

# Sebastien Rigali

## List of Publications by Year in descending order

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60  
papers

3,165  
citations

168829

31  
h-index

182931

54  
g-index

72  
all docs

72  
docs citations

72  
times ranked

2693  
citing authors

#	ARTICLE	IF	CITATIONS
1	The virulome of <i>Streptomyces scabiei</i> in response to cello-oligosaccharide elicitors. <i>Microbial Genomics</i> , 2022, 8, .	1.0	8
2	Old Enzyme, New Role: The Î <sup>2</sup> -Glucosidase BglC of <i>Streptomyces scabiei</i> Interferes with the Plant Defense Mechanism by Hydrolyzing Scopolin. <i>Biophysica</i> , 2022, 2, 1-7.	0.6	6
3	Structure of New Ferroverdins Recruiting Unconventional Ferrous Iron Chelating Agents. <i>Biomolecules</i> , 2022, 12, 752.	1.8	3
4	Identification of Novel Rotihibin Analogues in <i>Streptomyces scabies</i> , Including Discovery of Its Biosynthetic Gene Cluster. <i>Microbiology Spectrum</i> , 2021, 9, e0057121.	1.2	14
5	Prodiginines Postpone the Onset of Sporulation in <i>Streptomyces coelicolor</i> . <i>Antibiotics</i> , 2020, 9, 847.	1.5	8
6	Deletion of bglC triggers a genetic compensation response by awakening the expression of alternative beta-glucosidase. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194615.	0.9	14
7	On the Risks of Phylogeny-Based Strain Prioritization for Drug Discovery: <i>Streptomyces lunaelactis</i> as a Case Study. <i>Biomolecules</i> , 2020, 10, 1027.	1.8	18
8	A Single Biosynthetic Gene Cluster Is Responsible for the Production of Bagremycin Antibiotics and Ferroverdin Iron Chelators. <i>MBio</i> , 2019, 10, .	1.8	40
9	Self-resistance mechanisms to DNA-damaging antitumor antibiotics in actinobacteria. <i>Current Opinion in Microbiology</i> , 2018, 45, 100-108.	2.3	32
10	Cracking the regulatory code of biosynthetic gene clusters as a strategy for natural product discovery. <i>Biochemical Pharmacology</i> , 2018, 153, 24-34.	2.0	64
11	Contribution of the Î <sup>2</sup> â€glucosidase BglC to the onset of the pathogenic lifestyle of <i>Streptomyces scabies</i>. <i>Molecular Plant Pathology</i> , 2018, 19, 1480-1490.	2.0	19
12	Proteomic Response to Thaxtomin Phytotoxin Elicitor Cellobiose and to Deletion of Cellulose Utilization Regulator CebR in <i>Streptomyces scabies</i>. <i>Journal of Proteome Research</i> , 2018, 17, 3837-3852.	1.8	14
13	High-Throughput Sequencing Analysis of the Actinobacterial Spatial Diversity in Moonmilk Deposits. <i>Antibiotics</i> , 2018, 7, 27.	1.5	22
14	Isolation, Characterization, and Antibacterial Activity of Hard-to-Culture Actinobacteria from Cave Moonmilk Deposits. <i>Antibiotics</i> , 2018, 7, 28.	1.5	68
15	Complete Genome Sequence of <i>Streptomyces lunaelactis</i> MM109 T , Isolated from Cave Moonmilk Deposits. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
16	NgcE&lt;sup&gt;S</sup>Sco&lt;sup&gt;S</sup>; Acts as a Lower-Affinity Binding Protein of an ABC Transporter for the Uptake of &lt;i>N,Nâ€²</i>-Diacetylchitobiose in &lt;i>Streptomyces coelicolor</i> A3(2). <i>Microbes and Environments</i> , 2018, 33, 272-281.	0.7	8
17	Production of Prodiginines Is Part of a Programmed Cell Death Process in <i>Streptomyces coelicolor</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1742.	1.5	47
18	Tracking the Subtle Mutations Driving Host Sensing by the Plant Pathogen <i>Streptomyces scabies</i>. <i>MSphere</i> , 2017, 2, .	1.3	15

