

MarÃ-a Elena Ãlvarez-Buylla Roces

List of Publications by Year in descending order

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155
papers

8,155
citations

38742

50
h-index

58581

82
g-index

170
all docs

170
docs citations

170
times ranked

6978
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Regulatory Network Dynamical Logical Models for. <i>Methods in Molecular Biology</i> , 2022, 2395, 59-77.	0.9	1
2	Live Plant Cell Tracking: Fiji plugin to analyze cell proliferation dynamics and understand morphogenesis. <i>Plant Physiology</i> , 2022, 188, 846-860.	4.8	5
3	ORF8 and Health Complications of COVID-19 in Down Syndrome Patients. <i>Frontiers in Genetics</i> , 2022, 13, 830426.	2.3	1
4	Spatio-Temporal Dynamics of the Patterning of Arabidopsis Flower Meristem. <i>Frontiers in Plant Science</i> , 2021, 12, 585139.	3.6	3
5	The Epigenetic Faces of ULTRAPETALA1. <i>Frontiers in Plant Science</i> , 2021, 12, 637244.	3.6	8
6	Hormonal Regulation of Stem Cell Proliferation at the Arabidopsis thaliana Root Stem Cell Niche. <i>Frontiers in Plant Science</i> , 2021, 12, 628491.	3.6	5
7	Integrative Roles of Phytohormones on Cell Proliferation, Elongation and Differentiation in the Arabidopsis thaliana Primary Root. <i>Frontiers in Plant Science</i> , 2021, 12, 659155.	3.6	30
8	Beyond the Genetic Pathways, Flowering Regulation Complexity in Arabidopsis thaliana. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5716.	4.1	41
9	<i>In vivo</i> and <i>in vitro</i> human gene essentiality estimations capture contrasting functional constraints. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab063.	3.2	1
10	Unraveling the role of epigenetic regulation in asymmetric cell division during plant development. <i>Journal of Experimental Botany</i> , 2021, , .	4.8	3
11	Structural Analysis of SARS-CoV-2 ORF8 Protein: Pathogenic and Therapeutic Implications. <i>Frontiers in Genetics</i> , 2021, 12, 693227.	2.3	30
12	SARS-CoV-2 Nsp5 Protein Causes Acute Lung Inflammation, A Dynamical Mathematical Model. <i>Frontiers in Systems Biology</i> , 2021, 1, .	0.7	6
13	Maize yield in Mexico under climate change. <i>Agricultural Systems</i> , 2020, 177, 102697.	6.1	61
14	ULTRAPETALA1 maintains Arabidopsis root stem cell niche independently of ARABIDOPSIS TRITHORAX1. <i>New Phytologist</i> , 2020, 225, 1261-1272.	7.3	16
15	Interplay between Hormones and Several Abiotic Stress Conditions on Arabidopsis thaliana Primary Root Development. <i>Cells</i> , 2020, 9, 2576.	4.1	22
16	Beyond What Your Retina Can See: Similarities of Retinoblastoma Function between Plants and Animals, from Developmental Processes to Epigenetic Regulation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4925.	4.1	6
17	Multi-level gene regulatory network models to understand complex mechanisms underlying plant development. <i>Current Opinion in Plant Biology</i> , 2020, 57, 171-179.	7.1	10
18	A system-level mechanistic explanation for asymmetric stem cell fates: Arabidopsis thaliana root niche as a study system. <i>Scientific Reports</i> , 2020, 10, 3525.	3.3	15

