

Michael P Cummings

List of Publications by Year in descending order

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59
papers

5,258
citations

87888

38
h-index

149698

56
g-index

62
all docs

62
docs citations

62
times ranked

7473
citing authors

#	ARTICLE	IF	CITATIONS
1	BEAGLE: An Application Programming Interface and High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2012, 61, 170-173.	5.6	555
2	Independent Emergence of Artemisinin Resistance Mutations Among <i>Plasmodium falciparum</i> in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015, 211, 670-679.	4.0	368
3	Comparing Bootstrap and Posterior Probability Values in the Four-Taxon Case. <i>Systematic Biology</i> , 2003, 52, 477-487.	5.6	277
4	A Large-Scale, Higher-Level, Molecular Phylogenetic Study of the Insect Order Lepidoptera (Moths and Butterflies). <i>Systematic Biology</i> , 2015, 64, 100-110.	2.5	253
5	Genetic loci associated with delayed clearance of <i>Plasmodium falciparum</i> following artemisinin treatment in Southeast Asia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 240-245.	7.1	242
6	A GENEALOGICAL APPROACH TO QUANTIFYING LINEAGE DIVERGENCE. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, 2411-2422.	2.3	203
7	Toward reconstructing the evolution of advanced moths and butterflies (Lepidoptera: Ditrysia): an initial molecular study. <i>BMC Evolutionary Biology</i> , 2009, 9, 280.	3.2	202
8	A Gateway for Phylogenetic Analysis Powered by Grid Computing Featuring GARLI 2.0. <i>Systematic Biology</i> , 2014, 63, 812-818.	5.6	195
9	Phylogeny and Evolution of Lepidoptera. <i>Annual Review of Entomology</i> , 2017, 62, 265-283.	11.8	188
10	Resolving Arthropod Phylogeny: Exploring Phylogenetic Signal within 41 kb of Protein-Coding Nuclear Gene Sequence. <i>Systematic Biology</i> , 2008, 57, 920-938.	5.6	178
11	Extreme Polymorphism in a Vaccine Antigen and Risk of Clinical Malaria: Implications for Vaccine Development. <i>Science Translational Medicine</i> , 2009, 1, 2ra5.	12.4	154
12	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2019, 68, 1052-1061.	5.6	139
13	Phylogenetic Relationships of Acanthocephala Based on Analysis of 18S Ribosomal RNA Gene Sequences. <i>Journal of Molecular Evolution</i> , 2000, 50, 532-540.	1.8	116
14	Association of a Novel Mutation in the <i>Plasmodium falciparum</i> Chloroquine Resistance Transporter With Decreased Piperaquine Sensitivity. <i>Journal of Infectious Diseases</i> , 2017, 216, 468-476.	4.0	102
15	Biased data reduce efficiency and effectiveness of conservation reserve networks. <i>Ecology Letters</i> , 2007, 10, 364-374.	6.4	100
16	A molecular phylogeny for the pyraloid moths (Lepidoptera: Pyraloidea) and its implications for higher-level classification. <i>Systematic Entomology</i> , 2012, 37, 635-656.	3.9	96
17	Can RNA-Seq Resolve the Rapid Radiation of Advanced Moths and Butterflies (Hexapoda: Lepidoptera: Tortricidae)? <i>Systematic Biology</i> , 2015, 64, 111-121.	2.5	89
18	Can Deliberately Incomplete Gene Sample Augmentation Improve a Phylogeny Estimate for the Advanced Moths and Butterflies (Hexapoda: Lepidoptera)? <i>Systematic Biology</i> , 2011, 60, 782-796.	5.6	87

