

Krishan Gopal Thakur

List of Publications by Year in descending order

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37
papers

754
citations

471509
17
h-index

580821
25
g-index

44
all docs

44
docs citations

44
times ranked

1053
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular docking and dynamic simulation approach to decipher steroidal sapogenins (genus) <i>Tj ETQq1</i> 1 0.784314 rgBT /Overlock 107 and Dynamics, 2023, 41, 55-66.	3.5	4
2	A Microbe-Derived Efflux Pump Inhibitor of the Resistance-Nodulation-Cell Division Protein Restores Antibiotic Susceptibility in <i>Escherichia coli</i> and <i>Pseudomonas aeruginosa</i> . ACS Infectious Diseases, 2022, 8, 255-270.	3.8	19
3	A novel plant lectin, NTL-125, interferes with SARS-CoV-2 interaction with hACE2. Virus Research, 2022, 315, 198768.	2.2	5
4	Structural characterization of <i>Myxococcus xanthus</i> MglC, a component of the polarity control system, and its interactions with its paralog MglB. Journal of Biological Chemistry, 2021, 296, 100308.	3.4	7
5	Antifungal Azoles as Tetracycline Resistance Modifiers in <i>Staphylococcus aureus</i> . Applied and Environmental Microbiology, 2021, 87, e0015521.	3.1	17
6	Chlorhexidine: An effective anticovid mouth rinse. Journal of Indian Society of Periodontology, 2021, 25, 86-88.	0.7	16
7	Chlorhexidine: An effective anticovid mouth rinse. Journal of Indian Society of Periodontology, 2021, 25, 86.	0.7	42
8	Repurposing Approved Drugs as Fluoroquinolone Potentiators to Overcome Efflux Pump Resistance in <i>Staphylococcus aureus</i> . Microbiology Spectrum, 2021, 9, e0095121.	3.0	16
9	Biochemical and Taxonomic Characterization of Novel Haloarchaeal Strains and Purification of the Recombinant Halotolerant α -Amylase Discovered in the Isolate. Frontiers in Microbiology, 2020, 11, 2082.	3.5	7
10	Structure-Guided Designing and Evaluation of Peptides Targeting Bacterial Transcription. Frontiers in Bioengineering and Biotechnology, 2020, 8, 797.	4.1	6
11	Isolation and Taxonomic Characterization of Novel Haloarchaeal Isolates From Indian Solar Saltern: A Brief Review on Distribution of Bacteriorhodopsins and V-Type ATPases in Haloarchaea. Frontiers in Microbiology, 2020, 11, 554927.	3.5	5
12	VapBC22 toxin-antitoxin system from <i>Mycobacterium tuberculosis</i> is required for pathogenesis and modulation of host immune response. Science Advances, 2020, 6, eaba6944.	10.3	32
13	Molecular and Biochemical Characterization of YeeF/YezG, a Polymorphic Toxin-Immunity Protein Pair From <i>Bacillus subtilis</i> . Frontiers in Microbiology, 2020, 11, 95.	3.5	15
14	Microbe-Derived Indole Metabolite Demonstrates Potent Multidrug Efflux Pump Inhibition in <i>Staphylococcus aureus</i> . Frontiers in Microbiology, 2019, 10, 2153.	3.5	24
15	Structure Elucidation and Biochemical Characterization of Environmentally Relevant Novel Exradiol Dioxygenases Discovered by a Functional Metagenomics Approach. MSystems, 2019, 4, .	3.8	8
16	Discovery of bacteriorhodopsins in Haloarchaeal species isolated from Indian solar salterns: deciphering the role of the N-terminal residues in protein folding and functional expression. Microbial Biotechnology, 2019, 12, 434-446.	4.2	9
17	System-Wide Analysis Unravels the Differential Regulation and In Vivo Essentiality of Virulence-Associated Proteins B and C Toxin-Antitoxin Systems of <i>Mycobacterium tuberculosis</i> . Journal of Infectious Diseases, 2018, 217, 1809-1820.	4.0	39
18	Structural, functional and biological insights into the role of <i>Mycobacterium tuberculosis</i> VapBC11 toxin-antitoxin system: targeting a tRNase to tackle mycobacterial adaptation. Nucleic Acids Research, 2018, 46, 11639-11655.	14.5	37

