Yogendra Singh

List of Publications by Year
in descending order

68	1,961	236925 25	276875 41
papers	citations	h-index	g-index

74	74	74	2519
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Bacterial Virulence Factors: Secreted for Survival. Indian Journal of Microbiology, 2017, 57, 1-10.	2.7	126
2	Gut microbiome contributes to impairment of immunity in pulmonary tuberculosis patients by alteration of butyrate and propionate producers. Environmental Microbiology, 2018, 20, 402-419.	3.8	120
3	Role ofMycobacterium tuberculosisSer/Thr Kinase PknF: Implications in Glucose Transport and Cell Division. Journal of Bacteriology, 2005, 187, 3415-3420.	2.2	87
4	Interaction of Mycobacterium tuberculosis Elongation Factor Tu with GTP Is Regulated by Phosphorylation. Journal of Bacteriology, 2011, 193, 5347-5358.	2.2	86
5	Serine threonine protein kinases of mycobacterial genus: phylogeny to function. Physiological Genomics, 2007, 29, 66-75.	2.3	76
6	Comparative Genomic Analysis Reveals Habitat-Specific Genes and Regulatory Hubs within the Genus Novosphingobium. MSystems, 2017, 2, .	3.8	75
7	Protein Phosphatases of Pathogenic Bacteria: Role in Physiology and Virulence. Annual Review of Microbiology, 2015, 69, 527-547.	7.3	74
8	HupB, a Nucleoid-Associated Protein of Mycobacterium tuberculosis, Is Modified by Serine/Threonine Protein Kinases In Vivo. Journal of Bacteriology, 2014, 196, 2646-2657.	2.2	63
9	Computational tools for modern vaccine development. Human Vaccines and Immunotherapeutics, 2020, 16, 723-735.	3.3	61
10	Comparative Genomic Analysis of Rapidly Evolving SARS-CoV-2 Reveals Mosaic Pattern of Phylogeographical Distribution. MSystems, 2020, 5, .	3.8	60
11	Forkhead-associated Domain-containing Protein Rv0019c and Polyketide-associated Protein PapA5, from Substrates of Serine/Threonine Protein Kinase PknB to Interacting Proteins of Mycobacterium tuberculosis. Journal of Biological Chemistry, 2009, 284, 34723-34734.	3.4	55
12	Microbial taxonomy in the era of OMICS: application of DNA sequences, computational tools and techniques. Antonie Van Leeuwenhoek, 2017, 110, 1357-1371.	1.7	54
13	Systematic Analysis of Mycobacterial Acylation Reveals First Example of Acylation-mediated Regulation of Enzyme Activity of a Bacterial Phosphatase. Journal of Biological Chemistry, 2015, 290, 26218-26234.	3.4	53
14	Identification and characterization of a laminin-binding protein of Aspergillus fumigatus: extracellular thaumatin domain protein (AfCalAp). Journal of Medical Microbiology, 2009, 58, 714-722.	1.8	51
15	Understanding the Role of PknJ in Mycobacterium tuberculosis: Biochemical Characterization and Identification of Novel Substrate Pyruvate Kinase A. PLoS ONE, 2010, 5, e10772.	2.5	45
16	Regulation of homocysteine metabolism by Mycobacterium tuberculosis S-adenosylhomocysteine hydrolase. Scientific Reports, 2013, 3, 2264.	3.3	42
17	Modification of Rifamycin Polyketide Backbone Leads to Improved Drug Activity against Rifampicin-resistant Mycobacterium tuberculosis. Journal of Biological Chemistry, 2014, 289, 21142-21152.	3.4	40
18	Serine/Threonine Protein Phosphatase PstP of Mycobacterium tuberculosis Is Necessary for Accurate Cell Division and Survival of Pathogen. Journal of Biological Chemistry, 2016, 291, 24215-24230.	3.4	40

