Nicolas B Langlade

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. Nature, 2017, 546, 148-152.	13.7	579
2	Physiological Aspects of Cluster Root Function and Development in Phosphorus-deficient White Lupin (Lupinus albus L.). Annals of Botany, 2000, 85, 909-919.	1.4	304
3	Targeted mRNA Oxidation Regulates Sunflower Seed Dormancy Alleviation during Dry After-Ripening Â. Plant Cell, 2011, 23, 2196-2208.	3.1	180
4	Sunflower pan-genome analysis shows that hybridization altered gene content and disease resistance. Nature Plants, 2019, 5, 54-62.	4.7	172
5	Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. BioTechniques, 2016, 61, 203-205.	0.8	162
6	Evolution through genetically controlled allometry space. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10221-10226.	3.3	159
7	Evolutionary Paths Underlying Flower Color Variation in Antirrhinum. Science, 2006, 313, 963-966.	6.0	153
8	Reactive oxygen species, abscisic acid and ethylene interact to regulate sunflower seed germination. Plant, Cell and Environment, 2015, 38, 364-374.	2.8	125
9	Metabolic changes associated with cluster root development in white lupin (Lupinus albus L.): relationship between organic acid excretion, sucrose metabolism and energy status. Planta, 2001, 213, 534-542.	1.6	103
10	Sunflower crop and climate change: vulnerability, adaptation, and mitigation potential from case-studies in Europe. OCL - Oilseeds and Fats, Crops and Lipids, 2017, 24, D102.	0.6	95
11	Tinkering with the C-Function: A Molecular Frame for the Selection of Double Flowers in Cultivated Roses. PLoS ONE, 2010, 5, e9288.	1.1	94
12	Fortune telling: metabolic markers of plant performance. Metabolomics, 2016, 12, 158.	1.4	89
13	Progress towards a reference genome for sunflower. Botany, 2011, 89, 429-437.	0.5	67
14	Genetic control of plasticity of oil yield for combined abiotic stresses using a joint approach of crop modelling and genomeâ€wide association. Plant, Cell and Environment, 2017, 40, 2276-2291.	2.8	66
15	Isoflavonoid exudation from white lupin roots is influenced by phosphate supply, root type and clusterâ€root stage. New Phytologist, 2006, 171, 657-668.	3.5	65
16	A Gene-Phenotype Network Based on Genetic Variability for Drought Responses Reveals Key Physiological Processes in Controlled and Natural Environments. PLoS ONE, 2012, 7, e45249.	1.1	58
17	Phosphorus deficiency-induced modifications in citrate catabolism and in cytosolic pH as related to citrate exudation in cluster roots of white lupin. Plant and Soil, 2003, 248, 117-127.	1.8	52
18	Genetic Control of Water Use Efficiency and Leaf Carbon Isotope Discrimination in Sunflower (Helianthus annuus L) Subjected to Two Drought Scenarios, PLoS ONE, 2014, 9, e101218	1.1	50

