MarÃa Elena Ã€lvarez-Buylla Roces

List of Publications by Year
in descending order

155 papers	8,155 citations
50 h-index (38742)	82 g-index (58581)
170 all docs	170 docs citations
170 times ranked	6978 citing authors

#	Article	IF	Citations
1	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
2	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
3	Conversion of leaves into petals in Arabidopsis. Current Biology, 2001, 11, 182-184.	3.9	318
4	MADS-box gene evolution beyond flowers: expression in pollen, endosperm, guard cells, roots and trichomes. Plant Journal, 2000, 24, 457-466.	5.7	296
5	Dynamics of the Genetic Regulatory Network for Arabidopsis thaliana Flower Morphogenesis. Journal of Theoretical Biology, 1998, 193, 307-319.	1.7	235
6	Flower Development. The Arabidopsis Book, 2010, 8, e0127.	0.5	227
7	Demography and Allometry of Cecropia Obtusifolia, a Neotropical Pioneer Tree - An Evaluation of the Climax-Pioneer Paradigm for Tropical Rain Forests. Journal of Ecology, 1992, 80, 275.	4.0	195
8	An *AGAMOUS*-Related MADS-Box Gene, *XAL1* (*AGL12*), Regulates Root Meristem Cell Proliferation and Flowering Transition in Arabidopsis Â Â. Plant Physiology, 2008, 146, 1182-1192.	4.8	188
9	Phylogenetics of Pinus (Pinaceae) Based on Nuclear Ribosomal DNA Internal Transcribed Spacer Region Sequences. Molecular Phylogenetics and Evolution, 1999, 11, 95-109.	2.7	179
10	Critical Dynamics in Genetic Regulatory Networks: Examples from Four Kingdoms. PLoS ONE, 2008, 3, e2456.	2.5	178
11	Seed bank versus seed rain in the regeneration of a tropical pioneer tree. Oecologia, 1990, 84, 314-325.	2.0	155
12	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
13	MADS-box gene expression in lateral primordia, meristems and differentiated tissues of Arabidopsis thaliana roots. Planta, 2002, 214, 365-372.	3.2	120
14	Floral Morphogenesis: Stochastic Explorations of a Gene Network Epigenetic Landscape. PLoS ONE, 2008, 3, e3626.	2.5	120
15	MADS-Box Genes Are Key Components of Genetic Regulatory Networks Involved in Abiotic Stress and Plastic Developmental Responses in Plants. Frontiers in Plant Science, 2019, 10, 853.	3.6	119
16	Sustainable Harvesting of Tropical Trees: Demography and Matrix Models of Two Palm Species in Mexico. , 1995, 5, 484-500.		117
17	Transgenes in Mexican maize: molecular evidence and methodological considerations for GMO detection in landrace populations. Molecular Ecology, 2009, 18, 750-761.	3.9	113
18	Length Variation in the Nuclear Ribosomal DNA Internal Transcribed Spacer Region of Non-Flowering Seed Plants. Systematic Botany, 1996, 21, 109.	0.5	112

