Ian Holmes

List of Publications by Year
in descending order

45 papers	10,788 citations	236925 25 h-index	243625 44 g-index
53 all docs	53 docs citations	53 times ranked	18098 citing authors

#	Article	IF	Citations
1	GrainGenes: a data-rich repository for small grains genetics and genomics. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	22
2	Machine Boss: rapid prototyping of bioinformatic automata. Bioinformatics, 2021, 37, 29-35.	4.1	1
3	Pair consensus decoding improves accuracy of neural network basecallers for nanopore sequencing. Genome Biology, 2021, 22, 38.	8.8	37
4	JBrowseR: an R interface to the JBrowse 2 genome browser. Bioinformatics, 2021, 37, 3914-3915.	4.1	14
5	CNVpytor: a tool for copy number variation detection and analysis from read depth and allele imbalance in whole-genome sequencing. GigaScience, 2021, 10, .	6.4	38
6	JBrowse Connect: A server API to connect JBrowse instances and users. PLoS Computational Biology, 2020, 16, e1007261.	3.2	1
7	A Model of Indel Evolution by Finite-State, Continuous-Time Machines. Genetics, 2020, 216, 1187-1204.	2.9	7
8	Cram-JS: reference-based decompression in node and the browser. Bioinformatics, 2019, 35, 4451-4452.	4.1	3
9	Linking Statistical and Ecological Theory: Hubbell's Unified Neutral Theory of Biodiversity as a Hierarchical Dirichlet Process. Proceedings of the IEEE, 2017, 105, 516-529.	21.3	55
10	Solving the master equation for Indels. BMC Bioinformatics, 2017, 18, 255.	2.6	17
11	JBrowse: a dynamic web platform for genome visualization and analysis. Genome Biology, 2016, 17, 66.	8.8	690
12	Estimating Empirical Codon Hidden Markov Models. Molecular Biology and Evolution, 2013, 30, 725-736.	8.9	51
13	Visualizing next-generation sequencing data with JBrowse. Briefings in Bioinformatics, 2013, 14, 172-177.	6.5	62
14	Fitting birth–death processes to panel data with applications to bacterial DNA fingerprinting. Annals of Applied Statistics, 2013, 7, 2315-2335.	1.1	11
15	Evaluating bacterial gene-finding HMM structures as probabilistic logic programs. Bioinformatics, 2012, 28, 636-642.	4.1	13
16	HandAlign: Bayesian multiple sequence alignment, phylogeny and ancestral reconstruction. Bioinformatics, 2012, 28, 1170-1171.	4.1	18
17	Developing and Applying Heterogeneous Phylogenetic Models with XRate. PLoS ONE, 2012, 7, e36898.	2.5	5
18	Dirichlet Multinomial Mixtures: Generative Models for Microbial Metagenomics. PLoS ONE, 2012, 7, e30126.	2.5	653

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19	Accurate Reconstruction of Insertion-Deletion Histories by Statistical Phylogenetics. PLoS ONE, 2012, 7, e34572.	2.5	28
20	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	3.5	67
21	Evolutionary Modeling and Prediction of Non-Coding RNAs in Drosophila. PLoS ONE, 2009, 4, e6478.	2.5	13
22	Accurate Estimation of Gene Evolutionary Rates Using XRATE, with an Application to Transmembrane Proteins. Molecular Biology and Evolution, 2009, 26, 1715-1721.	8.9	9
23	Accurate Detection of Recombinant Breakpoints in Whole-Genome Alignments. PLoS Computational Biology, 2009, 5, e1000318.	3.2	31
24	Fast Statistical Alignment. PLoS Computational Biology, 2009, 5, e1000392.	3.2	302
25	Evolutionary Triplet Models of Structured RNA. PLoS Computational Biology, 2009, 5, e1000483.	3.2	6
26	JBrowse: A next-generation genome browser. Genome Research, 2009, 19, 1630-1638.	5.5	724
27	xREI: a phylo-grammar visualization webserver. Nucleic Acids Research, 2008, 36, W65-W69.	14.5	3
28	Specific alignment of structured RNA: stochastic grammars and sequence annealing. Bioinformatics, 2008, 24, 2677-2683.	4.1	35
29	Genome-wide nucleotide-level mammalian ancestor reconstruction. Genome Research, 2008, 18, 1829-1843.	5.5	164
30	Transducers: an emerging probabilistic framework for modeling indels on trees. Bioinformatics, 2007, 23, 3258-3262.	4.1	33
31	Phylocomposer and phylodirector: analysis and visualization of transducer indel models. Bioinformatics, 2007, 23, 3263-3264.	4.1	6
32	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
33	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
34	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
35	An Empirical Codon Model for Protein Sequence Evolution. Molecular Biology and Evolution, 2007, 24, 1464-1479.	8.9	166
36	XRate: a fast prototyping, training and annotation tool for phylo-grammars. BMC Bioinformatics, 2006, 7, 428.	2.6	49

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37	Accelerated probabilistic inference of RNA structure evolution. BMC Bioinformatics, 2005, 6, 73.	2.6	105
38	Using evolutionary Expectation Maximization to estimate indel rates. Bioinformatics, 2005, 21, 2294-2300.	4.1	61
39	A probabilistic model for the evolution of RNA structure. BMC Bioinformatics, 2004, 5, 166.	2.6	43
40	A "Long Indel" Model For Evolutionary Sequence Alignment. Molecular Biology and Evolution, 2003, 21, 529-540.	8.9	106
41	Transcendent Elements: Whole-Genome Transposon Screens and Open Evolutionary Questions. Genome Research, 2002, 12, 1152-1155.	5.5	19
42	An expectation maximization algorithm for training hidden substitution models 1 1Edited by F. Cohen. Journal of Molecular Biology, 2002, 317, 753-764.	4.2	68
43	Evolutionary HMMs: a Bayesian approach to multiple alignment. Bioinformatics, 2001, 17, 803-820.	4.1	169
44	Dynamic Programming Alignment Accuracy. Journal of Computational Biology, 1998, 5, 493-504.	1.6	97
45	WTFgenes:ÂWhat's The Function of these genes? Static sites for model-based gene set analysis. F1000Research, 0, 6, 423.	1.6	0