Pascal Gamas

List of Publications by Year
in descending order

51 papers	5,593 citations	93792 39 h-index	214428 50 g-index
54 all docs	54 docs citations	54 times ranked	5397 citing authors

#	Article	IF	Citations
1	MtEFD and MtEFD2: Two transcription factors with distinct neofunctionalization in symbiotic nodule development. Plant Physiology, 2022, 189, 1587-1607.	2.3	9
2	MtExpress, a Comprehensive and Curated RNAseq-based Gene Expression Atlas for the Model Legume <i>Medicago truncatula</i>. Plant and Cell Physiology, 2021, 62, 1494-1500.	1.5	48
3	NIN-like protein transcription factors regulate leghemoglobin genes in legume nodules. Science, 2021, 374, 625-628.	6.0	61
4	LeGOO: An Expertized Knowledge Database for the Model Legume Medicago truncatula. Plant and Cell Physiology, 2020, 61, 203-211.	1.5	19
5	Diversification of cytokinin phosphotransfer signaling genes in Medicago truncatula and other legume genomes. BMC Genomics, 2019, 20, 373.	1.2	14
6	Whole-genome landscape of Medicago truncatula symbiotic genes. Nature Plants, 2018, 4, 1017-1025.	4.7	192
7	Laser Capture Micro-Dissection Coupled to RNA Sequencing: A Powerful Approach Applied to the Model Legume Medicago truncatula in Interaction with Sinorhizobium meliloti. Methods in Molecular Biology, 2018, 1830, 191-224.	0.4	11
8	Regulation of Differentiation of Nitrogen-Fixing Bacteria by Microsymbiont Targeting of Plant Thioredoxin s1. Current Biology, 2017, 27, 250-256.	1.8	51
9	Cytokinins in Symbiotic Nodulation: When, Where, What For?. Trends in Plant Science, 2017, 22, 792-802.	4.3	128
10	Different cytokinin histidine kinase receptors regulate nodule initiation as well as later nodule developmental stages in <i>Medicago truncatula</i>. Plant, Cell and Environment, 2016, 39, 2198-2209.	2.8	49
11	A Laser Dissection-RNAseq Analysis Highlights the Activation of Cytokinin Pathways by Nod Factors in the <i>Medicago truncatula</i> Root Epidermis. Plant Physiology, 2016, 171, 2256-2276.	2.3	128
12	Reprogramming of DNA methylation is critical for nodule development in Medicago truncatula. Nature Plants, 2016, 2, 16166.	4.7	99
13	Fullâ€length <i>de novo</i> assembly of RNAâ€seq data in pea (<i><scp>P</scp>isum sativum</i> L.) provides a gene expression atlas and gives insights into root nodulation in this species. Plant Journal, 2015, 84, 1-19.	2.8	173
14	Combined genetic and transcriptomic analysis reveals three major signalling pathways activated by Mycâ€<scp>LCO</scp>s in <i>Medicago truncatula</i>. New Phytologist, 2015, 208, 224-240.	3.5	61
15	A phylogenetically conserved group of NF-Y transcription factors interact to control nodulation in legumes. Plant Physiology, 2015, 169, pp.01144.2015.	2.3	72
16	The CCAAT box-binding transcription factor NF-YA1 controls rhizobial infection. Journal of Experimental Botany, 2014, 65, 481-494.	2.4	117
17	An integrated analysis of plant and bacterial gene expression in symbiotic root nodules using laserâ€capture microdissection coupled to <scp>RNA</scp> sequencing. Plant Journal, 2014, 77, 817-837.	2.8	447
18	Two <scp>CCAAT</scp>â€boxâ€binding transcription factors redundantly regulate early steps of the legumeâ€rhizobia endosymbiosis. Plant Journal, 2014, 79, 757-768.	2.8	105

