Gilles P Van Wezel

List of Publications by Year
in descending order

181 papers	14,895 citations	30070 54 h-index	24258 110 g-index
226 all docs	226 docs citations	226 times ranked	12900 citing authors

#	Article	IF	Citations
1	antiSMASH 6.0: improving cluster detection and comparison capabilities. Nucleic Acids Research, 2021, 49, W29-W35.	14.5	1,520
2	Taxonomy, Physiology, and Natural Products of Actinobacteria. Microbiology and Molecular Biology Reviews, 2016, 80, 1-43.	6.6	1,395
3	Objective comparison of particle tracking methods. Nature Methods, 2014, 11, 281-289.	19.0	805
4	Minimum Information about a Biosynthetic Gene cluster. Nature Chemical Biology, 2015, 11, 625-631.	8.0	715
5	Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. Science, 2019, 366, 606-612.	12.6	621
6	New developments in RiPP discovery, enzymology and engineering. Natural Product Reports, 2021, 38, 130-239.	10.3	412
7	The regulation of the secondary metabolism of Streptomyces: new links and experimental advances. Natural Product Reports, 2011, 28, 1311.	10.3	390
8	Bacterial solutions to multicellularity: a tale of biofilms, filaments and fruiting bodies. Nature Reviews Microbiology, 2014, 12, 115-124.	28.6	379
9	Feast or famine: the global regulator DasR links nutrient stress to antibiotic production by <i>Streptomyces</i>. EMBO Reports, 2008, 9, 670-675.	4.5	358
10	Chemical ecology of antibiotic production by actinomycetes. FEMS Microbiology Reviews, 2017, 41, 392-416.	8.6	337
11	The Square-Planar Cytotoxic [CuII(pyrimol)Cl] Complex Acts as an Efficient DNA Cleaver without Reductant. Journal of the American Chemical Society, 2006, 128, 710-711.	13.7	216
12	Regulation of antibiotic production in Actinobacteria: new perspectives from the post-genomic era. Natural Product Reports, 2018, 35, 575-604.	10.3	203
13	Socially mediated induction and suppression of antibiosis during bacterial coexistence. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11054-11059.	7.1	198
14	The sugar phosphotransferase system of <i>Streptomyces coelicolor</i> is regulated by the GntRâ€family regulator DasR and links <i>N</i>â€acetylglucosamine metabolism to the control of development. Molecular Microbiology, 2006, 61, 1237-1251.	2.5	188
15	Ecology and genomics of Actinobacteria: new concepts for natural product discovery. Nature Reviews Microbiology, 2020, 18, 546-558.	28.6	188
16	Positive control of cell division: FtsZ is recruited by SsgB during sporulation of <i>Streptomyces</i>. Genes and Development, 2011, 25, 89-99.	5.9	176
17	Diversity and functions of volatile organic compounds produced by Streptomyces from a disease-suppressive soil. Frontiers in Microbiology, 2015, 6, 1081.	3.5	174
18	Triggers and cues that activate antibiotic production by actinomycetes. Journal of Industrial Microbiology and Biotechnology, 2014, 41, 371-386.	3.0	162

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19	Cell division and DNA segregation in <i>Streptomyces</i>: how to build a septum in the middle of nowhere?. Molecular Microbiology, 2012, 85, 393-404.	2.5	128
20	ssgA Is Essential for Sporulation ofStreptomyces coelicolor A3(2) and Affects Hyphal Development by Stimulating Septum Formation. Journal of Bacteriology, 2000, 182, 5653-5662.	2.2	119
21	Structure, Cytotoxicity, and DNA-Cleavage Properties of the Complex [Cu^{II}(pbt)Br₂]. Inorganic Chemistry, 2008, 47, 3719-3727.	4.0	118
22	Unlocking Streptomyces spp. for Use as Sustainable Industrial Production Platforms by Morphological Engineering. Applied and Environmental Microbiology, 2006, 72, 5283-5288.	3.1	117
23	Phenanthroline Derivatives with Improved Selectivity as DNAâ€Targeting Anticancer or Antimicrobial Drugs. ChemMedChem, 2008, 3, 1427-1434.	3.2	111
24	The Genome Sequence of Streptomyces lividans 66 Reveals a Novel tRNA-Dependent Peptide Biosynthetic System within a Metal-Related Genomic Island. Genome Biology and Evolution, 2013, 5, 1165-1175.	2.5	99
