

Sylvain Raffaele

List of Publications by Year in descending order

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57
papers

9,526
citations

94433

37
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144013

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69
all docs

69
docs citations

69
times ranked

8633
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional response to host chemical cues underpins the expansion of host range in a fungal plant pathogen lineage. <i>ISME Journal</i> , 2022, 16, 138-148.	9.8	17
2	Genome-wide alternative splicing profiling in the fungal plant pathogen <i>Sclerotinia sclerotiorum</i> during the colonization of diverse host families. <i>Molecular Plant Pathology</i> , 2021, 22, 31-47.	4.2	25
3	Silent control: microbial plant pathogens evade host immunity without coding sequence changes. <i>FEMS Microbiology Reviews</i> , 2021, 45, .	8.6	12
4	Patterns of Sequence and Expression Diversification Associate Members of the PADRE Gene Family With Response to Fungal Pathogens. <i>Frontiers in Genetics</i> , 2020, 11, 491.	2.3	9
5	Rapid identification of an <i>Arabidopsis</i> NLR gene as a candidate conferring susceptibility to <i>Sclerotinia sclerotiorum</i> using time-resolved automated phenotyping. <i>Plant Journal</i> , 2020, 103, 903-917.	5.7	31
6	Phylotranscriptomics of the Pentapetalae Reveals Frequent Regulatory Variation in Plant Local Responses to the Fungal Pathogen <i>Sclerotinia sclerotiorum</i> . <i>Plant Cell</i> , 2020, 32, 1820-1844.	6.6	21
7	A Chromosome-Scale Genome Assembly Resource for <i>Myriosclerotinia sulcatula</i> Infecting Sedge Grass (<i>Carex</i> sp.). <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 880-883.	2.6	2
8	Small RNAs from the plant pathogenic fungus <i>Sclerotinia sclerotiorum</i> highlight host candidate genes associated with quantitative disease resistance. <i>Molecular Plant Pathology</i> , 2019, 20, 1279-1297.	4.2	78
9	A whole genome scan of SNP data suggests a lack of abundant hard selective sweeps in the genome of the broad host range plant pathogenic fungus <i>Sclerotinia sclerotiorum</i> . <i>PLoS ONE</i> , 2019, 14, e0214201.	2.5	23
10	Intercellular cooperation in a fungal plant pathogen facilitates host colonization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3193-3201.	7.1	52
11	Expression polymorphism at the <i>scp>ARPC</scp>4</i> locus links the actin cytoskeleton with quantitative disease resistance to <i>Sclerotinia sclerotiorum</i> in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2019, 222, 480-496.	7.3	30
12	Shifts in diversification rates and host jump frequencies shaped the diversity of host range among <i>Sclerotiniaceae</i> fungal plant pathogens. <i>Molecular Ecology</i> , 2018, 27, 1309-1323.	3.9	40
13	The genetics underlying natural variation of plant–plant interactions, a beloved but forgotten member of the family of biotic interactions. <i>Plant Journal</i> , 2018, 93, 747-770.	5.7	65
14	Advances on plant–pathogen interactions from molecular toward systems biology perspectives. <i>Plant Journal</i> , 2017, 90, 720-737.	5.7	81
15	The Complete Genome Sequence of the Phytopathogenic Fungus <i>Sclerotinia sclerotiorum</i> Reveals Insights into the Genome Architecture of Broad Host Range Pathogens. <i>Genome Biology and Evolution</i> , 2017, 9, 593-618.	2.5	187
16	Structural basis for plant plasma membrane protein dynamics and organization into functional nanodomains. <i>ELife</i> , 2017, 6, .	6.0	135
17	Parallel evolution of the POQR prolyl oligo peptidase gene conferring plant quantitative disease resistance. <i>PLoS Genetics</i> , 2017, 13, e1007143.	3.5	38
18	Codon optimization underpins generalist parasitism in fungi. <i>ELife</i> , 2017, 6, .	6.0	36

