

Mathieu Blanchette

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

4,677
citations

201674

27
h-index

168389

53
g-index

58
all docs

58
docs citations

58
times ranked

7705
citing authors

#	ARTICLE	IF	CITATIONS
1	PhyloPGM: boosting regulatory function prediction accuracy using evolutionary information. <i>Bioinformatics</i> , 2022, 38, i299-i306.	4.1	1
2	Reconstruction of full-length LINE-1 progenitors from ancestral genomes. <i>Genetics</i> , 2022, 221, .	2.9	6
3	ETS1, ELK1, and ETV4 Transcription Factors Regulate Angiotensin-1 Signaling and the Angiogenic Response in Endothelial Cells. <i>Frontiers in Physiology</i> , 2021, 12, 683651.	2.8	9
4	Profiling Chromatin Landscape at High Resolution and Throughput with 2C-ChIP. <i>Methods in Molecular Biology</i> , 2021, 2157, 127-157.	0.9	0
5	oRNAmont: a database of putative RNA binding protein target sites in the transcriptomes of model species. <i>Nucleic Acids Research</i> , 2020, 48, D166-D173.	14.5	52
6	Mycorrhiza: genotype assignment using phylogenetic networks. <i>Bioinformatics</i> , 2020, 36, 212-220.	4.1	4
7	Upstream ORF-Encoded ASDURF Is a Novel Prefoldin-like Subunit of the PAQosome. <i>Journal of Proteome Research</i> , 2020, 19, 18-27.	3.7	37
8	EvoLSTM: context-dependent models of sequence evolution using a sequence-to-sequence LSTM. <i>Bioinformatics</i> , 2020, 36, i353-i361.	4.1	4
9	Graph neural representational learning of RNA secondary structures for predicting RNA-protein interactions. <i>Bioinformatics</i> , 2020, 36, i276-i284.	4.1	36
10	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. <i>Cell</i> , 2020, 183, 1617-1633.e22.	28.9	93
11	LAMPS: an analysis pipeline for sequence-specific ligation-mediated amplification reads. <i>BMC Research Notes</i> , 2020, 13, 273.	1.4	3
12	Inter-dependent Centrosomal Co-localization of the cen and ik2 cis-Natural Antisense mRNAs in <i>Drosophila</i> . <i>Cell Reports</i> , 2020, 30, 3339-3352.e6.	6.4	27
13	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , 2020, 11, 1018.	12.8	98
14	HIFI: estimating DNA-DNA interaction frequency from Hi-C data at restriction-fragment resolution. <i>Genome Biology</i> , 2020, 21, 11.	8.8	24
15	Supervised learning on phylogenetically distributed data. <i>Bioinformatics</i> , 2020, 36, i895-i902.	4.1	2
16	Prediction of mRNA subcellular localization using deep recurrent neural networks. <i>Bioinformatics</i> , 2019, 35, i333-i342.	4.1	53
17	Large-scale mammalian genome rearrangements coincide with chromatin interactions. <i>Bioinformatics</i> , 2019, 35, i117-i126.	4.1	4
18	Rapid Genetic Code Evolution in Green Algal Mitochondrial Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 766-783.	8.9	22