25	MreB of Streptomyces coelicolor is not essential for vegetative growth but is required for the integrity of aerial hyphae and spores. Molecular Microbiology, 2006, 60, 838-852.	2.5	98
26	PREDetector: A new tool to identify regulatory elements in bacterial genomes. Biochemical and Biophysical Research Communications, 2007, 357, 861-864.	2.1	97
27	Substrate induction and glucose repression of maltose utilization by <i>Streptomyces coelicolor</i> A3(2) is controlled by <i>malR</i>, a member of the <i>lacIâ€“galR</i> family of regulatory genes. Molecular Microbiology, 1997, 23, 537-549.	2.5	95
28	Morphogenesis of Streptomyces in Submerged Cultures. Advances in Applied Microbiology, 2014, 89, 1-45.	2.4	92
29	Functional Analysis of the N-Acetylglucosamine Metabolic Genes of Streptomyces coelicolor and Role in Control of Development and Antibiotic Production. Journal of Bacteriology, 2012, 194, 1136-1144.	2.2	87
30	Eliciting antibiotics active against the ESKAPE pathogens in a collection of actinomycetes isolated from mountain soils. Microbiology (United Kingdom), 2014, 160, 1714-1725.	1.8	87
31	Intertwining nutrientâ€sensory networks and the control of antibiotic production in <i>Streptomyces</i>. Molecular Microbiology, 2016, 102, 183-195.	2.5	87
32	A community resource for paired genomic and metabolomic data mining. Nature Chemical Biology, 2021, 17, 363-368.	8.0	81
33	Relative quantification of proteasome activity by activity-based protein profiling and LC-MS/MS. Nature Protocols, 2013, 8, 1155-1168.	12.0	77
34	Expansion of RiPP biosynthetic space through integration of pan-genomics and machine learning uncovers a novel class of lanthipeptides. PLoS Biology, 2020, 18, e3001026.	5.6	75
35	Conserved <i>cis</i>-Acting Elements Upstream of Genes Composing the Chitinolytic System of Streptomycetes Are DasR-Responsive Elements. Journal of Molecular Microbiology and Biotechnology, 2007, 12, 60-66.	1.0	74
36	Expanding the chemical space for natural products by Aspergillus-Streptomyces co-cultivation and biotransformation. Scientific Reports, 2015, 5, 10868.	3.3	74

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37	The permease gene<i>nagE2</i>is the key to<i>N</i>â€acetylglucosamine sensing and utilization in<i>Streptomyces coelicolor</i>and is subject to multiâ€level control. Molecular Microbiology, 2010, 75, 1133-1144.	2.5	73
38	Metabolomics in the natural products field â€" a gateway to novel antibiotics. Drug Discovery Today: Technologies, 2015, 13, 11-17.	4.0	73
39	Unique Ligand-Based Oxidative DNA Cleavage by Zinc(II) Complexes of Hpyramol and Hpyrimol. Chemistry - A European Journal, 2007, 13, 5213-5222.	3.3	72
40	The chitobiose-binding protein, DasA, acts as a link between chitin utilization and morphogenesis in Streptomyces coelicolor. Microbiology (United Kingdom), 2008, 154, 373-382.	1.8	72
41	From Dormant to Germinating Spores ofStreptomycescoelicolorA3(2):Â New Perspectives from thecrpNull Mutant. Journal of Proteome Research, 2005, 4, 1699-1708.	3.7	71
42	GlcP constitutes the major glucose uptake system of <i>Streptomyces coelicolor</i> A3(2). Molecular Microbiology, 2005, 55, 624-636.	2.5	70
43	SsgA-like proteins determine the fate of peptidoglycan during sporulation ofStreptomyces coelicolor. Molecular Microbiology, 2005, 58, 929-944.	2.5	70
44	Chapter 5 Applying the Genetics of Secondary Metabolism in Model Actinomycetes to the Discovery of New Antibiotics. Methods in Enzymology, 2009, 458, 117-141.	1.0	70
45	TheStreptomyces coelicolor ssgBgene is required for early stages of sporulation. FEMS Microbiology Letters, 2003, 225, 59-67.	1.8	69
46	The SsgA-like proteins in actinomycetes: small proteins up to a big task. Antonie Van Leeuwenhoek, 2008, 94, 85-97.	1.7	67
47	A novel taxonomic marker that discriminates between morphologically complex actinomycetes. Open Biology, 2013, 3, 130073.	3.6	66
