

Leonardo Miguel Galindo

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8157962/publications.pdf>

Version: 2024-02-01

17
papers

914
citations

758635

12
h-index

887659

17
g-index

17
all docs

17
docs citations

17
times ranked

1297
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of flax (<i>Linum usitatissimum</i>) assembled <i>de novo</i> from short shotgun sequence reads. <i>Plant Journal</i> , 2012, 72, 461-473.	2.8	415
2	LTR-retrotransposons in plants: Engines of evolution. <i>Gene</i> , 2017, 626, 14-25.	1.0	177
3	RNA-seq Transcriptome Response of Flax (<i>Linum usitatissimum</i> L.) to the Pathogenic Fungus <i>Fusarium oxysporum</i> f. sp. <i>lini</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1766.	1.7	67
4	Response of <i>Brassica napus</i> to <i>Plasmodiophora brassicae</i> Involves Salicylic Acid-Mediated Immunity: An RNA-Seq-Based Study. <i>Frontiers in Plant Science</i> , 2020, 11, 1025.	1.7	42
5	Integrated transcriptomic and proteomic profiling of white spruce stems during the transition from active growth to dormancy. <i>Plant, Cell and Environment</i> , 2012, 35, 682-701.	2.8	40
6	Identification, characterization and distribution of transposable elements in the flax (<i>Linum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 T	1.2	30
7	Influence of water deficit on the molecular responses of <i>Pinus contorta</i> x <i>Pinus banksiana</i> mature trees to infection by the mountain pine beetle fungal associate, <i>Grosmannia clavigera</i> . <i>Tree Physiology</i> , 2014, 34, 1220-1239.	1.4	25
8	Shaping Plant Adaptability, Genome Structure and Gene Expression through Transposable Element Epigenetic Control: Focus on Methylation. <i>Agronomy</i> , 2018, 8, 180.	1.3	25
9	Comparative Transcriptome Analysis of Rutabaga (<i>Brassica napus</i>) Cultivars Indicates Activation of Salicylic Acid and Ethylene-Mediated Defenses in Response to <i>Plasmodiophora brassicae</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 8381.	1.8	19
10	Ion Torrent sequencing as a tool for mutation discovery in the flax (<i>Linum usitatissimum</i> L.) genome. <i>Plant Methods</i> , 2015, 11, 19.	1.9	18
11	Diverse chitinases are invoked during the activity-dormancy transition in spruce. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	16
12	Isolation and characterization of RNase LTR sequences of Ty1-copia retrotransposons in common bean (<i>Phaseolus vulgaris</i> L.). <i>Genome</i> , 2004, 47, 84-95.	0.9	12
13	Ty1-copia elements reveal diverse insertion sites linked to polymorphisms among flax (<i>Linum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	9
14	Current and Future Pathotyping Platforms for <i>Plasmodiophora brassicae</i> in Canada. <i>Plants</i> , 2021, 10, 1446.	1.6	7
15	Candidate Effectors of <i>Plasmodiophora brassicae</i> Pathotype 5X During Infection of Two <i>Brassica napus</i> Genotypes. <i>Frontiers in Microbiology</i> , 2021, 12, 742268.	1.5	7
16	Protocol: rhPCR and SNaPshot assays to distinguish <i>Plasmodiophora brassicae</i> pathotype clusters. <i>Plant Methods</i> , 2022, 18, .	1.9	4
17	Influence of water deficit on the induced and constitutive responses of pines to infection by mountain pine beetle fungal associates. <i>BMC Proceedings</i> , 2011, 5, .	1.8	1