Pascal Gamas

List of Publications by Year in descending order

51 papers	5,593 citations	81900 39 h-index	189892 50 g-index
54 all docs	54 docs citations	54 times ranked	4872 citing authors

#	Article	IF	Citations
1	MtHAP2-1 is a key transcriptional regulator of symbiotic nodule development regulated by microRNA169 in Medicago truncatula. Genes and Development, 2006, 20, 3084-3088.	5.9	450
2	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.	5.7	447
3	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.	7.1	316
4	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.	4.8	269
5	CCAAT-box binding transcription factors in plants: Y so many?. Trends in Plant Science, 2013, 18, 157-166.	8.8	265
6	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.	2.6	263
7	Exploring root symbiotic programs in the model legume Medicago truncatula using EST analysis. Nucleic Acids Research, 2002, 30, 5579-5592.	14.5	193
8	Whole-genome landscape of Medicago truncatula symbiotic genes. Nature Plants, 2018, 4, 1017-1025.	9.3	192
9	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.	5.7	173
10	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.	6.6	172
11	Tn7 transposition in vitro proceeds through an excised transposon intermediate generated by staggered breaks in DNA. Cell, 1991, 65, 805-816.	28.9	167
12	Genome-Wide Annotation of Remorins, a Plant-Specific Protein Family: Evolutionary and Functional Perspectives. Plant Physiology, 2007, 145, 593-600.	4.8	164
13	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.	4.8	155
14	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.	4.8	128
15	Cytokinins in Symbiotic Nodulation: When, Where, What For?. Trends in Plant Science, 2017, 22, 792-802.	8.8	128
16	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.	4.2	126
17	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.	2.6	117
18	The CCAAT box-binding transcription factor NF-YA1 controls rhizobial infection. Journal of Experimental Botany, 2014, 65, 481-494.	4.8	117

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19	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
20	Two <scp>CCAAT</scp>â€boxâ€binding transcription factors redundantly regulate early steps of the legumeâ€rhizobia endosymbiosis. Plant Journal, 2014, 79, 757-768.	5.7	105
21	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.	3.8	103
22	<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.	5.9	103
23	Transcription Reprogramming during Root Nodule Development in Medicago truncatula. PLoS ONE, 2011, 6, e16463.	2.5	102
24	Reprogramming of DNA methylation is critical for nodule development in Medicago truncatula. Nature Plants, 2016, 2, 16166.	9.3	99
25	Next-Generation Annotation of Prokaryotic Genomes with EuGene-P: Application to Sinorhizobium meliloti 2011. DNA Research, 2013, 20, 339-354.	3.4	90
26	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.	2.6	78
27	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.	2.6	74
28	A phylogenetically conserved group of NF-Y transcription factors interact to control nodulation in legumes. Plant Physiology, 2015, 169, pp.01144.2015.	4.8	72
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.	2.6	68
30	Specificity of insertion of IS1. Journal of Molecular Biology, 1985, 185, 517-524.	4.2	64
31	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.	7.3	61
32	NIN-like protein transcription factors regulate leghemoglobin genes in legume nodules. Science, 2021, 374, 625-628.	12.6	61
33	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.	1.8	55
34	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.	4.8	53
35	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.	7.3	53
36	Regulation of Differentiation of Nitrogen-Fixing Bacteria by Microsymbiont Targeting of Plant Thioredoxin s1. Current Biology, 2017, 27, 250-256.	3.9	51

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37	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.	5.7	49
38	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.	3.1	48
39	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.	7.3	43
40	Purification and characterization of TnsC, a Tn7 transposition protein that binds ATP and DNA. Nucleic Acids Research, 1992, 20, 2525-2532.	14.5	42
41	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.	2.6	35
42	DNA sequence at the end of IS1 required for transposition. Nature, 1985, 317, 458-460.	27.8	30
43	Artificial transposable elements in the study of the ends of IS1. Gene, 1987, 61, 91-101.	2.2	25
44	LeGOO: An Expertized Knowledge Database for the Model Legume Medicago truncatula. Plant and Cell Physiology, 2020, 61, 203-211.	3.1	19
45	Diversification of cytokinin phosphotransfer signaling genes in Medicago truncatula and other legume genomes. BMC Genomics, 2019, 20, 373.	2.8	14
46	Analysis and modeling of the integrative response of Medicago truncatula to nitrogen constraints. Comptes Rendus - Biologies, 2009, 332, 1022-1033.	0.2	12
47	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.	0.9	11
48	MtEFD and MtEFD2: Two transcription factors with distinct neofunctionalization in symbiotic nodule development. Plant Physiology, 2022, 189, 1587-1607.	4.8	9
49	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
50	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
51	Identification of New Medicago truncatula Nodulin Genes: Comparison of Two Molecular Approaches. , 1997, , 77-81.		0