

Michael P Cummings

List of Publications by Citations

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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.

60
papers

4,121
citations

36
h-index

62
g-index

62
ext. papers

4,692
ext. citations

5.5
avg, IF

5.18
L-index

#	Paper	IF	Citations
60	BEAGLE: an application programming interface and high-performance computing library for statistical phylogenetics. <i>Systematic Biology</i> , 2012 , 61, 170-3	8.4	374
59	Independent emergence of artemisinin resistance mutations among <i>Plasmodium falciparum</i> in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015 , 211, 670-9	7	307
58	Comparing bootstrap and posterior probability values in the four-taxon case. <i>Systematic Biology</i> , 2003 , 52, 477-87	8.4	237
57	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, 240-5	11.5	214
56	A large-scale, higher-level, molecular phylogenetic study of the insect order Lepidoptera (moths and butterflies). <i>PLoS ONE</i> , 2013 , 8, e58568	3.7	201
55	A genealogical approach to quantifying lineage divergence. <i>Evolution; International Journal of Organic Evolution</i> , 2008 , 62, 2411-22	3.8	192
54	A gateway for phylogenetic analysis powered by grid computing featuring GARLI 2.0. <i>Systematic Biology</i> , 2014 , 63, 812-8	8.4	167
53	Toward reconstructing the evolution of advanced moths and butterflies (Lepidoptera: Ditrysia): an initial molecular study. <i>BMC Evolutionary Biology</i> , 2009 , 9, 280	3	163
52	Resolving arthropod phylogeny: exploring phylogenetic signal within 41 kb of protein-coding nuclear gene sequence. <i>Systematic Biology</i> , 2008 , 57, 920-38	8.4	162
51	Extreme polymorphism in a vaccine antigen and risk of clinical malaria: implications for vaccine development. <i>Science Translational Medicine</i> , 2009 , 1, 2ra5	17.5	129
50	Phylogeny and Evolution of Lepidoptera. <i>Annual Review of Entomology</i> , 2017 , 62, 265-283	21.8	121
49	Phylogenetic relationships of Acanthocephala based on analysis of 18S ribosomal RNA gene sequences. <i>Journal of Molecular Evolution</i> , 2000 , 50, 532-40	3.1	91
48	Biased data reduce efficiency and effectiveness of conservation reserve networks. <i>Ecology Letters</i> , 2007 , 10, 364-74	10	87
47	Can deliberately incomplete gene sample augmentation improve a phylogeny estimate for the advanced moths and butterflies (Hexapoda: Lepidoptera)? <i>Systematic Biology</i> , 2011 , 60, 782-96	8.4	78
46	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	7	75
45	Can RNA-Seq resolve the rapid radiation of advanced moths and butterflies (Hexapoda: Lepidoptera: Apoditrysia)? An exploratory study. <i>PLoS ONE</i> , 2013 , 8, e82615	3.7	72
44	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , 2019 , 68, 1052-1061	8.4	71

43	Phylogenetic relationships of Phytophthora species based on ribosomal ITS I DNA sequence analysis with emphasis on Waterhouse groups V and VI. <i>Mycological Research</i> , 2000 , 104, 1055-1061		70
42	A molecular phylogeny for the pyraloid moths (Lepidoptera: Pyraloidea) and its implications for higher-level classification. <i>Systematic Entomology</i> , 2012 , 37, 635-656	3.4	67
41	Effectiveness of Conservation Targets in Capturing Genetic Diversity. <i>Conservation Biology</i> , 2003 , 17, 219-229	6	63
40	Increased gene sampling yields robust support for higher-level clades within Bombycoidea (Lepidoptera). <i>Systematic Entomology</i> , 2011 , 36, 31-43	3.4	58
39	Phylogenetic analysis reveals five independent transfers of the chloroplast gene rbcL to the mitochondrial genome in angiosperms. <i>Current Genetics</i> , 2003 , 43, 131-8	2.9	58
38	A case for evolutionary genomics and the comprehensive examination of sequence biodiversity. <i>Molecular Biology and Evolution</i> , 2000 , 17, 1776-88	8.3	57
37	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	3.4	53
36	Phylogenetic analysis based on 18S ribosomal RNA gene sequences supports the existence of class polyacanthocephala (acanthocephala). <i>Molecular Phylogenetics and Evolution</i> , 2002 , 23, 288-92	4.1	53
35	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	3.7	52
34	Phylogenetic relationships of platyhelminthes based on 18S ribosomal gene sequences. <i>Molecular Phylogenetics and Evolution</i> , 1998 , 10, 1-10	4.1	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, 1622-5	11.5	44
32	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	3.7	43
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	40
30	Magic bullets and golden rules: data sampling in molecular phylogenetics. <i>Zoology</i> , 2005 , 108, 329-36	1.7	38
29	Relating amino acid sequence to phenotype: analysis of peptide-binding data. <i>Biometrics</i> , 2001 , 57, 632-428		38
28	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	37
27	Genetic consequences of ecological reserve design guidelines: An empirical investigation. <i>Conservation Genetics</i> , 2003 , 4, 427-439	2.6	37
26	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	36