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19	Increased gene sampling yields robust support for higher-level clades within Bombycoidea (Lepidoptera). <i>Systematic Entomology</i> , 2011, 36, 31-43.	3.9	83
20	A molecular phylogeny for the oldest (nonditrysian) lineages of extant Lepidoptera, with implications for classification, comparative morphology and life-history evolution. <i>Systematic Entomology</i> , 2015, 40, 671-704.	3.9	82
21	Phylogenetic relationships of <i>Phytophthora</i> species based on ribosomal ITS 1 DNA sequence analysis with emphasis on Waterhouse groups V and VI. <i>Mycological Research</i> , 2000, 104, 1055-1061.	2.5	80
22	Effectiveness of Conservation Targets in Capturing Genetic Diversity. <i>Conservation Biology</i> , 2003, 17, 219-229.	4.7	76
23	A Molecular Phylogeny for the Leaf-Roller Moths (Lepidoptera: Tortricidae) and Its Implications for Classification and Life History Evolution. <i>PLoS ONE</i> , 2012, 7, e35574.	2.5	71
24	A Molecular Phylogeny for Yponomeutoidea (Insecta, Lepidoptera, Ditrysia) and Its Implications for Classification, Biogeography and the Evolution of Host Plant Use. <i>PLoS ONE</i> , 2013, 8, e55066.	2.5	70
25	Phylogenetic analysis based on 18S ribosomal RNA gene sequences supports the existence of class polyacanthocephala (acanthocephala). <i>Molecular Phylogenetics and Evolution</i> , 2002, 23, 288-292.	2.7	67
26	Phylogenetic analysis reveals five independent transfers of the chloroplast gene <i>rbcl</i> to the mitochondrial genome in angiosperms. <i>Current Genetics</i> , 2003, 43, 131-138.	1.7	65
27	Phylogenetic Relationships of Platyhelminthes Based on 18S Ribosomal Gene Sequences. <i>Molecular Phylogenetics and Evolution</i> , 1998, 10, 1-10.	2.7	63
28	A Case for Evolutionary Genomics and the Comprehensive Examination of Sequence Biodiversity. <i>Molecular Biology and Evolution</i> , 2000, 17, 1776-1788.	8.9	63
29	Further progress on the phylogeny of Notopteroidea (Insecta: Lepidoptera). <i>Systematic Entomology</i> , 2015, 40, 671-704.	3.9	54
30	Prey preference follows phylogeny: evolutionary dietary patterns within the marine gastropod group Cladobranchia (Gastropoda: Heterobranchia: Nudibranchia). <i>BMC Evolutionary Biology</i> , 2017, 17, 221.	3.2	53
31	Increased gene sampling strengthens support for higher-level groups within leaf-mining moths and relatives (Lepidoptera: Gracillariidae). <i>BMC Evolutionary Biology</i> , 2011, 11, 182.	3.2	52
32	A molecular phylogeny and revised classification for the oldest ditrysian moth lineages (Lepidoptera: Ditrysia: Tortricidae), with implications for ancestral feeding habits of the mega-diverse Ditrysia. <i>Systematic Entomology</i> , 2015, 40, 409-432.	3.9	52
33	Divergent gene copies in the asexual class Bdelloidea (Rotifera) separated before the bdelloid radiation or within bdelloid families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1622-1625.	7.1	50
34	Relating Amino Acid Sequence to Phenotype: Analysis of Peptide-Binding Data. <i>Biometrics</i> , 2001, 57, 632-643.	1.4	48
35	Genetic consequences of ecological reserve design guidelines: An empirical investigation. <i>Conservation Genetics</i> , 2003, 4, 427-439.	1.5	44
36	Relationships within Cladobranchia (Gastropoda: Nudibranchia) based on RNA-Seq data: an initial investigation. <i>Royal Society Open Science</i> , 2015, 2, 150196.	2.4	44

