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	Genomics ofActinobacteria: Tracing the Evolutionary History of an Ancient Phylum. Microbiology and Molecular Biology Reviews, 2007, 71, 495-548.	6.6	852
2	Molecular Regulation of Antibiotic Biosynthesis in Streptomyces. Microbiology and Molecular Biology Reviews, 2013, 77, 112-143.	6.6	611
3	Stability and succession of the rhizosphere microbiota depends upon plant type and soil composition. ISME Journal, 2015, 9, 2349-2359.	9.8	302
4	Î» Red-Mediated Genetic Manipulation of Antibiotic-Producing Streptomyces. Advances in Applied Microbiology, 2004, 54, 107-128.	2.4	251
5	Genes essential for morphological development and antibiotic production in Streptomyces coelicolor are targets of BldD during vegetative growth. Molecular Microbiology, 2010, 78, 361-379.	2.5	193
6	P_{II}signal transduction proteins: nitrogen regulation and beyond. FEMS Microbiology Reviews, 2013, 37, 251-283.	8.6	178
7	Sensing and responding to diverse extracellular signals? Analysis of the sensor kinases and response regulators of Streptomyces coelicolor A3(2). Microbiology (United Kingdom), 2004, 150, 2795-2806.	1.8	147
8	Unexpected and widespread connections between bacterial glycogen and trehalose metabolism. Microbiology (United Kingdom), 2011, 157, 1565-1572.	1.8	136
9	The twin-arginine translocation pathway is a major route of protein export in Streptomyces coelicolor. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17927-17932.	7.1	134
10	The evolution of development inStreptomycesanalysed by genome comparisons. FEMS Microbiology Reviews, 2006, 30, 651-672.	8.6	130
11	Genome-wide analysis of the role of GlnR in Streptomyces venezuelae provides new insights into global nitrogen regulation in actinomycetes. BMC Genomics, 2011, 12, 175.	2.8	127
12	The use of the rare UUA codon to define â€œExpression Spaceâ€•for genes involved in secondary metabolism, development and environmental adaptation in Streptomyces. Journal of Microbiology, 2008, 46, 1-11.	2.8	123
13	Genes Required for Aerial Growth, Cell Division, and Chromosome Segregation Are Targets of WhiA before Sporulation in Streptomyces venezuelae. MBio, 2013, 4, e00684-13.	4.1	121
14	The Transcriptional Repressor Protein NsrR Senses Nitric Oxide Directly via a [2Fe-2S] Cluster. PLoS ONE, 2008, 3, e3623.	2.5	121
15	Developmental biology ofStreptomycesfrom the perspective of 100 actinobacterial genome sequences. FEMS Microbiology Reviews, 2014, 38, 345-379.	8.6	120
16	Expression of the chaplin and rodlin hydrophobic sheath proteins in Streptomyces venezuelae is controlled by Ïƒ^{BldN} and a cognate antiâ€sigma factor, RsbN. Molecular Microbiology, 2012, 84, 1033-1049.	2.5	106
17	Developmentally regulated volatiles geosmin and 2-methylisoborneol attract a soil arthropod to Streptomyces bacteria promoting spore dispersal. Nature Microbiology, 2020, 5, 821-829.	13.3	102
18	Uncovering the unexplored diversity of thioamidated ribosomal peptides in Actinobacteria using the RiPPER genome mining tool. Nucleic Acids Research, 2019, 47, 4624-4637.	14.5	98

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19	The actinobacteria-specific gene wblA controls major developmental transitions in Streptomyces coelicolor A3(2). Microbiology (United Kingdom), 2011, 157, 1312-1328.	1.8	82
20	Response Regulator Heterodimer Formation Controls a Key Stage in Streptomyces Development. PLoS Genetics, 2014, 10, e1004554.	3.5	82
21	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 Streptomyces. MBio, 2016, 7, e00523-16.	4.1	81
22	New Insights into Chloramphenicol Biosynthesis in Streptomyces venezuelae ATCC 10712. Antimicrobial Agents and Chemotherapy, 2014, 58, 7441-7450.	3.2	74
23	The twin arginine protein transport pathway exports multiple virulence proteins in the plant pathogen Streptomyces scabies. Molecular Microbiology, 2010, 77, 252-271.	2.5	71
