

# Jana Sperschneider

## List of Publications by Year in Descending Order

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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	Physical separation of haplotypes in dikaryons allows benchmarking of phasing accuracy in Nanopore and HiFi assemblies with Hi-C data.. <i>Genome Biology</i> , <b>2022</b> , 23, 84	18.3	2
46	Seeing is believing: Exploiting advances in structural biology to understand and engineer plant immunity.. <i>Current Opinion in Plant Biology</i> , <b>2022</b> , 67, 102210	9.9	1
45	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> , <b>2021</b> ,	9.8	6
44	EffectorP 3.0: prediction of apoplastic and cytoplasmic effectors in fungi and oomycetes. <i>Molecular Plant-Microbe Interactions</i> , <b>2021</b> ,	3.6	16
43	<i>Austropuccinia psidii</i> , causing myrtle rust, has a gigabase-sized genome shaped by transposable elements. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	2
42	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> , <b>2021</b> , 231, 2282-2296	9.8	10
41	Genomics accelerated isolation of a new stem rust avirulence gene-wheat resistance gene pair. <i>Nature Plants</i> , <b>2021</b> , 7, 1220-1228	11.5	12
40	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> , <b>2021</b> , 19, 203	7.3	5
39	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> , <b>2020</b> , 12, 597-617	3.9	14
38	Machine learning in plant-pathogen interactions: empowering biological predictions from field scale to genome scale. <i>New Phytologist</i> , <b>2020</b> , 228, 35-41	9.8	32
37	Emergence of the Ug99 lineage of the wheat stem rust pathogen through somatic hybridisation. <i>Nature Communications</i> , <b>2019</b> , 10, 5068	17.4	47
36	Flax rust infection transcriptomics reveals a transcriptional profile that may be indicative for rust Avr genes. <i>PLoS ONE</i> , <b>2019</b> , 14, e0226106	3.7	5
35	A Near-Complete Haplotype-Phased Genome of the Dikaryotic Wheat Stripe Rust Fungus f. sp. Reveals High Interhaplotype Diversity. <i>MBio</i> , <b>2018</b> , 9,	7.8	54
34	Improved prediction of fungal effector proteins from secretomes with EffectorP 2.0. <i>Molecular Plant Pathology</i> , <b>2018</b> , 19, 2094-2110	5.7	179
33	Assembly and Phasing of Dikaryotic Genomes from Two Isolates of f. sp. , the Causal Agent of Oat Crown Rust. <i>MBio</i> , <b>2018</b> , 9,	7.8	27
32	ApoplastP: prediction of effectors and plant proteins in the apoplast using machine learning. <i>New Phytologist</i> , <b>2018</b> , 217, 1764-1778	9.8	80
31	LOCALIZER: subcellular localization prediction of both plant and effector proteins in the plant cell. <i>Scientific Reports</i> , <b>2017</b> , 7, 44598	4.9	171

30	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> , <b>2017</b> , 7, 10410	4.9	32
29	Loss of by somatic exchange in stem rust leads to virulence for resistance in wheat. <i>Science</i> , <b>2017</b> , 358, 1607-1610	33.3	101
28	Computational Methods for Predicting Effectors in Rust Pathogens. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1659, 73-83	1.4	10
27	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> , <b>2016</b> , 17, 191	4.5	68
26	EffectorP: predicting fungal effector proteins from secretomes using machine learning. <i>New Phytologist</i> , <b>2016</b> , 210, 743-61	9.8	234
25	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> , <b>2016</b> , 7, 205	6.2	31
24	Advances and challenges in computational prediction of effectors from plant pathogenic fungi. <i>PLoS Pathogens</i> , <b>2015</b> , 11, e1004806	7.6	111
23	Evaluation of Secretion Prediction Highlights Differing Approaches Needed for Oomycete and Fungal Effectors. <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 1168	6.2	42
22	Genome-Wide Analysis in Three <i>Fusarium</i> Pathogens Identifies Rapidly Evolving Chromosomes and Genes Associated with Pathogenicity. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 1613-27	3.9	68
21	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> , <b>2014</b> , 5, 759	6.2	64
20	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> , <b>2014</b> , 5, 372	6.2	37
19	Genome sequencing and comparative genomics of the broad host-range pathogen <i>Rhizoctonia solani</i> AG8. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004281	6	102
18	A comparative hidden Markov model analysis pipeline identifies proteins characteristic of cereal-infecting fungi. <i>BMC Genomics</i> , <b>2013</b> , 14, 807	4.5	21
17	Predicting pseudoknotted structures across two RNA sequences. <i>Bioinformatics</i> , <b>2012</b> , 28, 3058-65	7.2	4
16	Heuristic RNA pseudoknot prediction including intramolecular kissing hairpins. <i>Rna</i> , <b>2011</b> , 17, 27-38	5.8	38
15	DotKnot: pseudoknot prediction using the probability dot plot under a refined energy model. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, e103	20.1	70
14	An Introduction to RNA Structure and Pseudoknot Prediction <b>2010</b> , 521-546		
13	KnotSeeker: heuristic pseudoknot detection in long RNA sequences. <i>Rna</i> , <b>2008</b> , 14, 630-40	5.8	25

12	Improved prediction of fungal effector proteins from secretomes with EffectorP 2.0	1
11	<i>Austropuccinia psidii</i> , causing myrtle rust, has a gigabase-sized genome shaped by transposable elements	1
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	ApoplastP: prediction of effectors and plant proteins in the apoplast using machine learning	5
8	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
7	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
6	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
5	Emergence of the Ug99 lineage of the wheat stem rust pathogen through somatic hybridisation	3
4	Distinct life histories impact dikaryotic genome evolution in the rust fungus <i>Puccinia striiformis</i> causing stripe rust in wheat	1
3	LOCALIZER: subcellular localization prediction of both plant and effector proteins in the plant cell	1
2	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
1	EffectorP 3.0: prediction of apoplastic and cytoplasmic effectors in fungi and oomycetes	4