

Govind Chandra

List of Publications by Year in descending order

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70
papers

5,501
citations

101543

36
h-index

98798

67
g-index

89
all docs

89
docs citations

89
times ranked

5648
citing authors

#	ARTICLE	IF	CITATIONS
1	Hyphal compartmentalization and sporulation in <i>Streptomyces</i> require the conserved cell division protein SepX. <i>Nature Communications</i> , 2022, 13, 71.	12.8	9
2	How do <i>Streptomyces</i> coordinate DNA repair and cell division following DNA damage?. <i>Access Microbiology</i> , 2022, 4, .	0.5	0
3	Genome-Wide Identification of the LexA-Mediated DNA Damage Response in <i>Streptomyces venezuelae</i> . <i>Journal of Bacteriology</i> , 2022, 204, .	2.2	3
4	A User Guide for the Identification of New RiPP Biosynthetic Gene Clusters Using a RiPPER-Based Workflow. <i>Methods in Molecular Biology</i> , 2021, 2296, 227-247.	0.9	8
5	A conserved cell division protein directly regulates FtsZ dynamics in filamentous and unicellular actinobacteria. <i>ELife</i> , 2021, 10, .	6.0	12
6	Re-wiring the regulation of the formicamycin biosynthetic gene cluster to enable the development of promising antibacterial compounds. <i>Cell Chemical Biology</i> , 2021, 28, 515-523.e5.	5.2	16
7	<i>Streptomyces venezuelae</i> NRRL B-65442: genome sequence of a model strain used to study morphological differentiation in filamentous actinobacteria. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2021, , .	3.0	14
8	Evolution of a c -di-GMP anti- σ switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	11
9	The microbiome of a shell mound: ancient anthropogenic waste as a source of <i>Streptomyces</i> degrading recalcitrant polysaccharides. <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 210.	3.6	1
10	Pan-genome analysis identifies intersecting roles for <i>Pseudomonas</i> specialized metabolites in potato pathogen inhibition. <i>ELife</i> , 2021, 10, .	6.0	25
11	c -di-GMP Arms an Anti- σ to Control Progression of Multicellular Differentiation in <i>Streptomyces</i> . <i>Molecular Cell</i> , 2020, 77, 586-599.e6.	9.7	58
12	The novel ECF56 SigG1-RsfG system modulates morphological differentiation and metal-ion homeostasis in <i>Streptomyces tsukubaensis</i> . <i>Scientific Reports</i> , 2020, 10, 21728.	3.3	4
13	Regulation of Bottromycin Biosynthesis Involves an Internal Transcriptional Start Site and a Cluster-Situated Modulator. <i>Frontiers in Microbiology</i> , 2020, 11, 495.	3.5	7
14	Developmentally regulated volatiles geosmin and 2-methylisoborneol attract a soil arthropod to <i>Streptomyces</i> bacteria promoting spore dispersal. <i>Nature Microbiology</i> , 2020, 5, 821-829.	13.3	102
15	Control of mRNA translation by dynamic ribosome modification. <i>PLoS Genetics</i> , 2020, 16, e1008837.	3.5	13
16	Control of mRNA translation by dynamic ribosome modification. , 2020, 16, e1008837.		0
17	Control of mRNA translation by dynamic ribosome modification. , 2020, 16, e1008837.		0
18	Control of mRNA translation by dynamic ribosome modification. , 2020, 16, e1008837.		0

