing bioinformatics applications. BMC Research Notes, 2015, 8, 628.	0.6	3
20	RECORD: Reference-Assisted Genome Assembly for Closely Related Genomes. International Journal of Genomics, 2015, 2015, 1-10.	0.8	2
21	Genome-Wide Analysis of <i>Drosophila</i> Rb2 Protein Highlights the Diversity of RB Family Targets and Possible Role in Regulation of Ribosome Biosynthesis. G3: Genes, Genomes, Genetics, 2015, 5, 1503-1515.	0.8	15
22	A specialized histone H1 variant is required for adaptive responses to complex abiotic stress and related DNA methylation in Arabidopsis. Plant Physiology, 2015, 169, pp.00493.2015.	2.3	101
23	Optimally choosing PWM motif databases and sequence scanning approaches based on ChIP-seq data. BMC Bioinformatics, 2015, 16, 140.	1.2	12
24	Supervised learning method for predicting chromatin boundary associated insulator elements. Journal of Bioinformatics and Computational Biology, 2014, 12, 1442006.	0.3	8
25	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. Development (Cambridge), 2014, 141, 2633-2643.	1.2	25
26	Coordinated repression and activation of two transcriptional programs stabilizes cell fate during myogenesis. Journal of Cell Science, 2014, 127, e1-e1.	1.2	0
27	Active enhancer positions can be accurately predicted from chromatin marks and collective sequence motif data. BMC Systems Biology, 2013, 7, S16.	3.0	15
28	BNFinder2: Faster Bayesian network learning and Bayesian classification. Bioinformatics, 2013, 29, 2068-2070.	1.8	24
29	Predicting Spatial and Temporal Gene Expression Using an Integrative Model of Transcription Factor Occupancy and Chromatin State. PLoS Computational Biology, 2012, 8, e1002798.	1.5	38
30	Tissue-specific analysis of chromatin state identifies temporal signatures of enhancer activity during embryonic development. Nature Genetics, 2012, 44, 148-156.	9.4	453
31	Dynamic CRM occupancy reflects a temporal map of developmental progression. Molecular Systems Biology, 2010, 6, 383.	3.2	44
32	A Computer Scientist's Guide to the Regulatory Genome. Fundamenta Informaticae, 2010, 103, 323-332.	0.3	2
33	Challenges for modeling global gene regulatory networks during development: Insights from <i>Drosophila</i> . Developmental Biology, 2010, 340, 161-169.	0.9	57
34	Finding evolutionarily conserved cis-regulatory modules with a universal set of motifs. BMC Bioinformatics, 2009, 10, 82.	1.2	24
35	Biopython: freely available Python tools for computational molecular biology and bioinformatics. Bioinformatics, 2009, 25, 1422-1423.	1.8	4,097
36	BNFinder: exact and efficient method for learning Bayesian networks. Bioinformatics, 2009, 25, 286-287.	1.8	89

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37	MEMOFinder: combining de novo motif prediction methods with a database of known motifs. Nature Precedings, 2008, , .	0.1	3
38	Reconstruction of Mammalian Cell Cycle Regulatory Network from Microarray Data Using Stochastic Logical Networks. Lecture Notes in Computer Science, 2007, , 121-135.	1.0	2
39	Applying dynamic Bayesian networks to perturbed gene expression data. BMC Bioinformatics, 2006, 7, 249.	1.2	133
40	Using local gene expression similarities to discover regulatory binding site modules. BMC Bioinformatics, 2006, 7, 505.	1.2	12
41	Regulatory Network Reconstruction Using Stochastic Logical Networks. Lecture Notes in Computer Science, 2006, , 142-154.	1.0	3
42	Discovering regulatory binding-site modules using rule-based learning. Genome Research, 2005, 15, 856-866.	2.4	41
43	A stochastic extension of R. Thomas regulatory network modelling. , 0, , .		0