Michael G B Blum

List of Publications by Year
in descending order

57 papers	6,743 citations	136950 32 h-index	149698 56 g-index
72 all docs	72 docs citations	72 times ranked	10653 citing authors

#	ARTICLE	IF	CITATIONS
1	Integrating deep learning CT-scan model, biological and clinical variables to predict severity of COVID-19 patients. Nature Communications, 2021, 12, 634.	12.8	126
2	Efficient toolkit implementing best practices for principal component analysis of population genetic data. Bioinformatics, 2020, 36, 4449-4457.	4.1	76
3	Guidelines for cell-type heterogeneity quantification based on a comparative analysis of reference-free DNA methylation deconvolution software. BMC Bioinformatics, 2020, 21, 16.	2.6	34
4	Performing Highly Efficient Genome Scans for Local Adaptation with R Package pcadapt Version 4. Molecular Biology and Evolution, 2020, 37, 2153-2154.	8.9	133
5	Cold adaptation in the Asian tiger mosquito's native range precedes its invasion success in temperate regions. Evolution; International Journal of Organic Evolution, 2019, 73, 1793-1808.	2.3	28
6	Predicting the success of an invader: Niche shift versus niche conservatism. Ecology and Evolution, 2019, 9, 12658-12675.	1.9	20
7	Efficient Implementation of Penalized Regression for Genetic Risk Prediction. Genetics, 2019, 212, 65-74.	2.9	51
8	Unravelling the invasion history of the Asian tiger mosquito in Europe. Molecular Ecology, 2019, 28, 2360-2377.	3.9	82
9	Making the Most of Clumping and Thresholding for Polygenic Scores. American Journal of Human Genetics, 2019, 105, 1213-1221.	6.2	123
10	Efficient analysis of large-scale genome-wide data with two R packages: bigstatsr and bigsnpr. Bioinformatics, 2018, 34, 2781-2787.	4.1	217
11	Evaluation of redundancy analysis to identify signatures of local adaptation. Molecular Ecology Resources, 2018, 18, 1223-1233.	4.8	118
12	Loter: A Software Package to Infer Local Ancestry for a Wide Range of Species. Molecular Biology and Evolution, 2018, 35, 2318-2326.	8.9	70
13	Can secondary contact following range expansion be distinguished from barriers to gene flow?. PeerJ, 2018, 6, e5325.	2.0	8
14	Ultradeep sequencing of B and non-B HIV-1 subtypes: Viral diversity and drug resistance mutations before and after one month of antiretroviral therapy in naive patients. Journal of Clinical Virology, 2017, 95, 13-19.	3.1	4
15	*pcadapt*: an <scp>R</scp> package to perform genome scans for selection based on principal component analysis. Molecular Ecology Resources, 2017, 17, 67-77.	4.8	647
16	Hepatitis C virus whole genome sequencing: Current methods/issues and future challenges. Critical Reviews in Clinical Laboratory Sciences, 2016, 53, 341-351.	6.1	12
17	Identifying outlier loci in admixed and in continuous populations using ancestral population differentiation statistics. Molecular Ecology, 2016, 25, 5029-5042.	3.9	38
18	Individuality of breathing during volitional moderate hyperventilation. European Journal of Applied Physiology, 2016, 116, 217-225.	2.5	2