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19	Ser/Thr protein kinase PrkC-mediated regulation of GroEL is critical for biofilm formation in Bacillus anthracis. Npj Biofilms and Microbiomes, 2017, 3, 7.	6.4	40
20	Interplay of Human Gut Microbiome in Health and Wellness. Indian Journal of Microbiology, 2020, 60, 26-36.	2.7	40
21	Unveiling the Novel Dual Specificity Protein Kinases in Bacillus anthracis. Journal of Biological Chemistry, 2012, 287, 26749-26763.	3.4	35
22	Zinc regulates the activity of kinase-phosphatase pair (BasPrkC/BasPrpC) in Bacillus anthracis. BioMetals, 2013, 26, 715-730.	4.1	34
23	Comparative genomic analysis of novel Acinetobacter symbionts: A combined systems biology and genomics approach. Scientific Reports, 2016, 6, 29043.	3.3	33
24	The Ser/Thr protein kinase PrkC imprints phenotypic memory in Bacillus anthracis spores by phosphorylating the glycolytic enzyme enolase. Journal of Biological Chemistry, 2019, 294, 8930-8941.	3.4	30
25	Bacterial and Archaeal Viruses of Himalayan Hot Springs at Manikaran Modulate Host Genomes. Frontiers in Microbiology, 2018, 9, 3095.	3.5	27
26	Fictibacillus halophilus sp. nov., from a microbial mat of a hot spring atop the Himalayan Range. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2409-2416.	1.7	24
27	Comparative Genomics and Integrated Network Approach Unveiled Undirected Phylogeny Patterns, Co-mutational Hot Spots, Functional Cross Talk, and Regulatory Interactions in SARS-CoV-2. MSystems, 2021, 6, .	3.8	23
28	clpC operon regulates cell architecture and sporulation in Bacillus anthracis. Environmental Microbiology, 2015, 17, 855-865.	3.8	22
29	Identification of Ser/Thr kinase and Forkhead Associated Domains in Mycobacterium ulcerans: Characterization of Novel Association between Protein Kinase Q and MupFHA. PLoS Neglected Tropical Diseases, 2014, 8, e3315.	3.0	20
30	Genome Organization of Sphingobium indicum B90A: An Archetypal Hexachlorocyclohexane (HCH) Degrading Genotype. Genome Biology and Evolution, 2017, 9, 2191-2197.	2.5	17
31	Suppression of Toll-like receptor 2â€“mediated proinflammatory responses by Mycobacterium tuberculosis protein Rv3529c. Journal of Leukocyte Biology, 2017, 102, 1249-1259.	3.3	17
32	Comparative genomics of Sphingopyxis spp. unravelled functional attributes. Genomics, 2020, 112, 1956-1969.	2.9	17
33	Diagnostic performance of non-invasive, stool-based molecular assays in patients with paucibacillary tuberculosis. Scientific Reports, 2020, 10, 7102.	3.3	17
34	Compromised base excision repair pathway in Mycobacterium tuberculosis imparts superior adaptability in the host. PLoS Pathogens, 2021, 17, e1009452.	4.7	16
35	Suppression of Protective Responses upon Activation of L-Type Voltage Gated Calcium Channel in Macrophages during Mycobacterium bovis BCG Infection. PLoS ONE, 2016, 11, e0163845.	2.5	15
36	Corynebacterium pollutisoli sp. nov., isolated from hexachlorocyclohexane-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3531-3537.	1.7	15

