

Claudia Elizabeth Thompson

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

929
citations

430874

18
h-index

501196

28
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48
all docs

48
docs citations

48
times ranked

1761
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome of the Avirulent Human-Infective Trypanosome "Trypanosoma rangeli". PLoS Neglected Tropical Diseases, 2014, 8, e3176.	3.0	72
2	New insights on the biology of swine respiratory tract mycoplasmas from a comparative genome analysis. BMC Genomics, 2013, 14, 175.	2.8	63
3	Metagenomic Analysis of the Microbiota from the Crop of an Invasive Snail Reveals a Rich Reservoir of Novel Genes. PLoS ONE, 2012, 7, e48505.	2.5	62
4	E484K as an innovative phylogenetic event for viral evolution: Genomic analysis of the E484K spike mutation in SARS-CoV-2 lineages from Brazil. Infection, Genetics and Evolution, 2021, 93, 104941.	2.3	58
5	Predicting the Proteins of Angomonas deanei, Strigomonas culicis and Their Respective Endosymbionts Reveals New Aspects of the Trypanosomatidae Family. PLoS ONE, 2013, 8, e60209.	2.5	55
6	Comparative genome analysis of entomopathogenic fungi reveals a complex set of secreted proteins. BMC Genomics, 2014, 15, 822.	2.8	49
7	Taxonomic and functional profiles of soil samples from Atlantic forest and Caatinga biomes in northeastern Brazil. MicrobiologyOpen, 2014, 3, 299-315.	3.0	48
8	A potential source for cellulolytic enzyme discovery and environmental aspects revealed through metagenomics of Brazilian mangroves. AMB Express, 2013, 3, 65.	3.0	40
9	Increased LPS levels coexist with systemic inflammation and result in monocyte activation in severe COVID-19 patients. International Immunopharmacology, 2021, 100, 108125.	3.8	40
10	Population-based prevalence surveys during the Covid-19 pandemic: A systematic review. Reviews in Medical Virology, 2021, 31, e2200.	8.3	33
11	Genomic Analyses and Transcriptional Profiles of the Glycoside Hydrolase Family 18 Genes of the Entomopathogenic Fungus Metarhizium anisopliae. PLoS ONE, 2014, 9, e107864.	2.5	28
12	Evaluation of the impact of functional diversification on Poaceae, Brassicaceae, Fabaceae, and Pinaceae alcohol dehydrogenase enzymes. Journal of Molecular Modeling, 2010, 16, 919-928.	1.8	25
13	Sequence and structural aspects of the functional diversification of plant alcohol dehydrogenases. Gene, 2007, 396, 108-115.	2.2	23
14	Polyurethanases: Three-dimensional structures and molecular dynamics simulations of enzymes that degrade polyurethane. Journal of Molecular Graphics and Modelling, 2019, 89, 82-95.	2.4	23
15	Genome-Wide Analysis of Secondary Metabolite Gene Clusters in Ophiostoma ulmi and Ophiostoma novo-ulmi Reveals a Fujikurin-Like Gene Cluster with a Putative Role in Infection. Frontiers in Microbiology, 2017, 8, 1063.	3.5	22
16	Comparative metagenomics reveals different hydrocarbon degradative abilities from enriched oil-drilling waste. Chemosphere, 2018, 209, 7-16.	8.2	22
17	Genomic epidemiology of SARS-CoV-2 in Esteio, Rio Grande do Sul, Brazil. BMC Genomics, 2021, 22, 371.	2.8	22
18	Patterns of molecular evolution in pathogenesis-related proteins. Genetics and Molecular Biology, 2005, 28, 645-653.	1.3	20