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19	A Computational Model of the Endothelial to Mesenchymal Transition. <i>Frontiers in Genetics</i> , 2020, 11, 40.	2.3	24
20	The COVID-19 Pandemic and Paradigm Change in Global Scientific Research. <i>MEDICC Review</i> , 2020, 22, 14.	0.7	2
21	Dynamical modeling predicts an inflammation-inducible CXCR7+ B cell precursor with potential implications in lymphoid blockage pathologies. <i>PeerJ</i> , 2020, 8, e9902.	2.0	7
22	A new scientific agenda for Mexico. <i>Science</i> , 2019, 365, 1257-1258.	12.6	1
23	MADS-Box Genes Are Key Components of Genetic Regulatory Networks Involved in Abiotic Stress and Plastic Developmental Responses in Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 853.	3.6	119
24	MADS-box genes underground becoming mainstream: plant root developmental mechanisms. <i>New Phytologist</i> , 2019, 223, 1143-1158.	7.3	57
25	Natural Root Cellular Variation in Responses to Osmotic Stress in <i>Arabidopsis thaliana</i> Accessions. <i>Genes</i> , 2019, 10, 983.	2.4	17
26	Identifying the transition to the maturation zone in three ecotypes of <i>Arabidopsis thaliana</i> roots. <i>Communicative and Integrative Biology</i> , 2018, 11, e1395993.	1.4	19
27	Role of Cytokine Combinations on CD4+ T Cell Differentiation, Partial Polarization, and Plasticity: Continuous Network Modeling Approach. <i>Frontiers in Physiology</i> , 2018, 9, 877.	2.8	52
28	Modeling the Epigenetic Landscape in Plant Development. <i>Methods in Molecular Biology</i> , 2018, 1819, 357-383.	0.9	5
29	Structural robustness of mammalian transcription factor networks reveals plasticity across development. <i>Scientific Reports</i> , 2018, 8, 13922.	3.3	3
30	Spatial dynamics of floral organ formation. <i>Journal of Theoretical Biology</i> , 2018, 454, 30-40.	1.7	5
31	Modeling Procedures. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1069, 35-134.	1.6	2
32	Genome mining of <i>Streptomyces scabrisporus</i> NF3 reveals symbiotic features including genes related to plant interactions. <i>PLoS ONE</i> , 2018, 13, e0192618.	2.5	28
33	Medical Systems Biology. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1069, 1-33.	1.6	2
34	Case Studies. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1069, 135-209.	1.6	0
35	Gene regulatory network underlying the immortalization of epithelial cells. <i>BMC Systems Biology</i> , 2017, 11, 24.	3.0	33
36	The combination of the functionalities of feedback circuits is determinant for the attractors' number and size in pathway-like Boolean networks. <i>Scientific Reports</i> , 2017, 7, 42023.	3.3	21

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37	Model of polar auxin transport coupled to mechanical forces retrieves robust morphogenesis along the $\sqrt{\text{Arabidopsis}}$ root. <i>Physical Review E</i> , 2017, 95, 032410.	2.1	10
38	The CD4+ T cell regulatory network mediates inflammatory responses during acute hyperinsulinemia: a simulation study. <i>BMC Systems Biology</i> , 2017, 11, 64.	3.0	13
39	Boolean Dynamic Modeling Approaches to Study Plant Gene Regulatory Networks: Integration, Validation, and Prediction. <i>Methods in Molecular Biology</i> , 2017, 1629, 297-315.	0.9	7
40	A dynamic genetic-hormonal regulatory network model explains multiple cellular behaviors of the root apical meristem of <i>Arabidopsis thaliana</i> . <i>PLoS Computational Biology</i> , 2017, 13, e1005488.	3.2	36
41	Root Architecture Diversity and Meristem Dynamics in Different Populations of <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 858.	3.6	18
42	Dynamic network modelling to understand flowering transition and floral patterning. <i>Journal of Experimental Botany</i> , 2016, 67, 2565-2572.	4.8	16
43	Systems Biology Approaches to Development beyond Bioinformatics: Nonlinear Mechanistic Models Using Plant Systems. <i>BioScience</i> , 2016, 66, 371-383.	4.9	27
44	The MADS-box <i>XAANTAL1</i> increases proliferation at the <i>Arabidopsis</i> root stem-cell niche and participates in transition to differentiation by regulating cell-cycle components. <i>Annals of Botany</i> , 2016, 118, 787-796.	2.9	15
45	Retroactivity effects dependency on the transcription factors binding mechanisms. <i>Journal of Theoretical Biology</i> , 2016, 410, 77-106.	1.7	0
46	Finding potential high-yield areas for Mexican maize under current and climate change conditions. <i>Journal of Agricultural Science</i> , 2016, 154, 782-794.	1.3	9
47	Longitudinal zonation pattern in <i>Arabidopsis</i> root tip defined by a multiple structural change algorithm. <i>Annals of Botany</i> , 2016, 118, 763-776.	2.9	30
48	The impact of Polycomb group (PcG) and Trithorax group (TrxG) epigenetic factors in plant plasticity. <i>New Phytologist</i> , 2015, 208, 684-694.	7.3	60
49	Modeling the epigenetic attractors landscape: toward a post-genomic mechanistic understanding of development. <i>Frontiers in Genetics</i> , 2015, 6, 160.	2.3	51
50	A Minimal Regulatory Network of Extrinsic and Intrinsic Factors Recovers Observed Patterns of CD4+ T Cell Differentiation and Plasticity. <i>PLoS Computational Biology</i> , 2015, 11, e1004324.	3.2	75
51	A Dynamic Gene Regulatory Network Model That Recovers the Cyclic Behavior of <i>Arabidopsis thaliana</i> Cell Cycle. <i>PLoS Computational Biology</i> , 2015, 11, e1004486.	3.2	42
52	Descriptive vs. Mechanistic Network Models in Plant Development in the Post-Genomic Era. <i>Methods in Molecular Biology</i> , 2015, 1284, 455-479.	0.9	6
53	<i>XAANTAL2</i> (AGL14) Is an Important Component of the Complex Gene Regulatory Network that Underlies <i>Arabidopsis</i> Shoot Apical Meristem Transitions. <i>Molecular Plant</i> , 2015, 8, 796-813.	8.3	68
54	A model of the regulatory network involved in the control of the cell cycle and cell differentiation in the <i>Caenorhabditis elegans</i> vulva. <i>BMC Bioinformatics</i> , 2015, 16, 81.	2.6	11