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37	Magic bullets and golden rules: Data sampling in molecular phylogenetics. <i>Zoology</i> , 2005, 108, 329-336.	1.2	43
38	Broader incorporation of bioinformatics in education: opportunities and challenges. <i>Briefings in Bioinformatics</i> , 2010, 11, 537-543.	6.5	43
39	Grid Services Base Library: A high-level, procedural application programming interface for writing Globus-based Grid services. <i>Future Generation Computer Systems</i> , 2007, 23, 517-522.	7.5	42
40	Phylogeny and feeding trait evolution of the mega-diverse Gelechioidea (Lepidoptera: Obtectomera): new insight from 19 nuclear genes. <i>Systematic Entomology</i> , 2016, 41, 112-132.	3.9	39
41	Phylotranscriptomics resolves ancient divergences in the Lepidoptera. <i>Systematic Entomology</i> , 2017, 42, 305-316.	3.9	38
42	Simple statistical models predict C-to-U edited sites in plant mitochondrial RNA. <i>BMC Bioinformatics</i> , 2004, 5, 132.	2.6	37
43	Necessity is the mother of invention: a simple grid computing system using commodity tools. <i>Journal of Parallel and Distributed Computing</i> , 2003, 63, 578-589.	4.1	35
44	Bio-STEER: A Semantic Web workflow tool for Grid computing in the life sciences. <i>Future Generation Computer Systems</i> , 2007, 23, 497-509.	7.5	34
45	DNA SEQUENCE VARIATION IN THE RIBOSOMAL INTERNAL TRANSCRIBED SPACER REGION OF FRESHWATER CLADOPHORA SPECIES (CHLOROPHYTA)1. <i>Journal of Phycology</i> , 1996, 32, 1035-1042.	2.3	33
46	Comparative morphology and evolution of the cnidosac in Cladobranchia (Gastropoda:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,382 Td (H</i>	2.0	33
47	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. <i>Microbiome</i> , 2017, 5, 11.	11.1	31
48	Pigment composition of putatively achlorophyllous angiosperms. <i>Plant Systematics and Evolution</i> , 1998, 210, 105-111.	0.9	29
49	Computing the Tree of Life: Leveraging the Power of Desktop and Service Grids. , 2011, , .		29
50	Few amino acid positions in rpoB are associated with most of the rifampin resistance in <i>Mycobacterium tuberculosis</i> . <i>BMC Bioinformatics</i> , 2004, 5, 137.	2.6	19
51	A Molecular Footprint of Limb Loss: Sequence Variation of the Autopodial Identity Gene Hoxa-13. <i>Journal of Molecular Evolution</i> , 2008, 67, 581-593.	1.8	18
52	<i>Plasmodium falciparum</i> field isolates from areas of repeated emergence of drug resistant malaria show no evidence of hypermutator phenotype. <i>Infection, Genetics and Evolution</i> , 2015, 30, 318-322.	2.3	18
53	Section-level relationships of North American Agalinis (Orobanchaceae) based on DNA sequence analysis of three chloroplast gene regions. <i>BMC Evolutionary Biology</i> , 2004, 4, 15.	3.2	16
54	A critical assessment of gene catalogs for metagenomic analysis. <i>Bioinformatics</i> , 2021, 37, 2848-2857.	4.1	15

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55	Subdividing Long-Running, Variable-Length Analyses Into Short, Fixed-Length BOINC Workunits. Journal of Grid Computing, 2016, 14, 429-441.	3.9	9
56	Validating the systematic position of Plationus Segers, Murugan & Dumont, 1993 (Rotifera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 C oxidase. Hydrobiologia, 2010, 644, 361-370.	2.0	7
57	Heterogeneous Hardware Support in BEAGLE, a High-Performance Computing Library for Statistical Phylogenetics. , 2017, , .		6
58	Configuring Concurrent Computation of Phylogenetic Partial Likelihoods: Accelerating Analyses Using the BEAGLE Library. Lecture Notes in Computer Science, 2017, , 533-547.	1.3	6
59	Rerooting Trees Increases Opportunities for Concurrent Computation and Results in Markedly Improved Performance for Phylogenetic Inference. , 2018, , .		2