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37	Computational approaches in epitope design using DNA binding proteins as vaccine candidate in Mycobacterium tuberculosis. Infection, Genetics and Evolution, 2020, 83, 104357.	2.3	14
38	Systems Biology Approaches for Therapeutics Development Against COVID-19. Frontiers in Cellular and Infection Microbiology, 2020, 10, 560240.	3.9	13
39	Comparative metagenomic analyses of a high-altitude Himalayan geothermal spring revealed temperature-constrained habitat-specific microbial community and metabolic dynamics. Archives of Microbiology, 2019, 201, 377-388.	2.2	12
40	Comparative Genomic Analysis of Mycobacteriaceae Reveals Horizontal Gene Transfer-Mediated Evolution of the CRISPR-Cas System in the Mycobacterium tuberculosis Complex. MSystems, 2021, 6, .	3.8	11
41	Adhesins in the virulence of opportunistic fungal pathogens of human. Mycology, 2021, 12, 296-324.	4.4	11
42	Gut microbiome of endangered Tor putitora (Ham.) as a reservoir of antibiotic resistance genes and pathogens associated with fish health. BMC Microbiology, 2020, 20, 249.	3.3	10
43	Mycobacterium tuberculosis exploits host ATM kinase for survival advantage through SecA2 secretome. ELife, 2020, 9, .	6.0	10
44	Harnessing taxonomically diverse and metabolically versatile genus Paracoccus for bioplastic synthesis and xenobiotic biodegradation. Journal of Applied Microbiology, 2022, 132, 4208-4224.	3.1	10
45	Phylogenetic and Structural Analysis of Polyketide Synthases inAspergilli. Evolutionary Bioinformatics, 2016, 12, EBO.S32694.	1.2	9
46	Complete genome sequence of Paracoccus sp. strain AK26: Insights into multipartite genome architecture and methylotropy. Genomics, 2020, 112, 2572-2582.	2.9	9
47	Mycobacterium tuberculosis Peptidyl Prolyl Isomerase A Interacts With Host Integrin Receptor to Exacerbate Disease Progression. Journal of Infectious Diseases, 2021, 224, 1383-1393.	4.0	9
48	Draft genome sequence of Lampropedia cohaerens strain CT6T isolated from arsenic rich microbial mats of a Himalayan hot water spring. Standards in Genomic Sciences, 2016, 11, 64.	1.5	8
49	Highlight on Engineering Mycobacterium smegmatis for testosterone production. Microbial Biotechnology, 2017, 10, 73-75.	4.2	8
50	Methylation of two-component response regulator MtrA in mycobacteria negatively modulates its DNA binding and transcriptional activation. Biochemical Journal, 2020, 477, 4473-4489.	3.7	7
51	Human Milk Microbiota: Transferring the Antibiotic Resistome to Infants. Indian Journal of Microbiology, 2019, 59, 410-416.	2.7	6
52	Prediction of Transcription Factors and Their Involvement in Regulating Rifamycin Production in Amycolatopsis mediterranei S699. Indian Journal of Microbiology, 2020, 60, 310-317.	2.7	6
53	Comparative proteomics unravelled the hexachlorocyclohexane (HCH) isomers specific responses in an archetypical HCH degrading bacterium Sphingobium indicum B90A. Environmental Science and Pollution Research, 2021, 28, 41380-41395.	5.3	6
54	Differential mass spectrometry-based proteome analyses unveil major regulatory hubs in rifamycin B production in Amycolatopsis mediterranei. Journal of Proteomics, 2021, 239, 104168.	2.4	6

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55	Effect of Homocysteine on Biofilm Formation by Mycobacteria. Indian Journal of Microbiology, 2018, 58, 287-293.	2.7	5
56	Comparison of DNA Extraction Methods for Optimal Recovery of Metagenomic DNA from Human and Environmental Samples. Indian Journal of Microbiology, 2019, 59, 482-489.	2.7	5
57	PrkC, a Transmembrane Serine/Threonine Protein Kinase, Regulates Bacterial Chain Length in Bacillus anthracis. Journal of Bacteriology, 2021, 203, .	2.2	5
58	Recent Developments in Anti-dotes Against Anthrax. Recent Patents on Anti-infective Drug Discovery, 2015, 9, 83-96.	0.8	5
59	Regulation of Interferon-Î³ receptor (IFN-Î³R) expression in macrophages during Mycobacterium tuberculosis infection. Biomolecular Concepts, 2020, 11, 76-85.	2.2	5
60	GroEL Mediates Folding of Bacillus anthracis Serine/Threonine Protein Kinase, PrkC. Indian Journal of Microbiology, 2018, 58, 520-524.	2.7	4
61	Quorum Sensing Inhibition: A Target for Treating Chronic Wounds. , 2018, , 111-126.		3
62	Draft Genome Sequence of Deinococcus sp. Strain S9, Isolated from Microbial Mat Deposits of Hot Springs Located atop the Himalayan Ranges at Manikaran, India. Microbiology Resource Announcements, 2019, 8, .	0.6	3
63	Phylogenomic Framework for Taxonomic Delineation of Paracoccus spp. and Exploration of Core-Pan Genome. Indian Journal of Microbiology, 2021, 61, 180-194.	2.7	3
64	ClpC-Mediated Sporulation Regulation at Engulfment Stage in Bacillus anthracis. Indian Journal of Microbiology, 2021, 61, 170-179.	2.7	3
65	Recent developments in systems biology and genetic engineering toward design of vaccines for TB. Critical Reviews in Biotechnology, 2021, , 1-16.	9.0	3
66	Evaluating the efficacy of stool sample on Xpert MTB/RIF Ultra and its comparison with other sample types by meta-analysis for TB diagnostics. European Journal of Clinical Microbiology and Infectious Diseases, 2022, 41, 893-906.	2.9	2
67	Deletion of serine/threonine-protein kinase pknL from Mycobacterium tuberculosis reduces the efficacy of isoniazid and ethambutol. Tuberculosis, 2021, 128, 102066.	1.9	1
68	Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences. Indian Journal of Microbiology, 2021, 61, 111-115.	2.7	0