

AndrÃ© O Hudson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/330273/publications.pdf>

Version: 2024-02-01

81
papers

1,682
citations

331259

21
h-index

315357

38
g-index

91
all docs

91
docs citations

91
times ranked

2219
citing authors

#	ARTICLE	IF	CITATIONS
1	A Three-Ring Circus: Metabolism of the Three Proteogenic Aromatic Amino Acids and Their Role in the Health of Plants and Animals. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 29.	1.6	214
2	L,L-diaminopimelate aminotransferase, a trans-kingdom enzyme shared by Chlamydia and plants for synthesis of diaminopimelate/lysine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17909-17914.	3.3	121
3	An L-Diaminopimelate Aminotransferase Defines a Novel Variant of the Lysine Biosynthesis Pathway in Plants. <i>Plant Physiology</i> , 2006, 140, 292-301.	2.3	115
4	The Synthesis and Role of β^2 -Alanine in Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 921.	1.7	112
5	Localization of Members of the β^3 -Glutamyl Transpeptidase Family Identifies Sites of Glutathione and Glutathione S-Conjugate Hydrolysis. <i>Plant Physiology</i> , 2007, 144, 1715-1732.	2.3	98
6	The Quest for Novel Antimicrobial Compounds: Emerging Trends in Research, Development, and Technologies. <i>Antibiotics</i> , 2019, 8, 8.	1.5	67
7	Comparative genomic analysis of six bacteria belonging to the genus <i>Novosphingobium</i> : insights into marine adaptation, cell-cell signaling and bioremediation. <i>BMC Genomics</i> , 2013, 14, 431.	1.2	65
8	Is Plastic Pollution in Aquatic and Terrestrial Environments a Driver for the Transmission of Pathogens and the Evolution of Antibiotic Resistance?. <i>Environmental Science & Technology</i> , 2019, 53, 1744-1745.	4.6	57
9	Identification and Partial Characterization of an L-Tyrosine Aminotransferase (TAT) from <i>Arabidopsis thaliana</i> . <i>Biochemistry Research International</i> , 2010, 2010, 1-11.	1.5	45
10	Whole genome sequencing and analysis reveal insights into the genetic structure, diversity and evolutionary relatedness of luxI and luxR homologs in bacteria belonging to the Sphingomonadaceae family. <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 188.	1.8	41
11	Biochemical and Phylogenetic Characterization of a Novel Diaminopimelate Biosynthesis Pathway in Prokaryotes Identifies a Diverged Form of <i>scpII</i> -Diaminopimelate Aminotransferase. <i>Journal of Bacteriology</i> , 2008, 190, 3256-3263.	1.0	38
12	Exploration of the <i>Neisseria</i> Resistome Reveals Resistance Mechanisms in Commensals That May Be Acquired by <i>N. gonorrhoeae</i> through Horizontal Gene Transfer. <i>Antibiotics</i> , 2020, 9, 656.	1.5	33
13	Chemical Composition and Disruption of Quorum Sensing Signaling in Geographically Diverse United States Propolis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2015, 2015, 1-10.	0.5	31
14	Amino acid-derived defense metabolites from plants: A potential source to facilitate novel antimicrobial development. <i>Journal of Biological Chemistry</i> , 2021, 296, 100438.	1.6	31
15	Identification of an <i>rshJ</i> Gene from a <i>Novosphingobium</i> sp. Necessary for Quorum-Sensing Signal Accumulation. <i>Journal of Bacteriology</i> , 2009, 191, 2551-2560.	1.0	30
16	A novel property of propolis (bee glue): Anti-pathogenic activity by inhibition of N-acyl-homoserine lactone mediated signaling in bacteria. <i>Journal of Ethnopharmacology</i> , 2011, 138, 788-797.	2.0	29
17	Synonymous codon bias and functional constraint on GC3-related DNA backbone dynamics in the prokaryotic nucleoid. <i>Nucleic Acids Research</i> , 2014, 42, 10915-10926.	6.5	29
18	Identification of Essential Genes in the Salmonella Phage SPN3US Reveals Novel Insights into Giant Phage Head Structure and Assembly. <i>Journal of Virology</i> , 2016, 90, 10284-10298.	1.5	29

