## Nishant A Dafale

List of Publications by Year in descending order

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Version: 2024-02-01

1163117 1372567 11 168 8 10 citations h-index g-index papers 11 11 11 90 citing authors docs citations times ranked all docs

#	Article	IF	CITATIONS
1	Genomically Defined Paenibacillus polymyxa ND24 for Efficient Cellulase Production Utilizing Sugarcane Bagasse as a Substrate. Applied Biochemistry and Biotechnology, 2019, 187, 266-281.	2.9	28
2	Environmental Distribution, Metabolic Fate, and Degradation Mechanism of Chlorpyrifos: Recent and Future Perspectives. Applied Biochemistry and Biotechnology, 2022, 194, 2301-2335.	2.9	25
3	Paenibacillus polymyxa ND25: candidate genome for lignocellulosic biomass utilization. 3 Biotech, 2018, 8, 248.	2.2	23
4	Understanding Ethanol Tolerance Mechanism in Saccharomyces cerevisiae to Enhance the Bioethanol Production: Current and Future Prospects. Bioenergy Research, 2021, 14, 670-688.	3.9	21
5	Unraveling the camel rumen microbiome through metaculturomics approach for agriculture waste hydrolytic potential. Archives of Microbiology, 2021, 203, 107-123.	2.2	18
6	Exploring the rearrangement of sensory intelligence in proteobacteria: insight of Pho regulon. World Journal of Microbiology and Biotechnology, 2018, 34, 172.	3.6	14
7	Regulatory rewiring through global gene regulations by PhoB and alarmone (p)ppGpp under various stress conditions. Microbiological Research, 2019, 227, 126309.	5.3	13
8	Exploring the eukaryotic diversity in rumen of Indian camel (Camelus dromedarius) using 18S rRNA amplicon sequencing. Archives of Microbiology, 2020, 202, 1861-1872.	2.2	12
9	Synergistic action of lytic polysaccharide monooxygenase with glycoside hydrolase for lignocellulosic waste valorization: a review. Biomass Conversion and Biorefinery, 2023, 13, 8727-8745.	4.6	8
10	Unique pool of carbohydrate-degrading enzymes in novel bacteria assembled from cow and buffalo rumen metagenomes. Applied Microbiology and Biotechnology, 2022, 106, 4643-4654.	3.6	4
11	Revealing the potential of Klebsiella pneumoniae PVN-1 for plant beneficial attributes by genome sequencing and analysis. 3 Biotech, 2021, 11, 473.	2.2	2