

James B Munro

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

4,358
citations

471509

17
h-index

552781

26
g-index

33
all docs

33
docs citations

33
times ranked

6620
citing authors

#	ARTICLE	IF	CITATIONS
1	The Human Disease Ontology 2022 update. <i>Nucleic Acids Research</i> , 2022, 50, D1255-D1261.	14.5	92
2	ECO: the Evidence and Conclusion Ontology, an update for 2022. <i>Nucleic Acids Research</i> , 2022, 50, D1515-D1521.	14.5	21
3	STRIDE: a command-line HMM-based identifier and sub-classifier of <i>Plasmodium falciparum</i> RIFIN and STEVOR variant surface antigen families. <i>BMC Bioinformatics</i> , 2022, 23, 15.	2.6	1
4	ECO-CollectF: A Corpus of Annotated Evidence-Based Assertions in Biomedical Manuscripts. <i>Frontiers in Research Metrics and Analytics</i> , 2021, 6, 674205.	1.9	2
5	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
6	Strains used in whole organism <i>Plasmodium falciparum</i> vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , 2020, 12, 6.	8.2	61
7	Rapid evolution of genome-wide gene expression and plasticity during saline to freshwater invasions by the copepod <i>Eurytemora affinis</i> species complex. <i>Molecular Ecology</i> , 2020, 29, 4835-4856.	3.9	19
8	Signature of adaptive evolution in olfactory receptor genes in Cory's Shearwater supports molecular basis for smell in procellariiform seabirds. <i>Scientific Reports</i> , 2020, 10, 543.	3.3	13
9	Capture-based enrichment of <i>Theileria parva</i> DNA enables full genome assembly of first buffalo-derived strain and reveals exceptional intra-specific genetic diversity. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008781.	3.0	6
10	Title is missing!. , 2020, 14, e0008781.		0
11	Title is missing!. , 2020, 14, e0008781.		0
12	Title is missing!. , 2020, 14, e0008781.		0
13	Title is missing!. , 2020, 14, e0008781.		0
14	Human Disease Ontology 2018 update: classification, content and workflow expansion. <i>Nucleic Acids Research</i> , 2019, 47, D955-D962.	14.5	383
15	ECO, the Evidence & Conclusion Ontology: community standard for evidence information. <i>Nucleic Acids Research</i> , 2019, 47, D1186-D1194.	14.5	67
16	<i>Haemophilus influenzae</i> genome evolution during persistence in the human airways in chronic obstructive pulmonary disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3256-E3265.	7.1	57
17	Using Core Genome Alignments To Assign Bacterial Species. <i>MSystems</i> , 2018, 3, .	3.8	54
18	Discovery of a novel species, <i>Theileria haneyi</i> n. sp., infective to equids, highlights exceptional genomic diversity within the genus <i>Theileria</i> : implications for apicomplexan parasite surveillance. <i>International Journal for Parasitology</i> , 2018, 48, 679-690.	3.1	61

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19	Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. <i>Molecular Biology and Evolution</i> , 2017, 34, 1838-1862.	8.9	157
20	Absolute Quantification of the Host-To-Parasite DNA Ratio in <i>Theileria parva</i> -Infected Lymphocyte Cell Lines. <i>PLoS ONE</i> , 2016, 11, e0150401.	2.5	17
21	The Microbiota of Freshwater Fish and Freshwater Niches Contain Omega-3 Fatty Acid-Producing <i>Shewanella</i> Species. <i>Applied and Environmental Microbiology</i> , 2016, 82, 218-231.	3.1	53
22	A Novel Clade of Unique Eukaryotic Ribonucleotide Reductase R2 Subunits is Exclusive to Apicomplexan Parasites. <i>Journal of Molecular Evolution</i> , 2013, 77, 92-106.	1.8	7
23	A phylogenetic analysis of the megadiverse Chalcidoidea (Hymenoptera). <i>Cladistics</i> , 2013, 29, 466-542.	3.3	205
24	Ribonucleotide reductase as a target to control apicomplexan diseases. <i>Current Issues in Molecular Biology</i> , 2012, 14, 9-26.	2.4	9
25	A Molecular Phylogeny of the Chalcidoidea (Hymenoptera). <i>PLoS ONE</i> , 2011, 6, e27023.	2.5	134
26	Genome sequences reveal divergence times of malaria parasite lineages. <i>Parasitology</i> , 2011, 138, 1737-1749.	1.5	50
27	Evolution of the hymenopteran megaradiation. <i>Molecular Phylogenetics and Evolution</i> , 2011, 60, 73-88.	2.7	171
28	Molecular phylogeny of the assassin bugs (Hemiptera: Reduviidae), based on mitochondrial and nuclear ribosomal genes. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 287-299.	2.7	127
29	Forkhead transcription factors regulate mosquito reproduction. <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 985-997.	2.7	69
30	A Secondary Structural Model of the 28S rRNA Expansion Segments D2 and D3 for Chalcidoid Wasps (Hymenoptera: Chalcidoidea). <i>Molecular Biology and Evolution</i> , 2005, 22, 1593-1608.	8.9	102