48	Transcription of the sporulation gene ssgA is activated by the IclR-type regulator SsgR in a whi-independent manner in Streptomyces coelicolor A3(2). Molecular Microbiology, 2004, 53, 985-1000.	2.5	65
49	Developmental Regulation of the Streptomyces lividans ram Genes: Involvement of RamR in Regulation of the ramCSAB Operon. Journal of Bacteriology, 2002, 184, 4420-4429.	2.2	64
50	The evolution of no-cost resistance at sub-MIC concentrations of streptomycin in <i>Streptomyces coelicolor</i>. ISME Journal, 2017, 11, 1168-1178.	9.8	64
51	Cracking the regulatory code of biosynthetic gene clusters as a strategy for natural product discovery. Biochemical Pharmacology, 2018, 153, 24-34.	4.4	64
52	The DyP-type peroxidase DtpA is a Tat-substrate required for GlxA maturation and morphogenesis in <i>Streptomyces</i>. Open Biology, 2016, 6, 150149.	3.6	63
53	Streptomyces leeuwenhoekii sp. nov., the producer of chaxalactins and chaxamycins, forms a distinct branch in Streptomyces gene trees. Antonie Van Leeuwenhoek, 2014, 105, 849-861.	1.7	62
54	Metabolomics-Driven Discovery of a Prenylated Isatin Antibiotic Produced by <i>Streptomyces</i> Species MBT28. Journal of Natural Products, 2015, 78, 2355-2363.	3.0	60

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55	RRE-Finder: a Genome-Mining Tool for Class-Independent RiPP Discovery. MSystems, 2020, 5, .	3.8	60
56	Antibiotic production in <i>Streptomyces</i> is organized by a division of labor through terminal genomic differentiation. Science Advances, 2020, 6, eaay5781.	10.3	60
57	A New Piece of an Old Jigsaw: Glucose Kinase Is Activated Posttranslationally in a Glucose Transport-Dependent Manner in <i>Streptomyces coelicolor </i>A3(2). Journal of Molecular Microbiology and Biotechnology, 2007, 12, 67-74.	1.0	57
58	Unsuspected control of siderophore production by <i>N</i>â€acetylglucosamine in streptomycetes. Environmental Microbiology Reports, 2012, 4, 512-521.	2.4	57
59	Multidimensional View of the Bacterial Cytoskeleton. Journal of Bacteriology, 2013, 195, 1627-1636.	2.2	57
60	Loss of the controlled localization of growth stage-specific cell-wall synthesis pleiotropically affects developmental gene expression in an ssgA mutant of Streptomyces coelicolor. Molecular Microbiology, 2007, 64, 1244-1259.	2.5	55
61	Goodbye to brute force in antibiotic discovery?. Nature Microbiology, 2016, 1, 15020.	13.3	55
62	Healthy scents: microbial volatiles as new frontier in antibiotic research?. Current Opinion in Microbiology, 2018, 45, 84-91.	5.1	55
63	A novel locus for mycelial aggregation forms a gateway to improved Streptomyces cell factories. Microbial Cell Factories, 2015, 14, 44.	4.0	54
64	New approaches to achieve high level enzyme production in Streptomyces lividans. Microbial Cell Factories, 2016, 15, 28.	4.0	54
65	Inter- and intracellular colonization of Arabidopsis roots by endophytic actinobacteria and the impact of plant hormones on their antimicrobial activity. Antonie Van Leeuwenhoek, 2018, 111, 679-690.	1.7	54
66	The ROK Family Regulator Rok7B7 Pleiotropically Affects Xylose Utilization, Carbon Catabolite Repression, and Antibiotic Production in Streptomyces coelicolor. Journal of Bacteriology, 2013, 195, 1236-1248.	2.2	53
67	Stress-induced formation of cell wall-deficient cells in filamentous actinomycetes. Nature Communications, 2018, 9, 5164.	12.8	52
68	Production of ammonia as a low-cost and long-distance antibiotic strategy by <i>Streptomyces</i> species. ISME Journal, 2020, 14, 569-583.	9.8	52
69	The malEFG gene cluster of Streptomyces coelicolor A3(2): characterization, disruption and transcriptional analysis. Molecular Genetics and Genomics, 1997, 254, 604-608.	2.4	51
70	Natural Product Proteomining, a Quantitative Proteomics Platform, Allows Rapid Discovery of Biosynthetic Gene Clusters for Different Classes of Natural Products. Chemistry and Biology, 2014, 21, 707-718.	6.0	51