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19	Density Dependence and Patch Dynamics in Tropical Rain Forests: Matrix Models and Applications to a Tree Species. American Naturalist, 1994, 143, 155-191.	2.1	108
20	LIMITED SEED DISPERSAL AND GENETIC STRUCTURE IN LIFE STAGES OF*CECROPIA OBTUSIFOLIA*. Evolution; International Journal of Organic Evolution, 1997, 51, 275-282.	2.3	102
21	POPULATION GENETIC STRUCTURE OF *CECROPIA OBTUSIFOLIA* , A TROPICAL PIONEER TREE SPECIES. Evolution; International Journal of Organic Evolution, 1994, 48, 437-453.	2.3	97
22	How old are tropical rain forest trees?. Trends in Plant Science, 1998, 3, 400-405.	8.8	95
23	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
24	Gene regulatory network models for plant development. Current Opinion in Plant Biology, 2007, 10, 83-91.	7.1	89
25	The MADS transcription factor XAL2/AGL14 modulates auxin transport during Arabidopsis root development by regulating PIN expression. EMBO Journal, 2013, 32, 2884-2895.	7.8	87
26	Seed and Forest Dynamics: A Theoretical Framework and an Example from the Neotropics. American Naturalist, 1991, 137, 133-154.	2.1	86
27	Finding Confidence Limits on Population Growth Rates: Three Real Examples Revised. Ecology, 1994, 75, 255-260.	3.2	81
28	Hormone symphony during root growth and development. Developmental Dynamics, 2012, 241, 1867-1885.	1.8	76
29	A Minimal Regulatory Network of Extrinsic and Intrinsic Factors Recovers Observed Patterns of CD4+ T Cell Differentiation and Plasticity. PLoS Computational Biology, 2015, 11, e1004324.	3.2	75
30	Single-cell and coupled GRN models of cell patterning in the Arabidopsis thaliana root stem cell niche. BMC Systems Biology, 2010, 4, 134.	3.0	72
31	An efficient flat-surface collar-free grafting method for Arabidopsis thaliana seedlings. Plant Methods, 2013, 9, 14.	4.3	71
32	*AGAMOUS–LIKE 17*, a novel flowering promoter, acts in a *FT*–independent photoperiod pathway. Plant Journal, 2008, 55, 253-265.	5.7	70
33	Recent long-distance transgene flow into wild populations conforms to historical patterns of gene flow in cotton (Gossypium hirsutum) at its centre of origin. Molecular Ecology, 2011, 20, 4182-4194.	3.9	69
34	Projecting the effects of climate change on the distribution of maize races and their wild relatives in Mexico. Global Change Biology, 2012, 18, 1073-1082.	9.5	69
35	XAANTAL2 (AGL14) Is an Important Component of the Complex Gene Regulatory Network that Underlies Arabidopsis Shoot Apical Meristem Transitions. Molecular Plant, 2015, 8, 796-813.	8.3	68
36	DEMOGRAPHIC GENETICS OF A PIONEER TROPICAL TREE SPECIES: PATCH DYNAMICS, SEED DISPERSAL, AND SEED BANKS. Evolution; International Journal of Organic Evolution, 1996, 50, 1155-1166.	2.3	66

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37	Molecular evolution of flower development. Trends in Ecology and Evolution, 2000, 15, 144-149.	8.7	64
38	Finding confidence limits on population growth rates. Trends in Ecology and Evolution, 1991, 6, 221-224.	8.7	63
39	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
40	Homegardens of a humid tropical region in Southeast Mexico: an example of an agroforestry cropping system in a recently established community. Agroforestry Systems, 1989, 8, 133-156.	2.0	62
41	Dispersal of Transgenes through Maize Seed Systems in Mexico. PLoS ONE, 2009, 4, e5734.	2.5	62
42	Pollen-mediated gene flow and differential male reproductive success in a tropical pioneer tree, Cecropia obtusifolia Bertol. (Moraceae): a paternity analysis. Heredity, 1998, 81, 164-173.	2.6	61
43	Maize yield in Mexico under climate change. Agricultural Systems, 2020, 177, 102697.	6.1	61
44	The impact of Polycomb group (PcG) and Trithorax group (TrxG) epigenetic factors in plant plasticity. New Phytologist, 2015, 208, 684-694.	7.3	60
45	Finding Confidence Limits on Population Growth Rates: Monte Carlo Test of a Simple Analytic Method. Oikos, 1993, 68, 273.	2.7	59
46	Characterization of the expression patterns of *LEAFY/FLORICAULA* and *NEEDLY* orthologs in female and male cones of the conifer genera *Picea*, *Podocarpus*, and *Taxus*: implications for current evo€devo hypotheses for gymnosperms. Evolution & Development, 2007, 9, 446-459.	2.0	59
47	High population differentiation and genetic variation in the endangered Mexican pinePinus Rzedowskii(Pinaceae). American Journal of Botany, 1999, 86, 669-676.	1.7	57
48	MADS€box genes underground becoming mainstream: plant root developmental mechanisms. New Phytologist, 2019, 223, 1143-1158.	7.3	57
49	The Arabidopsis thaliana flower organ specification gene regulatory network determines a robust differentiation process. Journal of Theoretical Biology, 2010, 264, 971-983.	1.7	56
50	From ABC genes to regulatory networks, epigenetic landscapes and flower morphogenesis: Making biological sense of theoretical approaches. Seminars in Cell and Developmental Biology, 2010, 21, 108-117.	5.0	56
51	Genetic Regulation of Root Hair Development in Arabidopsis Thaliana: A Network Model. Journal of Theoretical Biology, 2000, 204, 311-326.	1.7	55
52	Phylogenetics of*Lophodermium*from pine. Mycologia, 2003, 95, 846-859.	1.9	55
53	General Theory of Genotype to Phenotype Mapping: Derivation of Epigenetic Landscapes from N-Node Complex Gene Regulatory Networks. Physical Review Letters, 2012, 109, 118102.	7.8	54
54	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