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19	Molecular Modeling of Pathogenesis-Related Proteins of Family 5. <i>Cell Biochemistry and Biophysics</i> , 2006, 44, 385-394.	1.8	18
20	Molecular evolution and functional divergence of alcohol dehydrogenases in animals, fungi and plants. <i>Genetics and Molecular Biology</i> , 2018, 41, 341-354.	1.3	16
21	Mutation hotspots and spatiotemporal distribution of SARS-CoV-2 lineages in Brazil, February 2020-2021. <i>Virus Research</i> , 2021, 304, 198532.	2.2	15
22	Diversification and distinctive structural features of S-RNase alleles in the genus <i>Solanum</i> . <i>Molecular Genetics and Genomics</i> , 2015, 290, 987-1002.	2.1	13
23	Contribution of WUSCHEL-related homeobox (WOX) genes to identify the phylogenetic relationships among <i>Petunia</i> species. <i>Genetics and Molecular Biology</i> , 2016, 39, 658-664.	1.3	11
24	Predominance of the SARS-CoV-2 Lineage P.1 and Its Sublineage P.1.2 in Patients from the Metropolitan Region of Porto Alegre, Southern Brazil in March 2021. <i>Pathogens</i> , 2021, 10, 988.	2.8	11
25	Molecular evolution analysis of WUSCHEL-related homeobox transcription factor family reveals functional divergence among clades in the homeobox region. <i>Development Genes and Evolution</i> , 2016, 226, 259-268.	0.9	10
26	Comparative Genomics and Characterization of SARS-CoV-2 P.1 (Gamma) Variant of Concern From Amazonas, Brazil. <i>Frontiers in Medicine</i> , 2022, 9, 806611.	2.6	10
27	First detection of bovine papillomavirus type 2 in cutaneous wart lesions from ovines. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 939-943.	3.0	9
28	Expression and <i>In Silico</i> Analysis of the Recombinant Bovine Papillomavirus E6 Protein as a Model for Viral Oncoproteins Studies. <i>BioMed Research International</i> , 2013, 2013, 1-9.	1.9	8
29	Molecular evolution of Pr1 proteases depicts ongoing diversification in <i>Metarhizium</i> spp. <i>Molecular Genetics and Genomics</i> , 2019, 294, 901-917.	2.1	8
30	Molecular evolution and transcriptional profile of GH3 and GH20 β -N-acetylglucosaminidases in the entomopathogenic fungus <i>Metarhizium anisopliae</i> . <i>Genetics and Molecular Biology</i> , 2018, 41, 843-857.	1.3	7
31	Crystal structure determination and dynamic studies of <i>Mycobacterium tuberculosis</i> Cytidine deaminase in complex with products. <i>Archives of Biochemistry and Biophysics</i> , 2011, 509, 108-115.	3.0	6
32	Prion protein conversion triggered by acidic condition: a molecular dynamics study through different force fields. <i>Journal of Computational Chemistry</i> , 2018, 39, 2000-2011.	3.3	6
33	Cestode strobilation: prediction of developmental genes and pathways. <i>BMC Genomics</i> , 2020, 21, 487.	2.8	5
34	Computational studies of polyurethanases from <i>Pseudomonas</i> . <i>Journal of Molecular Modeling</i> , 2021, 27, 46.	1.8	4
35	Evolution and function of the <i>Mycoplasma hyopneumoniae</i> peroxiredoxin, a 2-Cys-like enzyme with a single Cys residue. <i>Molecular Genetics and Genomics</i> , 2017, 292, 297-305.	2.1	3
36	Molecular evolution and structural analyses of the spike glycoprotein from Brazilian SARS-CoV-2 genomes: the impact of selected mutations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 3110-3128.	3.5	1

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37	Bos taurus papillomavirus (BPV) E6 protein: Sequence analysis and molecular evolution. <i>Veterinary Microbiology</i> , 2015, 181, 328-333.	1.9	0
38	Efficacy of Proxalutamide (GT0918) in Hospitalized COVID-19 Patients. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
39	Acute kidney injury associated with rhabdomyolysis in a patient with COVID-19. <i>Jornal Brasileiro De Nefrologia: Orgao Oficial De Sociedades Brasileira E Latino-Americana De Nefrologia</i> , 2021, , .	0.9	0
40	Metagenomic Analysis: A Pathway Toward Efficiency Using High-Performance Computing. <i>Lecture Notes in Networks and Systems</i> , 2022, , 555-565.	0.7	0