25	Relationships within Cladobanchia (Gastropoda: Nudibranchia) based on RNA-Seq data: an initial investigation. <i>Royal Society Open Science</i> , 2015 , 2, 150196	3.3	36
24	Broader incorporation of bioinformatics in education: opportunities and challenges. <i>Briefings in Bioinformatics</i> , 2010 , 11, 537-43	13.4	34
23	Simple statistical models predict C-to-U edited sites in plant mitochondrial RNA. <i>BMC Bioinformatics</i> , 2004 , 5, 132	3.6	33
22	Further progress on the phylogeny of Noctuoidea (Insecta: Lepidoptera) using an expanded gene sample. <i>Systematic Entomology</i> , 2017 , 42, 82-93	3.4	30
21	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	3	30
20	A molecular phylogeny and revised classification for the oldest ditrysian moth lineages (Lepidoptera: Tineoidea), with implications for ancestral feeding habits of the mega-diverse Ditrysia. <i>Systematic Entomology</i> , 2015 , 40, 409-432	3.4	29
19	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	3.4	28
18	Phylotranscriptomics resolves ancient divergences in the Lepidoptera. <i>Systematic Entomology</i> , 2017 , 42, 305-316	3.4	28
17	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	4.4	27
16	Computing the Tree of Life: Leveraging the Power of Desktop and Service Grids 2011 ,		26
15	Pigment composition of putatively achlorophyllous angiosperms. <i>Plant Systematics and Evolution</i> , 1998 , 210, 105-111	1.3	24
14	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. <i>Microbiome</i> , 2017 , 5, 11	16.6	23
13	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	23
12	Plasmodium falciparum 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	4.5	18
11	Few amino acid positions in rpoB are associated with most of the rifampin resistance in Mycobacterium tuberculosis. <i>BMC Bioinformatics</i> , 2004 , 5, 137	3.6	18
10	Comparative morphology and evolution of the cnidosac in Cladobanchia (Gastropoda: Heterobranchia: Nudibranchia). <i>Frontiers in Zoology</i> , 2018 , 15, 43	2.8	17
9	A molecular footprint of limb loss: sequence variation of the autopodial identity gene Hoxa-13. <i>Journal of Molecular Evolution</i> , 2008 , 67, 581-93	3.1	14
8	Section-level relationships of North American Agalini (Orobanchaceae) based on DNA sequence analysis of three chloroplast gene regions. <i>BMC Evolutionary Biology</i> , 2004 , 4, 15	3	10

7	Subdividing Long-Running, Variable-Length Analyses Into Short, Fixed-Length BOINC Workunits. <i>Journal of Grid Computing</i> , 2016 , 14, 429-441	4.2	9
6	Expanding the Reach of Grid Computing: Combining Globus- and BOINC-Based Systems 71-85		9
5	Heterogeneous Hardware Support in BEAGLE, a High-Performance Computing Library for Statistical Phylogenetics 2017 ,		4
4	Configuring Concurrent Computation of Phylogenetic Partial Likelihoods: Accelerating Analyses Using the BEAGLE Library. <i>Lecture Notes in Computer Science</i> , 2017 , 533-547	0.9	4
3	Validating the systematic position of <i>Plationus Segers, Murugan & Dumont, 1993</i> (Rotifera: Brachionidae) using sequences of the large subunit of the nuclear ribosomal DNA and of cytochrome C oxidase. <i>Hydrobiologia</i> , 2010 , 644, 361-370	2.4	4
2	A critical assessment of gene catalogs for metagenomic analysis. <i>Bioinformatics</i> , 2021 ,	7.2	3
1	Rerooting Trees Increases Opportunities for Concurrent Computation and Results in Markedly Improved Performance for Phylogenetic Inference 2018 ,		2