

Nicolas B Langlade

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

3,276
citations

185998

28
h-index

182168

51
g-index

60
all docs

60
docs citations

60
times ranked

4214
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Optimized cultivar deployment improves the efficiency and stability of sunflower crop production at national scale. <i>Theoretical and Applied Genetics</i> , 2022, 135, 4049-4063. | 1.8 | 4 |
| 2 | Expression complementation of gene presence/absence polymorphisms in hybrids contributes importantly to heterosis in sunflower. <i>Journal of Advanced Research</i> , 2022, 42, 83-98. | 4.4 | 12 |
| 3 | Maternal drought stress induces abiotic stress tolerance to the progeny at the germination stage in sunflower. <i>Environmental and Experimental Botany</i> , 2022, , 104939. | 2.0 | 7 |
| 4 | Gene regulatory network inference methodology for genomic and transcriptomic data acquired in genetically related heterozygote individuals. <i>Bioinformatics</i> , 2022, 38, 4127-4134. | 1.8 | 0 |
| 5 | New challenges for sunflower ideotyping in changing environments and more ecological cropping systems. <i>OCL - Oilseeds and Fats, Crops and Lipids</i> , 2021, 28, 29. | 0.6 | 15 |
| 6 | Leaf metabolomic data of eight sunflower lines and their sixteen hybrids under water deficit. <i>OCL - Oilseeds and Fats, Crops and Lipids</i> , 2021, 28, 42. | 0.6 | 2 |
| 7 | Proteomic data from leaves of twenty-four sunflower genotypes under water deficit. <i>OCL - Oilseeds and Fats, Crops and Lipids</i> , 2021, 28, 12. | 0.6 | 6 |
| 8 | Genome-wide and comparative phylogenetic analysis of senescence-associated NAC transcription factors in sunflower (<i>Helianthus annuus</i>). <i>BMC Genomics</i> , 2021, 22, 893. | 1.2 | 6 |
| 9 | RNA expression dataset of 384 sunflower hybrids in field condition. <i>OCL - Oilseeds and Fats, Crops and Lipids</i> , 2020, 27, 36. | 0.6 | 4 |
| 10 | Gene banks for wild and cultivated sunflower genetic resources. <i>OCL - Oilseeds and Fats, Crops and Lipids</i> , 2020, 27, 9. | 0.6 | 20 |
| 11 | A multiscale approach reveals regulatory players of water stress responses in seeds during germination. <i>Plant, Cell and Environment</i> , 2020, 43, 1300-1313. | 2.8 | 14 |
| 12 | Transcriptomic data of leaves from eight sunflower lines and their sixteen hybrids under water deficit. <i>OCL - Oilseeds and Fats, Crops and Lipids</i> , 2020, 27, 48. | 0.6 | 5 |
| 13 | Exploring gene networks in two sunflower lines with contrasting leaf senescence phenotype using a system biology approach. <i>BMC Plant Biology</i> , 2019, 19, 446. | 1.6 | 10 |
| 14 | Metabolomic characterization of sunflower leaf allows discriminating genotype groups or stress levels with a minimal set of metabolic markers. <i>Metabolomics</i> , 2019, 15, 56. | 1.4 | 17 |
| 15 | Sunflower pan-genome analysis shows that hybridization altered gene content and disease resistance. <i>Nature Plants</i> , 2019, 5, 54-62. | 4.7 | 172 |
| 16 | Comparison of GWAS models to identify non-additive genetic control of flowering time in sunflower hybrids. <i>Theoretical and Applied Genetics</i> , 2018, 131, 319-332. | 1.8 | 38 |
| 17 | Data describing the eco-physiological responses of twenty-four sunflower genotypes to water deficit. <i>Data in Brief</i> , 2018, 21, 1296-1301. | 0.5 | 16 |
| 18 | One Way to Achieve Germination: Common Molecular Mechanism Induced by Ethylene and After-Ripening in Sunflower Seeds. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2464. | 1.8 | 15 |