71	Genome-Wide Analysis of In Vivo Binding of the Master Regulator DasR in Streptomyces coelicolor Identifies Novel Non-Canonical Targets. PLoS ONE, 2015, 10, e0122479.	2.5	51
72	Identification of glucose kinaseâ€dependent and â€independent pathways for carbon control of primary metabolism, development and antibiotic production in <i><scp>S</scp>treptomyces coelicolor</i> by quantitative proteomics. Molecular Microbiology, 2012, 86, 1490-1507.	2.5	49

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73	Cross-membranes orchestrate compartmentalization and morphogenesis in Streptomyces. Nature Communications, 2016, 7, ncomms11836.	12.8	49
74	A comparative study of the ribosomal RNA operons ofStreptomyces coelicolorA3(2) and sequence analysis ofrrnA. Nucleic Acids Research, 1991, 19, 4399-4403.	14.5	48
75	A comparison of key aspects of gene regulation inStreptomyces coelicolorandEscherichia coliusing nucleotideâ€resolution transcription maps produced in parallel by global and differentialRNAsequencing. Molecular Microbiology, 2014, 94, 963-987.	2.5	48
76	Aggregation of germlings is a major contributing factor towards mycelial heterogeneity of Streptomyces. Scientific Reports, 2016, 6, 27045.	3.3	48
77	Metabolomics-guided analysis of isocoumarin production by Streptomyces species MBT76 and biotransformation of flavonoids and phenylpropanoids. Metabolomics, 2016, 12, 90.	3.0	48
78	Production of Prodiginines Is Part of a Programmed Cell Death Process in Streptomyces coelicolor. Frontiers in Microbiology, 2018, 9, 1742.	3.5	47
79	Modestobacter caceresii sp. nov., novel actinobacteria with an insight into their adaptive mechanisms for survival in extreme hyper-arid Atacama Desert soils. Systematic and Applied Microbiology, 2016, 39, 243-251.	2.8	46
80	Lugdunomycin, an Angucyclineâ€Derived Molecule with Unprecedented Chemical Architecture. Angewandte Chemie - International Edition, 2019, 58, 2809-2814.	13.8	46
81	Three tuf-like genes in the kirromycin producer Streptomyces ramocissimus. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	45
82	Glucose kinase of Streptomyces coelicolor A3(2): large-scale purification and biochemical analysis. Antonie Van Leeuwenhoek, 2000, 78, 253-261.	1.7	45
83	Anthracyclines: biosynthesis, engineering and clinical applications. Natural Product Reports, 2022, 39, 814-841.	10.3	45
84	DNA cleavage and antitumour activity of platinum(II) and copper(II) compounds derived from 4-methyl-2-N-(2-pyridylmethyl)aminophenol: spectroscopic, electrochemical and biological investigation. Dalton Transactions, 2009, , 10846.	3.3	44
85	Structure and DNA cleavage properties of two copper(ii) complexes of the pyridine-pyrazole-containing ligands mbpzbpy and Hmpzbpya. Dalton Transactions, 2007, , 3676.	3.3	43
86	Analysis of two distinct mycelial populations in liquid-grown Streptomyces cultures using a flow cytometry-based proteomics approach. Applied Microbiology and Biotechnology, 2012, 96, 1301-1312.	3.6	42
87	Structural and Proteomic Changes in Viable but Non-culturable Vibrio cholerae. Frontiers in Microbiology, 2019, 10, 793.	3.5	42
88	Structured morphological modeling as a framework for rational strain design of Streptomyces species. Antonie Van Leeuwenhoek, 2012, 102, 409-423.	1.7	41
89	A Single Biosynthetic Gene Cluster Is Responsible for the Production of Bagremycin Antibiotics and Ferroverdin Iron Chelators. MBio, 2019, 10, .	4.1	40
90	Biosynthesis, evolution and ecology of microbial terpenoids. Natural Product Reports, 2022, 39, 249-272.	10.3	40

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91	The tylosin resistance genetlrBofStreptomyces fradiaeencodes a methyltransferase that targets G748 in 23S rRNA. Molecular Microbiology, 2000, 37, 811-820.	2.5	39