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19	Intertwined Precursor Supply during Biosynthesis of the Catecholate- $\alpha$ -Hydroxamate Siderophores Qinchelins in <i>Streptomyces</i> sp. MBT76. <i>ACS Chemical Biology</i> , 2017, 12, 2756-2766.	1.6	33
20	Assessment of the Potential Role of <i>Streptomyces</i> in Cave Moonmilk Formation. <i>Frontiers in Microbiology</i> , 2017, 8, 1181.	1.5	63
21	A Phenotypic and Genotypic Analysis of the Antimicrobial Potential of Cultivable <i>Streptomyces</i> Isolated from Cave Moonmilk Deposits. <i>Frontiers in Microbiology</i> , 2016, 7, 1455.	1.5	64
22	Intertwining nutrient-sensory networks and the control of antibiotic production in <i>Streptomyces</i> . <i>Molecular Microbiology</i> , 2016, 102, 183-195.	1.2	87
23	The CebE/MsiK Transporter is a Doorway to the Cello-oligosaccharide-mediated Induction of <i>Streptomyces scabies</i> Pathogenicity. <i>Scientific Reports</i> , 2016, 6, 27144.	1.6	42
24	OsdR of <i>Streptomyces coelicolor</i> and the Dormancy Regulator DevR of <i>Mycobacterium tuberculosis</i> Control Overlapping Regulons. <i>MSystems</i> , 2016, 1, .	1.7	30
25	The Cellobiose Sensor CebR Is the Gatekeeper of <i>Streptomyces scabies</i> Pathogenicity. <i>MBio</i> , 2015, 6, e02018.	1.8	66
26	<i>Streptomyces lunaelactis</i> sp. nov., a novel feroverdin A-producing <i>Streptomyces</i> species isolated from a moonmilk speleothem. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 519-531.	0.7	38
27	Multiple allosteric effectors control the affinity of DasR for its target sites. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 324-329.	1.0	32
28	On the necessity and biological significance of threshold-free regulon prediction outputs. <i>Molecular BioSystems</i> , 2015, 11, 333-337.	2.9	9
29	Growth of desferrioxamine-deficient <i>Streptomyces</i> mutants through xenosiderophore piracy of airborne fungal contaminations. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv080.	1.3	25
30	DasR is a pleiotropic regulator required for antibiotic production, pigment biosynthesis, and morphological development in <i>Saccharopolyspora erythraea</i> . <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10215-10224.	1.7	19
31	Genome-Wide Analysis of In Vivo Binding of the Master Regulator DasR in <i>Streptomyces coelicolor</i> Identifies Novel Non-Canonical Targets. <i>PLoS ONE</i> , 2015, 10, e0122479.	1.1	51
32	Control of chitin and N-acetylglucosamine utilization in <i>Saccharopolyspora erythraea</i> . <i>Microbiology (United Kingdom)</i> , 2014, 160, 1914-1928.	0.7	20
33	Altered desferrioxamine-mediated iron utilization is a common trait of bald mutants of <i>Streptomyces coelicolor</i> . <i>Metallomics</i> , 2014, 6, 1390-1399.	1.0	36
34	GlnR-mediated regulation of nitrogen metabolism in the actinomycete <i>Saccharopolyspora erythraea</i> . <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7935-7948.	1.7	47
35	Use of red autofluorescence for monitoring prodiginine biosynthesis. <i>Journal of Microbiological Methods</i> , 2013, 93, 138-143.	0.7	29
36	Functional Analysis of the N-Acetylglucosamine Metabolic Genes of <i>Streptomyces coelicolor</i> and Role in Control of Development and Antibiotic Production. <i>Journal of Bacteriology</i> , 2012, 194, 1136-1144.	1.0	87

