

# Atmika Paudel

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

906  
citations

516215

16  
h-index

500791

28  
g-index

41  
all docs

41  
docs citations

41  
times ranked

888  
citing authors

#	ARTICLE	IF	CITATIONS
1	YjbH regulates virulence genes expression and oxidative stress resistance in <i>Staphylococcus aureus</i> . <i>Virulence</i> , 2021, 12, 470-480.	1.8	25
2	Silkworm model for <i>Bacillus anthracis</i> infection and virulence determination. <i>Virulence</i> , 2021, 12, 2285-2295.	1.8	5
3	Novel chromosomal insertions of ISEcp1-blaCTX-M-15 and diverse antimicrobial resistance genes in Zambian clinical isolates of <i>Enterobacter cloacae</i> and <i>Escherichia coli</i> . <i>Antimicrobial Resistance and Infection Control</i> , 2021, 10, 79.	1.5	24
4	Complete genome sequence and comparative genomic analysis of <i>Enterococcus faecalis</i> EF-2001, a probiotic bacterium. <i>Genomics</i> , 2021, 113, 1534-1542.	1.3	27
5	Direct Regulons of AtxA, the Master Virulence Regulator of <i>Bacillus anthracis</i> . <i>MSystems</i> , 2021, 6, e0029121.	1.7	5
6	Serum apolipoprotein A-I potentiates the therapeutic efficacy of lysocin E against <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2021, 12, 6364.	5.8	12
7	Novel Pathogenic Mucorales Identified Using the Silkworm Infection Model. <i>Journal of Fungi (Basel)</i> , 2021, 6, 10784314. Tj ETQq1 1 0.784314 rgBT /Overl	1.5	4
8	Large-Scale Screening and Identification of Novel Pathogenic <i>Staphylococcus aureus</i> Genes Using a Silkworm Infection Model. <i>Journal of Infectious Diseases</i> , 2020, 221, 1795-1804.	1.9	22
9	Discovery of gramicidin A analogues with altered activities by multidimensional screening of a one-bead-one-compound library. <i>Nature Communications</i> , 2020, 11, 4935.	5.8	21
10	Clinical and epidemiological features of COVID-19 deaths in Nepal. <i>New Microbes and New Infections</i> , 2020, 38, 100797.	0.8	13
11	COVID-19: the current situation in Nepal. <i>New Microbes and New Infections</i> , 2020, 37, 100737.	0.8	19
12	The Role of Amino Acid Substitution in HepT Toward Menaquinone Isoprenoid Chain Length Definition and Lysocin E Sensitivity in <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 2076.	1.5	6
13	A simple artificial diet available for research of silkworm disease models. <i>Drug Discoveries and Therapeutics</i> , 2020, 14, 177-180.	0.6	6
14	Complete Genome Sequence of <i>Weissella hellenica</i> 0916-4-2 and Its Comparative Genomic Analysis. <i>Frontiers in Microbiology</i> , 2019, 10, 1619.	1.5	28
15	Development of a high-throughput strategy for discovery of potent analogues of antibiotic lysocin E. <i>Nature Communications</i> , 2019, 10, 2992.	5.8	36
16	GPI0363 inhibits the interaction of RNA polymerase with DNA in <i>Staphylococcus aureus</i> . <i>RSC Advances</i> , 2019, 9, 37889-37894.	1.7	12
17	Pharmacokinetic parameters explain the therapeutic activity of antimicrobial agents in a silkworm infection model. <i>Scientific Reports</i> , 2018, 8, 1578.	1.6	22
18	Total Synthesis and Biological Mode of Action of WAP-8294A2: A Menaquinone-Targeting Antibiotic. <i>Journal of Organic Chemistry</i> , 2018, 83, 6924-6935.	1.7	32

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19	Utilization of Hybrid Assembly Approach to Determine the Genome of an Opportunistic Pathogenic Fungus, <i>Candida albicans</i> TIMM 1768. <i>Genome Biology and Evolution</i> , 2018, 10, 2017-2022.	1.1	30
20	Unified Total Synthesis of Polyoxinsâ€¦J, L, and Fluorinated Analogues on the Basis of Decarbonylative Radical Coupling Reactions. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 11865-11869.	7.2	36
21	Unified Total Synthesis of Polyoxinsâ€¦J, L, and Fluorinated Analogues on the Basis of Decarbonylative Radical Coupling Reactions. <i>Angewandte Chemie</i> , 2017, 129, 12027-12031.	1.6	8
22	Total Synthesis and Antibacterial Investigation of Plusbacin A <sub>3</sub> . <i>Organic Letters</i> , 2017, 19, 3771-3774.	2.4	19
23	Advantages of the Silkworm As an Animal Model for Developing Novel Antimicrobial Agents. <i>Frontiers in Microbiology</i> , 2017, 8, 373.	1.5	69
24	A Novel Spiro-Heterocyclic Compound Identified by the Silkworm Infection Model Inhibits Transcription in <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 712.	1.5	22
25	Genomic analysis of vancomycin-resistant &i>Staphylococcus aureus &i>VRS3b and its comparison with other VRSA isolates. <i>Drug Discoveries and Therapeutics</i> , 2017, 11, 78-83.	0.6	15
26	Draft Genome Sequence of the Vancomycin-Resistant Clinical Isolate <i>Staphylococcus aureus</i> VRS3b. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
27	<i>Lysobacter</i> species: a potential source of novel antibiotics. <i>Archives of Microbiology</i> , 2016, 198, 839-845.	1.0	85
28	Menaquinone as a potential target of antibacterial agents. <i>Drug Discoveries and Therapeutics</i> , 2016, 10, 123-128.	0.6	37
29	Analgesic, Anti-inflammatory and Other Pharmacological Activities of Methanol Extract of <i>Rhododendron campanulatum</i> from Nepal. <i>European Journal of Medicinal Plants</i> , 2016, 13, 1-7.	0.5	1
30	Lysocin E is a new antibiotic that targets menaquinone in the bacterial membrane. <i>Nature Chemical Biology</i> , 2015, 11, 127-133.	3.9	194
31	Structureâ€“activity relationship study of novel iminothiadiazolo-pyrimidinone antimicrobial agents. <i>Journal of Antibiotics</i> , 2013, 66, 663-667.	1.0	15
32	Identification of novel deoxyribofuranosyl indole antimicrobial agents. <i>Journal of Antibiotics</i> , 2012, 65, 53-57.	1.0	39