

# AndrÃ© O Hudson

## List of Publications by Year in descending order

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Version: 2024-02-01

81  
papers

1,682  
citations

331670

21  
h-index

315739

38  
g-index

91  
all docs

91  
docs citations

91  
times ranked

2219  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	3.5	12
2	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.	3.5	7
3	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.	2.5	8
4	Exploration of Chemical Biology Approaches to Facilitate the Discovery and Development of Novel Antibiotics. <i>Frontiers in Tropical Diseases</i> , 2022, 3, .	1.4	5
5	Amino acid-derived defense metabolites from plants: A potential source to facilitate novel antimicrobial development. <i>Journal of Biological Chemistry</i> , 2021, 296, 100438.	3.4	31
6	Whole-Genome Sequencing and Annotation of 10 Endophytic and Epiphytic Bacteria Isolated from <i>Lolium arundinaceum</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
7	Genomic characterization of bacteria from the ultra-oligotrophic Madison aquifer: insight into the archetypical LuxI/LuxR and identification of novel LuxR solos. <i>BMC Research Notes</i> , 2021, 14, 175.	1.4	3
8	<i>Exiguobacterium</i> sp. is endowed with antibiotic properties against Gram positive and negative bacteria. <i>BMC Research Notes</i> , 2021, 14, 230.	1.4	5
9	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.	0.6	1
10	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.	3.7	33
11	<i>Aeromonas hydrophila</i> RIT668 and <i>Citrobacter portucalensis</i> RIT669 Potential Zoonotic Pathogens Isolated from Spotted Turtles. <i>Microorganisms</i> , 2020, 8, 1805.	3.6	3
12	A Cut above the Rest: Characterization of the Assembly of a Large Viral Icosahedral Capsid. <i>Viruses</i> , 2020, 12, 725.	3.3	9
13	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.	3.6	14
14	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.	1.4	9
15	Differential Evolution of $\beta$ -Glucan Water Dikinase (GWD) in Plants. <i>Plants</i> , 2020, 9, 1101.	3.5	4
16	Whole-Genome Sequencing of <i>Pantoea</i> sp. Strain RIT388, a Potential Oral Opportunistic Pathogen Isolated from a Chewing Stick ( <i>Distemonanthus benthamianus</i> ). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
17	Structure-Function Studies of the Antibiotic Target <i>l</i> -Diaminopimelate Aminotransferase from <i>Verrucomicrobium spinosum</i> Reveal an Unusual Oligomeric Structure. <i>Biochemistry</i> , 2020, 59, 2274-2288.	2.5	0
18	Comparative Molecular Dynamics Simulations Provide Insight Into Antibiotic Interactions: A Case Study Using the Enzyme <i>L,L</i> -Diaminopimelate Aminotransferase (DapL). <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 46.	3.5	1

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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.	3.7	26
20	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. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
21	Insight into the resistome and quorum sensing system of a divergent <i>Acinetobacter pittii</i> isolate from an untouched site of the Lechuguilla Cave. <i>Access Microbiology</i> , 2020, 2, acmi000089.	0.5	2
22	The Synthesis and Role of Î²-Alanine in Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 921.	3.6	112
23	Computational Network Analysis Identifies Evolutionarily Conserved miRNA Gene Interactions Potentially Regulating Immune Response in Bovine Trypanosomosis. <i>Frontiers in Microbiology</i> , 2019, 10, 2010.	3.5	8
24	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.	3.5	15
25	The Quest for Novel Antimicrobial Compounds: Emerging Trends in Research, Development, and Technologies. <i>Antibiotics</i> , 2019, 8, 8.	3.7	67
26	Is Plastic Pollution in Aquatic and Terrestrial Environments a Driver for the Transmission of Pathogens and the Evolution of Antibiotic Resistance?. <i>Environmental Science &amp; Technology</i> , 2019, 53, 1744-1745.	10.0	57
27	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, .	0.6	0
28	Structureâ€‘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.	3.4	6
29	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.	0.9	5
30	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.	0.5	0
31	The <i>Arabidopsis thaliana</i> gene annotated by the locus tag At3g08860 encodes alanine aminotransferase. <i>Plant Direct</i> , 2019, 3, e00171.	1.9	11
32	Using Molecular Dynamics Simulations to Evaluate Ligand Binding of L, Î“diaminopimelate Aminotransferase, an Enzyme Involved in Protein and Peptidoglycan Biosynthesis. <i>FASEB Journal</i> , 2019, 33, 642.1.	0.5	1
33	Draft Genome Sequences of Five <i>Proteobacteria</i> Isolated from Lechuguilla Cave, New Mexico, USA, and Insights into Taxonomy and Quorum Sensing. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
34	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.	1.8	8
35	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. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	1
36	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.	0.9	8

