

# Michael P Cummings

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/11249508/michael-p-cummings-publications-by-year.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	A critical assessment of gene catalogs for metagenomic analysis. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	3
59	BEAGLE 3: Improved Performance, Scaling, and Usability for a High-Performance Computing Library for Statistical Phylogenetics. <i>Systematic Biology</i> , <b>2019</b> , 68, 1052-1061	8.4	71
58	Comparative morphology and evolution of the cnidosac in Cladobranchia (Gastropoda: Heterobranchia: Nudibranchia). <i>Frontiers in Zoology</i> , <b>2018</b> , 15, 43	2.8	17
57	Rerooting Trees Increases Opportunities for Concurrent Computation and Results in Markedly Improved Performance for Phylogenetic Inference <b>2018</b> ,		2
56	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. <i>Microbiome</i> , <b>2017</b> , 5, 11	16.6	23
55	Prey preference follows phylogeny: evolutionary dietary patterns within the marine gastropod group Cladobranchia (Gastropoda: Heterobranchia: Nudibranchia). <i>BMC Evolutionary Biology</i> , <b>2017</b> , 17, 221	3	36
54	Heterogeneous Hardware Support in BEAGLE, a High-Performance Computing Library for Statistical Phylogenetics <b>2017</b> ,		4
53	Association of a Novel Mutation in the Plasmodium falciparum Chloroquine Resistance Transporter With Decreased Piperaquine Sensitivity. <i>Journal of Infectious Diseases</i> , <b>2017</b> , 216, 468-476	7	75
52	Configuring Concurrent Computation of Phylogenetic Partial Likelihoods: Accelerating Analyses Using the BEAGLE Library. <i>Lecture Notes in Computer Science</i> , <b>2017</b> , 533-547	0.9	4
51	Phylogeny and Evolution of Lepidoptera. <i>Annual Review of Entomology</i> , <b>2017</b> , 62, 265-283	21.8	121
50	Further progress on the phylogeny of Noctuoidea (Insecta: Lepidoptera) using an expanded gene sample. <i>Systematic Entomology</i> , <b>2017</b> , 42, 82-93	3.4	30
49	Phylotranscriptomics resolves ancient divergences in the Lepidoptera. <i>Systematic Entomology</i> , <b>2017</b> , 42, 305-316	3.4	28
48	Phylogeny and feeding trait evolution of the mega-diverse Gelechioidea (Lepidoptera: Obtectomera): new insight from 19 nuclear genes. <i>Systematic Entomology</i> , <b>2016</b> , 41, 112-132	3.4	28
47	Subdividing Long-Running, Variable-Length Analyses Into Short, Fixed-Length BOINC Workunits. <i>Journal of Grid Computing</i> , <b>2016</b> , 14, 429-441	4.2	9
46	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> , <b>2015</b> , 30, 318-322	4.5	18
45	Independent emergence of artemisinin resistance mutations among Plasmodium falciparum in Southeast Asia. <i>Journal of Infectious Diseases</i> , <b>2015</b> , 211, 670-9	7	307
44	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> , <b>2015</b> , 40, 409-432	3.4	29

43	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> , <b>2015</b> , 40, 671-704	3.4	53
42	Relationships within Cladobranhia (Gastropoda: Nudibranchia) based on RNA-Seq data: an initial investigation. <i>Royal Society Open Science</i> , <b>2015</b> , 2, 150196	3.3	36
41	A gateway for phylogenetic analysis powered by grid computing featuring GARLI 2.0. <i>Systematic Biology</i> , <b>2014</b> , 63, 812-8	8.4	167
40	Genetic loci associated with delayed clearance of Plasmodium falciparum following artemisinin treatment in Southeast Asia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 240-5	11.5	214
39	A large-scale, higher-level, molecular phylogenetic study of the insect order Lepidoptera (moths and butterflies). <i>PLoS ONE</i> , <b>2013</b> , 8, e58568	3.7	201
38	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> , <b>2013</b> , 8, e55066	3.7	43
37	Can RNA-Seq resolve the rapid radiation of advanced moths and butterflies (Hexapoda: Lepidoptera: Apoditrysia)? An exploratory study. <i>PLoS ONE</i> , <b>2013</b> , 8, e82615	3.7	72
36	A molecular phylogeny for the pyraloid moths (Lepidoptera: Pyraloidea) and its implications for higher-level classification. <i>Systematic Entomology</i> , <b>2012</b> , 37, 635-656	3.4	67
35	BEAGLE: an application programming interface and high-performance computing library for statistical phylogenetics. <i>Systematic Biology</i> , <b>2012</b> , 61, 170-3	8.4	374
34	A molecular phylogeny for the leaf-roller moths (Lepidoptera: Tortricidae) and its implications for classification and life history evolution. <i>PLoS ONE</i> , <b>2012</b> , 7, e35574	3.7	52
33	Increased gene sampling yields robust support for higher-level clades within Bombycoidea (Lepidoptera). <i>Systematic Entomology</i> , <b>2011</b> , 36, 31-43	3.4	58
32	Increased gene sampling strengthens support for higher-level groups within leaf-mining moths and relatives (Lepidoptera: Gracillariidae). <i>BMC Evolutionary Biology</i> , <b>2011</b> , 11, 182	3	40
31	Computing the Tree of Life: Leveraging the Power of Desktop and Service Grids <b>2011</b> ,		26
30	Can deliberately incomplete gene sample augmentation improve a phylogeny estimate for the advanced moths and butterflies (Hexapoda: Lepidoptera)? <i>Systematic Biology</i> , <b>2011</b> , 60, 782-96	8.4	78
29	Broader incorporation of bioinformatics in education: opportunities and challenges. <i>Briefings in Bioinformatics</i> , <b>2010</b> , 11, 537-43	13.4	34
28	Validating the systematic position of Plationus Segers, Murugan & Dumont, 1993 (Rotifera: Brachionidae) using sequences of the large subunit of the nuclear ribosomal DNA and of cytochrome C oxidase. <i>Hydrobiologia</i> , <b>2010</b> , 644, 361-370	2.4	4
27	Extreme polymorphism in a vaccine antigen and risk of clinical malaria: implications for vaccine development. <i>Science Translational Medicine</i> , <b>2009</b> , 1, 2ra5	17.5	129
26	Toward reconstructing the evolution of advanced moths and butterflies (Lepidoptera: Ditrysia): an initial molecular study. <i>BMC Evolutionary Biology</i> , <b>2009</b> , 9, 280	3	163