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55	Role of Cytokine Combinations on CD4+ T Cell Differentiation, Partial Polarization, and Plasticity: Continuous Network Modeling Approach. Frontiers in Physiology, 2018, 9, 877.	2.8	52
56	Modeling the epigenetic attractors landscape: toward a post-genomic mechanistic understanding of development. Frontiers in Genetics, 2015, 6, 160.	2.3	51
57	Finding Missing Interactions of the Arabidopsis thaliana Root Stem Cell Niche Gene Regulatory Network. Frontiers in Plant Science, 2013, 4, 110.	3.6	50
58	B-Function Expression in the Flower Center Underlies the Homeotic Phenotype of <i>Lacandonia schismatica</i> (Triuridaceae) Â Â. Plant Cell, 2010, 22, 3543-3559.	6.6	49
59	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
60	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
61	Molecular Evolution and Patterns of Duplication in the SEP/AGL6-Like Lineage of the Zingiberales: A Proposed Mechanism for Floral Diversification. Molecular Biology and Evolution, 2013, 30, 2401-2422.	8.9	42
62	A Dynamic Gene Regulatory Network Model That Recovers the Cyclic Behavior of Arabidopsis thaliana Cell Cycle. PLoS Computational Biology, 2015, 11, e1004486.	3.2	42
63	Cell Patterns Emerge from Coupled Chemical and Physical Fields with Cell Proliferation Dynamics: The Arabidopsis thaliana Root as a Study System. PLoS Computational Biology, 2013, 9, e1003026.	3.2	41
64	Beyond the Genetic Pathways, Flowering Regulation Complexity in Arabidopsis thaliana. International Journal of Molecular Sciences, 2021, 22, 5716.	4.1	41
65	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
66	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
67	Co-option of the polarity gene network shapes filament morphology in angiosperms. Scientific Reports, 2014, 4, 6194.	3.3	37
68	MADSâ€box gene evolution beyond flowers: expression in pollen, endosperm, guard cells, roots and trichomes. Plant Journal, 2000, 24, 457-466.	5.7	36
69	"Antelope": a hybrid-logic model checker for branching-time Boolean GRN analysis. BMC Bioinformatics, 2011, 12, 490.	2.6	36
70	Reshaping the epigenetic landscape during early flower development: induction of attractor transitions by relative differences in gene decay rates. BMC Systems Biology, 2015, 9, 20.	3.0	36
71	A dynamic genetic-hormonal regulatory network model explains multiple cellular behaviors of the root apical meristem of Arabidopsis thaliana. PLoS Computational Biology, 2017, 13, e1005488.	3.2	36
72	ARACNe-based inference, using curated microarray data, of Arabidopsis thaliana root transcriptional regulatory networks. BMC Plant Biology, 2014, 14, 97.	3.6	35

