# Leonardo Miguel Galindo

## List of Publications by Year in Descending Order

**Source:** https://exaly.com/author-pdf/8157962/leonardo-miguel-galindo-publications-by-year.pdf
**Version:** 2024-04-23

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|---|---|---|---|
| 14<br>papers | 627<br>citations | 10<br>h-index | 17<br>g-index |
| 17<br>ext. papers | 819<br>ext. citations | 4.7<br>avg, IF | 3.82<br>L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 14 | Candidate Effectors of Pathotype 5X During Infection of Two Genotypes. *Frontiers in Microbiology*, **2021**, 12, 742268 | 5.7 | 0 |
| 13 | Comparative Transcriptome Analysis of Rutabaga () Cultivars Indicates Activation of Salicylic Acid and Ethylene-Mediated Defenses in Response to. *International Journal of Molecular Sciences*, **2020**, 21, | 6.3 | 7 |
| 12 | Response of to Involves Salicylic Acid-Mediated Immunity: An RNA-Seq-Based Study. *Frontiers in Plant Science*, **2020**, 11, 1025 | 6.2 | 15 |
| 11 | Shaping Plant Adaptability, Genome Structure and Gene Expression through Transposable Element Epigenetic Control: Focus on Methylation. *Agronomy*, **2018**, 8, 180 | 3.6 | 19 |
| 10 | LTR-retrotransposons in plants: Engines of evolution. *Gene*, **2017**, 626, 14-25 | 3.8 | 101 |
| 9 | RNA-seq Transcriptome Response of Flax ( L.) to the Pathogenic Fungus f. sp.. *Frontiers in Plant Science*, **2016**, 7, 1766 | 6.2 | 42 |
| 8 | Ty1-copia elements reveal diverse insertion sites linked to polymorphisms among flax (Linum usitatissimum L.) accessions. *BMC Genomics*, **2016**, 17, 1002 | 4.5 | 7 |
| 7 | Ion Torrent sequencing as a tool for mutation discovery in the flax (Linum usitatissimum L.) genome. *Plant Methods*, **2015**, 11, 19 | 5.8 | 16 |
| 6 | Diverse chitinases are invoked during the activity-dormancy transition in spruce. *Tree Genetics and Genomes*, **2015**, 11, 1 | 2.1 | 9 |
| 5 | Influence of water deficit on the molecular responses of Pinus contorta □Pinus banksiana mature trees to infection by the mountain pine beetle fungal associate, Grosmannia clavigera. *Tree Physiology*, **2014**, 34, 1220-39 | 4.2 | 22 |
| 4 | The genome of flax (Linum usitatissimum) assembled de novo from short shotgun sequence reads. *Plant Journal*, **2012**, 72, 461-73 | 6.9 | 315 |
| 3 | Identification, characterization and distribution of transposable elements in the flax (Linum usitatissimum L.) genome. *BMC Genomics*, **2012**, 13, 644 | 4.5 | 25 |
| 2 | Integrated transcriptomic and proteomic profiling of white spruce stems during the transition from active growth to dormancy. *Plant, Cell and Environment*, **2012**, 35, 682-701 | 8.4 | 38 |
| 1 | Isolation and characterization of RNase LTR sequences of Ty1-copia retrotransposons in common bean (Phaseolus vulgaris L). *Genome*, **2004**, 47, 84-95 | 2.4 | 11 |