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55	Role of transcriptional regulation in the evolution of plant phenotype: A dynamic systems approach. <i>Developmental Dynamics</i> , 2015, 244, 1074-1095.	1.8	15
56	Reshaping the epigenetic landscape during early flower development: induction of attractor transitions by relative differences in gene decay rates. <i>BMC Systems Biology</i> , 2015, 9, 20.	3.0	36
57	Mechanical forces as information: an integrated approach to plant and animal development. <i>Frontiers in Plant Science</i> , 2014, 5, 265.	3.6	19
58	Tetramer formation in Arabidopsis MADS domain proteins: analysis of a protein-protein interaction network. <i>BMC Systems Biology</i> , 2014, 8, 9.	3.0	28
59	Molecular Evolution Constraints in the Floral Organ Specification Gene Regulatory Network Module across 18 Angiosperm Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 560-573.	8.9	34
60	ARACNe-based inference, using curated microarray data, of Arabidopsis thaliana root transcriptional regulatory networks. <i>BMC Plant Biology</i> , 2014, 14, 97.	3.6	35
61	Co-option of the polarity gene network shapes filament morphology in angiosperms. <i>Scientific Reports</i> , 2014, 4, 6194.	3.3	37
62	Gene Regulatory Network Models for Floral Organ Determination. <i>Methods in Molecular Biology</i> , 2014, 1110, 441-469.	0.9	27
63	An efficient flat-surface collar-free grafting method for Arabidopsis thaliana seedlings. <i>Plant Methods</i> , 2013, 9, 14.	4.3	71
64	Environmental and social factors account for Mexican maize richness and distribution: A data mining approach. <i>Agriculture, Ecosystems and Environment</i> , 2013, 179, 25-34.	5.3	25
65	The MADS transcription factor XAL2/AGL14 modulates auxin transport during Arabidopsis root development by regulating PIN expression. <i>EMBO Journal</i> , 2013, 32, 2884-2895.	7.8	87
66	Dynamic models of epidermal patterning as an approach to plant eco-evo-devo. <i>Current Opinion in Plant Biology</i> , 2013, 16, 11-18.	7.1	7
67	Cell Patterns Emerge from Coupled Chemical and Physical Fields with Cell Proliferation Dynamics: The Arabidopsis thaliana Root as a Study System. <i>PLoS Computational Biology</i> , 2013, 9, e1003026.	3.2	41
68	Molecular Evolution and Patterns of Duplication in the SEP/AGL6-Like Lineage of the Zingiberales: A Proposed Mechanism for Floral Diversification. <i>Molecular Biology and Evolution</i> , 2013, 30, 2401-2422.	8.9	42
69	Finding Missing Interactions of the Arabidopsis thaliana Root Stem Cell Niche Gene Regulatory Network. <i>Frontiers in Plant Science</i> , 2013, 4, 110.	3.6	50
70	Finding Missing Interactions in Gene Regulatory Networks Using Boolean Models. <i>Springer Proceedings in Complexity</i> , 2013, , 543-551.	0.3	0
71	New Genes in Traditional Seed Systems: Diffusion, Detectability and Persistence of Transgenes in a Maize Metapopulation. <i>PLoS ONE</i> , 2012, 7, e46123.	2.5	20
72	Arabidopsis thaliana AtUTr7 Encodes a Golgi-Localized UDP-Glucose/UDP-Galactose Transporter that Affects Lateral Root Emergence. <i>Molecular Plant</i> , 2012, 5, 1263-1280.	8.3	31