24	Two dynamin-like proteins stabilize FtsZ rings during Streptomyces sporulation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6176-E6183.	7.1	70
25	Genome Sequence of the Fleming Strain of Micrococcus luteus , a Simple Free-Living Actinobacterium. Journal of Bacteriology, 2010, 192, 841-860.	2.2	68
26	The MtrAB two-component system controls antibiotic production in Streptomyces coelicolor A3(2). Microbiology (United Kingdom), 2017, 163, 1415-1419.	1.8	62
27	The Streptomyces leeuwenhoekii genome: de novo sequencing and assembly in single contigs of the chromosome, circular plasmid pSLE1 and linear plasmid pSLE2. BMC Genomics, 2015, 16, 485.	2.8	61
28	c-di-GMP Arms an Anti-Ïƒ to Control Progression of Multicellular Differentiation in Streptomyces. Molecular Cell, 2020, 77, 586-599.e6.	9.7	58
29	Investigating lipoprotein biogenesis and function in the model Gramâ€positive bacterium Streptomyces coelicolor. Molecular Microbiology, 2010, 77, 943-957.	2.5	56
30	Discovery of Unusual Biaryl Polyketides by Activation of a Silent Streptomyces venezuelae Biosynthetic Gene Cluster. ChemBioChem, 2016, 17, 2189-2198.	2.6	50
31	A holin and an endopeptidase are essential for chitinolytic protein secretion in Serratia marcescens. Journal of Cell Biology, 2014, 207, 615-626.	5.2	47
32	Metabolic Network for the Biosynthesis of Intra- and Extracellular Î±-Glucans Required for Virulence of Mycobacterium tuberculosis. PLoS Pathogens, 2016, 12, e1005768.	4.7	46
33	The Conserved Actinobacterial Two-Component System MtrAB Coordinates Chloramphenicol Production with Sporulation in Streptomyces venezuelae NRRL B-65442. Frontiers in Microbiology, 2017, 8, 1145.	3.5	44
34	A genetic and bioinformatic analysis ofStreptomyces coelicolorgenes containing TTA codons, possible targets for regulation by a developmentally significant tRNA. FEMS Microbiology Letters, 2007, 266, 20-28.	1.8	43
35	Dissecting the complete lipoprotein biogenesis pathway in Streptomyces scabies. Molecular Microbiology, 2011, 80, 1395-1412.	2.5	42
36	Evolutionary flux of potentially bldA-dependent Streptomyces genes containing the rare leucine codon TTA. Antonie Van Leeuwenhoek, 2008, 94, 111-126.	1.7	41

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37	Topoisomerase I (TopA) Is Recruited to ParB Complexes and Is Required for Proper Chromosome Organization during Streptomyces coelicolor Sporulation. Journal of Bacteriology, 2013, 195, 4445-4455.	2.2	39
38	Investigation of DNA sequence recognition by a streptomycete MarR family transcriptional regulator through surface plasmon resonance and X-ray crystallography. Nucleic Acids Research, 2013, 41, 7009-7022.	14.5	39
39	One ligand, two regulators and three binding sites: How KDPG controls primary carbon metabolism in Pseudomonas. PLoS Genetics, 2017, 13, e1006839.	3.5	39
40	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. Nucleic Acids Research, 2004, 32, e113-e113.	14.5	37
41	Discovery and Biosynthesis of the Antibiotic Bicyclomycin in Distantly Related Bacterial Classes. Applied and Environmental Microbiology, 2018, 84, .	3.1	36
42	BldC Delays Entry into Development To Produce a Sustained Period of Vegetative Growth in Streptomyces venezuelae. MBio, 2019, 10, .	4.1	36
43	Draft Genome Sequence of the Human Pathogen Streptomyces somaliensis, a Significant Cause of Actinomycetoma. Journal of Bacteriology, 2012, 194, 3544-3545.	2.2	33
44	Defining the regulon of genes controlled by Ïƒ^E, a key regulator of the cell envelope stress response in Streptomyces coelicolor. Molecular Microbiology, 2019, 112, 461-481.	2.5	27
45	The MerR-like protein BldC binds DNA direct repeats as cooperative multimers to regulate Streptomyces development. Nature Communications, 2018, 9, 1139.	12.8	26