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19	Detecting Genomic Signatures of Natural Selection with Principal Component Analysis: Application to the 1000 Genomes Data. Molecular Biology and Evolution, 2016, 33, 1082-1093.	8.9	123
20	Reimagining Electronic Clinical Communication in the Post-Pager, Smartphone Era. JAMA - Journal of the American Medical Association, 2016, 315, 21.	7.4	16
21	Fine-scale human genetic structure in Western France. European Journal of Human Genetics, 2015, 23, 831-836.	2.8	31
22	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. Nature Genetics, 2015, 47, 242-249.	21.4	466
23	Ultradeep Pyrosequencing of NS3 To Predict Response to Triple Therapy with Protease Inhibitors in Previously Treated Chronic Hepatitis C Patients. Journal of Clinical Microbiology, 2015, 53, 389-397.	3.9	6
24	HaploPOP: a software that improves population assignment by combining markers into haplotypes. BMC Bioinformatics, 2015, 16, 242.	2.6	8
25	POPS: A Software for Prediction of Population Genetic Structure Using Latent Regression Models. Journal of Statistical Software, 2015, 68, .	3.7	11
26	Diagnostic tools for approximate Bayesian computation using the coverage property. Australian and New Zealand Journal of Statistics, 2014, 56, 309-329.	0.9	37
27	Genome Scans for Detecting Footprints of Local Adaptation Using a Bayesian Factor Model. Molecular Biology and Evolution, 2014, 31, 2483-2495.	8.9	94
28	NONSTATIONARY PATTERNS OF ISOLATIONâ€BYâ€DISTANCE: INFERRING MEASURES OF LOCAL GENETIC DIFFERENTIATION WITH BAYESIAN KRIGING. Evolution; International Journal of Organic Evolution, 2014, 68, 1110-1123.	2.3	42
29	Inferring population size changes with sequence and SNP data: lessons from human bottlenecks. Heredity, 2013, 110, 409-419.	2.6	84
30	Anisotropic Isolation by Distance: The Main Orientations of Human Genetic Differentiation. Molecular Biology and Evolution, 2013, 30, 513-525.	8.9	35
31	A Comparative Review of Dimension Reduction Methods in Approximate Bayesian Computation. Statistical Science, 2013, 28, .	2.8	232
32	Resequencing Data Provide No Evidence for a Human Bottleneck in Africa during the Penultimate Glacial Period. Molecular Biology and Evolution, 2012, 29, 1851-1860.	8.9	43
33	Identification of a new recurrent Aurora kinase C mutation in both European and African men with macrozoospermia. Human Reproduction, 2012, 27, 3337-3346.	0.9	52
34	Genomic Variation in Seven Khoe-San Groups Reveals Adaptation and Complex African History. Science, 2012, 338, 374-379.	12.6	364
35	abc: an R package for approximate Bayesian computation (ABC). Methods in Ecology and Evolution, 2012, 3, 475-479.	5.2	617
36	Deep Divergences of Human Gene Trees and Models of Human Origins. Molecular Biology and Evolution, 2011, 28, 889-898.	8.9	60

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37	Predictions of Native American Population Structure Using Linguistic Covariates in a Hidden Regression Framework. PLoS ONE, 2011, 6, e16227.	2.5	9
38	Non-linear regression models for Approximate Bayesian Computation. Statistics and Computing, 2010, 20, 63-73.	1.5	331
39	Approximate Bayesian Computation: A Nonparametric Perspective. Journal of the American Statistical Association, 2010, 105, 1178-1187.	3.1	153
40	HIV with contact tracing: a case study in approximate Bayesian computation. Biostatistics, 2010, 11, 644-660.	1.5	60
41	Approximate Bayesian Computation (ABC) in practice. Trends in Ecology and Evolution, 2010, 25, 410-418.	8.7	943
42	Invalid arguments against ABC: Reply to A.R. Templeton. Trends in Ecology and Evolution, 2010, 25, 490-491.	8.7	12
43	Choosing the Summary Statistics and the Acceptance Rate in Approximate Bayesian Computation. , 2010, , 47-56.		13
44	A deterministic model of admixture and genetic introgression: The case of Neanderthal and Cro-Magnon. Mathematical Biosciences, 2008, 216, 71-76.	1.9	6
45	The goat domestication process inferred from large-scale mitochondrial DNA analysis of wild and domestic individuals. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17659-17664.	7.1	279
46	Demographic History of European Populations of Arabidopsis thaliana. PLoS Genetics, 2008, 4, e1000075.	3.5	182
47	Estimating the Number of Ancestral Lineages Using a Maximum-Likelihood Method Based on Rejection Sampling. Genetics, 2007, 176, 1741-1757.	2.9	8
48	Sampling properties of homozygosity-based statistics for linkage disequilibrium. Mathematical Biosciences, 2007, 208, 33-47.	1.9	8
49	Prediction of group patterns in social mammals based on a coalescent model. Journal of Theoretical Biology, 2007, 249, 262-270.	1.7	10
50	The mean, variance and limiting distribution of two statistics sensitive to phylogenetic tree balance. Annals of Applied Probability, 2006, 16, 2195.	1.3	69
51	Low Levels of Genetic Divergence across Geographically and Linguistically Diverse Populations from India. PLoS Genetics, 2006, 2, e215.	3.5	82
52	Which Random Processes Describe the Tree of Life? A Large-Scale Study of Phylogenetic Tree Imbalance. Systematic Biology, 2006, 55, 685-691.	5.6	154
53	apTreeshape: statistical analysis of phylogenetic tree shape. Bioinformatics, 2006, 22, 363-364.	4.1	109
54	Matrilineal Fertility Inheritance Detected in Hunter–Gatherer Populations Using the Imbalance of Gene Genealogies. PLoS Genetics, 2006, 2, e122.	3.5	30

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55	Minimal clade size and external branch length under the neutral coalescent. Advances in Applied Probability, 2005, 37, 647-662.	0.7	29
56	On statistical tests of phylogenetic tree imbalance: The Sackin and other indices revisited. Mathematical Biosciences, 2005, 195, 141-153.	1.9	93
57	Brownian models and coalescent structures. Theoretical Population Biology, 2004, 65, 249-261.	1.1	10