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73	When ABC becomes ACB. <i>Journal of Experimental Botany</i> , 2012, 63, 2377-2395.	4.8	10
74	Hormone symphony during root growth and development. <i>Developmental Dynamics</i> , 2012, 241, 1867-1885.	1.8	76
75	A complex systems approach to Arabidopsis root stem-cell niche developmental mechanisms: from molecules, to networks, to morphogenesis. <i>Plant Molecular Biology</i> , 2012, 80, 351-363.	3.9	13
76	General Theory of Genotype to Phenotype Mapping: Derivation of Epigenetic Landscapes from N-Node Complex Gene Regulatory Networks. <i>Physical Review Letters</i> , 2012, 109, 118102.	7.8	54
77	An Epigenetic Model for Pigment Patterning Based on Mechanical and Cellular Interactions. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2012, 318, 209-223.	1.3	11
78	Projecting the effects of climate change on the distribution of maize races and their wild relatives in Mexico. <i>Global Change Biology</i> , 2012, 18, 1073-1082.	9.5	69
79	Dynamic network-based epistasis analysis: Boolean examples. <i>Frontiers in Plant Science</i> , 2011, 2, 92.	3.6	25
80	Recent long-distance transgene flow into wild populations conforms to historical patterns of gene flow in cotton (<i>Gossypium hirsutum</i>) at its centre of origin. <i>Molecular Ecology</i> , 2011, 20, 4182-4194.	3.9	69
81	Mutually reinforcing patterning mechanisms. <i>Nature Reviews Molecular Cell Biology</i> , 2011, 12, 533-533.	37.0	3
82	"Antelope": a hybrid-logic model checker for branching-time Boolean GRN analysis. <i>BMC Bioinformatics</i> , 2011, 12, 490.	2.6	36
83	Epidermal patterning in Arabidopsis: models make a difference. , 2011, 316B, 241-253.		24
84	Single-cell and coupled GRN models of cell patterning in the Arabidopsis thaliana root stem cell niche. <i>BMC Systems Biology</i> , 2010, 4, 134.	3.0	72
85	The Arabidopsis thaliana flower organ specification gene regulatory network determines a robust differentiation process. <i>Journal of Theoretical Biology</i> , 2010, 264, 971-983.	1.7	56
86	Dynamic-module redundancy confers robustness to the gene regulatory network involved in hair patterning of Arabidopsis epidermis. <i>BioSystems</i> , 2010, 102, 11-15.	2.0	26
87	Flower Development. <i>The Arabidopsis Book</i> , 2010, 8, e0127.	0.5	227
88	B-Function Expression in the Flower Center Underlies the Homeotic Phenotype of <i>Lacandonia schismatica</i> (Triuridaceae). <i>Plant Cell</i> , 2010, 22, 3543-3559.	6.6	49
89	From ABC genes to regulatory networks, epigenetic landscapes and flower morphogenesis: Making biological sense of theoretical approaches. <i>Seminars in Cell and Developmental Biology</i> , 2010, 21, 108-117.	5.0	56
90	Flower Development as an Interplay between Dynamical Physical Fields and Genetic Networks. <i>PLoS ONE</i> , 2010, 5, e13523.	2.5	29

