

Jana Sperschneider

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

47
papers

1,751
citations

21
h-index

41
g-index

51
ext. papers

2,931
ext. citations

7.9
avg, IF

5.16
L-index

#	Paper	IF	Citations
47	EffectorP: predicting fungal effector proteins from secretomes using machine learning. <i>New Phytologist</i> , 2016 , 210, 743-61	9.8	234
46	Improved prediction of fungal effector proteins from secretomes with EffectorP 2.0. <i>Molecular Plant Pathology</i> , 2018 , 19, 2094-2110	5.7	179
45	LOCALIZER: subcellular localization prediction of both plant and effector proteins in the plant cell. <i>Scientific Reports</i> , 2017 , 7, 44598	4.9	171
44	Advances and challenges in computational prediction of effectors from plant pathogenic fungi. <i>PLoS Pathogens</i> , 2015 , 11, e1004806	7.6	111
43	Genome sequencing and comparative genomics of the broad host-range pathogen <i>Rhizoctonia solani</i> AG8. <i>PLoS Genetics</i> , 2014 , 10, e1004281	6	102
42	Loss of by somatic exchange in stem rust leads to virulence for resistance in wheat. <i>Science</i> , 2017 , 358, 1607-1610	33.3	101
41	ApoplastP: prediction of effectors and plant proteins in the apoplast using machine learning. <i>New Phytologist</i> , 2018 , 217, 1764-1778	9.8	80
40	DotKnot: pseudoknot prediction using the probability dot plot under a refined energy model. <i>Nucleic Acids Research</i> , 2010 , 38, e103	20.1	70
39	Comparative genomics and prediction of conditionally dispensable sequences in legume-infecting <i>Fusarium oxysporum</i> formae speciales facilitates identification of candidate effectors. <i>BMC Genomics</i> , 2016 , 17, 191	4.5	68
38	Genome-Wide Analysis in Three <i>Fusarium</i> Pathogens Identifies Rapidly Evolving Chromosomes and Genes Associated with Pathogenicity. <i>Genome Biology and Evolution</i> , 2015 , 7, 1613-27	3.9	68
37	Comparative genomics of Australian isolates of the wheat stem rust pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> reveals extensive polymorphism in candidate effector genes. <i>Frontiers in Plant Science</i> , 2014 , 5, 759	6.2	64
36	A Near-Complete Haplotype-Phased Genome of the Dikaryotic Wheat Stripe Rust Fungus f. sp. Reveals High Interhaplotype Diversity. <i>MBio</i> , 2018 , 9,	7.8	54
35	Emergence of the Ug99 lineage of the wheat stem rust pathogen through somatic hybridisation. <i>Nature Communications</i> , 2019 , 10, 5068	17.4	47
34	Evaluation of Secretion Prediction Highlights Differing Approaches Needed for Oomycete and Fungal Effectors. <i>Frontiers in Plant Science</i> , 2015 , 6, 1168	6.2	42
33	Heuristic RNA pseudoknot prediction including intramolecular kissing hairpins. <i>Rna</i> , 2011 , 17, 27-38	5.8	38
32	Diversifying selection in the wheat stem rust fungus acts predominantly on pathogen-associated gene families and reveals candidate effectors. <i>Frontiers in Plant Science</i> , 2014 , 5, 372	6.2	37
31	Comparative secretome analysis of <i>Rhizoctonia solani</i> isolates with different host ranges reveals unique secretomes and cell death inducing effectors. <i>Scientific Reports</i> , 2017 , 7, 10410	4.9	32