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|----|---|------|-----------|
| 19 | Heliaphen, an Outdoor High-Throughput Phenotyping Platform for Genetic Studies and Crop Modeling. <i>Frontiers in Plant Science</i> , 2018, 9, 1908. | 1.7 | 34 |
| 20 | Molecular diversity of sunflower populations maintained as genetic resources is affected by multiplication processes and breeding for major traits. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1099-1112. | 1.8 | 12 |
| 21 | Genetic control of plasticity of oil yield for combined abiotic stresses using a joint approach of crop modelling and genome-wide association. <i>Plant, Cell and Environment</i> , 2017, 40, 2276-2291. | 2.8 | 66 |
| 22 | Sunflower crop and climate change: vulnerability, adaptation, and mitigation potential from case-studies in Europe. <i>OCL - Oilseeds and Fats, Crops and Lipids</i> , 2017, 24, D102. | 0.6 | 95 |
| 23 | The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. <i>Nature</i> , 2017, 546, 148-152. | 13.7 | 579 |
| 24 | Genomic Prediction of Sunflower Hybrids Oil Content. <i>Frontiers in Plant Science</i> , 2017, 8, 1633. | 1.7 | 31 |
| 25 | Different genetic architectures underlie crop responses to the same pathogen: the { <i>Helianthus annuus</i> * <i>Phoma macdonaldii</i> } interaction case for black stem disease and premature ripening. <i>BMC Plant Biology</i> , 2017, 17, 167. | 1.6 | 7 |
| 26 | Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. <i>BioTechniques</i> , 2017, 62, xv. | 0.8 | 6 |
| 27 | Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. <i>BioTechniques</i> , 2016, 61, 203-205. | 0.8 | 162 |
| 28 | Effects of plant growth stage and leaf aging on the response of transpiration and photosynthesis to water deficit in sunflower. <i>Functional Plant Biology</i> , 2016, 43, 797. | 1.1 | 31 |
| 29 | Fortune telling: metabolic markers of plant performance. <i>Metabolomics</i> , 2016, 12, 158. | 1.4 | 89 |
| 30 | Reactive oxygen species, abscisic acid and ethylene interact to regulate sunflower seed germination. <i>Plant, Cell and Environment</i> , 2015, 38, 364-374. | 2.8 | 125 |
| 31 | Genetic Control of Water Use Efficiency and Leaf Carbon Isotope Discrimination in Sunflower (<i>Helianthus annuus</i> L.) Subjected to Two Drought Scenarios. <i>PLoS ONE</i> , 2014, 9, e101218. | 1.1 | 50 |
| 32 | Translatome profiling in dormant and nondormant sunflower (<i>Helianthus annuus</i>) seeds highlights post-transcriptional regulation of germination. <i>New Phytologist</i> , 2014, 204, 864-872. | 3.5 | 36 |
| 33 | Bridging physiological and evolutionary time-scales in a gene regulatory network. <i>New Phytologist</i> , 2014, 203, 685-696. | 3.5 | 15 |
| 34 | Is Gene Transcription Involved in Seed Dry After-Ripening?. <i>PLoS ONE</i> , 2014, 9, e86442. | 1.1 | 38 |
| 35 | A biomarker based on gene expression indicates plant water status in controlled and natural environments. <i>Plant, Cell and Environment</i> , 2013, 36, 2175-2189. | 2.8 | 25 |
| 36 | Combined linkage and association mapping of flowering time in Sunflower (<i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1337-1356. | 1.8 | 48 |

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|----|--|-----|-----------|
| 37 | Consensus mapping of major resistance genes and independent QTL for quantitative resistance to sunflower downy mildew. <i>Theoretical and Applied Genetics</i> , 2012, 125, 909-920. | 1.8 | 48 |
| 38 | Genetic analysis of phytosterol content in sunflower seeds. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1589-1601. | 1.8 | 45 |
| 39 | The genetic basis for natural variation in heteroblasty in <i>Antirrhinum</i> . <i>New Phytologist</i> , 2012, 196, 1251-1259. | 3.5 | 24 |
| 40 | A Gene-Phenotype Network Based on Genetic Variability for Drought Responses Reveals Key Physiological Processes in Controlled and Natural Environments. <i>PLoS ONE</i> , 2012, 7, e45249. | 1.1 | 58 |
| 41 | Genetic dissection of tocopherol and phytosterol in recombinant inbred lines of sunflower through quantitative trait locus analysis and the candidate gene approach. <i>Molecular Breeding</i> , 2012, 29, 717-729. | 1.0 | 25 |
| 42 | Targeted mRNA Oxidation Regulates Sunflower Seed Dormancy Alleviation during Dry After-Ripening. <i>Plant Cell</i> , 2011, 23, 2196-2208. | 3.1 | 180 |
| 43 | Progress towards a reference genome for sunflower. <i>Botany</i> , 2011, 89, 429-437. | 0.5 | 67 |
| 44 | Tinkering with the C-Function: A Molecular Frame for the Selection of Double Flowers in Cultivated Roses. <i>PLoS ONE</i> , 2010, 5, e9288. | 1.1 | 94 |
| 45 | Mutational spaces for leaf shape and size. <i>HFSP Journal</i> , 2008, 2, 110-120. | 2.5 | 45 |
| 46 | Isoflavonoid exudation from white lupin roots is influenced by phosphate supply, root type and cluster root stage. <i>New Phytologist</i> , 2006, 171, 657-668. | 3.5 | 65 |
| 47 | Evolutionary Paths Underlying Flower Color Variation in <i>Antirrhinum</i> . <i>Science</i> , 2006, 313, 963-966. | 6.0 | 153 |
| 48 | Evolution through genetically controlled allometry space. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10221-10226. | 3.3 | 159 |
| 49 | Phosphorus deficiency-induced modifications in citrate catabolism and in cytosolic pH as related to citrate exudation in cluster roots of white lupin. <i>Plant and Soil</i> , 2003, 248, 117-127. | 1.8 | 52 |
| 50 | Phosphorus deficiency-induced modifications in citrate catabolism and in cytosolic pH as related to citrate exudation in cluster roots of white lupin. , 2003, , 117-127. | | 2 |
| 51 | ATP citrate lyase: cloning, heterologous expression and possible implication in root organic acid metabolism and excretion. <i>Plant, Cell and Environment</i> , 2002, 25, 1561-1569. | 2.8 | 30 |
| 52 | Metabolic changes associated with cluster root development in white lupin (<i>Lupinus albus</i> L.): relationship between organic acid excretion, sucrose metabolism and energy status. <i>Planta</i> , 2001, 213, 534-542. | 1.6 | 103 |
| 53 | Physiological Aspects of Cluster Root Function and Development in Phosphorus-deficient White Lupin (<i>Lupinus albus</i> L.). <i>Annals of Botany</i> , 2000, 85, 909-919. | 1.4 | 304 |