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91	Information flow during gene activation by signaling molecules: ethylene transduction in Arabidopsis cells as a study system. BMC Systems Biology, 2009, 3, 48.	3.0	15
92	Transgenes in Mexican maize: molecular evidence and methodological considerations for GMO detection in landrace populations. Molecular Ecology, 2009, 18, 750-761.	3.9	113
93	Resolution of the Mexican transgene detection controversy: error sources and scientific practice in commercial and ecological contexts. Molecular Ecology, 2009, 18, 4145-4150.	3.9	14
94	Dispersal of Transgenes through Maize Seed Systems in Mexico. PLoS ONE, 2009, 4, e5734.	2.5	62
95	Complexity of Boolean Dynamics in Simple Models of Signaling Networks and in Real Genetic Networks. World Scientific Lecture Notes in Complex Systems, 2009, , 79-101.	0.1	0
96	Using phylogenetic, genetic and demographic evidence for setting conservation priorities for Mexican rare pines. Biodiversity and Conservation, 2008, 17, 121-137.	2.6	13
97	<i>AGAMOUS</i> -LIKE 17, a novel flowering promoter, acts in a FT-independent photoperiod pathway. Plant Journal, 2008, 55, 253-265.	5.7	70
98	Interlinked nonlinear subnetworks underlie the formation of robust cellular patterns in Arabidopsis epidermis: a dynamic spatial model. BMC Systems Biology, 2008, 2, 98.	3.0	52
99	An <i>AGAMOUS</i> -Related MADS-Box Gene, <i>XAL1</i> (<i>AGL12</i>), Regulates Root Meristem Cell Proliferation and Flowering Transition in Arabidopsis. Plant Physiology, 2008, 146, 1182-1192.	4.8	188
100	Critical Dynamics in Genetic Regulatory Networks: Examples from Four Kingdoms. PLoS ONE, 2008, 3, e2456.	2.5	178
101	Floral Morphogenesis: Stochastic Explorations of a Gene Network Epigenetic Landscape. PLoS ONE, 2008, 3, e3626.	2.5	120
102	Functional Diversification of B MADS-Box Homeotic Regulators of Flower Development: Adaptive Evolution in Protein-Protein Interaction Domains after Major Gene Duplication Events. Molecular Biology and Evolution, 2007, 24, 465-481.	8.9	95
103	Introgressive Hybridization in <i>Pinus montezumae</i> Lamb and <i>Pinus pseudostrobus</i> Lindl. (Pinaceae): Morphological and Molecular (cpSSR) Evidence. International Journal of Plant Sciences, 2007, 168, 861-875.	1.3	40
104	Equivalent genetic regulatory networks in different contexts recover contrasting spatial cell patterns that resemble those in Arabidopsis root and leaf epidermis: a dynamic model. International Journal of Developmental Biology, 2007, 51, 139-155.	0.6	45
105	Characterization of the expression patterns of <i>LEAFY/FLORICAULA</i> and <i>NEEDLY</i> orthologs in female and male cones of the conifer genera <i>Picea</i> , <i>Podocarpus</i> , and <i>Taxus</i> : implications for current evo-devo hypotheses for gymnosperms. Evolution & Development, 2007, 9, 446-459.	2.0	59
106	Gene regulatory network models for plant development. Current Opinion in Plant Biology, 2007, 10, 83-91.	7.1	89
107	From Genes to Flower Patterns and Evolution: Dynamic Models of Gene Regulatory Networks. Journal of Plant Growth Regulation, 2006, 25, 278-289.	5.1	63
108	A model of the ethylene signaling pathway and its gene response in Arabidopsis thaliana: Pathway cross-talk and noise-filtering properties. Chaos, 2006, 16, 023112.	2.5	28