#	ARTICLE	IF	CITATIONS
19	Creation of an electrokinetic characterization library for the detection and identification of biological cells. <i>Analytical and Bioanalytical Chemistry</i> , 2020, 412, 3935-3945.	1.9	26
20	Whole-Genome Sequences of 13 Endophytic Bacteria Isolated from Shrub Willow (<i>Salix</i>) Grown in Geneva, New York. <i>Genome Announcements</i> , 2014, 2, .	0.8	25
21	L,L-Diaminopimelate Aminotransferase from <i>Chlamydomonas reinhardtii</i> : A Target for Algaecide Development. <i>PLoS ONE</i> , 2011, 6, e20439.	1.1	24
22	Whole genome sequencing of <i>Rhodotorula mucilaginosa</i> isolated from the chewing stick (<i>Distemonanthus benthamianus</i>): insights into <i>Rhodotorula</i> phylogeny, mitogenome dynamics and carotenoid biosynthesis. <i>PeerJ</i> , 2017, 5, e4030.	0.9	20
23	Genome Sequence of <i>Novosphingobium</i> sp. Strain Rr 2-17, a Nopaline Crown Gall-Associated Bacterium Isolated from <i>Vitis vinifera</i> L. Grapevine. <i>Journal of Bacteriology</i> , 2012, 194, 5137-5138.	1.0	18
24	Dual diaminopimelate biosynthesis pathways in <i>Bacteroides fragilis</i> and <i>Clostridium thermocellum</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1162-1168.	1.1	17
25	Genome Sequence of <i>Methylobacterium</i> sp. Strain GXF4, a Xylem-Associated Bacterium Isolated from <i>Vitis vinifera</i> L. Grapevine. <i>Journal of Bacteriology</i> , 2012, 194, 5157-5158.	1.0	17
26	Whole-Genome Sequences of Five Oligotrophic Bacteria Isolated from Deep within Lechuguilla Cave, New Mexico. <i>Genome Announcements</i> , 2014, 2, .	0.8	17
27	L,L-diaminopimelate aminotransferase (DapL): a putative target for the development of narrow-spectrum antibacterial compounds. <i>Frontiers in Microbiology</i> , 2014, 5, 509.	1.5	16
28	Dihydrodipicolinate Synthase: Structure, Dynamics, Function, and Evolution. <i>Sub-Cellular Biochemistry</i> , 2017, 83, 271-289.	1.0	15
29	Insight Into the Microbial Co-occurrence and Diversity of 73 Grapevine (<i>Vitis vinifera</i>) Crown Galls Collected Across the Northern Hemisphere. <i>Frontiers in Microbiology</i> , 2019, 10, 1896.	1.5	15
30	Genomic and Biochemical Analysis of the Diaminopimelate and Lysine Biosynthesis Pathway in <i>Verrucomicrobium spinosum</i> : Identification and Partial Characterization of L,L-Diaminopimelate Aminotransferase and UDP-N-Acetylmuramoylalanyl-D-glutamyl-2,6-meso-Diaminopimelate Ligase. <i>Frontiers in Microbiology</i> , 2012, 3, 183.	1.5	14
31	Expression of a Shiga-Like Toxin during Plastic Colonization by Two Multidrug-Resistant Bacteria, <i>Aeromonas hydrophila</i> RIT668 and <i>Citrobacter freundii</i> RIT669, Isolated from Endangered Turtles (<i>Clemmys guttata</i>). <i>Microorganisms</i> , 2020, 8, 1172.	1.6	14
32	Genome sequencing-assisted identification and the first functional validation of N-acyl-homoserine-lactone synthases from the Sphingomonadaceae family. <i>PeerJ</i> , 2016, 4, e2332.	0.9	13
33	Whole-Genome Sequence and Annotation of Octopine-Utilizing <i>Pseudomonas kilonensis</i> (Previously P.) Tj ETQq1 1,0,784314 rgBT / Overlock 10 Tf 50 62 Td (<	0,8	12
34	Function and evolution of B-Raf loop dynamics relevant to cancer recurrence under drug inhibition. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 468-483.	2.0	12
35	Cloning, expression, purification, crystallization and preliminary X-ray diffraction studies of N-acetylneuraminidase from methicillin-resistant <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 306-312.	0.7	11
36	Whole-Genome Sequence and Classification of 11 Endophytic Bacteria from Poison Ivy () Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 62 Td (<	0,8	11