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19	Immunity-Guided Identification of Threonyl-tRNA Synthetase as the Molecular Target of Obaflourin, a β -Lactone Antibiotic. <i>ACS Chemical Biology</i> , 2019, 14, 2663-2671.	3.4	13
20	Uncovering the unexplored diversity of thioamidated ribosomal peptides in Actinobacteria using the RiPPER genome mining tool. <i>Nucleic Acids Research</i> , 2019, 47, 4624-4637.	14.5	98
21	Defining the regulon of genes controlled by σ^E , a key regulator of the cell envelope stress response in <i>Streptomyces coelicolor</i> . <i>Molecular Microbiology</i> , 2019, 112, 461-481.	2.5	27
22	BldC Delays Entry into Development To Produce a Sustained Period of Vegetative Growth in <i>Streptomyces venezuelae</i> . <i>MBio</i> , 2019, 10, .	4.1	36
23	Discovery and Biosynthesis of the Antibiotic Bicyclomycin in Distantly Related Bacterial Classes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	36
24	The MerR-like protein BldC binds DNA direct repeats as cooperative multimers to regulate <i>Streptomyces</i> development. <i>Nature Communications</i> , 2018, 9, 1139.	12.8	26
25	Hierarchical interactions between Fnr orthologs allows fine-tuning of transcription in response to oxygen in <i>Herbaspirillum seropedicae</i> . <i>Nucleic Acids Research</i> , 2018, 46, 3953-3966.	14.5	5
26	The crystal structure of the RsbN- σ^E complex from <i>Streptomyces venezuelae</i> defines a new structural class of anti- σ factor. <i>Nucleic Acids Research</i> , 2018, 46, 7405-7417.	14.5	10
27	Genome wide identification and experimental validation of <i>Pseudomonas aeruginosa</i> Tat substrates. <i>Scientific Reports</i> , 2018, 8, 11950.	3.3	11
28	Multi-layered inhibition of <i>Streptomyces</i> development: BldO is a dedicated repressor of σ^B . <i>Molecular Microbiology</i> , 2017, 104, 700-711.	2.5	20
29	Translational Control of the SigR-Directed Oxidative Stress Response in <i>Streptomyces</i> via IF3-Mediated Repression of a Noncanonical GTC Start Codon. <i>MBio</i> , 2017, 8, .	4.1	25
30	Two dynamin-like proteins stabilize FtsZ rings during <i>Streptomyces</i> sporulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6176-E6183.	7.1	70
31	The Conserved Actinobacterial Two-Component System MtrAB Coordinates Chloramphenicol Production with Sporulation in <i>Streptomyces venezuelae</i> NRRL B-65442. <i>Frontiers in Microbiology</i> , 2017, 8, 1145.	3.5	44
32	Analyzing the Complex Regulatory Landscape of Hfq – an Integrative, Multi-Omics Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 1784.	3.5	17
33	The MtrAB two-component system controls antibiotic production in <i>Streptomyces coelicolor</i> A3(2). <i>Microbiology (United Kingdom)</i> , 2017, 163, 1415-1419.	1.8	62
34	One ligand, two regulators and three binding sites: How KDPG controls primary carbon metabolism in <i>Pseudomonas</i> . <i>PLoS Genetics</i> , 2017, 13, e1006839.	3.5	39
35	A unifying mechanism for the biogenesis of membrane proteins co-operatively integrated by the Sec and Tat pathways. <i>ELife</i> , 2017, 6, .	6.0	11
36	Discovery of Unusual Biaryl Polyketides by Activation of a Silent <i>Streptomyces venezuelae</i> Biosynthetic Gene Cluster. <i>ChemBioChem</i> , 2016, 17, 2189-2198.	2.6	50

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37	Cosmid based mutagenesis causes genetic instability in <i>Streptomyces coelicolor</i> , as shown by targeting of the lipoprotein signal peptidase gene. <i>Scientific Reports</i> , 2016, 6, 29495.	3.3	4
38	Genome-Wide Chromatin Immunoprecipitation Sequencing Analysis Shows that WhiB Is a Transcription Factor That Cocontrols Its Regulon with WhiA To Initiate Developmental Cell Division in <i>Streptomyces</i> . <i>MBio</i> , 2016, 7, e00523-16.	4.1	81
39	Metabolic Network for the Biosynthesis of Intra- and Extracellular β -Glucans Required for Virulence of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005768.	4.7	46
40	Stability and succession of the rhizosphere microbiota depends upon plant type and soil composition. <i>ISME Journal</i> , 2015, 9, 2349-2359.	9.8	302
41	The <i>Streptomyces leeuwenhoekii</i> genome: de novo sequencing and assembly in single contigs of the chromosome, circular plasmid pSLE1 and linear plasmid pSLE2. <i>BMC Genomics</i> , 2015, 16, 485.	2.8	61
42	New Insights into Chloramphenicol Biosynthesis in <i>Streptomyces venezuelae</i> ATCC 10712. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 7441-7450.	3.2	74
43	Response Regulator Heterodimer Formation Controls a Key Stage in <i>Streptomyces</i> Development. <i>PLoS Genetics</i> , 2014, 10, e1004554.	3.5	82
44	A holin and an endopeptidase are essential for chitinolytic protein secretion in <i>Serratia marcescens</i> . <i>Journal of Cell Biology</i> , 2014, 207, 615-626.	5.2	47
45	Developmental biology of <i>Streptomyces</i> from the perspective of 100 actinobacterial genome sequences. <i>FEMS Microbiology Reviews</i> , 2014, 38, 345-379.	8.6	120
46	Molecular Regulation of Antibiotic Biosynthesis in <i>Streptomyces</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2013, 77, 112-143.	6.6	611
47	P _{ll} signal transduction proteins: nitrogen regulation and beyond. <i>FEMS Microbiology Reviews</i> , 2013, 37, 251-283.	8.6	178
48	Genes Required for Aerial Growth, Cell Division, and Chromosome Segregation Are Targets of WhiA before Sporulation in <i>Streptomyces venezuelae</i> . <i>MBio</i> , 2013, 4, e00684-13.	4.1	121
49	Topoisomerase I (TopA) Is Recruited to ParB Complexes and Is Required for Proper Chromosome Organization during <i>Streptomyces coelicolor</i> Sporulation. <i>Journal of Bacteriology</i> , 2013, 195, 4445-4455.	2.2	39
50	Investigation of DNA sequence recognition by a streptomycete MarR family transcriptional regulator through surface plasmon resonance and X-ray crystallography. <i>Nucleic Acids Research</i> , 2013, 41, 7009-7022.	14.5	39
51	Draft Genome Sequence of the Human Pathogen <i>Streptomyces somaliensis</i> , a Significant Cause of Actinomycetoma. <i>Journal of Bacteriology</i> , 2012, 194, 3544-3545.	2.2	33
52	Expression of the chaplin and rodlin hydrophobic sheath proteins in <i>Streptomyces venezuelae</i> is controlled by σ^{BldN} and a cognate anti- σ factor, RsbN. <i>Molecular Microbiology</i> , 2012, 84, 1033-1049.	2.5	106
53	Dissecting the complete lipoprotein biogenesis pathway in <i>Streptomyces scabies</i> . <i>Molecular Microbiology</i> , 2011, 80, 1395-1412.	2.5	42
54	Genome-wide analysis of the role of GlnR in <i>Streptomyces venezuelae</i> provides new insights into global nitrogen regulation in actinomycetes. <i>BMC Genomics</i> , 2011, 12, 175.	2.8	127

