

Claudia Elizabeth Thompson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8923216/publications.pdf>

Version: 2024-02-01

40
papers

929
citations

430874

18
h-index

501196

28
g-index

48
all docs

48
docs citations

48
times ranked

1761
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Metagenomic Analysis: A Pathway Toward Efficiency Using High-Performance Computing. <i>Lecture Notes in Networks and Systems</i> , 2022, , 555-565.	0.7	0
3	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
4	Population-based prevalence surveys during the Covid-19 pandemic: A systematic review. <i>Reviews in Medical Virology</i> , 2021, 31, e2200.	8.3	33
5	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
6	Genomic epidemiology of SARS-CoV-2 in Esteio, Rio Grande do Sul, Brazil. <i>BMC Genomics</i> , 2021, 22, 371.	2.8	22
7	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
8	E484K as an innovative phylogenetic event for viral evolution: Genomic analysis of the E484K spike mutation in SARS-CoV-2 lineages from Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104941.	2.3	58
9	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
10	Increased LPS levels coexist with systemic inflammation and result in monocyte activation in severe COVID-19 patients. <i>International Immunopharmacology</i> , 2021, 100, 108125.	3.8	40
11	Computational studies of polyurethanases from <i>Pseudomonas</i> . <i>Journal of Molecular Modeling</i> , 2021, 27, 46.	1.8	4
12	Cestode strobilation: prediction of developmental genes and pathways. <i>BMC Genomics</i> , 2020, 21, 487.	2.8	5
13	Polyurethanases: Three-dimensional structures and molecular dynamics simulations of enzymes that degrade polyurethane. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 89, 82-95.	2.4	23
14	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
15	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
16	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Comparative metagenomics reveals different hydrocarbon degradative abilities from enriched oil-drilling waste. <i>Chemosphere</i> , 2018, 209, 7-16.	8.2	22
20	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
21	Genome-Wide Analysis of Secondary Metabolite Gene Clusters in <i>Ophiostoma ulmi</i> and <i>Ophiostoma novo-ulmi</i> Reveals a Fujikurin-Like Gene Cluster with a Putative Role in Infection. <i>Frontiers in Microbiology</i> , 2017, 8, 1063.	3.5	22
22	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
23	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
24	<i>Bos taurus</i> papillomavirus (BPV) E6 protein: Sequence analysis and molecular evolution. <i>Veterinary Microbiology</i> , 2015, 181, 328-333.	1.9	0
25	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
26	Genomic Analyses and Transcriptional Profiles of the Glycoside Hydrolase Family 18 Genes of the Entomopathogenic Fungus <i>Metarhizium anisopliae</i> . <i>PLoS ONE</i> , 2014, 9, e107864.	2.5	28
27	Comparative genome analysis of entomopathogenic fungi reveals a complex set of secreted proteins. <i>BMC Genomics</i> , 2014, 15, 822.	2.8	49
28	Genome of the Avirulent Human-Infective Trypanosome "Trypanosoma rangeli". <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3176.	3.0	72
29	Taxonomic and functional profiles of soil samples from Atlantic forest and Caatinga biomes in northeastern Brazil. <i>MicrobiologyOpen</i> , 2014, 3, 299-315.	3.0	48
30	New insights on the biology of swine respiratory tract mycoplasmas from a comparative genome analysis. <i>BMC Genomics</i> , 2013, 14, 175.	2.8	63
31	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
32	A potential source for cellulolytic enzyme discovery and environmental aspects revealed through metagenomics of Brazilian mangroves. <i>AMB Express</i> , 2013, 3, 65.	3.0	40
33	Predicting the Proteins of <i>Angomonas deanei</i> , <i>Strigomonas culicis</i> and Their Respective Endosymbionts Reveals New Aspects of the Trypanosomatidae Family. <i>PLoS ONE</i> , 2013, 8, e60209.	2.5	55
34	Metagenomic Analysis of the Microbiota from the Crop of an Invasive Snail Reveals a Rich Reservoir of Novel Genes. <i>PLoS ONE</i> , 2012, 7, e48505.	2.5	62
35	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
36	Evaluation of the impact of functional diversification on Poaceae, Brassicaceae, Fabaceae, and Pinaceae alcohol dehydrogenase enzymes. <i>Journal of Molecular Modeling</i> , 2010, 16, 919-928.	1.8	25

#	ARTICLE	IF	CITATIONS
37	Sequence and structural aspects of the functional diversification of plant alcohol dehydrogenases. <i>Gene</i> , 2007, 396, 108-115.	2.2	23
38	Molecular Modeling of Pathogenesis-Related Proteins of Family 5. <i>Cell Biochemistry and Biophysics</i> , 2006, 44, 385-394.	1.8	18
39	Patterns of molecular evolution in pathogenesis-related proteins. <i>Genetics and Molecular Biology</i> , 2005, 28, 645-653.	1.3	20
40	Efficacy of Proxalutamide (GT0918) in Hospitalized COVID-19 Patients. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0