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73	Molecular Evolution Constraints in the Floral Organ Specification Gene Regulatory Network Module across 18 Angiosperm Genomes. Molecular Biology and Evolution, 2014, 31, 560-573.	8.9	34
74	Demographic Genetics of a Pioneer Tropical Tree Species: Patch Dynamics, Seed Dispersal, and Seed Banks. Evolution; International Journal of Organic Evolution, 1996, 50, 1155.	2.3	33
75	Gene regulatory network underlying the immortalization of epithelial cells. BMC Systems Biology, 2017, 11, 24.	3.0	33
76	The ribosomal ITS region as a marker to detect hybridization in pines. Molecular Ecology, 1997, 6, 995-996.	3.9	31
77	Arabidopsis thaliana AtUTr7 Encodes a Golgi-Localized UDP–Glucose/UDP–Galactose Transporter that Affects Lateral Root Emergence. Molecular Plant, 2012, 5, 1263-1280.	8.3	31
78	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
79	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
80	Longitudinal zonation pattern in *Arabidopsis* root tip defined by a multiple structural change algorithm. Annals of Botany, 2016, 118, 763-776.	2.9	30
81	Integrative Roles of Phytohormones on Cell Proliferation, Elongation and Differentiation in the Arabidopsis thaliana Primary Root. Frontiers in Plant Science, 2021, 12, 659155.	3.6	30
82	Structural Analysis of SARS-CoV-2 ORF8 Protein: Pathogenic and Therapeutic Implications. Frontiers in Genetics, 2021, 12, 693227.	2.3	30
83	Flower Development as an Interplay between Dynamical Physical Fields and Genetic Networks. PLoS ONE, 2010, 5, e13523.	2.5	29
84	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
85	Tetramer formation in Arabidopsis MADS domain proteins: analysis of a protein-protein interaction network. BMC Systems Biology, 2014, 8, 9.	3.0	28
86	Genome mining of Streptomyces scabrisporus NF3 reveals symbiotic features including genes related to plant interactions. PLoS ONE, 2018, 13, e0192618.	2.5	28
87	Systems Biology Approaches to Development beyond Bioinformatics: Nonlinear Mechanistic Models Using Plant Systems. BioScience, 2016, 66, 371-383.	4.9	27
88	Gene Regulatory Network Models for Floral Organ Determination. Methods in Molecular Biology, 2014, 1110, 441-469.	0.9	27
89	Dynamic-module redundancy confers robustness to the gene regulatory network involved in hair patterning of Arabidopsis epidermis. BioSystems, 2010, 102, 11-15.	2.0	26
90	Dynamic network-based epistasis analysis: Boolean examples. Frontiers in Plant Science, 2011, 2, 92.	3.6	25

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91	Environmental and social factors account for Mexican maize richness and distribution: A data mining approach. Agriculture, Ecosystems and Environment, 2013, 179, 25-34.	5.3	25
92	Phylogenetics of Lophodermium from Pine. Mycologia, 2003, 95, 846.	1.9	24
93	Epidermal patterning in Arabidopsis: models make a difference. , 2011, 316B, 241-253.		24
94	A Computational Model of the Endothelial to Mesenchymal Transition. Frontiers in Genetics, 2020, 11, 40.	2.3	24
95	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
96	Interplay between Hormones and Several Abiotic Stress Conditions on Arabidopsis thaliana Primary Root Development. Cells, 2020, 9, 2576.	4.1	22
97	Variation in the nuclear ribosomal DNA internal transcribed spacer (ITS) region of Pinus rzedowskii revealed by PCR-RFLP. Theoretical and Applied Genetics, 1998, 96, 539-544.	3.6	21
98	MADS-BOX GENES: DEVELOPMENT AND EVOLUTION OF PLANT BODY PLANS. Journal of Phycology, 2000, 36, 803-812.	2.3	21
99	The combination of the functionalities of feedback circuits is determinant for the attractors' number and size in pathway-like Boolean networks. Scientific Reports, 2017, 7, 42023.	3.3	21
100	New Genes in Traditional Seed Systems: Diffusion, Detectability and Persistence of Transgenes in a Maize Metapopulation. PLoS ONE, 2012, 7, e46123.	2.5	20
101	Mechanical forces as information: an integrated approach to plant and animal development. Frontiers in Plant Science, 2014, 5, 265.	3.6	19
102	Identifying the transition to the maturation zone in three ecotypes of *Arabidopsis thaliana* roots. Communicative and Integrative Biology, 2018, 11, e1395993.	1.4	19
103	Root Architecture Diversity and Meristem Dynamics in Different Populations of Arabidopsis thaliana. Frontiers in Plant Science, 2016, 7, 858.	3.6	18
104	Models of patch dynamics in tropical forests. Trends in Ecology and Evolution, 1993, 8, 201-204.	8.7	17
105	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
106	Natural Root Cellular Variation in Responses to Osmotic Stress in Arabidopsis thaliana Accessions. Genes, 2019, 10, 983.	2.4	17
107	Dynamic network modelling to understand flowering transition and floral patterning. Journal of Experimental Botany, 2016, 67, 2565-2572.	4.8	16
108	*ULTRAPETALA1* maintains *Arabidopsis* root stem cell niche independently of *ARABIDOPSIS TRITHORAX1*. New Phytologist, 2020, 225, 1261-1272.	7.3	16