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109	Unique and redundant functional domains of APETALA1 and CAULIFLOWER, two recently duplicated Arabidopsis thaliana floral MADS-box genes. Journal of Experimental Botany, 2006, 57, 3099-3107.	4.8	43
110	Comparative developmental series of the Mexican triurids support a euanthial interpretation for the unusual reproductive axes of <i>Lacandonia schismatica</i> (Triuridaceae). American Journal of Botany, 2006, 93, 15-35.	1.7	37
111	A Gene Regulatory Network Model for Cell-Fate Determination during Arabidopsis thaliana Flower Development That Is Robust and Recovers Experimental Gene Expression Profiles[W]. Plant Cell, 2004, 16, 2923-2939.	6.6	389
112	FLOR1, a putative interaction partner of the floral homeotic protein AGAMOUS, is a plant-specific intracellular LRR. Plant Science, 2004, 167, 225-231.	3.6	17
113	Inside-Out Flowers Characteristic of Lacandonia schismatica Evolved at Least before Its Divergence from a Closely Related Taxon, Triuris brevistylis. International Journal of Plant Sciences, 2003, 164, 345-357.	1.3	30
114	Adaptive evolution in the Arabidopsis MADS-box gene family inferred from its complete resolved phylogeny. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13407-13412.	7.1	127
115	Phylogenetics of Lophodermium from Pine. Mycologia, 2003, 95, 846.	1.9	24
116	Phylogenetics of <i>Lophodermium</i> from pine. Mycologia, 2003, 95, 846-859.	1.9	55
117	MADS-box gene expression in lateral primordia, meristems and differentiated tissues of Arabidopsis thaliana roots. Planta, 2002, 214, 365-372.	3.2	120
118	Population dynamics of Zea diploperennis, an endangered perennial herb: effect of slash and burn practice. Journal of Ecology, 2002, 90, 684-692.	4.0	23
119	Floral Transcription Factor AGAMOUS Interacts in Vitro with a Leucine-Rich Repeat and an Acid Phosphatase Protein Complex. Biochemical and Biophysical Research Communications, 2001, 288, 1018-1026.	2.1	30
120	Conversion of leaves into petals in Arabidopsis. Current Biology, 2001, 11, 182-184.	3.9	318
121	A cDNA for Nuclear-encoded Chloroplast Translational Initiation Factor 2 from a Higher Plant Is Able to Complement an <i>infB</i> Escherichia coli Null Mutant. Journal of Biological Chemistry, 2001, 276, 28388-28394.	3.4	10
122	Do rare pines need different conservation strategies? Evidence from three Mexican species. Canadian Journal of Botany, 2001, 79, 131-138.	1.1	14
123	Genetic Regulation of Root Hair Development in Arabidopsis Thaliana: A Network Model. Journal of Theoretical Biology, 2000, 204, 311-326.	1.7	55
124	MADS-BOX GENES: DEVELOPMENT AND EVOLUTION OF PLANT BODY PLANS. Journal of Phycology, 2000, 36, 803-812.	2.3	21
125	An ancestral MADS-box gene duplication occurred before the divergence of plants and animals. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 5328-5333.	7.1	459
126	Molecular evolution of flower development. Trends in Ecology and Evolution, 2000, 15, 144-149.	8.7	64