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19	Emerging Trends in Molecular Interactions between Plants and the Broad Host Range Fungal Pathogens <i>Botrytis cinerea</i> and <i>Sclerotinia sclerotiorum</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 422.	3.6	105
20	Cuticle Structure in Relation to Chemical Composition: Re-assessing the Prevailing Model. <i>Frontiers in Plant Science</i> , 2016, 7, 427.	3.6	185
21	Comparative Genomic Analysis of <i>Drechmeria coniospora</i> Reveals Core and Specific Genetic Requirements for Fungal Endoparasitism of Nematodes. <i>PLoS Genetics</i> , 2016, 12, e1006017.	3.5	45
22	Common protein sequence signatures associate with <i>Sclerotinia borealis</i> lifestyle and secretion in fungal pathogens of the Sclerotiniaceae. <i>Frontiers in Plant Science</i> , 2015, 6, 776.	3.6	16
23	A Receptor Pair with an Integrated Decoy Converts Pathogen Disabling of Transcription Factors to Immunity. <i>Cell</i> , 2015, 161, 1074-1088.	28.9	401
24	A Recent Expansion of the RXLR Effector Gene <i>Avrblb2</i> Is Maintained in Global Populations of <i>Phytophthora infestans</i> Indicating Different Contributions to Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 901-912.	2.6	44
25	The two-speed genomes of filamentous pathogens: waltz with plants. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 57-65.	3.3	503
26	The Plant Membrane-Associated REMORIN1.3 Accumulates in Discrete Perihaustorial Domains and Enhances Susceptibility to <i>Phytophthora infestans</i> . <i>Plant Physiology</i> , 2014, 165, 1005-1018.	4.8	116
27	Resistance to phytopathogens <i>e tutti quanti</i> : placing plant quantitative disease resistance on the map. <i>Molecular Plant Pathology</i> , 2014, 15, 427-432.	4.2	135
28	Identification and phylogenetic analyses of VASt, an uncharacterized protein domain associated with lipid-binding domains in Eukaryotes. <i>BMC Bioinformatics</i> , 2014, 15, 222.	2.6	38
29	Secretome analysis reveals effector candidates associated with broad host range necrotrophy in the fungal plant pathogen <i>Sclerotinia sclerotiorum</i> . <i>BMC Genomics</i> , 2014, 15, 336.	2.8	241
30	Two-Dimensional Data Binning for the Analysis of Genome Architecture in Filamentous Plant Pathogens and Other Eukaryotes. <i>Methods in Molecular Biology</i> , 2014, 1127, 29-51.	0.9	44
31	From pathogen genomes to host plant processes: the power of plant parasitic oomycetes. <i>Genome Biology</i> , 2013, 14, 211.	8.8	64
32	Regulate and be regulated: integration of defense and other signals by the AtMYB30 transcription factor. <i>Frontiers in Plant Science</i> , 2013, 4, 98.	3.6	38
33	Searching algorithm for type IV secretion system effectors 1.0: a tool for predicting type IV effectors and exploring their genomic context. <i>Nucleic Acids Research</i> , 2013, 41, 9218-9229.	14.5	50
34	The Remorin C-terminal Anchor was shaped by convergent evolution among membrane binding domains. <i>Plant Signaling and Behavior</i> , 2013, 8, e23207.	2.4	12
35	Major Transcriptome Reprogramming Underlies Floral Mimicry Induced by the Rust Fungus <i>Puccinia monoica</i> in <i>Boechera stricta</i> . <i>PLoS ONE</i> , 2013, 8, e75293.	2.5	25
36	Genome Analyses of an Aggressive and Invasive Lineage of the Irish Potato Famine Pathogen. <i>PLoS Pathogens</i> , 2012, 8, e1002940.	4.7	321

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37	Genome evolution in filamentous plant pathogens: why bigger can be better. <i>Nature Reviews Microbiology</i> , 2012, 10, 417-430.	28.6	735
38	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	2.6	264
39	Using Hierarchical Clustering of Secreted Protein Families to Classify and Rank Candidate Effectors of Rust Fungi. <i>PLoS ONE</i> , 2012, 7, e29847.	2.5	235
40	Natural Variation in Seed Very Long Chain Fatty Acid Content Is Controlled by a New Isoform of KCS18 in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2012, 7, e49261.	2.5	28
41	Plasma Membrane Localization of <i>Solanum tuberosum</i> Remorin from Group 1, Homolog 3 Is Mediated by Conformational Changes in a Novel C-Terminal Anchor and Required for the Restriction of Potato Virus X Movement. <i>Plant Physiology</i> , 2012, 160, 624-637.	4.8	132
42	Understanding and Exploiting Late Blight Resistance in the Age of Effectors. <i>Annual Review of Phytopathology</i> , 2011, 49, 507-531.	7.8	369
43	Analyses of genome architecture and gene expression reveal novel candidate virulence factors in the secretome of <i>Phytophthora infestans</i> . <i>BMC Genomics</i> , 2010, 11, 637.	2.8	188
44	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 705-715.	2.1	108
45	Recent developments in effector biology of filamentous plant pathogens. <i>Cellular Microbiology</i> , 2010, 12, 1015-1015.	2.1	11
46	A remorin protein interacts with symbiotic receptors and regulates bacterial infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2343-2348.	7.1	316
47	Genome Evolution Following Host Jumps in the Irish Potato Famine Pathogen Lineage. <i>Science</i> , 2010, 330, 1540-1543.	12.6	440
48	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	9.6	391
49	Remorin, a Solanaceae Protein Resident in Membrane Rafts and Plasmodesmata, Impairs <i>Potato virus X</i> Movement. <i>Plant Cell</i> , 2009, 21, 1541-1555.	6.6	352
50	Up regulation of the plant protein remorin correlates with dehiscence and cell maturation; a link with the maturation of plasmodesmata?. <i>Plant Signaling and Behavior</i> , 2009, 4, 915-919.	2.4	23
51	Ten things to know about oomycete effectors. <i>Molecular Plant Pathology</i> , 2009, 10, 795-803.	4.2	185
52	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	27.8	1,405
53	Very long chain fatty acid and lipid signaling in the response of plants to pathogens. <i>Plant Signaling and Behavior</i> , 2009, 4, 94-99.	2.4	98
54	The VLCFA elongase gene family in <i>Arabidopsis thaliana</i> : phylogenetic analysis, 3D modelling and expression profiling. <i>Plant Molecular Biology</i> , 2008, 67, 547-566.	3.9	317

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55	A MYB Transcription Factor Regulates Very-Long-Chain Fatty Acid Biosynthesis for Activation of the Hypersensitive Cell Death Response in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2008, 20, 752-767.	6.6	343
56	Genome-Wide Annotation of Remorins, a Plant-Specific Protein Family: Evolutionary and Functional Perspectives. <i>Plant Physiology</i> , 2007, 145, 593-600.	4.8	164
57	An essential role for salicylic acid in AtMYB30-mediated control of the hypersensitive cell death program in <i>Arabidopsis</i> . <i>FEBS Letters</i> , 2006, 580, 3498-3504.	2.8	134