#	ARTICLE	IF	CITATIONS
37	The <i>Arabidopsis thaliana</i> gene annotated by the locus tag At3g08860 encodes alanine aminotransferase. <i>Plant Direct</i> , 2019, 3, e00171.	0.8	11
38	Can all heritable biology really be reduced to a single dimension?. <i>Gene</i> , 2016, 578, 162-168.	1.0	10
39	Biochemical Characterization of UDP-N-acetylmuramoyl-L-alanyl-D-glutamate: meso-2,6-diaminopimelate ligase (MurE) from <i>Verrucomicrobium spinosum</i> DSM 4136T. <i>PLoS ONE</i> , 2013, 8, e66458.	1.1	9
40	Differential response of orthologous l,diaminopimelate aminotransferases (DapL) to enzyme inhibitory antibiotic lead compounds. <i>Bioorganic and Medicinal Chemistry</i> , 2014, 22, 523-530.	1.4	9
41	A Cut above the Rest: Characterization of the Assembly of a Large Viral Icosahedral Capsid. <i>Viruses</i> , 2020, 12, 725.	1.5	9
42	Isolation and whole-genome sequencing of <i>Pseudomonas</i> sp. RIT 623, a slow-growing bacterium endowed with antibiotic properties. <i>BMC Research Notes</i> , 2020, 13, 370.	0.6	9
43	Triplet-Based Codon Organization Optimizes the Impact of Synonymous Mutation on Nucleic Acid Molecular Dynamics. <i>Journal of Molecular Evolution</i> , 2018, 86, 91-102.	0.8	8
44	Isolation and genomic characterization of six endophytic bacteria isolated from <i>Saccharum</i> sp (sugarcane): Insights into antibiotic, secondary metabolite and quorum sensing metabolism. <i>Journal of Genomics</i> , 2018, 6, 117-121.	0.6	8
45	Computational Network Analysis Identifies Evolutionarily Conserved miRNA Gene Interactions Potentially Regulating Immune Response in Bovine Trypanosomosis. <i>Frontiers in Microbiology</i> , 2019, 10, 2010.	1.5	8
46	Evolutionary paths to macrolide resistance in a <i>Neisseria</i> commensal converge on ribosomal genes through short sequence duplications. <i>PLoS ONE</i> , 2022, 17, e0262370.	1.1	8
47	Crystallization and preliminary X-ray diffraction analysis of <i>ScpL</i> , <i>ScpL</i> -diaminopimelate aminotransferase (DapL) from <i>Chlamydomonas reinhardtii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 140-143.	0.7	7
48	Genomic characterization of eight <i>Ensifer</i> strains isolated from pristine caves and a whole genome phylogeny of <i>Ensifer</i> (<i>Sinorhizobium</i>). <i>Journal of Genomics</i> , 2017, 5, 12-15.	0.6	7
49	Functional binding dynamics relevant to the evolution of zoonotic spillovers in endemic and emergent <i>Betacoronavirus</i> strains. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 10978-10996.	2.0	7
50	Identification and Partial Characterization of a Novel UDP-N-Acetylenolpyruvoylglucosamine Reductase/UDP-N-Acetylmuramate:l-Alanine Ligase Fusion Enzyme from <i>Verrucomicrobium spinosum</i> DSM 4136T. <i>Frontiers in Microbiology</i> , 2016, 7, 362.	1.5	6
51	Structure-function analyses of two plant meso-diaminopimelate decarboxylase isoforms reveal that active-site gating provides stereochemical control. <i>Journal of Biological Chemistry</i> , 2019, 294, 8505-8515.	1.6	6
52	Whole-Genome Sequence of <i>Enterobacter</i> sp. Strain SST3, an Endophyte Isolated from Jamaican Sugarcane (<i>Saccharum</i> sp.) Stalk Tissue. <i>Journal of Bacteriology</i> , 2012, 194, 5981-5982.	1.0	5
53	Cloning, expression, purification, crystallization and X-ray diffraction analysis of dihydrodipicolinate synthase from the human pathogenic bacterium <i>Bartonella henselae</i> strain Houston-1 at 2.1 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 2-9.	0.4	5
54	SELFies and CELLfies: Whole Genome Sequencing and Annotation of Five Antibiotic Resistant Bacteria Isolated from the Surfaces of Smartphones, An Inquiry Based Laboratory Exercise in a Genomics Undergraduate Course at the Rochester Institute of Technology. <i>Journal of Genomics</i> , 2019, 7, 26-30.	0.6	5

