

Ian Holmes

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

45
papers

8,707
citations

24
h-index

53
g-index

53
ext. papers

10,072
ext. citations

8.7
avg, IF

5.28
L-index

#	Paper	IF	Citations
45	CNVpytor: a tool for copy number variation detection and analysis from read depth and allele imbalance in whole-genome sequencing. <i>GigaScience</i> , 2021 , 10,	7.6	6
44	JBrowseR: An R Interface to the JBrowse 2 Genome Browser. <i>Bioinformatics</i> , 2021 ,	7.2	2
43	Machine Boss: rapid prototyping of bioinformatic automata. <i>Bioinformatics</i> , 2021 , 37, 29-35	7.2	1
42	Pair consensus decoding improves accuracy of neural network basecallers for nanopore sequencing. <i>Genome Biology</i> , 2021 , 22, 38	18.3	12
41	A Model of Indel Evolution by Finite-State, Continuous-Time Machines. <i>Genetics</i> , 2020 , 216, 1187-1204	4	0
40	JBrowse Connect: A server API to connect JBrowse instances and users. <i>PLoS Computational Biology</i> , 2020 , 16, e1007261	5	1
39	Cram-JS: reference-based decompression in node and the browser. <i>Bioinformatics</i> , 2019 , 35, 4451-4452	7.2	1
38	Consensus Decoding of Recurrent Neural Network Basecallers. <i>Lecture Notes in Computer Science</i> , 2018 , 128-139	0.9	1
37	Linking Statistical and Ecological Theory: Hubbell's Unified Neutral Theory of Biodiversity as a Hierarchical Dirichlet Process. <i>Proceedings of the IEEE</i> , 2017 , 105, 516-529	14.3	36
36	JBrowse: a dynamic web platform for genome visualization and analysis. <i>Genome Biology</i> , 2016 , 17, 66	18.3	393
35	Estimating empirical codon hidden Markov models. <i>Molecular Biology and Evolution</i> , 2013 , 30, 725-36	8.3	43
34	Visualizing next-generation sequencing data with JBrowse. <i>Briefings in Bioinformatics</i> , 2013 , 14, 172-7	13.4	57
33	Fitting Birth-Death Processes to Panel Data with Applications to Bacterial DNA Fingerprinting. <i>Annals of Applied Statistics</i> , 2013 , 7, 2315-2335	2.1	9
32	Developing and applying heterogeneous phylogenetic models with XRate. <i>PLoS ONE</i> , 2012 , 7, e36898	3.7	3
31	Evaluating bacterial gene-finding HMM structures as probabilistic logic programs. <i>Bioinformatics</i> , 2012 , 28, 636-42	7.2	10
30	HandAlign: Bayesian multiple sequence alignment, phylogeny and ancestral reconstruction. <i>Bioinformatics</i> , 2012 , 28, 1170-1	7.2	12
29	Dirichlet multinomial mixtures: generative models for microbial metagenomics. <i>PLoS ONE</i> , 2012 , 7, e30136	13.6	385

28	Accurate reconstruction of insertion-deletion histories by statistical phylogenetics. <i>PLoS ONE</i> , 2012 , 7, e34572	3.7	23
27	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011 , 17, 1941-6	5.8	54
26	Evolutionary modeling and prediction of non-coding RNAs in Drosophila. <i>PLoS ONE</i> , 2009 , 4, e6478	3.7	10
25	Accurate estimation of gene evolutionary rates using XRATE, with an application to transmembrane proteins. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1715-21	8.3	7
24	Accurate detection of recombinant breakpoints in whole-genome alignments. <i>PLoS Computational Biology</i> , 2009 , 5, e1000318	5	25
23	Fast statistical alignment. <i>PLoS Computational Biology</i> , 2009 , 5, e1000392	5	252
22	Evolutionary triplet models of structured RNA. <i>PLoS Computational Biology</i> , 2009 , 5, e1000483	5	4
21	JBrowse: a next-generation genome browser. <i>Genome Research</i> , 2009 , 19, 1630-8	9.7	550
20	xREI: a phylo-grammar visualization webserver. <i>Nucleic Acids Research</i> , 2008 , 36, W65-9	20.1	2
19	Specific alignment of structured RNA: stochastic grammars and sequence annealing. <i>Bioinformatics</i> , 2008 , 24, 2677-83	7.2	31
18	Genome-wide nucleotide-level mammalian ancestor reconstruction. <i>Genome Research</i> , 2008 , 18, 1829-43	9.7	136
17	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007 , 17, 760-74	9.7	163
16	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
15	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
14	An empirical codon model for protein sequence evolution. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1464-79	8.3	139
13	Transducers: an emerging probabilistic framework for modeling indels on trees. <i>Bioinformatics</i> , 2007 , 23, 3258-62	7.2	29
12	Phylocomposer and phylodirector: analysis and visualization of transducer indel models. <i>Bioinformatics</i> , 2007 , 23, 3263-4	7.2	6
11	XRate: a fast prototyping, training and annotation tool for phylo-grammars. <i>BMC Bioinformatics</i> , 2006 , 7, 428	3.6	40

10	Accelerated probabilistic inference of RNA structure evolution. <i>BMC Bioinformatics</i> , 2005 , 6, 73	3.6	95
9	Using evolutionary Expectation Maximization to estimate indel rates. <i>Bioinformatics</i> , 2005 , 21, 2294-3007.2		30
8	A probabilistic model for the evolution of RNA structure. <i>BMC Bioinformatics</i> , 2004 , 5, 166	3.6	38
7	A "Long Indel" model for evolutionary sequence alignment. <i>Molecular Biology and Evolution</i> , 2004 , 21, 529-40	8.3	91
6	Transcendent elements: whole-genome transposon screens and open evolutionary questions. <i>Genome Research</i> , 2002 , 12, 1152-5	9.7	15
5	An expectation maximization algorithm for training hidden substitution models. <i>Journal of Molecular Biology</i> , 2002 , 317, 753-64	6.5	59
4	Evolutionary HMMs: a Bayesian approach to multiple alignment. <i>Bioinformatics</i> , 2001 , 17, 803-20	7.2	133
3	Dynamic programming alignment accuracy. <i>Journal of Computational Biology</i> , 1998 , 5, 493-504	1.7	84
2	Modular non-repeating codes for DNA storage		1
1	WTFgenes: What's The Function of these genes? Static sites for model-based gene set analysis. <i>F1000Research</i> , 6 , 423	3.6	