25	Resolving arthropod phylogeny: exploring phylogenetic signal within 41 kb of protein-coding nuclear gene sequence. <i>Systematic Biology</i> , <b>2008</b> , 57, 920-38	8.4	162
24	A molecular footprint of limb loss: sequence variation of the autopodial identity gene Hoxa-13. <i>Journal of Molecular Evolution</i> , <b>2008</b> , 67, 581-93	3.1	14
23	A genealogical approach to quantifying lineage divergence. <i>Evolution; International Journal of Organic Evolution</i> , <b>2008</b> , 62, 2411-22	3.8	192
22	Bio-STEER: A Semantic Web workflow tool for Grid computing in the life sciences. <i>Future Generation Computer Systems</i> , <b>2007</b> , 23, 497-509	7.5	23
21	Biased data reduce efficiency and effectiveness of conservation reserve networks. <i>Ecology Letters</i> , <b>2007</b> , 10, 364-74	10	87
20	Grid Services Base Library: A high-level, procedural application programming interface for writing Globus-based Grid services. <i>Future Generation Computer Systems</i> , <b>2007</b> , 23, 517-522	7.5	37
19	Magic bullets and golden rules: data sampling in molecular phylogenetics. <i>Zoology</i> , <b>2005</b> , 108, 329-36	1.7	38
18	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> , <b>2004</b> , 101, 1622-5	11.5	44
17	Simple statistical models predict C-to-U edited sites in plant mitochondrial RNA. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 132	3.6	33
16	Few amino acid positions in rpoB are associated with most of the rifampin resistance in <i>Mycobacterium tuberculosis</i> . <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 137	3.6	18
15	Section-level relationships of North American Agalinis (Orobanchaceae) based on DNA sequence analysis of three chloroplast gene regions. <i>BMC Evolutionary Biology</i> , <b>2004</b> , 4, 15	3	10
14	Genetic consequences of ecological reserve design guidelines: An empirical investigation. <i>Conservation Genetics</i> , <b>2003</b> , 4, 427-439	2.6	37
13	Phylogenetic analysis reveals five independent transfers of the chloroplast gene rbcL to the mitochondrial genome in angiosperms. <i>Current Genetics</i> , <b>2003</b> , 43, 131-8	2.9	58
12	Necessity is the mother of invention: a simple grid computing system using commodity tools. <i>Journal of Parallel and Distributed Computing</i> , <b>2003</b> , 63, 578-589	4.4	27
11	Effectiveness of Conservation Targets in Capturing Genetic Diversity. <i>Conservation Biology</i> , <b>2003</b> , 17, 219-229	6	63
10	Comparing bootstrap and posterior probability values in the four-taxon case. <i>Systematic Biology</i> , <b>2003</b> , 52, 477-87	8.4	237
9	Phylogenetic analysis based on 18S ribosomal RNA gene sequences supports the existence of class polyacanthocephala (acanthocephala). <i>Molecular Phylogenetics and Evolution</i> , <b>2002</b> , 23, 288-92	4.1	53
8	Relating amino acid sequence to phenotype: analysis of peptide-binding data. <i>Biometrics</i> , <b>2001</b> , 57, 632-42		38

7	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> , <b>2000</b> , 104, 1055-1061		70
6	Phylogenetic relationships of Acanthocephala based on analysis of 18S ribosomal RNA gene sequences. <i>Journal of Molecular Evolution</i> , <b>2000</b> , 50, 532-40	3.1	91
5	A case for evolutionary genomics and the comprehensive examination of sequence biodiversity. <i>Molecular Biology and Evolution</i> , <b>2000</b> , 17, 1776-88	8.3	57
4	Phylogenetic relationships of platyhelminthes based on 18S ribosomal gene sequences. <i>Molecular Phylogenetics and Evolution</i> , <b>1998</b> , 10, 1-10	4.1	52
3	Pigment composition of putatively achlorophyllous angiosperms. <i>Plant Systematics and Evolution</i> , <b>1998</b> , 210, 105-111	1.3	24
2	DNA SEQUENCE VARIATION IN THE RIBOSOMAL INTERNAL TRANSCRIBED SPACER REGION OF FRESHWATER CLADOPHORA SPECIES (CHLOROPHYTA)1. <i>Journal of Phycology</i> , <b>1996</b> , 32, 1035-1042	3	30
1	Expanding the Reach of Grid Computing: Combining Globus- and BOINC-Based Systems71-85		9