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109	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
110	Role of transcriptional regulation in the evolution of plant phenotype: A dynamic systems approach. Developmental Dynamics, 2015, 244, 1074-1095.	1.8	15
111	The MADS-box *XAANTAL1* increases proliferation at the Arabidopsis root stem-cell niche and participates in transition to differentiation by regulating cell-cycle components. Annals of Botany, 2016, 118, 787-796.	2.9	15
112	A system-level mechanistic explanation for asymmetric stem cell fates: Arabidopsis thaliana root niche as a study system. Scientific Reports, 2020, 10, 3525.	3.3	15
113	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
114	Do rare pines need different conservation strategies? Evidence from three MeÃ—ican species. Canadian Journal of Botany, 2001, 79, 131-138.	1.1	14
115	Seed dispersal and patch dynamics in tropical rain forests: A demographic approach. Ecoscience, 1995, 2, 223-229.	1.4	13
116	Using phylogenetic, genetic and demographic evidence for setting conservation priorities for Mexican rare pines. Biodiversity and Conservation, 2008, 17, 121-137.	2.6	13
117	A complex systems approach to Arabidopsis root stem-cell niche developmental mechanisms: from molecules, to networks, to morphogenesis. Plant Molecular Biology, 2012, 80, 351-363.	3.9	13
118	The CD4+ T cell regulatory network mediates inflammatory responses during acute hyperinsulinemia: a simulation study. BMC Systems Biology, 2017, 11, 64.	3.0	13
119	An Epigenetic Model for Pigment Patterning Based on Mechanical and Cellular Interactions. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2012, 318, 209-223.	1.3	11
120	A model of the regulatory network involved in the control of the cell cycle and cell differentiation in the Caenorhabditis elegans vulva. BMC Bioinformatics, 2015, 16, 81.	2.6	11
121	Isozyme Variation in a Tropical Pioneer Tree Species (Cecropia obtusifolia, Moraceae) with High Contents of Secondary Compounds1. Biotropica, 1997, 29, 280-290.	1.6	10
122	A cDNA for Nuclear-encoded Chloroplast Translational Initiation Factor 2 from a Higher Plant Is Able to Complement an infB Escherichia coli Null Mutant. Journal of Biological Chemistry, 2001, 276, 28388-28394.	3.4	10
123	When ABC becomes ACB. Journal of Experimental Botany, 2012, 63, 2377-2395.	4.8	10
124	Model of polar auxin transport coupled to mechanical forces retrieves robust morphogenesis along the $Arabidopsis$ root. Physical Review E, 2017, 95, 032410.	2.1	10
125	Multi-level gene regulatory network models to understand complex mechanisms underlying plant development. Current Opinion in Plant Biology, 2020, 57, 171-179.	7.1	10
126	Finding potential high-yield areas for Mexican maize under current and climate change conditions. Journal of Agricultural Science, 2016, 154, 782-794.	1.3	9