30	Machine learning in plant-pathogen interactions: empowering biological predictions from field scale to genome scale. <i>New Phytologist</i> , 2020 , 228, 35-41	9.8	32
29	Changing the Game: Using Integrative Genomics to Probe Virulence Mechanisms of the Stem Rust Pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> . <i>Frontiers in Plant Science</i> , 2016 , 7, 205	6.2	31
28	Assembly and Phasing of Dikaryotic Genomes from Two Isolates of f. sp. , the Causal Agent of Oat Crown Rust. <i>MBio</i> , 2018 , 9,	7.8	27
27	KnotSeeker: heuristic pseudoknot detection in long RNA sequences. <i>Rna</i> , 2008 , 14, 630-40	5.8	25
26	A comparative hidden Markov model analysis pipeline identifies proteins characteristic of cereal-infecting fungi. <i>BMC Genomics</i> , 2013 , 14, 807	4.5	21
25	EffectorP 3.0: prediction of apoplastic and cytoplasmic effectors in fungi and oomycetes. <i>Molecular Plant-Microbe Interactions</i> , 2021 ,	3.6	16
24	Distinct Life Histories Impact Dikaryotic Genome Evolution in the Rust Fungus <i>Puccinia striiformis</i> Causing Stripe Rust in Wheat. <i>Genome Biology and Evolution</i> , 2020 , 12, 597-617	3.9	14
23	Genomics accelerated isolation of a new stem rust avirulence gene-wheat resistance gene pair. <i>Nature Plants</i> , 2021 , 7, 1220-1228	11.5	12
22	Computational Methods for Predicting Effectors in Rust Pathogens. <i>Methods in Molecular Biology</i> , 2017 , 1659, 73-83	1.4	10
21	The crystal structure of SnTox3 from the necrotrophic fungus <i>Parastagonospora nodorum</i> reveals a unique effector fold and provides insight into Snn3 recognition and pro-domain protease processing of fungal effectors. <i>New Phytologist</i> , 2021 , 231, 2282-2296	9.8	10
20	Long reads and Hi-C sequencing illuminate the two-compartment genome of the model arbuscular mycorrhizal symbiont <i>Rhizophagus irregularis</i> . <i>New Phytologist</i> , 2021 ,	9.8	6
19	ApoplastP: prediction of effectors and plant proteins in the apoplast using machine learning		5
18	Flax rust infection transcriptomics reveals a transcriptional profile that may be indicative for rust Avr genes. <i>PLoS ONE</i> , 2019 , 14, e0226106	3.7	5
17	The stem rust fungus <i>Puccinia graminis</i> f. sp. <i>tritici</i> induces centromeric small RNAs during late infection that are associated with genome-wide DNA methylation. <i>BMC Biology</i> , 2021 , 19, 203	7.3	5
16	Predicting pseudoknotted structures across two RNA sequences. <i>Bioinformatics</i> , 2012 , 28, 3058-65	7.2	4
15	The stem rust fungus <i>Puccinia graminis</i> f. sp. <i>tritici</i> induces centromeric small RNAs during late infection that direct genome-wide DNA methylation		4
14	EffectorP 3.0: prediction of apoplastic and cytoplasmic effectors in fungi and oomycetes		4
13	The crystal structure of SnTox3 from the necrotrophic fungus <i>Parastagonospora nodorum</i> reveals a unique effector fold and insights into Kex2 protease processing of fungal effectors		3

12	Emergence of the Ug99 lineage of the wheat stem rust pathogen through somatic hybridisation		3
11	<i>Austropuccinia psidii</i> , causing myrtle rust, has a gigabase-sized genome shaped by transposable elements. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	2
10	De novo assembly and phasing of dikaryotic genomes from two isolates of <i>Puccinia coronata</i> f. sp. <i>avenae</i> , the causal agent of oat crown rust		2
9	A near complete haplotype-phased genome of the dikaryotic wheat stripe rust fungus <i>Puccinia striiformis</i> f. sp. <i>tritici</i> reveals high inter-haplotype diversity		2
8	Physical separation of haplotypes in dikaryons allows benchmarking of phasing accuracy in Nanopore and HiFi assemblies with Hi-C data.. <i>Genome Biology</i> , 2022 , 23, 84	18.3	2
7	Improved prediction of fungal effector proteins from secretomes with EffectorP 2.0		1
6	<i>Austropuccinia psidii</i> , causing myrtle rust, has a gigabase-sized genome shaped by transposable elements		1
5	Distinct life histories impact dikaryotic genome evolution in the rust fungus <i>Puccinia striiformis</i> causing stripe rust in wheat		1
4	LOCALIZER: subcellular localization prediction of both plant and effector proteins in the plant cell		1
3	Identification and correction of phase switches with Hi-C data in the Nanopore and HiFi chromosome-scale assemblies of the dikaryotic leaf rust fungus <i>Puccinia triticina</i>		1
2	Seeing is believing: Exploiting advances in structural biology to understand and engineer plant immunity.. <i>Current Opinion in Plant Biology</i> , 2022 , 67, 102210	9.9	1
1	An Introduction to RNA Structure and Pseudoknot Prediction 2010 , 521-546		