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55	The actinobacteria-specific gene <i>wblA</i> controls major developmental transitions in <i>Streptomyces coelicolor</i> A3(2). <i>Microbiology (United Kingdom)</i> , 2011, 157, 1312-1328.	1.8	82
56	Unexpected and widespread connections between bacterial glycogen and trehalose metabolism. <i>Microbiology (United Kingdom)</i> , 2011, 157, 1565-1572.	1.8	136
57	The twin arginine protein transport pathway exports multiple virulence proteins in the plant pathogen <i>Streptomyces scabies</i> . <i>Molecular Microbiology</i> , 2010, 77, 252-271.	2.5	71
58	Investigating lipoprotein biogenesis and function in the model Gram-positive bacterium <i>Streptomyces coelicolor</i> . <i>Molecular Microbiology</i> , 2010, 77, 943-957.	2.5	56
59	Genes essential for morphological development and antibiotic production in <i>Streptomyces coelicolor</i> are targets of BldD during vegetative growth. <i>Molecular Microbiology</i> , 2010, 78, 361-379.	2.5	193
60	Genome Sequence of the Fleming Strain of <i>Micrococcus luteus</i> , a Simple Free-Living Actinobacterium. <i>Journal of Bacteriology</i> , 2010, 192, 841-860.	2.2	68
61	The use of the rare UUA codon to define "Expression Space" for genes involved in secondary metabolism, development and environmental adaptation in <i>Streptomyces</i> . <i>Journal of Microbiology</i> , 2008, 46, 1-11.	2.8	123
62	Evolutionary flux of potentially <i>bldA</i> -dependent <i>Streptomyces</i> genes containing the rare leucine codon TTA. <i>Antonie Van Leeuwenhoek</i> , 2008, 94, 111-126.	1.7	41
63	The Transcriptional Repressor Protein NsrR Senses Nitric Oxide Directly via a [2Fe-2S] Cluster. <i>PLoS ONE</i> , 2008, 3, e3623.	2.5	121
64	Genomics of <i>Actinobacteria</i> : Tracing the Evolutionary History of an Ancient Phylum. <i>Microbiology and Molecular Biology Reviews</i> , 2007, 71, 495-548.	6.6	852
65	A genetic and bioinformatic analysis of <i>Streptomyces coelicolor</i> genes containing TTA codons, possible targets for regulation by a developmentally significant tRNA. <i>FEMS Microbiology Letters</i> , 2007, 266, 20-28.	1.8	43
66	The evolution of development in <i>Streptomyces</i> analysed by genome comparisons. <i>FEMS Microbiology Reviews</i> , 2006, 30, 651-672.	8.6	130
67	The twin-arginine translocation pathway is a major route of protein export in <i>Streptomyces coelicolor</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17927-17932.	7.1	134
68	Transposon Express, a software application to report the identity of insertions obtained by comprehensive transposon mutagenesis of sequenced genomes: analysis of the preference for in vitro Tn5 transposition into GC-rich DNA. <i>Nucleic Acids Research</i> , 2004, 32, e113-e113.	14.5	37
69	Sensing and responding to diverse extracellular signals? Analysis of the sensor kinases and response regulators of <i>Streptomyces coelicolor</i> A3(2). <i>Microbiology (United Kingdom)</i> , 2004, 150, 2795-2806.	1.8	147
70	Red-Mediated Genetic Manipulation of Antibiotic-Producing <i>Streptomyces</i> . <i>Advances in Applied Microbiology</i> , 2004, 54, 107-128.	2.4	251