

Joelle Amselem

List of Publications by Year in descending order

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35
papers

6,344
citations

172457

29
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361022

35
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35
all docs

35
docs citations

35
times ranked

7565
citing authors

#	ARTICLE	IF	CITATIONS
1	At the nexus of three kingdoms: the genome of the mycorrhizal fungus <i>Gigaspora margarita</i> provides insights into plant, endobacterial and fungal interactions. <i>Environmental Microbiology</i> , 2020, 22, 122-141.	3.8	84
2	pH effect on strain-specific transcriptomes of the take-all fungus. <i>PLoS ONE</i> , 2020, 15, e0236429.	2.5	2
3	RepetDB: a unified resource for transposable element references. <i>Mobile DNA</i> , 2019, 10, 6.	3.6	43
4	Population Genome Sequencing of the Scab Fungal Species <i>Venturia inaequalis</i> , <i>Venturia pirina</i> , <i>Venturia aucupariae</i> and <i>Venturia asperata</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2405-2414.	1.8	33
5	Ten steps to get started in Genome Assembly and Annotation. <i>F1000Research</i> , 2018, 7, 148.	1.6	85
6	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	9.3	303
7	A small secreted protein in <i>Zymoseptoria tritici</i> is responsible for avirulence on wheat cultivars carrying the <i>Stb6</i> resistance gene. <i>New Phytologist</i> , 2017, 214, 619-631.	7.3	218
8	Two genomes of highly polyphagous lepidopteran pests (<i>Spodoptera frugiperda</i> , Noctuidae) with different host-plant ranges. <i>Scientific Reports</i> , 2017, 7, 11816.	3.3	242
9	Gapless genome assembly of <i>Colletotrichum higginsianum</i> reveals chromosome structure and association of transposable elements with secondary metabolite gene clusters. <i>BMC Genomics</i> , 2017, 18, 667.	2.8	111
10	Comparative genomics of <i>Coniophora olivacea</i> reveals different patterns of genome expansion in Boletales. <i>BMC Genomics</i> , 2017, 18, 883.	2.8	20
11	The botrydial biosynthetic gene cluster of <i>Botrytis cinerea</i> displays a bipartite genomic structure and is positively regulated by the putative Zn(II)2Cys6 transcription factor BcBot6. <i>Fungal Genetics and Biology</i> , 2016, 96, 33-46.	2.1	60
12	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016, 16, 254-265.	4.8	108
13	Evolution of the EKA family of powdery mildew avirulence-effector genes from the ORF 1 of a LINE retrotransposon. <i>BMC Genomics</i> , 2015, 16, 917.	2.8	33
14	Deciphering Genome Content and Evolutionary Relationships of Isolates from the Fungus <i>Magnaporthe oryzae</i> Attacking Different Host Plants. <i>Genome Biology and Evolution</i> , 2015, 7, 2896-2912.	2.5	96
15	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. <i>Scientific Reports</i> , 2015, 5, 11571.	3.3	50
16	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. <i>BMC Genomics</i> , 2015, 16, 112.	2.8	49
17	Whole genome comparative analysis of transposable elements provides new insight into mechanisms of their inactivation in fungal genomes. <i>BMC Genomics</i> , 2015, 16, 141.	2.8	105
18	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus. <i>BMC Genomics</i> , 2015, 16, 461.	2.8	58

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19	The first set of expressed sequence tags (EST) from the medicinal mushroom <i>Agaricus subrufescens</i> delivers resource for gene discovery and marker development. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7879-7892.	3.6	13
20	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. <i>Nature Genetics</i> , 2013, 45, 1092-1096.	21.4	236
21	GnPS: an information system to integrate genetic and genomic data from plants and fungi. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat058.	3.0	43
22	LINKAGE TO THE MATING-TYPE LOCUS ACROSS THE GENUS <i>MICROBOTRYUM</i> : INSIGHTS INTO NONRECOMBINING CHROMOSOMES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3519-3533.	2.3	32
23	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	3.5	902
24	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	7.1	640
25	Effector diversification within compartments of the <i>Leptosphaeria maculans</i> genome affected by Repeat-Induced Point mutations. <i>Nature Communications</i> , 2011, 2, 202.	12.8	481
26	<i>Pã</i> rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	27.8	641
27	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. <i>Science</i> , 2010, 330, 1543-1546.	12.6	725
28	Hunting down fungal secretomes using liquidâ€phase IEF prior to high resolution 2â€DE. <i>Electrophoresis</i> , 2009, 30, 4118-4136.	2.4	31
29	Genome Annotation in Plants and Fungi: EuGene as a Model Platform. <i>Current Bioinformatics</i> , 2008, 3, 87-97.	1.5	102
30	Systemic response to aphid infestation by <i>Myzus persicae</i> in the phloem of <i>Apium graveolens</i> . <i>Plant Molecular Biology</i> , 2005, 57, 517-540.	3.9	137
31	Gene identification in the oomycete pathogen <i>Phytophthora parasitica</i> during in vitro vegetative growth through expressed sequence tags. <i>Fungal Genetics and Biology</i> , 2005, 42, 611-623.	2.1	46
32	Differential gene expression in <i>Arabidopsis</i> monitored using cDNA arrays. <i>Plant Journal</i> , 1998, 14, 643-652.	5.7	111
33	Further progress towards a catalogue of all <i>Arabidopsis</i> genes: analysis of a set of 5000 non-redundant ESTs. <i>Plant Journal</i> , 1996, 9, 101-124.	5.7	208
34	An inventory of 1152 expressed sequence tags obtained by partial sequencing of cDNAs from <i>Arabidopsis thaliana</i> +. <i>Plant Journal</i> , 1993, 4, 1051-1061.	5.7	254
35	Molecular basis for novel root phenotypes induced by <i>Agrobacterium rhizogenes</i> A4 on cucumber. <i>Plant Molecular Biology</i> , 1992, 19, 421-432.	3.9	42