92	Altered desferrioxamine-mediated iron utilization is a common trait of bald mutants of Streptomyces coelicolor. Metallomics, 2014, 6, 1390-1399.	2.4	36
93	Discovery of C-Glycosylpyranonaphthoquinones in Streptomyces sp. MBT76 by a Combined NMR-Based Metabolomics and Bioinformatics Workflow. Journal of Natural Products, 2017, 80, 269-277.	3.0	36
94	Engineering of N-acetylglucosamine metabolism for improved antibiotic production in Streptomyces coelicolor A3(2) and an unsuspected role of NagA in glucosamine metabolism. Bioengineered, 2012, 3, 280-285.	3.2	35
95	Distance-dependent danger responses in bacteria. Current Opinion in Microbiology, 2017, 36, 95-101.	5.1	35
96	High-Resolution Analysis of the Peptidoglycan Composition in Streptomyces coelicolor. Journal of Bacteriology, 2018, 200, .	2.2	35
97	Analysis of novel kitasatosporae reveals significant evolutionary changes in conserved developmental genes between Kitasatospora and Streptomyces. Antonie Van Leeuwenhoek, 2014, 106, 365-380.	1.7	34
98	Metabolic profiling as a tool for prioritizing antimicrobial compounds. Journal of Industrial Microbiology and Biotechnology, 2016, 43, 299-312.	3.0	34
99	Dynamic and Functional Profiling of Xylan-Degrading Enzymes in <i>Aspergillus</i> Secretomes Using Activity-Based Probes. ACS Central Science, 2019, 5, 1067-1078.	11.3	34
100	Imaging of Streptomyces coelicolor A3(2) with Reduced Autofluorescence Reveals a Novel Stage of FtsZ Localization. PLoS ONE, 2009, 4, e4242.	2.5	34
101	Intertwined Precursor Supply during Biosynthesis of the Catecholateâ€"Hydroxamate Siderophores Qinichelins in <i>Streptomyces</i> sp. MBT76. ACS Chemical Biology, 2017, 12, 2756-2766.	3.4	33
102	Mining for Microbial Gems: Integrating Proteomics in the Postgenomic Natural Product Discovery Pipeline. Proteomics, 2018, 18, e1700332.	2.2	33
103	Rational Design of Mechanism-Based Inhibitors and Activity-Based Probes for the Identification of Retaining Î±-<scp>l</scp>-Arabinofuranosidases. Journal of the American Chemical Society, 2020, 142, 4648-4662.	13.7	33
104	Multiple allosteric effectors control the affinity of DasR for its target sites. Biochemical and Biophysical Research Communications, 2015, 464, 324-329.	2.1	32
105	Correlative Cryo-Fluorescence Light Microscopy and Cryo-Electron Tomography of Streptomyces. Methods in Cell Biology, 2014, 124, 217-239.	1.1	31
106	Subcompartmentalization by cross-membranes during early growth of Streptomyces hyphae. Nature Communications, 2016, 7, 12467.	12.8	31
107	SepG coordinates sporulation-specific cell division and nucleoid organization in <i>Streptomyces coelicolor</i>. Open Biology, 2016, 6, 150164.	3.6	30
108	OsdR of Streptomyces coelicolor and the Dormancy Regulator DevR of Mycobacterium tuberculosis Control Overlapping Regulons. MSystems, 2016, 1, .	3.8	30

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109	Omics-based strategies to discover novel classes of RiPP natural products. Current Opinion in Biotechnology, 2021, 69, 60-67.	6.6	30
110	Enzyme-Constrained Models and Omics Analysis of Streptomyces coelicolor Reveal Metabolic Changes that Enhance Heterologous Production. IScience, 2020, 23, 101525.	4.1	30
111	Effects of increased and deregulated expression of cell division genes on the morphology and on antibiotic production of streptomycetes. Antonie Van Leeuwenhoek, 2000, 78, 269-276.	1.7	29
112	Competition Sensing Changes Antibiotic Production in <i>Streptomyces</i>. MBio, 2021, 12, .	4.1	29
113	Phylogenomic analyses and distribution of terpene synthases amongStreptomyces. Beilstein Journal of Organic Chemistry, 2019, 15, 1181-1193.	2.2	28
114	Mammalian cell entry genes in Streptomyces may provide clues to the evolution of bacterial virulence. Scientific Reports, 2013, 3, 1109.	3.3	27
115	Dissecting Disease-Suppressive Rhizosphere Microbiomes by Functional Amplicon Sequencing and 10Ã— Metagenomics. MSystems, 2021, 6, e0111620.	3.8	27
