Mathieu Blanchette

List of Publications by Year
in descending order

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	Aligning Multiple Genomic Sequences With the Threaded Blockset Aligner. Genome Research, 2004, 14, 708-715.	5.5	1,290
2	Systematic Analysis of the Protein Interaction Network for the Human Transcription Machinery Reveals the Identity of the 7SK Capping Enzyme. Molecular Cell, 2007, 27, 262-274.	9.7	404
3	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. Nature Genetics, 2013, 45, 891-898.	21.4	350
4	Discovery of Regulatory Elements by a Computational Method for Phylogenetic Footprinting. Genome Research, 2002, 12, 739-748.	5.5	268
5	Reconstructing contiguous regions of an ancestral genome. Genome Research, 2006, 16, 1557-1565.	5.5	246
6	Genome-wide computational prediction of transcriptional regulatory modules reveals new insights into human gene expression. Genome Research, 2006, 16, 656-668.	5.5	229
7	Gene Order Breakpoint Evidence in Animal Mitochondrial Phylogeny. Journal of Molecular Evolution, 1999, 49, 193-203.	1.8	159
8	Algorithms for Phylogenetic Footprinting. Journal of Computational Biology, 2002, 9, 211-223.	1.6	138
9	Evidence for Widespread Positive and Negative Selection in Coding and Conserved Noncoding Regions of Capsella grandiflora. PLoS Genetics, 2014, 10, e1004622.	3.5	128
10	Reconstructing large regions of an ancestral mammalian genome in silico. Genome Research, 2004, 14, 2412-2423.	5.5	121
11	A critical assessment of topologically associating domain prediction tools. Nucleic Acids Research, 2017, 45, 2994-3005.	14.5	121
12	Chromatin conformation signatures of cellular differentiation. Genome Biology, 2009, 10, R37.	9.6	108
13	RADICL-seq identifies general and cell typeâ€“specific principles of genome-wide RNA-chromatin interactions. Nature Communications, 2020, 11, 1018.	12.8	98
14	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. Cell, 2020, 183, 1617-1633.e22.	28.9	93
15	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. Genome Biology, 2015, 16, 290.	8.8	90
16	A call for benchmarking transposable element annotation methods. Mobile DNA, 2015, 6, 13.	3.6	83
17	CeFra-seq reveals broad asymmetric mRNA and noncoding RNA distribution profiles in Drosophila and human cells. Rna, 2018, 24, 98-113.	3.5	75
18	Prediction of mRNA subcellular localization using deep recurrent neural networks. Bioinformatics, 2019, 35, i333-i342.	4.1	53

#	Article	IF	Citations
19	PAM multiplicity marks genomic target sites as inhibitory to CRISPR-Cas9 editing. Nature Communications, 2015, 6, 10124.	12.8	52
20	oRNAment: a database of putative RNA binding protein target sites in the transcriptomes of model species. Nucleic Acids Research, 2020, 48, D166-D173.	14.5	52
21	Ancestors 1.0: a web server for ancestral sequence reconstruction. Bioinformatics, 2010, 26, 130-131.	4.1	38
22	Upstream ORF-Encoded ASDURF Is a Novel Prefoldin-like Subunit of the PAQosome. Journal of Proteome Research, 2020, 19, 18-27.	3.7	37
23	Methylation of the DNA/RNA-binding protein Kin17 by METTL22 affects its association with chromatin. Journal of Proteomics, 2014, 100, 115-124.	2.4	36
24	Graph neural representational learning of RNA secondary structures for predicting RNA-protein interactions. Bioinformatics, 2020, 36, i276-i284.	4.1	36
25	Prediction of human miRNA target genes using computationally reconstructed ancestral mammalian sequences. Nucleic Acids Research, 2017, 45, 556-566.	14.5	34
26	Exact and Heuristic Algorithms for the Indel Maximum Likelihood Problem. Journal of Computational Biology, 2007, 14, 446-461.	1.6	33
27	Phylogenetic Invariants for Genome Rearrangements. Journal of Computational Biology, 1999, 6, 431-445.	1.6	31
28	Computation and Analysis of Genomic Multi-Sequence Alignments. Annual Review of Genomics and Human Genetics, 2007, 8, 193-213.	6.2	30
29	Inter-dependent Centrosomal Co-localization of the cen and ik2 cis-Natural Antisense mRNAs in Drosophila. Cell Reports, 2020, 30, 3339-3352.e6.	6.4	27
30	Phylogenetic and Genomic Analyses Resolve the Origin of Important Plant Genes Derived from Transposable Elements. Molecular Biology and Evolution, 2016, 33, 1937-1956.	8.9	26
31	HIFI: estimating DNA-DNA interaction frequency from Hi-C data at restriction-fragment resolution. Genome Biology, 2020, 21, 11.	8.8	24
32	Rapid Genetic Code Evolution in Green Algal Mitochondrial Genomes. Molecular Biology and Evolution, 2019, 36, 766-783.	8.9	22
33	Specific Dysregulation of IFNÎ³ Production by Natural Killer Cells Confers Susceptibility to Viral Infection. PLoS Pathogens, 2014, 10, e1004511.	4.7	13
34	Detection of Locally Over-Represented GO Terms in Protein-Protein Interaction Networks. Journal of Computational Biology, 2010, 17, 443-457.	1.6	12
35	CoreTracker: accurate codon reassignment prediction, applied to mitochondrial genomes. Bioinformatics, 2017, 33, 3331-3339.	4.1	12
36	Double-Stranded Biotinylated Donor Enhances Homology-Directed Repair in Combination with Cas9 Monoavidin in Mammalian Cells. CRISPR Journal, 2018, 1, 414-430.	2.9	12