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37	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.	3.5	214
38	Dihydrodipicolinate Synthase: Structure, Dynamics, Function, and Evolution. <i>Sub-Cellular Biochemistry</i> , 2017, 83, 271-289.	2.4	15
39	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
40	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.	0.9	7
41	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.	2.0	20
42	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.	0.8	5
43	Identification and Partial Characterization of a Novel UDP-N-Acetylenolpyruvoylglucosamine Reductase/UDP-N-Acetylmuramate:Alanine Ligase Fusion Enzyme from <i>Verrucomicrobium spinosum</i> DSM 4136T. <i>Frontiers in Microbiology</i> , 2016, 7, 362.	3.5	6
44	Isolation, Total Synthesis, and Biological Activities of 1-Aminocyclopropane-1-Carboxylic Acid (ACC) Containing Natural Compounds. <i>Studies in Natural Products Chemistry</i> , 2016, 47, 405-430.	1.8	3
45	Identification of Essential Genes in the <i>Salmonella</i> Phage SPN3US Reveals Novel Insights into Giant Phage Head Structure and Assembly. <i>Journal of Virology</i> , 2016, 90, 10284-10298.	3.4	29
46	Functional Complementation Analysis (FCA): A Laboratory Exercise Designed and Implemented to Supplement the Teaching of Biochemical Pathways. <i>Journal of Visualized Experiments</i> , 2016, .	0.3	0
47	Whole-Genome Sequencing Reveals a New Genospecies of <i>Methylobacterium</i> sp. GX513, Isolated from <i>Vitis vinifera</i> L. Xylem Sap. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
48	Can all heritable biology really be reduced to a single dimension?. <i>Gene</i> , 2016, 578, 162-168.	2.2	10
49	The crystal structure of dihydrodipicolinate reductase from the human-pathogenic bacterium <i>Bartonella henselae</i> strain Houston-1 at 2.3 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 885-891.	0.8	4
50	Genome sequencing-assisted identification and the first functional validation of <i>N</i> -acyl-homoserine-lactone synthases from the Sphingomonadaceae family. <i>PeerJ</i> , 2016, 4, e2332.	2.0	13
51	Whole-Genome Sequence and Classification of 11 Endophytic Bacteria from Poison Ivy ( <i>Rhus typhina</i> ) Tissues. <i>Journal of Microbiology and Biotechnology</i> , 2016, 10, 1028-1035.	0.8	11
52	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.	1.2	31
53	Isolation, Identification, Whole-Genome Sequencing, and Annotation of Four <i>Bacillus</i> Species, <i>B. anthracis</i> RIT375, <i>B. circulans</i> RIT379, <i>B. altitudinis</i> RIT380, and <i>B. megaterium</i> RIT381, from Internal Stem Tissue of the Insulin Plant <i>Costus igneus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	4
54	Whole-Genome Sequencing and Annotation of <i>Bacillus safensis</i> RIT372 and <i>Pseudomonas oryzae</i> RIT370 from <i>Capsicum annuum</i> (Bird's Eye Chili) and <i>Capsicum chinense</i> (Yellow Lantern Chili), Respectively. <i>Genome Announcements</i> , 2015, 3, .	0.8	2