46	Translational Control of the SigR-Directed Oxidative Stress Response in Streptomyces via IF3-Mediated Repression of a Noncanonical GTC Start Codon. MBio, 2017, 8, .	4.1	25
47	Pan-genome analysis identifies intersecting roles for Pseudomonas specialized metabolites in potato pathogen inhibition. ELife, 2021, 10, .	6.0	25
48	Multiâ€layered inhibition of Streptomyces development: BldO is a dedicated repressor of whiB. Molecular Microbiology, 2017, 104, 700-711.	2.5	20
49	Analyzing the Complex Regulatory Landscape of Hfq â€“ an Integrative, Multi-Omics Approach. Frontiers in Microbiology, 2017, 8, 1784.	3.5	17
50	Re-wiring the regulation of the formicamycin biosynthetic gene cluster to enable the development of promising antibacterial compounds. Cell Chemical Biology, 2021, 28, 515-523.e5.	5.2	16
51	Streptomyces venezuelae NRRL B-65442: genome sequence of a model strain used to study morphological differentiation in filamentous actinobacteria. Journal of Industrial Microbiology and Biotechnology, 2021, , .	3.0	14
52	Immunity-Guided Identification of Threonyl-tRNA Synthetase as the Molecular Target of Obafluorin, a Î²-Lactone Antibiotic. ACS Chemical Biology, 2019, 14, 2663-2671.	3.4	13
53	Control of mRNA translation by dynamic ribosome modification. PLoS Genetics, 2020, 16, e1008837.	3.5	13
54	A conserved cell division protein directly regulates FtsZ dynamics in filamentous and unicellular actinobacteria. ELife, 2021, 10, .	6.0	12

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55	Genome wide identification and experimental validation of Pseudomonas aeruginosa Tat substrates. Scientific Reports, 2018, 8, 11950.	3.3	11
56	Evolution of a Ïƒâ€“(c-di-GMP)â€“anti-Ïƒ switch. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	11
57	A unifying mechanism for the biogenesis of membrane proteins co-operatively integrated by the Sec and Tat pathways. ELife, 2017, 6, .	6.0	11
58	The crystal structure of the RsbNâ€“ÏƒBldN complex from Streptomyces venezuelae defines a new structural class of anti-Ïƒ factor. Nucleic Acids Research, 2018, 46, 7405-7417.	14.5	10
59	Hyphal compartmentalization and sporulation in Streptomyces require the conserved cell division protein SepX. Nature Communications, 2022, 13, 71.	12.8	9
60	A User Guide for the Identification of New RiPP Biosynthetic Gene Clusters Using a RiPPER-Based Workflow. Methods in Molecular Biology, 2021, 2296, 227-247.	0.9	8
61	Regulation of Bottromycin Biosynthesis Involves an Internal Transcriptional Start Site and a Cluster-Situated Modulator. Frontiers in Microbiology, 2020, 11, 495.	3.5	7
62	Hierarchical interactions between Fnr orthologs allows fine-tuning of transcription in response to oxygen in Herbaspirillum seropedicae. Nucleic Acids Research, 2018, 46, 3953-3966.	14.5	5
63	Cosmid based mutagenesis causes genetic instability in Streptomyces coelicolor, as shown by targeting of the lipoprotein signal peptidase gene. Scientific Reports, 2016, 6, 29495.	3.3	4
64	The novel ECF56 SigG1-RsfG system modulates morphological differentiation and metal-ion homeostasis in Streptomyces tsukubaensis. Scientific Reports, 2020, 10, 21728.	3.3	4
65	Genome-Wide Identification of the LexA-Mediated DNA Damage Response in Streptomyces venezuelae. Journal of Bacteriology, 2022, 204, .	2.2	3
66	The microbiome of a shell mound: ancient anthropogenic waste as a source of Streptomyces degrading recalcitrant polysaccharides. World Journal of Microbiology and Biotechnology, 2021, 37, 210.	3.6	1
67	Control of mRNA translation by dynamic ribosome modification. , 2020, 16, e1008837.		0
68	Control of mRNA translation by dynamic ribosome modification. , 2020, 16, e1008837.		0
69	Control of mRNA translation by dynamic ribosome modification. , 2020, 16, e1008837.		0
70	How do Streptomyces coordinate DNA repair and cell division following DNA damage?. Access Microbiology, 2022, 4, .	0.5	0