NICOLAS B LANGLADE

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19	Consensus mapping of major resistance genes and independent QTL for quantitative resistance to sunflower downy mildew. Theoretical and Applied Genetics, 2012, 125, 909-920.	1.8	48
20	Combined linkage and association mapping of flowering time in Sunflower (Helianthus annuus L.). Theoretical and Applied Genetics, 2013, 126, 1337-1356.	1.8	48
21	Mutational spaces for leaf shape and size. HFSP Journal, 2008, 2, 110-120.	2.5	45
22	Genetic analysis of phytosterol content in sunflower seeds. Theoretical and Applied Genetics, 2012, 125, 1589-1601.	1.8	45
23	Comparison of GWAS models to identify non-additive genetic control of flowering time in sunflower hybrids. Theoretical and Applied Genetics, 2018, 131, 319-332.	1.8	38
24	Is Gene Transcription Involved in Seed Dry After-Ripening?. PLoS ONE, 2014, 9, e86442.	1.1	38
25	Translatome profiling in dormant and nondormant sunflower (<i>Helianthus annuus</i>) seeds highlights postâ€transcriptional regulation of germination. New Phytologist, 2014, 204, 864-872.	3.5	36
26	Heliaphen, an Outdoor High-Throughput Phenotyping Platform for Genetic Studies and Crop Modeling. Frontiers in Plant Science, 2018, 9, 1908.	1.7	34
27	Effects of plant growth stage and leaf aging on the response of transpiration and photosynthesis to water deficit in sunflower. Functional Plant Biology, 2016, 43, 797.	1.1	31
28	Genomic Prediction of Sunflower Hybrids Oil Content. Frontiers in Plant Science, 2017, 8, 1633.	1.7	31
29	ATP citrate lyase: cloning, heterologous expression and possible implication in root organic acid metabolism and excretion. Plant, Cell and Environment, 2002, 25, 1561-1569.	2.8	30
30	Genetic dissection of tocopherol and phytosterol in recombinant inbred lines of sunflower through quantitative trait locus analysis and the candidate gene approach. Molecular Breeding, 2012, 29, 717-729.	1.0	25
31	A biomarker based on gene expression indicates plant water status in controlled and natural environments. Plant, Cell and Environment, 2013, 36, 2175-2189.	2.8	25
32	The genetic basis for natural variation in heteroblasty in <i>Antirrhinum</i> . New Phytologist, 2012, 196, 1251-1259.	3.5	24
33	Gene banks for wild and cultivated sunflower genetic resources. OCL - Oilseeds and Fats, Crops and Lipids, 2020, 27, 9.	0.6	20
34	Metabolomic characterization of sunflower leaf allows discriminating genotype groups or stress levels with a minimal set of metabolic markers. Metabolomics, 2019, 15, 56.	1.4	17
35	Data describing the eco-physiological responses of twenty-four sunflower genotypes to water deficit. Data in Brief, 2018, 21, 1296-1301.	0.5	16
36	Bridging physiological and evolutionary timeâ€scales in a gene regulatory network. New Phytologist, 2014, 203, 685-696.	3.5	15

NICOLAS B LANGLADE

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37	One Way to Achieve Germination: Common Molecular Mechanism Induced by Ethylene and After-Ripening in Sunflower Seeds. International Journal of Molecular Sciences, 2018, 19, 2464.	1.8	15
38	New challenges for sunflower ideotyping in changing environments and more ecological cropping systems. OCL - Oilseeds and Fats, Crops and Lipids, 2021, 28, 29.	0.6	15
39	A multiscale approach reveals regulatory players of water stress responses in seeds during germination. Plant, Cell and Environment, 2020, 43, 1300-1313.	2.8	14
40	Molecular diversity of sunflower populations maintained as genetic resources is affected by multiplication processes and breeding for major traits. Theoretical and Applied Genetics, 2017, 130, 1099-1112.	1.8	12
41	Expression complementation of gene presence/absence polymorphisms in hybrids contributes importantly to heterosis in sunflower. Journal of Advanced Research, 2022, 42, 83-98.	4.4	12
42	Exploring gene networks in two sunflower lines with contrasting leaf senescence phenotype using a system biology approach. BMC Plant Biology, 2019, 19, 446.	1.6	10
43	Different genetic architectures underlie crop responses to the same pathogen: the {Helianthus annuus * Phoma macdonaldii} interaction case for black stem disease and premature ripening. BMC Plant Biology, 2017, 17, 167.	1.6	7
44	Maternal drought stress induces abiotic stress tolerance to the progeny at the germination stage in sunflower. Environmental and Experimental Botany, 2022, , 104939.	2.0	7
45	Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. BioTechniques, 2017, 62, xv.	0.8	6
46	Proteomic data from leaves of twenty-four sunflower genotypes under water deficit. OCL - Oilseeds and Fats, Crops and Lipids, 2021, 28, 12.	0.6	6
47	Genome-wide and comparative phylogenetic analysis of senescence-associated NAC transcription factors in sunflower (Helianthus annuus). BMC Genomics, 2021, 22, 893.	1.2	6
48	Transcriptomic data of leaves from eight sunflower lines and their sixteen hybrids under water deficit. OCL - Oilseeds and Fats, Crops and Lipids, 2020, 27, 48.	0.6	5
49	RNA expression dataset of 384 sunflower hybrids in field condition. OCL - Oilseeds and Fats, Crops and Lipids, 2020, 27, 36.	0.6	4
50	Optimized cultivar deployment improves the efficiency and stability of sunflower crop production at national scale. Theoretical and Applied Genetics, 2022, 135, 4049-4063.	1.8	4
51	Leaf metabolomic data of eight sunflower lines and their sixteen hybrids under water deficit. OCL - Oilseeds and Fats, Crops and Lipids, 2021, 28, 42.	0.6	2
52	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
53	Gene regulatory network inference methodology for genomic and transcriptomic data acquired in genetically related heterozygote individuals. Bioinformatics, 2022, 38, 4127-4134.	1.8	0