

# Sebastien Cunnac

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

2,526  
citations

394390

19  
h-index

580810

25  
g-index

29  
all docs

29  
docs citations

29  
times ranked

2312  
citing authors

#	ARTICLE	IF	CITATIONS
1	Broad-spectrum resistance to bacterial blight in rice using genome editing. <i>Nature Biotechnology</i> , 2019, 37, 1344-1350.	17.5	470
2	<i>Pseudomonas syringae</i> type III effector repertoires: last words in endless arguments. <i>Trends in Microbiology</i> , 2012, 20, 199-208.	7.7	256
3	<i>Pseudomonas syringae</i> type III secretion system effectors: repertoires in search of functions. <i>Current Opinion in Microbiology</i> , 2009, 12, 53-60.	5.1	236
4	Inventory and functional analysis of the large Hrp regulon in <i>Ralstonia solanacearum</i> : identification of novel effector proteins translocated to plant host cells through the type III secretion system. <i>Molecular Microbiology</i> , 2004, 53, 115-128.	2.5	223
5	Genetic disassembly and combinatorial reassembly identify a minimal functional repertoire of type III effectors in <i>Pseudomonas syringae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2975-2980.	7.1	212
6	Targeted promoter editing for rice resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> reveals differential activities for <i>SWEET14</i> inducing <i>TAL</i> effectors. <i>Plant Biotechnology Journal</i> , 2017, 15, 306-317.	8.3	176
7	Two Type III Secretion System Effectors from <i>Ralstonia solanacearum</i> GMI1000 Determine Host-Range Specificity on Tobacco. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 538-550.	2.6	139
8	Characterization of the cis-Acting Regulatory Element Controlling HrpB-Mediated Activation of the Type III Secretion System and Effector Genes in <i>Ralstonia solanacearum</i> . <i>Journal of Bacteriology</i> , 2004, 186, 2309-2318.	2.2	116
9	An Improved Method for TAL Effectors DNA-Binding Sites Prediction Reveals Functional Convergence in TAL Repertoires of <i>Xanthomonas oryzae</i> Strains. <i>PLoS ONE</i> , 2013, 8, e68464.	2.5	102
10	The evolution of <i>Pseudomonas syringae</i> host specificity and type III effector repertoires. <i>Molecular Plant Pathology</i> , 2009, 10, 767-775.	4.2	97
11	Genome-Wide Analysis of Gene Expression in <i>Ralstonia solanacearum</i> Reveals That the <i>hrpB</i> Gene Acts as a Regulatory Switch Controlling Multiple Virulence Pathways. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 938-949.	2.6	92
12	Functional analysis of African <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> TALomes reveals a new susceptibility gene in bacterial leaf blight of rice. <i>PLoS Pathogens</i> , 2018, 14, e1007092.	4.7	86
13	QueTAL: a suite of tools to classify and compare TAL effectors functionally and phylogenetically. <i>Frontiers in Plant Science</i> , 2015, 6, 545.	3.6	62
14	PopF1 and PopF2, Two Proteins Secreted by the Type III Protein Secretion System of <i>Ralstonia solanacearum</i> , Are Translocators Belonging to the HrpF/NopX Family. <i>Journal of Bacteriology</i> , 2006, 188, 4903-4917.	2.2	43
15	Functional and Genome Sequence-Driven Characterization of tal Effector Gene Repertoires Reveals Novel Variants With Altered Specificities in Closely Related Malian <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 1657.	3.5	40
16	Virus-Bacteria Rice Co-Infection in Africa: Field Estimation, Reciprocal Effects, Molecular Mechanisms, and Evolutionary Implications. <i>Frontiers in Plant Science</i> , 2017, 8, 645.	3.6	32
17	Salt distribution in the Senegal middle valley. <i>Agricultural Water Management</i> , 2001, 46, 201-213.	5.6	27
18	High-Quality Draft Genome Sequence of the <i>Xanthomonas translucens</i> pv. <i>cerealis</i> Pathotype Strain CFBP 2541. <i>Genome Announcements</i> , 2015, 3, .	0.8	24

#	ARTICLE	IF	CITATIONS
19	daTALbase: A Database for Genomic and Transcriptomic Data Related to TAL Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 471-480.	2.6	22
20	Complete Genome Assemblies of All <i>Xanthomonas translucens</i> Pathotype Strains Reveal Three Genetically Distinct Clades. <i>Frontiers in Microbiology</i> , 2021, 12, 817815.	3.5	19
21	Polyphasic origin of salinity in the Senegal delta and middle valley. <i>Catena</i> , 2004, 58, 101-124.	5.0	16
22	Improved bacterial leaf blight disease resistance in the major elite Vietnamese rice cultivar TBR225 via editing of the OsSWEET14 promoter. <i>PLoS ONE</i> , 2021, 16, e0255470.	2.5	13
23	Draft Genome Sequence of <i>Xanthomonas translucens</i> pv. <i>graminis</i> Pathotype Strain CFBP 2053. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
24	An atypical class of non-coding small RNAs is produced in rice leaves upon bacterial infection. <i>Scientific Reports</i> , 2021, 11, 24141.	3.3	3
25	The Rice ILI2 Locus Is a Bidirectional Target of the African <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Major Transcription Activator-like Effector TalC but Does Not Contribute to Disease Susceptibility. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5559.	4.1	1