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19	2C-ChIP: measuring chromatin immunoprecipitation signal from defined genomic regions with deep sequencing. <i>BMC Genomics</i> , 2019, 20, 162.	2.8	4
20	Bioinformatics Approaches to Gain Insights into cis-Regulatory Motifs Involved in mRNA Localization. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1203, 165-194.	1.6	2
21	An analytic approach for interpretable predictive models in high-dimensional data in the presence of interactions with exposures. <i>Genetic Epidemiology</i> , 2018, 42, 233-249.	1.3	8
22	CeFra-seq reveals broad asymmetric mRNA and noncoding RNA distribution profiles in <i>Drosophila</i> and human cells. <i>Rna</i> , 2018, 24, 98-113.	3.5	75
23	[Regular Paper] Detection of Errors in Multi-genome Alignments Using Machine Learning Approaches. , 2018, , .		0
24	RLALIGN: A Reinforcement Learning Approach for Multiple Sequence Alignment. , 2018, , .		5
25	Double-Stranded Biotinylated Donor Enhances Homology-Directed Repair in Combination with Cas9 Monoavidin in Mammalian Cells. <i>CRISPR Journal</i> , 2018, 1, 414-430.	2.9	12
26	A critical assessment of topologically associating domain prediction tools. <i>Nucleic Acids Research</i> , 2017, 45, 2994-3005.	14.5	121
27	CoreTracker: accurate codon reassignment prediction, applied to mitochondrial genomes. <i>Bioinformatics</i> , 2017, 33, 3331-3339.	4.1	12
28	Prediction of human miRNA target genes using computationally reconstructed ancestral mammalian sequences. <i>Nucleic Acids Research</i> , 2017, 45, 556-566.	14.5	34
29	Functional 5' UTR motif discovery with LESMoN: Local Enrichment of Sequence Motifs in biological Networks. <i>Nucleic Acids Research</i> , 2017, 45, 10415-10427.	14.5	9
30	Models and algorithms for genome rearrangement with positional constraints. <i>Algorithms for Molecular Biology</i> , 2016, 11, 13.	1.2	9
31	Phylogenetic and Genomic Analyses Resolve the Origin of Important Plant Genes Derived from Transposable Elements. <i>Molecular Biology and Evolution</i> , 2016, 33, 1937-1956.	8.9	26
32	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. <i>Genome Biology</i> , 2015, 16, 290.	8.8	90
33	A low-latency, big database system and browser for storage, querying and visualization of 3D genomic data. <i>Nucleic Acids Research</i> , 2015, 43, e103-e103.	14.5	8
34	PAM multiplicity marks genomic target sites as inhibitory to CRISPR-Cas9 editing. <i>Nature Communications</i> , 2015, 6, 10124.	12.8	52
35	A call for benchmarking transposable element annotation methods. <i>Mobile DNA</i> , 2015, 6, 13.	3.6	83
36	Specific Dysregulation of IFN β Production by Natural Killer Cells Confers Susceptibility to Viral Infection. <i>PLoS Pathogens</i> , 2014, 10, e1004511.	4.7	13

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37	Evidence for Widespread Positive and Negative Selection in Coding and Conserved Noncoding Regions of <i>Capsella grandiflora</i> . <i>PLoS Genetics</i> , 2014, 10, e1004622.	3.5	128
38	Methylation of the DNA/RNA-binding protein Kin17 by METTL22 affects its association with chromatin. <i>Journal of Proteomics</i> , 2014, 100, 115-124.	2.4	36
39	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. <i>Nature Genetics</i> , 2013, 45, 891-898.	21.4	350
40	Exploiting ancestral mammalian genomes for the prediction of human transcription factor binding sites. <i>BMC Bioinformatics</i> , 2012, 13, S2.	2.6	1
41	A Probabilistic Model for Sequence Alignment with Context-Sensitive Indels. <i>Journal of Computational Biology</i> , 2011, 18, 1449-1464.	1.6	10
42	Ancestors 1.0: a web server for ancestral sequence reconstruction. <i>Bioinformatics</i> , 2010, 26, 130-131.	4.1	38
43	Detection of Locally Over-Represented GO Terms in Protein-Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2010, 17, 443-457.	1.6	12
44	Chromatin conformation signatures of cellular differentiation. <i>Genome Biology</i> , 2009, 10, R37.	9.6	108
45	Computation and Analysis of Genomic Multi-Sequence Alignments. <i>Annual Review of Genomics and Human Genetics</i> , 2007, 8, 193-213.	6.2	30
46	Systematic Analysis of the Protein Interaction Network for the Human Transcription Machinery Reveals the Identity of the 7SK Capping Enzyme. <i>Molecular Cell</i> , 2007, 27, 262-274.	9.7	404
47	Exact and Heuristic Algorithms for the Indel Maximum Likelihood Problem. <i>Journal of Computational Biology</i> , 2007, 14, 446-461.	1.6	33
48	Reconstructing contiguous regions of an ancestral genome. <i>Genome Research</i> , 2006, 16, 1557-1565.	5.5	246
49	Genome-wide computational prediction of transcriptional regulatory modules reveals new insights into human gene expression. <i>Genome Research</i> , 2006, 16, 656-668.	5.5	229
50	Reconstructing large regions of an ancestral mammalian genome in silico. <i>Genome Research</i> , 2004, 14, 2412-2423.	5.5	121
51	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. <i>Genome Research</i> , 2004, 14, 708-715.	5.5	1,290
52	Algorithms for Phylogenetic Footprinting. <i>Journal of Computational Biology</i> , 2002, 9, 211-223.	1.6	138
53	Discovery of Regulatory Elements by a Computational Method for Phylogenetic Footprinting. <i>Genome Research</i> , 2002, 12, 739-748.	5.5	268
54	Phylogenetic Invariants for Genome Rearrangements. <i>Journal of Computational Biology</i> , 1999, 6, 431-445.	1.6	31

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55	Gene Order Breakpoint Evidence in Animal Mitochondrial Phylogeny. <i>Journal of Molecular Evolution</i> , 1999, 49, 193-203.	1.8	159