#	ARTICLE	IF	CITATIONS
55	Exiguobacterium sp. is endowed with antibiotic properties against Gram positive and negative bacteria. BMC Research Notes, 2021, 14, 230.	0.6	5
56	Exploration of Chemical Biology Approaches to Facilitate the Discovery and Development of Novel Antibiotics. Frontiers in Tropical Diseases, 2022, 3, .	0.5	5
57	Isolation, Identification, Whole-Genome Sequencing, and Annotation of Four Bacillus Species, B. anthracis RIT375, B. circulans RIT379, B. altitudinis RIT380, and B. megaterium RIT381, from Internal Stem Tissue of the Insulin Plant Costus igneus. Genome Announcements, 2015, 3, .	0.8	4
58	Differential Evolution of β -Glucan Water Dikinase (GWD) in Plants. Plants, 2020, 9, 1101.	1.6	4
59	The crystal structure of dihydrodipicolinate reductase from the human-pathogenic bacterium <i>Bartonella henselae</i> strain Houston-1 at 2.3 Å resolution. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 885-891.	0.4	4
60	Isolation, Total Synthesis, and Biological Activities of 1-Aminocyclopropane-1-Carboxylic Acid (ACC) Containing Natural Compounds. Studies in Natural Products Chemistry, 2016, 47, 405-430.	0.8	3
61	<i>Aeromonas hydrophila</i> RIT668 and <i>Citrobacter portucalensis</i> RIT669 Potential Zoonotic Pathogens Isolated from Spotted Turtles. Microorganisms, 2020, 8, 1805.	1.6	3
62	Isolation and Whole-Genome Sequencing of 12 Mushroom-Associated Bacterial Strains: an Inquiry-Based Laboratory Exercise in a Genomics Course at the Rochester Institute of Technology. Microbiology Resource Announcements, 2020, 9, .	0.3	3
63	Genomic characterization of bacteria from the ultra-oligotrophic Madison aquifer: insight into the archetypical LuxI/LuxR and identification of novel LuxR solos. BMC Research Notes, 2021, 14, 175.	0.6	3
64	Propolis, a product of the bee hive, has an antagonistic affect on quorum sensing regulated bioluminescence, gene transcription and motility. FASEB Journal, 2011, 25, 948.1.	0.2	3
65	The purification, crystallization and preliminary X-ray diffraction analysis of two isoforms of meso-diaminopimelate decarboxylase from <i>Arabidopsis thaliana</i> . Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 663-668.	0.4	2
66	Whole-Genome Sequencing and Annotation of <i>Bacillus safensis</i> RIT372 and <i>Pseudomonas oryzihabitans</i> RIT370 from <i>Capsicum annuum</i> (Bird's Eye Chili) and <i>Capsicum chinense</i> (Yellow Lantern Chili), Respectively. Genome Announcements, 2015, 3, .	0.8	2
67	Whole-Genome Sequencing Reveals a New Genospecies of <i>Methylobacterium</i> sp. CXS13, Isolated from <i>Vitis vinifera</i> L. Xylem Sap. Genome Announcements, 2016, 4, .	0.8	2
68	Draft Genome Sequences of Five Proteobacteria Isolated from Lechuguilla Cave, New Mexico, USA, and Insights into Taxonomy and Quorum Sensing. Microbiology Resource Announcements, 2019, 8, .	0.3	2
69	Insight into the resistome and quorum sensing system of a divergent <i>Acinetobacter pittii</i> isolate from an untouched site of the Lechuguilla Cave. Access Microbiology, 2020, 2, acmi000089.	0.2	2
70	High-Quality Draft Whole-Genome Sequences of Three Strains of <i>Enterobacter</i> Isolated from Jamaican <i>Dioscorea cayenensis</i> (Yellow Yam). Genome Announcements, 2014, 2, .	0.8	1
71	Whole-Genome Sequencing and Annotation of <i>Exiguobacterium</i> sp. RIT 452, an Antibiotic-Producing Strain Isolated from a Pond Located on the Campus of the Rochester Institute of Technology. Microbiology Resource Announcements, 2018, 7, .	0.3	1
72	Whole-Genome Sequencing of <i>Pantoea</i> sp. Strain RIT388, a Potential Oral Opportunistic Pathogen Isolated from a Chewing Stick (<i>Distemonanthus benthamianus</i>). Microbiology Resource Announcements, 2020, 9, .	0.3	1

