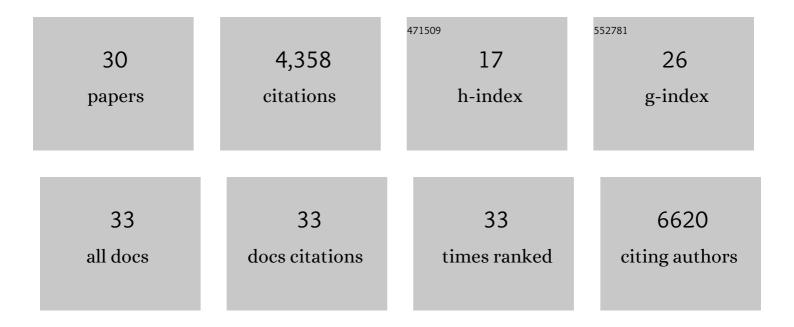
James B Munro

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8649498/publications.pdf

Version: 2024-02-01



IAMES R MUNDO

#	Article	IF	CITATIONS
1	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	14.5	2,416
2	Human Disease Ontology 2018 update: classification, content and workflow expansion. Nucleic Acids Research, 2019, 47, D955-D962.	14.5	383
3	A phylogenetic analysis of the megadiverse <scp>C</scp> halcidoidea (<scp>H</scp> ymenoptera). Cladistics, 2013, 29, 466-542.	3.3	205
4	Evolution of the hymenopteran megaradiation. Molecular Phylogenetics and Evolution, 2011, 60, 73-88.	2.7	171
5	Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. Molecular Biology and Evolution, 2017, 34, 1838-1862.	8.9	157
6	A Molecular Phylogeny of the Chalcidoidea (Hymenoptera). PLoS ONE, 2011, 6, e27023.	2.5	134
7	Molecular phylogeny of the assassin bugs (Hemiptera: Reduviidae), based on mitochondrial and nuclear ribosomal genes. Molecular Phylogenetics and Evolution, 2009, 53, 287-299.	2.7	127
8	A Secondary Structural Model of the 28S rRNA Expansion Segments D2 and D3 for Chalcidoid Wasps (Hymenoptera: Chalcidoidea). Molecular Biology and Evolution, 2005, 22, 1593-1608.	8.9	102
9	The Human Disease Ontology 2022 update. Nucleic Acids Research, 2022, 50, D1255-D1261.	14.5	92
10	Forkhead transcription factors regulate mosquito reproduction. Insect Biochemistry and Molecular Biology, 2007, 37, 985-997.	2.7	69
11	ECO, the Evidence & Conclusion Ontology: community standard for evidence information. Nucleic Acids Research, 2019, 47, D1186-D1194.	14.5	67
12	Discovery of a novel species, Theileria haneyi n. sp., infective to equids, highlights exceptional genomic diversity within the genus Theileria: implications for apicomplexan parasite surveillance. International Journal for Parasitology, 2018, 48, 679-690.	3.1	61
13	Strains used in whole organism Plasmodium falciparum vaccine trials differ in genome structure, sequence, and immunogenic potential. Genome Medicine, 2020, 12, 6.	8.2	61
14	<i>Haemophilus influenzae</i> genome evolution during persistence in the human airways in chronic obstructive pulmonary disease. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3256-E3265.	7.1	57
15	Using Core Genome Alignments To Assign Bacterial Species. MSystems, 2018, 3, .	3.8	54
16	The Microbiota of Freshwater Fish and Freshwater Niches Contain Omega-3 Fatty Acid-Producing Shewanella Species. Applied and Environmental Microbiology, 2016, 82, 218-231.	3.1	53
17	Genome sequences reveal divergence times of malaria parasite lineages. Parasitology, 2011, 138, 1737-1749.	1.5	50
18	ECO: the Evidence and Conclusion Ontology, an update for 2022. Nucleic Acids Research, 2022, 50, D1515-D1521.	14.5	21

JAMES B MUNRO

#	Article	IF	CITATIONS
19	Rapid evolution of genomeâ€wide gene expression and plasticity during saline to freshwater invasions by the copepod <i>Eurytemora affinis</i> species complex. Molecular Ecology, 2020, 29, 4835-4856.	3.9	19
20	Absolute Quantification of the Host-To-Parasite DNA Ratio in Theileria parva-Infected Lymphocyte Cell Lines. PLoS ONE, 2016, 11, e0150401.	2.5	17
21	Signature of adaptive evolution in olfactory receptor genes in Cory's Shearwater supports molecular basis for smell in procellariiform seabirds. Scientific Reports, 2020, 10, 543.	3.3	13
22	Ribonucleotide reductase as a target to control apicomplexan diseases. Current Issues in Molecular Biology, 2012, 14, 9-26.	2.4	9
23	A Novel Clade of Unique Eukaryotic Ribonucleotide Reductase R2 Subunits is Exclusive to Apicomplexan Parasites. Journal of Molecular Evolution, 2013, 77, 92-106.	1.8	7
24	Capture-based enrichment of Theileria parva DNA enables full genome assembly of first buffalo-derived strain and reveals exceptional intra-specific genetic diversity. PLoS Neglected Tropical Diseases, 2020, 14, e0008781.	3.0	6
25	ECO-CollecTF: A Corpus of Annotated Evidence-Based Assertions in Biomedical Manuscripts. Frontiers in Research Metrics and Analytics, 2021, 6, 674205.	1.9	2
26	STRIDE: a command-line HMM-based identifier and sub-classifier of Plasmodium falciparum RIFIN and STEVOR variant surface antigen families. BMC Bioinformatics, 2022, 23, 15.	2.6	1
27	Title is missing!. , 2020, 14, e0008781.		0
28	Title is missing!. , 2020, 14, e0008781.		0
29	Title is missing!. , 2020, 14, e0008781.		0
30	Title is missing!. , 2020, 14, e0008781.		0