#	Article	IF	Citations
37	A Probabilistic Model for Sequence Alignment with Context-Sensitive Indels. Journal of Computational Biology, 2011, 18, 1449-1464.	1.6	10
38	Models and algorithms for genome rearrangement with positional constraints. Algorithms for Molecular Biology, 2016, 11, 13.	1.2	9
39	Functional 5â€² UTR motif discovery with LESMoN: Local Enrichment of Sequence Motifs in biological Networks. Nucleic Acids Research, 2017, 45, 10415-10427.	14.5	9
40	ETS1, ELK1, and ETV4 Transcription Factors Regulate Angiopoietin-1 Signaling and the Angiogenic Response in Endothelial Cells. Frontiers in Physiology, 2021, 12, 683651.	2.8	9
41	A low-latency, big database system and browser for storage, querying and visualization of 3D genomic data. Nucleic Acids Research, 2015, 43, e103-e103.	14.5	8
42	An analytic approach for interpretable predictive models in highâ€dimensional data in the presence of interactions with exposures. Genetic Epidemiology, 2018, 42, 233-249.	1.3	8
43	Reconstruction of full-length LINE-1 progenitors from ancestral genomes. Genetics, 2022, 221, .	2.9	6
44	RLALIGN: A Reinforcement Learning Approach for Multiple Sequence Alignment. , 2018, , .		5
45	Large-scale mammalian genome rearrangements coincide with chromatin interactions. Bioinformatics, 2019, 35, i117-i126.	4.1	4
46	2C-ChIP: measuring chromatin immunoprecipitation signal from defined genomic regions with deep sequencing. BMC Genomics, 2019, 20, 162.	2.8	4
47	Mycorrhiza: genotype assignment using phylogenetic networks. Bioinformatics, 2020, 36, 212-220.	4.1	4
48	EvoLSTM: context-dependent models of sequence evolution using a sequence-to-sequence LSTM. Bioinformatics, 2020, 36, i353-i361.	4.1	4
49	LAMPS: an analysis pipeline for sequence-specific ligation-mediated amplification reads. BMC Research Notes, 2020, 13, 273.	1.4	3
50	Bioinformatics Approaches to Gain Insights into cis-Regulatory Motifs Involved in mRNA Localization. Advances in Experimental Medicine and Biology, 2019, 1203, 165-194.	1.6	2
51	Supervised learning on phylogenetically distributed data. Bioinformatics, 2020, 36, i895-i902.	4.1	2
52	Exploiting ancestral mammalian genomes for the prediction of human transcription factor binding sites. BMC Bioinformatics, 2012, 13, S2.	2.6	1
53	PhyloPGM: boosting regulatory function prediction accuracy using evolutionary information. Bioinformatics, 2022, 38, i299-i306.	4.1	1
54	[Regular Paper] Detection of Errors in Multi-genome Alignments Using Machine Learning Approaches. , 2018, , .		0

#	Article	IF	Citations
55	Profiling Chromatin Landscape at High Resolution and Throughput with 2C-ChIP. Methods in Molecular Biology, 2021, 2157, 127-157.	0.9	0