#	ARTICLE	IF	CITATIONS
73	Comparative Molecular Dynamics Simulations Provide Insight Into Antibiotic Interactions: A Case Study Using the Enzyme L,L-Diaminopimelate Aminotransferase (DapL). <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 46.	1.6	1
74	Whole-Genome Sequencing and Annotation of 10 Endophytic and Epiphytic Bacteria Isolated from <i>Lolium arundinaceum</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
75	Using Molecular Dynamics Simulations to Evaluate Ligand Binding of L, L-diaminopimelate Aminotransferase, an Enzyme Involved in Protein and Peptidoglycan Biosynthesis. <i>FASEB Journal</i> , 2019, 33, 642.1.	0.2	1
76	Isolation, Whole-Genome Sequencing, and Annotation of Three Unclassified Antibiotic-Producing Bacteria, <i>Enterobacter</i> sp. Strain RIT 637, <i>Pseudomonas</i> sp. Strain RIT 778, and <i>Deinococcus</i> sp. Strain RIT 780. <i>Microbiology Resource Announcements</i> , 2021, 10, e0086321.	0.3	1
77	Functional Complementation Analysis (FCA): A Laboratory Exercise Designed and Implemented to Supplement the Teaching of Biochemical Pathways. <i>Journal of Visualized Experiments</i> , 2016, .	0.2	0
78	Whole-Genome Sequences of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Typhimurium Strains TT6675 and TT9097 Employed in the Isolation and Characterization of a Giant Phage Mutant Collection. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
79	Isolation, Whole-Genome Sequencing, and Annotation of <i>Yimella</i> sp. RIT 621, a Strain That Produces Antibiotic Compounds against <i>Escherichia coli</i> ATCC 25922 and <i>Bacillus subtilis</i> BGSC 168. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
80	Comparative Molecular Dynamics Dynamics of the BRAF Activation Loop Reveals a Biophysical Mechanism of Cancer Recurrence Under Drug Inhibition. <i>Biophysical Journal</i> , 2019, 116, 434a.	0.2	0
81	Structure-Function Studies of the Antibiotic Target L,D-Diaminopimelate Aminotransferase from <i>Verrucomicrobium spinosum</i> Reveal an Unusual Oligomeric Structure. <i>Biochemistry</i> , 2020, 59, 2274-2288.	1.2	0