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19	Mycobacterium tuberculosis CarD, an essential global transcriptional regulator forms amyloid-like fibrils. Scientific Reports, 2018, 8, 10124.	3.3	22
20	Escherichia coli Î²-clamp slows down DNA polymerase I dependent nick translation while accelerating ligation. PLoS ONE, 2018, 13, e0199559.	2.5	7
21	Structural insights into the mechanism of Type IVa pilus extension and retraction ATPase motors. FEBS Journal, 2018, 285, 3402-3421.	4.7	21
22	Bacillus subtilis HelD, an RNA Polymerase Interacting Helicase, Forms Amyloid-Like Fibrils. Frontiers in Microbiology, 2018, 9, 1934.	3.5	12
23	Crystal structure of <i>Mycobacterium tuberculosis</i> VapC20 toxin and its interactions with cognate antitoxin, VapB20, suggest a model for toxin-antitoxin assembly. FEBS Journal, 2017, 284, 4066-4082.	4.7	23
24	Facile fabrication of lipase to amine functionalized gold nanoparticles to enhance stability and activity. RSC Advances, 2017, 7, 42845-42855.	3.6	34
25	Functional and Structural Characterization of Purine Nucleoside Phosphorylase from Kluyveromyces lactis and Its Potential Applications in Reducing Purine Content in Food. PLoS ONE, 2016, 11, e0164279.	2.5	23
26	Crystal structure of the N-terminal domain of human SIRT7 reveals a three-helical domain architecture. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1558-1563.	2.6	22
27	Dual Role of a Biosynthetic Enzyme, CysK, in Contact Dependent Growth Inhibition in Bacteria. PLoS ONE, 2016, 11, e0159844.	2.5	16
28	The intramolecular disulfide-stapled structure of laterosporulin, a class II bacteriocin, conceals a human defensin-like structural module. FEBS Journal, 2015, 282, 203-214.	4.7	32
29	Structural basis for the redox sensitivity of the <i>Mycobacterium tuberculosis</i> SigK-RskA Îf-anti-Îf complex. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1026-1036.	2.5	35
30	Crystal structure of <i>Mycobacterium tuberculosis</i> CarD, an essential RNA polymerase binding protein, reveals a quasidomain-swapped dimeric structural architecture. Proteins: Structure, Function and Bioinformatics, 2014, 82, 879-884.	2.6	21
31	<i>Mycobacterium tuberculosis</i> Keto-Mycolic Acid and Macrophage Nuclear Receptor TR4 Modulate Foamy Biogenesis in Granulomas: A Case of a Heterologous and Noncanonical Ligand-Receptor Pair. Journal of Immunology, 2014, 193, 295-305.	0.8	61
32	<i>Mycobacterium tuberculosis</i> Rv2704 is a member of the YjgF/YER057c/UK114 family. Proteins: Structure, Function and Bioinformatics, 2010, 78, 773-778.	2.6	17
33	X-ray crystallographic and NMR studies of pantothenate synthetase provide insights into the mechanism of homotropic inhibition by pantoate. FEBS Journal, 2010, 277, 697-712.	4.7	3
34	Structural and Biochemical Bases for the Redox Sensitivity of Mycobacterium tuberculosis RslA. Journal of Molecular Biology, 2010, 397, 1199-1208.	4.2	43
35	Over-expression and purification strategies for recombinant multi-protein oligomers: A case study of Mycobacterium tuberculosis Îf/anti-Îf factor protein complexes. Protein Expression and Purification, 2010, 74, 223-230.	1.3	12
36	Structural and Biophysical Studies on Two Promoter Recognition Domains of the Extra-cytoplasmic Function Îf Factor ÎfC from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2007, 282, 4711-4718.	3.4	29

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37	Crystallization and preliminary X-ray diffraction studies of two domains of a bilobed extra-cytoplasmic function sigma factor SigC from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 779-781.	0.7	3