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55	Whole-Genome Sequence and Annotation of Octopine-Utilizing <i>Pseudomonas kilonensis</i> (Previously <i>P. Tj ETQq1</i> ) <a href="#">10.784314</a> <a href="#">rgBT / Ove</a> <a href="#">125</a>	0.8	125
56	L,L-diaminopimelate aminotransferase (DapL): a putative target for the development of narrow-spectrum antibacterial compounds. <i>Frontiers in Microbiology</i> , 2014, 5, 509.	3.5	16
57	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
58	High-Quality Draft Whole-Genome Sequences of Three Strains of <i>Enterobacter</i> Isolated from Jamaican <i>Dioscorea cayenensis</i> (Yellow Yam). <i>Genome Announcements</i> , 2014, 2, .	0.8	1
59	Whole-Genome Sequences of Five Oligotrophic Bacteria Isolated from Deep within Lechuguilla Cave, New Mexico. <i>Genome Announcements</i> , 2014, 2, .	0.8	17
60	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.	14.5	29
61	The purification, crystallization and preliminary X-ray diffraction analysis of two isoforms of meso-diaminopimelate decarboxylase from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 663-668.	0.8	2
62	Differential response of orthologous L,L-diaminopimelate aminotransferases (DapL) to enzyme inhibitory antibiotic lead compounds. <i>Bioorganic and Medicinal Chemistry</i> , 2014, 22, 523-530.	3.0	9
63	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.	3.9	41
64	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.	2.8	65
65	Cloning, expression, purification, crystallization and preliminary X-ray diffraction studies of N-acetylneuraminate lyase from methicillin-resistant <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 306-312.	0.7	11
66	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.	2.5	9
67	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.	2.2	17
68	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.	2.2	18
69	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.	2.2	5
70	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-Acetylmuramoyl-L-alanyl-D-glutamyl-2,6-meso-Diaminopimelate Ligase. <i>Frontiers in Microbiology</i> , 2012, 3, 183.	3.5	14
71	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.	4.1	29
72	L,L-Diaminopimelate Aminotransferase from <i>Chlamydomonas reinhardtii</i> : A Target for Algaecide Development. <i>PLoS ONE</i> , 2011, 6, e20439.	2.5	24

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73	Crystallization and preliminary X-ray diffraction analysis of <i>L</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
74	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.	2.3	17
75	Propolis, a product of the bee hive, has an antagonistic affect on quorum-sensing regulated bioluminescence, gene transcription and motility. <i>FASEB Journal</i> , 2011, 25, 948.1.	0.5	3
76	Identification and Partial Characterization of an L-Tyrosine Aminotransferase (TAT) from <i>Arabidopsis thaliana</i> . <i>Biochemistry Research International</i> , 2010, 2010, 1-11.	3.3	45
77	Identification of an <i>rsh</i> Gene from a <i>Novosphingobium</i> sp. Necessary for Quorum-Sensing Signal Accumulation. <i>Journal of Bacteriology</i> , 2009, 191, 2551-2560.	2.2	30
78	Biochemical and Phylogenetic Characterization of a Novel Diaminopimelate Biosynthesis Pathway in Prokaryotes Identifies a Diverged Form of <i>ll</i> -Diaminopimelate Aminotransferase. <i>Journal of Bacteriology</i> , 2008, 190, 3256-3263.	2.2	38
79	Localization of Members of the $\hat{3}$ -Glutamyl Transpeptidase Family Identifies Sites of Glutathione and Glutathione S-Conjugate Hydrolysis. <i>Plant Physiology</i> , 2007, 144, 1715-1732.	4.8	98
80	An <i>ll</i> -Diaminopimelate Aminotransferase Defines a Novel Variant of the Lysine Biosynthesis Pathway in Plants. <i>Plant Physiology</i> , 2006, 140, 292-301.	4.8	115
81	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.	7.1	121