

Joelle Amselem

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

6,344
citations

172457

29
h-index

361022

35
g-index

35
all docs

35
docs citations

35
times ranked

7565
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism. <i>Science</i> , 2010, 330, 1543-1546.	12.6	725
3	P ^Å origord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	27.8	641
4	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
5	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
6	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	9.3	303
7	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
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	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. <i>Nature Genetics</i> , 2013, 45, 1092-1096.	21.4	236
10	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
11	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
12	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
13	Differential gene expression in <i>Arabidopsis</i> monitored using cDNA arrays. <i>Plant Journal</i> , 1998, 14, 643-652.	5.7	111
14	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
15	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
16	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
17	Genome Annotation in Plants and Fungi: EuGene as a Model Platform. <i>Current Bioinformatics</i> , 2008, 3, 87-97.	1.5	102
18	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

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19	Ten steps to get started in Genome Assembly and Annotation. F1000Research, 2018, 7, 148.	1.6	85
20	At the nexus of three kingdoms: the genome of the mycorrhizal fungus <i>Gigaspora margarita</i> provides insights into plant, endobacterial and fungal interactions. Environmental Microbiology, 2020, 22, 122-141.	3.8	84
21	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. Fungal Genetics and Biology, 2016, 96, 33-46.	2.1	60
22	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus. BMC Genomics, 2015, 16, 461.	2.8	58
23	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. Scientific Reports, 2015, 5, 11571.	3.3	50
24	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. BMC Genomics, 2015, 16, 112.	2.8	49
25	Gene identification in the oomycete pathogen <i>Phytophthora parasitica</i> during in vitro vegetative growth through expressed sequence tags. Fungal Genetics and Biology, 2005, 42, 611-623.	2.1	46
26	GnPLS: an information system to integrate genetic and genomic data from plants and fungi. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat058.	3.0	43
27	RepetDB: a unified resource for transposable element references. Mobile DNA, 2019, 10, 6.	3.6	43
28	Molecular basis for novel root phenotypes induced by <i>Agrobacterium rhizogenes</i> A4 on cucumber. Plant Molecular Biology, 1992, 19, 421-432.	3.9	42
29	Evolution of the EKA family of powdery mildew avirulence-effector genes from the ORF 1 of a LINE retrotransposon. BMC Genomics, 2015, 16, 917.	2.8	33
30	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> . G3: Genes, Genomes, Genetics, 2019, 9, 2405-2414.	1.8	33
31	LINKAGE TO THE MATING-TYPE LOCUS ACROSS THE GENUS <i>MICROBOTRYUM</i> : INSIGHTS INTO NONRECOMBINING CHROMOSOMES. Evolution; International Journal of Organic Evolution, 2012, 66, 3519-3533.	2.3	32
32	Hunting down fungal secretomes using liquid-phase IEF prior to high resolution 2D-E. Electrophoresis, 2009, 30, 4118-4136.	2.4	31
33	Comparative genomics of <i>Coniophora olivacea</i> reveals different patterns of genome expansion in Boletales. BMC Genomics, 2017, 18, 883.	2.8	20
34	The first set of expressed sequence tags (EST) from the medicinal mushroom <i>Agaricus subrufescens</i> delivers resource for gene discovery and marker development. Applied Microbiology and Biotechnology, 2014, 98, 7879-7892.	3.6	13
35	pH effect on strain-specific transcriptomes of the take-all fungus. PLoS ONE, 2020, 15, e0236429.	2.5	2