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37	Response to Copper Stress in <i>Streptomyces lividans</i> Extends beyond Genes under Direct Control of a Copper-sensitive Operon Repressor Protein (CsoR). <i>Journal of Biological Chemistry</i> , 2012, 287, 17833-17847.	1.6	50
38	Engineering of N-acetylglucosamine metabolism for improved antibiotic production in <i>Streptomyces coelicolor</i> A3(2) and an unsuspected role of NagA in glucosamine metabolism. <i>Bioengineered</i> , 2012, 3, 280-285.	1.4	35
39	Extracellular sugar phosphates are assimilated by <i>Streptomyces</i> in a PhoP-dependent manner. <i>Antonie Van Leeuwenhoek</i> , 2012, 102, 425-433.	0.7	19
40	Unsuspected control of siderophore production by N-acetylglucosamine in streptomycetes. <i>Environmental Microbiology Reports</i> , 2012, 4, 512-521.	1.0	57
41	Role of the phenazine-inducing protein Pip in stress resistance of <i>Pseudomonas chlororaphis</i> . <i>Microbiology (United Kingdom)</i> , 2011, 157, 398-407.	0.7	16
42	Regulon of the N-Acetylglucosamine Utilization Regulator NagR in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 3525-3536.	1.0	52
43	The permease gene <i>nagE2</i> is the key to N-acetylglucosamine sensing and utilization in <i>Streptomyces coelicolor</i> and is subject to multi-level control. <i>Molecular Microbiology</i> , 2010, 75, 1133-1144.	1.2	73
44	Chapter 1 Variation in Form and Function. <i>Advances in Applied Microbiology</i> , 2009, 69, 1-22.	1.3	123
45	Feast or famine: the global regulator DasR links nutrient stress to antibiotic production by <i>Streptomyces</i> . <i>EMBO Reports</i> , 2008, 9, 670-675.	2.0	358
46	The chitobiose-binding protein, DasA, acts as a link between chitin utilization and morphogenesis in <i>Streptomyces coelicolor</i> . <i>Microbiology (United Kingdom)</i> , 2008, 154, 373-382.	0.7	72
47	The Secreted Signaling Protein Factor C Triggers the A-factor Response Regulon in <i>Streptomyces griseus</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1248-1256.	2.5	20
48	Conserved cis-Acting Elements Upstream of Genes Composing the Chitinolytic System of Streptomycetes Are DasR-Responsive Elements. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2007, 12, 60-66.	1.0	74
49	PREDetector: A new tool to identify regulatory elements in bacterial genomes. <i>Biochemical and Biophysical Research Communications</i> , 2007, 357, 861-864.	1.0	97
50	The sugar phosphotransferase system of <i>Streptomyces coelicolor</i> is regulated by the GntR-family regulator DasR and links N-acetylglucosamine metabolism to the control of development. <i>Molecular Microbiology</i> , 2006, 61, 1237-1251.	1.2	188
51	DevA, a GntR-Like Transcriptional Regulator Required for Development in <i>Streptomyces coelicolor</i> . <i>Journal of Bacteriology</i> , 2006, 188, 5014-5023.	1.0	51
52	Pip, a Novel Activator of Phenazine Biosynthesis in <i>Pseudomonas chlororaphis</i> PCL1391. <i>Journal of Bacteriology</i> , 2006, 188, 8283-8293.	1.0	33
53	Improving the alkalophilic performances of the Xyl1 xylanase from <i>Streptomyces</i> sp. S38: Structural comparison and mutational analysis. <i>Protein Science</i> , 2005, 14, 292-302.	3.1	29
54	From Dormant to Germinating Spores of <i>Streptomyces coelicolor</i> A3(2): A New Perspectives from the <i>chrpNull</i> Mutant. <i>Journal of Proteome Research</i> , 2005, 4, 1699-1708.	1.8	71

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55	Deletion of a Cyclic AMP Receptor Protein Homologue Diminishes Germination and Affects Morphological Development of <i>Streptomyces coelicolor</i> . <i>Journal of Bacteriology</i> , 2004, 186, 1893-1897.	1.0	62
56	Extending the classification of bacterial transcription factors beyond the helix-turn-helix motif as an alternative approach to discover new cis/trans relationships. <i>Nucleic Acids Research</i> , 2004, 32, 3418-3426.	6.5	74
57	Crp of <i>Streptomyces coelicolor</i> is the third transcription factor of the large CRP-FNR superfamily able to bind cAMP. <i>Biochemical and Biophysical Research Communications</i> , 2004, 325, 983-990.	1.0	35
58	Site-directed mutagenesis of conserved inverted repeat sequences in the xylanase C promoter region from <i>Streptomyces</i> sp. EC3. <i>Molecular Genetics and Genomics</i> , 2003, 270, 337-346.	1.0	6
59	PlmA, a New Member of the GntR Family, Has Plasmid Maintenance Functions in <i>Anabaena</i> sp. Strain PCC 7120. <i>Journal of Bacteriology</i> , 2003, 185, 4315-4325.	1.0	62
60	Subdivision of the Helix-Turn-Helix GntR Family of Bacterial Regulators in the FadR, HutC, MocR, and YtrA Subfamilies. <i>Journal of Biological Chemistry</i> , 2002, 277, 12507-12515.	1.6	311