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19	The symbiotic transcription factor <scp>M</scp>t<scp>EFD</scp> and cytokinins are positively acting in the <i><scp>M</scp>edicago truncatula</i> and <i><scp>R</scp>alstonia solanacearum</i> pathogenic interaction. New Phytologist, 2014, 201, 1343-1357.	3.5	43
20	Next-Generation Annotation of Prokaryotic Genomes with EuGene-P: Application to Sinorhizobium meliloti 2011. DNA Research, 2013, 20, 339-354.	1.5	90
21	CCAAT-box binding transcription factors in plants: Y so many?. Trends in Plant Science, 2013, 18, 157-166.	4.3	265
22	A Regulatory Network-Based Approach Dissects Late Maturation Processes Related to the Acquisition of Desiccation Tolerance and Longevity of Medicago truncatula Seeds. Plant Physiology, 2013, 163, 757-774.	2.3	155
23	Transcription Reprogramming during Root Nodule Development in Medicago truncatula. PLoS ONE, 2011, 6, e16463.	1.1	102
24	MtbHLH1, a bHLH transcription factor involved in <i>Medicago truncatula</i> nodule vascular patterning and nodule to plant metabolic exchanges. New Phytologist, 2011, 191, 391-404.	3.5	53
25	A remorin protein interacts with symbiotic receptors and regulates bacterial infection. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2343-2348.	3.3	316
26	Analysis and modeling of the integrative response of Medicago truncatula to nitrogen constraints. Comptes Rendus - Biologies, 2009, 332, 1022-1033.	0.1	12
27	EFD Is an ERF Transcription Factor Involved in the Control of Nodule Number and Differentiation in<i>Medicago truncatula</i>. Plant Cell, 2008, 20, 2696-2713.	3.1	172
28	<i>Trans</i>-regulation of the expression of the transcription factor <i>MtHAP2-1</i> by a uORF controls root nodule development. Genes and Development, 2008, 22, 1549-1559.	2.7	103
29	Evidence for the Involvement in Nodulation of the Two Small Putative Regulatory Peptide-Encoding Genes <i>MtRALFL1</i> and <i>MtDVL1</i>. Molecular Plant-Microbe Interactions, 2008, 21, 1118-1127.	1.4	68
30	Genome-Wide Annotation of Remorins, a Plant-Specific Protein Family: Evolutionary and Functional Perspectives. Plant Physiology, 2007, 145, 593-600.	2.3	164
31	Identification of New Potential Regulators of the Medicago truncatulaâ€"Sinorhizobium meliloti Symbiosis Using a Large-Scale Suppression Subtractive Hybridization Approach. Molecular Plant-Microbe Interactions, 2007, 20, 321-332.	1.4	35
32	The MtMMPL1 Early Nodulin Is a Novel Member of the Matrix Metalloendoproteinase Family with a Role in Medicago truncatula Infection by Sinorhizobium meliloti Â. Plant Physiology, 2007, 144, 703-716.	2.3	53
33	MtHAP2-1 is a key transcriptional regulator of symbiotic nodule development regulated by microRNA169 in Medicago truncatula. Genes and Development, 2006, 20, 3084-3088.	2.7	450
34	Expression Profiling in Medicago truncatula Identifies More Than 750 Genes Differentially Expressed during Nodulation, Including Many Potential Regulators of the Symbiotic Program. Plant Physiology, 2004, 136, 3159-3176.	2.3	269
35	Construction and validation of cDNA-based Mt6k-RIT macro- and microarrays to explore root endosymbioses in the model legume Medicago truncatula. Journal of Biotechnology, 2004, 108, 95-113.	1.9	103
36	Cytological, Genetic, and Molecular Analysis to Characterize Compatible and Incompatible Interactions Between Medicago truncatula and Colletotrichum trifolii. Molecular Plant-Microbe Interactions, 2004, 17, 909-920.	1.4	74

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37	Exploring root symbiotic programs in the model legume Medicago truncatula using EST analysis. Nucleic Acids Research, 2002, 30, 5579-5592.	6.5	193
38	Cloning of Gsi-Like Genes of Medicago truncatula: Support for the Paralogous Evolution of GSI and GSII Genes. Current Plant Science and Biotechnology in Agriculture, 2002, , 341-341.	0.0	0
39	GÃ©nomique de la lÃ©gumineuse modÃ¨le Medicago truncatula : Ã©tat des lieux et perspectives. Oleagineux Corps Gras Lipides, 2001, 8, 478-484.	0.2	6
40	The Presence of GSI-Like Genes in Higher Plants: Support for the Paralogous Evolution of GSI and GSII Genes. Journal of Molecular Evolution, 2000, 50, 116-122.	0.8	55
41	Symbiosis-Specific Expression of Two Medicago truncatula Nodulin Genes, MtN1 and MtN13, Encoding Products Homologous to Plant Defense Proteins. Molecular Plant-Microbe Interactions, 1998, 11, 393-403.	1.4	117
42	The Medicago truncatula MtAnn1 Gene Encoding an Annexin Is Induced by Nod Factors and During the Symbiotic Interaction with Rhizobium meliloti. Molecular Plant-Microbe Interactions, 1998, 11, 504-513.	1.4	78
43	Identification of New Medicago truncatula Nodulin Genes: Comparison of Two Molecular Approaches. , 1997, , 77-81.		0
44	Use of a Subtractive Hybridization Approach to Identify New<i>Medicago truncatula</i>Genes Induced During Root Nodule Development. Molecular Plant-Microbe Interactions, 1996, 9, 233.	1.4	263
45	Purification and characterization of TnsC, a Tn7 transposition protein that binds ATP and DNA. Nucleic Acids Research, 1992, 20, 2525-2532.	6.5	42
46	Tn7 transposition in vitro proceeds through an excised transposon intermediate generated by staggered breaks in DNA. Cell, 1991, 65, 805-816.	13.5	167
47	Escherichia coli integration host factor binds specifically to the ends of the insertion sequence IS1 and to its major insertion hot-spot in pBR322. Journal of Molecular Biology, 1987, 195, 261-272.	2.0	126
48	Artificial transposable elements in the study of the ends of IS1. Gene, 1987, 61, 91-101.	1.0	25
49	Replication of pSC101: effects of mutations in the E. coli DNA binding protein IHF. Molecular Genetics and Genomics, 1986, 204, 85-89.	2.4	107
50	DNA sequence at the end of IS1 required for transposition. Nature, 1985, 317, 458-460.	13.7	30
51	Specificity of insertion of IS1. Journal of Molecular Biology, 1985, 185, 517-524.	2.0	64