116	Leucanicidin and Endophenasides Result from Methyl-Rhamnosylation by the Same Tailoring Enzymes in <i>Kitasatospora</i> sp. MBT66. ACS Chemical Biology, 2016, 11, 478-490.	3.4	25
117	Teichoic acids anchor distinct cell wall lamellae in an apically growing bacterium. Communications Biology, 2020, 3, 314.	4.4	25
118	The tmRNAâ€tagging mechanism and the control of gene expression: a review. Wiley Interdisciplinary Reviews RNA, 2011, 2, 233-246.	6.4	24
119	Structural and Functional Characterizations of SsgB, a Conserved Activator of Developmental Cell Division in Morphologically Complex Actinomycetes. Journal of Biological Chemistry, 2009, 284, 25268-25279.	3.4	23
120	A novel function of Streptomyces integration host factor (sIHF) in the control of antibiotic production and sporulation in Streptomyces coelicolor. Antonie Van Leeuwenhoek, 2012, 101, 479-492.	1.7	23
121	Identification of novel endophenaside antibiotics produced by Kitasatospora sp. MBT66. Journal of Antibiotics, 2015, 68, 445-452.	2.0	23
122	Microbial and volatile profiling of soils suppressive to <i>Fusarium culmorum</i> of wheat. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20192527.	2.6	23
123	Production of poly-Î²-1,6-N-acetylglucosamine by MatAB is required for hyphal aggregation and hydrophilic surface adhesion by Streptomyces. Microbial Cell, 2018, 5, 269-279.	3.2	23
124	Platinum(II) compounds with chelating ligands based on pyridine and pyrimidine: DNA and protein binding studies. Journal of Inorganic Biochemistry, 2009, 103, 1288-1297.	3.5	22
125	Single particle tracking of dynamically localizing TatA complexes in Streptomyces coelicolor. Biochemical and Biophysical Research Communications, 2013, 438, 38-42.	2.1	22
126	Aromatic Polyketide GTRIâ€02 is a Previously Unidentified Product of the <i>act</i> Gene Cluster in <i>Streptomyces coelicolor</i>â€…A3(2). ChemBioChem, 2017, 18, 1428-1434.	2.6	22

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127	Discovery of novel glycerolated quinazolinones from <i>Streptomyces</i> sp. MBT27. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 483-492.	3.0	22
128	A novel plasmid vector that uses the glucose kinase gene (glkA) for the positive selection of stable gene disruptants in Streptomyces. Gene, 1996, 182, 229-230.	2.2	21
129	Transferâ€“messenger RNA controls the translation of cellâ€cycle and stress proteins in Streptomyces. EMBO Reports, 2010, 11, 119-125.	4.5	21
130	The Secreted Signaling Protein Factor C Triggers the A-factor Response Regulon in Streptomyces griseus. Molecular and Cellular Proteomics, 2007, 6, 1248-1256.	3.8	20
131	Dynamic Localization of Tat Protein Transport Machinery Components in Streptomyces coelicolor. Journal of Bacteriology, 2012, 194, 6272-6281.	2.2	19
132	Streptomyces coelicolor. Trends in Microbiology, 2019, 27, 468-469.	7.7	19
133	SParticle, an algorithm for the analysis of filamentous microorganisms in submerged cultures. Antonie Van Leeuwenhoek, 2018, 111, 171-182.	1.7	18
134	Characterization of the gene for factor C, an extracellular signal protein involved in morphological differentiation of Streptomyces griseus This paper is dedicated to the memory of Professor GÃ¡bor SzabÃ³. The GenBank accession number for the sequence reported in this paper is AF103943.. Microbiology (United Kingdom), 1999, 145, 2245-2253.	1.8	18
135	The tuf3 gene of Streptomyces coelicolor A3(2) encodes an inessential elongation factor Tu that is apparently subject to positive stringent control. Microbiology (United Kingdom), 1995, 141, 2519-2528.	1.8	17
136	Constitutive expression of ftsZ overrides the whi developmental genes to initiate sporulation of Streptomyces coelicolor. Antonie Van Leeuwenhoek, 2012, 101, 619-632.	1.7	17
137	Spatial structure increases the benefits of antibiotic production in<i>Streptomyces</i>*. Evolution; International Journal of Organic Evolution, 2020, 74, 179-187.	2.3	17