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127	MADS-box gene evolution beyond flowers: expression in pollen, endosperm, guard cells, roots and trichomes. <i>Plant Journal</i> , 2000, 24, 457-466.	5.7	36
128	MADS-box gene evolution beyond flowers: expression in pollen, endosperm, guard cells, roots and trichomes. <i>Plant Journal</i> , 2000, 24, 457-466.	5.7	296
129	High population differentiation and genetic variation in the endangered Mexican pine <i>Pinus Rzedowskii</i> (Pinaceae). <i>American Journal of Botany</i> , 1999, 86, 669-676.	1.7	57
130	Phylogenetics of <i>Pinus</i> (Pinaceae) Based on Nuclear Ribosomal DNA Internal Transcribed Spacer Region Sequences. <i>Molecular Phylogenetics and Evolution</i> , 1999, 11, 95-109.	2.7	179
131	Reply to Chambers and Trumbore: Tropical rain forest tree life-history diversity calls for more than one aging method. <i>Trends in Plant Science</i> , 1999, 4, 386.	8.8	3
132	Dynamics of the Genetic Regulatory Network for <i>Arabidopsis thaliana</i> Flower Morphogenesis. <i>Journal of Theoretical Biology</i> , 1998, 193, 307-319.	1.7	235
133	Variation in the nuclear ribosomal DNA internal transcribed spacer (ITS) region of <i>Pinus rzedowskii</i> revealed by PCR-RFLP. <i>Theoretical and Applied Genetics</i> , 1998, 96, 539-544.	3.6	21
134	Pollen-mediated gene flow and differential male reproductive success in a tropical pioneer tree, <i>Cecropia obtusifolia</i> Bertol. (Moraceae): a paternity analysis. <i>Heredity</i> , 1998, 81, 164-173.	2.6	61
135	How old are tropical rain forest trees?. <i>Trends in Plant Science</i> , 1998, 3, 400-405.	8.8	95
136	LIMITED SEED DISPERSAL AND GENETIC STRUCTURE IN LIFE STAGES OF <i>CECROPIA OBTUSIFOLIA</i> . Evolution; <i>International Journal of Organic Evolution</i> , 1997, 51, 275-282.	2.3	102
137	Isozyme Variation in a Tropical Pioneer Tree Species (<i>Cecropia obtusifolia</i> , Moraceae) with High Contents of Secondary Compounds. <i>Biotropica</i> , 1997, 29, 280-290.	1.6	10
138	The ribosomal ITS region as a marker to detect hybridization in pines. <i>Molecular Ecology</i> , 1997, 6, 995-996.	3.9	31
139	DEMOGRAPHIC GENETICS OF A PIONEER TROPICAL TREE SPECIES: PATCH DYNAMICS, SEED DISPERSAL, AND SEED BANKS. Evolution; <i>International Journal of Organic Evolution</i> , 1996, 50, 1155-1166.	2.3	66
140	Demographic Genetics of a Pioneer Tropical Tree Species: Patch Dynamics, Seed Dispersal, and Seed Banks. Evolution; <i>International Journal of Organic Evolution</i> , 1996, 50, 1155.	2.3	33
141	Length Variation in the Nuclear Ribosomal DNA Internal Transcribed Spacer Region of Non-Flowering Seed Plants. <i>Systematic Botany</i> , 1996, 21, 109.	0.5	112
142	Seed dispersal and patch dynamics in tropical rain forests: A demographic approach. <i>Ecoscience</i> , 1995, 2, 223-229.	1.4	13
143	Sustainable Harvesting of Tropical Trees: Demography and Matrix Models of Two Palm Species in Mexico. , 1995, 5, 484-500.		117
144	Finding Confidence Limits on Population Growth Rates: Three Real Examples Revised. <i>Ecology</i> , 1994, 75, 255-260.	3.2	81

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145	Density Dependence and Patch Dynamics in Tropical Rain Forests: Matrix Models and Applications to a Tree Species. <i>American Naturalist</i> , 1994, 143, 155-191.	2.1	108
146	POPULATION GENETIC STRUCTURE OF <i>CECROPIA OBTUSIFOLIA</i> , A TROPICAL PIONEER TREE SPECIES. Evolution; <i>International Journal of Organic Evolution</i> , 1994, 48, 437-453.	2.3	97
147	Models of patch dynamics in tropical forests. <i>Trends in Ecology and Evolution</i> , 1993, 8, 201-204.	8.7	17
148	Finding Confidence Limits on Population Growth Rates: Monte Carlo Test of a Simple Analytic Method. <i>Oikos</i> , 1993, 68, 273.	2.7	59
149	Demography and Allometry of <i>Cecropia Obtusifolia</i> , a Neotropical Pioneer Tree - An Evaluation of the Climax-Pioneer Paradigm for Tropical Rain Forests. <i>Journal of Ecology</i> , 1992, 80, 275.	4.0	195
150	Finding confidence limits on population growth rates. <i>Trends in Ecology and Evolution</i> , 1991, 6, 221-224.	8.7	63
151	Seed and Forest Dynamics: A Theoretical Framework and an Example from the Neotropics. <i>American Naturalist</i> , 1991, 137, 133-154.	2.1	86
152	Seed bank versus seed rain in the regeneration of a tropical pioneer tree. <i>Oecologia</i> , 1990, 84, 314-325.	2.0	155
153	Homegardens of a humid tropical region in Southeast Mexico: an example of an agroforestry cropping system in a recently established community. <i>Agroforestry Systems</i> , 1989, 8, 133-156.	2.0	62
154	Pervasive presence of transgenes and glyphosate in maize-derived food in Mexico. <i>Agroecology and Sustainable Food Systems</i> , 0, , 1-16.	1.9	8
155	There Is More to Corn than Popcorn and Corn on the Cob!. <i>Frontiers for Young Minds</i> , 0, 5, .	0.8	1