Ian Holmes

List of Publications by Year
in descending order

45 papers	10,788 citations	236612 25 h-index	243296 44 g-index
53 all docs	53 docs citations	53 times ranked	18098 citing authors

#	Article	IF	Citations
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
2	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
3	JBrowse: A next-generation genome browser. Genome Research, 2009, 19, 1630-1638.	2.4	724
4	JBrowse: a dynamic web platform for genome visualization and analysis. Genome Biology, 2016, 17, 66.	3.8	690
5	Dirichlet Multinomial Mixtures: Generative Models for Microbial Metagenomics. PLoS ONE, 2012, 7, e30126.	1.1	653
6	Fast Statistical Alignment. PLoS Computational Biology, 2009, 5, e1000392.	1.5	302
7	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	2.4	184
8	Evolutionary HMMs: a Bayesian approach to multiple alignment. Bioinformatics, 2001, 17, 803-820.	1.8	169
9	An Empirical Codon Model for Protein Sequence Evolution. Molecular Biology and Evolution, 2007, 24, 1464-1479.	3.5	166
10	Genome-wide nucleotide-level mammalian ancestor reconstruction. Genome Research, 2008, 18, 1829-1843.	2.4	164
11	A "Long Indel" Model For Evolutionary Sequence Alignment. Molecular Biology and Evolution, 2003, 21, 529-540.	3.5	106
12	Accelerated probabilistic inference of RNA structure evolution. BMC Bioinformatics, 2005, 6, 73.	1.2	105
13	Dynamic Programming Alignment Accuracy. Journal of Computational Biology, 1998, 5, 493-504.	0.8	97
14	An expectation maximization algorithm for training hidden substitution models 1 1Edited by F. Cohen. Journal of Molecular Biology, 2002, 317, 753-764.	2.0	68
15	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	1.6	67
16	Visualizing next-generation sequencing data with JBrowse. Briefings in Bioinformatics, 2013, 14, 172-177.	3.2	62
17	Using evolutionary Expectation Maximization to estimate indel rates. Bioinformatics, 2005, 21, 2294-2300.	1.8	61
18	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.	16.4	55

#	ARTICLE	IF	CITATIONS
19	Estimating Empirical Codon Hidden Markov Models. Molecular Biology and Evolution, 2013, 30, 725-736.	3.5	51
20	XRate: a fast prototyping, training and annotation tool for phylo-grammars. BMC Bioinformatics, 2006, 7, 428.	1.2	49
21	A probabilistic model for the evolution of RNA structure. BMC Bioinformatics, 2004, 5, 166.	1.2	43
22	CNVpytor: a tool for copy number variation detection and analysis from read depth and allele imbalance in whole-genome sequencing. GigaScience, 2021, 10, .	3.3	38
23	Pair consensus decoding improves accuracy of neural network basecallers for nanopore sequencing. Genome Biology, 2021, 22, 38.	3.8	37
24	Specific alignment of structured RNA: stochastic grammars and sequence annealing. Bioinformatics, 2008, 24, 2677-2683.	1.8	35
25	Transducers: an emerging probabilistic framework for modeling indels on trees. Bioinformatics, 2007, 23, 3258-3262.	1.8	33
26	Accurate Detection of Recombinant Breakpoints in Whole-Genome Alignments. PLoS Computational Biology, 2009, 5, e1000318.	1.5	31
27	Accurate Reconstruction of Insertion-Deletion Histories by Statistical Phylogenetics. PLoS ONE, 2012, 7, e34572.	1.1	28
28	GrainGenes: a data-rich repository for small grains genetics and genomics. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	22
29	Transcendent Elements: Whole-Genome Transposon Screens and Open Evolutionary Questions. Genome Research, 2002, 12, 1152-1155.	2.4	19
30	HandAlign: Bayesian multiple sequence alignment, phylogeny and ancestral reconstruction. Bioinformatics, 2012, 28, 1170-1171.	1.8	18
31	Solving the master equation for Indels. BMC Bioinformatics, 2017, 18, 255.	1.2	17
32	JBrowseR: an R interface to the JBrowse 2 genome browser. Bioinformatics, 2021, 37, 3914-3915.	1.8	14
33	Evolutionary Modeling and Prediction of Non-Coding RNAs in Drosophila. PLoS ONE, 2009, 4, e6478.	1.1	13
34	Evaluating bacterial gene-finding HMM structures as probabilistic logic programs. Bioinformatics, 2012, 28, 636-642.	1.8	13
35	Fitting birthâ€"death processes to panel data with applications to bacterial DNA fingerprinting. Annals of Applied Statistics, 2013, 7, 2315-2335.	0.5	11
36	Accurate Estimation of Gene Evolutionary Rates Using XRATE, with an Application to Transmembrane Proteins. Molecular Biology and Evolution, 2009, 26, 1715-1721.	3.5	9

#	Article	IF	Citations
37	A Model of Indel Evolution by Finite-State, Continuous-Time Machines. Genetics, 2020, 216, 1187-1204.	1.2	7
38	Phylocomposer and phylodirector: analysis and visualization of transducer indel models. Bioinformatics, 2007, 23, 3263-3264.	1.8	6
39	Evolutionary Triplet Models of Structured RNA. PLoS Computational Biology, 2009, 5, e1000483.	1.5	6
40	Developing and Applying Heterogeneous Phylogenetic Models with XRate. PLoS ONE, 2012, 7, e36898.	1.1	5
41	xREI: a phylo-grammar visualization webserver. Nucleic Acids Research, 2008, 36, W65-W69.	6.5	3
42	Cram-JS: reference-based decompression in node and the browser. Bioinformatics, 2019, 35, 4451-4452.	1.8	3
43	JBrowse Connect: A server API to connect JBrowse instances and users. PLoS Computational Biology, 2020, 16, e1007261.	1.5	1
44	Machine Boss: rapid prototyping of bioinformatic automata. Bioinformatics, 2021, 37, 29-35.	1.8	1
45	WTFgenes:ÂWhat's The Function of these genes? Static sites for model-based gene set analysis. F1000Research, 0, 6, 423.	0.8	0