138	Cloning and sequencing of the tuf genes of Streptomyces coelicolor A3(2). Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1994, 1219, 543-547.	2.4	16
139	Polyphasic classification of the gifted natural product producer Streptomyces roseifaciens sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 899-908.	1.7	16
140	Role for a Lytic Polysaccharide Monooxygenase in Cell Wall Remodeling in Streptomyces coelicolor. MBio, 2022, 13, e0045622.	4.1	16
141	Elongation Factor Tu3 (EF-Tu3) from the Kirromycin Producer Streptomyces ramocissimus Is Resistant to Three Classes of EF-Tu-Specific Inhibitors. Journal of Bacteriology, 2007, 189, 3581-3590.	2.2	15
142	Discovery of actinomycin L, a new member of the actinomycin family of antibiotics. Scientific Reports, 2022, 12, 2813.	3.3	15
143	Transcriptional analysis of the cell division-related ssg genes in Streptomyces coelicolor reveals direct control of ssgR by AtrA. Antonie Van Leeuwenhoek, 2015, 108, 201-213.	1.7	14
144	Structure of an MmyB-Like Regulator from C. aurantiacus, Member of a New Transcription Factor Family Linked to Antibiotic Metabolism in Actinomycetes. PLoS ONE, 2012, 7, e41359.	2.5	14

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145	Mapping of genes involved in macromolecular synthesis on the chromosome of Streptomyces coelicolor A3(2). Journal of Bacteriology, 1995, 177, 473-476.	2.2	13
146	Structural and functional characterization of the alanine racemase from Streptomyces coelicolor A3(2). Biochemical and Biophysical Research Communications, 2017, 483, 122-128.	2.1	13
147	Glycosylated cyclophellitol-derived activity-based probes and inhibitors for cellulases. RSC Chemical Biology, 2020, 1, 148-155.	4.1	13
148	Growth phase-dependent transcription of the Streptomyces ramocissimus tuf1 gene occurs from two promoters. Journal of Bacteriology, 1997, 179, 3619-3624.	2.2	12
149	Lack of A-factor Production Induces the Expression of Nutrient Scavenging and Stress-related Proteins in Streptomyces griseus>. Molecular and Cellular Proteomics, 2009, 8, 2396-2403.	3.8	12
150	Genome Sequence of the Filamentous Actinomycete <i>Kitasatospora viridifaciens</i>. Genome Announcements, 2017, 5, .	0.8	12
151	The <scp>ROK</scp>â€family regulator <scp>Rok7B7</scp> directly controls carbon catabolite repression, antibiotic biosynthesis, and morphological development in <i>Streptomyces avermitilis</i>. Environmental Microbiology, 2020, 22, 5090-5108.	3.8	11
152	Novel Aspects of Signaling in Streptomyces Development. Advances in Applied Microbiology, 2004, 56, 65-88.	2.4	10
153	Identification and isolation of lantibiotics from culture: a bioorthogonal chemistry approach. Organic and Biomolecular Chemistry, 2012, 10, 8677.	2.8	10
154	Substrate Inhibition of VanA by <scp>d</scp> -Alanine Reduces Vancomycin Resistance in a VanX-Dependent Manner. Antimicrobial Agents and Chemotherapy, 2016, 60, 4930-4939.	3.2	10
155	Atypical Spirotetronate Polyketides Identified in the Underexplored Genus <i>Streptacidiphilus</i>. Journal of Organic Chemistry, 2020, 85, 10648-10657.	3.2	10
156	Transcriptional and functional analysis of the gene for factor C, an extracellular signal protein involved in cytodifferentiation of Streptomyces griseus. Antonie Van Leeuwenhoek, 2000, 78, 277-285.	1.7	9
157	A microbial expression system for high-level production of scFv HIV-neutralizing antibody fragments in Escherichia coli. Applied Microbiology and Biotechnology, 2019, 103, 8875-8888.	3.6	9
158	The ubiquitous catechol moiety elicits siderophore and angucycline production in Streptomyces. Communications Chemistry, 2022, 5, .	4.5	9
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160	Complete Genome Sequence of Escherichia coli AS19, an Antibiotic-Sensitive Variant of E. coli Strain B REL606. Genome Announcements, 2018, 6, .	0.8	8
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