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127	Pervasive presence of transgenes and glyphosate in maize-derived food in Mexico. Agroecology and Sustainable Food Systems, 0, , 1-16.	1.9	8
128	The Epigenetic Faces of ULTRAPETALA1. Frontiers in Plant Science, 2021, 12, 637244.	3.6	8
129	Dynamic models of epidermal patterning as an approach to plant eco-evo-devo. Current Opinion in Plant Biology, 2013, 16, 11-18.	7.1	7
130	Boolean Dynamic Modeling Approaches to Study Plant Gene Regulatory Networks: Integration, Validation, and Prediction. Methods in Molecular Biology, 2017, 1629, 297-315.	0.9	7
131	Dynamical modeling predicts an inflammation-inducible CXCR7+ B cell precursor with potential implications in lymphoid blockage pathologies. PeerJ, 2020, 8, e9902.	2.0	7
132	Descriptive vs. Mechanistic Network Models in Plant Development in the Post-Genomic Era. Methods in Molecular Biology, 2015, 1284, 455-479.	0.9	6
133	Beyond What Your Retina Can See: Similarities of Retinoblastoma Function between Plants and Animals, from Developmental Processes to Epigenetic Regulation. International Journal of Molecular Sciences, 2020, 21, 4925.	4.1	6
134	SARS-CoV-2 Nsp5 Protein Causes Acute Lung Inflammation, A Dynamical Mathematical Model. Frontiers in Systems Biology, 2021, 1, .	0.7	6
135	Modeling the Epigenetic Landscape in Plant Development. Methods in Molecular Biology, 2018, 1819, 357-383.	0.9	5
136	Spatial dynamics of floral organ formation. Journal of Theoretical Biology, 2018, 454, 30-40.	1.7	5
137	Hormonal Regulation of Stem Cell Proliferation at the Arabidopsis thaliana Root Stem Cell Niche. Frontiers in Plant Science, 2021, 12, 628491.	3.6	5
138	Live Plant Cell Tracking: Fiji plugin to analyze cell proliferation dynamics and understand morphogenesis. Plant Physiology, 2022, 188, 846-860.	4.8	5
139	Reply to Chambers and Trumbore… Tropical rain forest tree life-history diversity calls for more than one aging method. Trends in Plant Science, 1999, 4, 386.	8.8	3
140	Mutually reinforcing patterning mechanisms. Nature Reviews Molecular Cell Biology, 2011, 12, 533-533.	37.0	3
141	Structural robustness of mammalian transcription factor networks reveals plasticity across development. Scientific Reports, 2018, 8, 13922.	3.3	3
142	Spatio-Temporal Dynamics of the Patterning of Arabidopsis Flower Meristem. Frontiers in Plant Science, 2021, 12, 585139.	3.6	3
143	Unraveling the role of epigenetic regulation in asymmetric cell division during plant development. Journal of Experimental Botany, 2021, , .	4.8	3
144	Modeling Procedures. Advances in Experimental Medicine and Biology, 2018, 1069, 35-134.	1.6	2

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145	Medical Systems Biology. Advances in Experimental Medicine and Biology, 2018, 1069, 1-33.	1.6	2
146	The COVID-19 Pandemic and Paradigm Change in Global Scientific Research. MEDICC Review, 2020, 22, 14.	0.7	2
147	There Is More to Corn than Popcorn and Corn on the Cob!. Frontiers for Young Minds, 0, 5, .	0.8	1
148	A new scientific agenda for Mexico. Science, 2019, 365, 1257-1258.	12.6	1
149	*In vivo* and *in vitro* human gene essentiality estimations capture contrasting functional constraints. NAR Genomics and Bioinformatics, 2021, 3, lqab063.	3.2	1
150	Gene Regulatory Network Dynamical Logical Models for. Methods in Molecular Biology, 2022, 2395, 59-77.	0.9	1
151	ORF8 and Health Complications of COVID-19 in Down Syndrome Patients. Frontiers in Genetics, 2022, 13, 830426.	2.3	1
152	Retroactivity effects dependency on the transcription factors binding mechanisms. Journal of Theoretical Biology, 2016, 410, 77-106.	1.7	0
153	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
154	Finding Missing Interactions in Gene Regulatory Networks Using Boolean Models. Springer Proceedings in Complexity, 2013, , 543-551.	0.3	0
155	Case Studies. Advances in Experimental Medicine and Biology, 2018, 1069, 135-209.	1.6	0