Victoria Mironova

List of Publications by Year
in descending order

47 papers	1,228 citations	361296 20 h-index	395590 33 g-index
54 all docs	54 docs citations	54 times ranked	1468 citing authors

#	Article	IF	Citations
1	Meet your MAKR: the membraneâ€associated kinase regulator protein family in the regulation of plant development. FEBS Journal, 2022, 289, 6172-6186.	2.2	7
2	A PLETHORA/PIN-FORMED/auxin network mediates prehaustorium formation in the parasitic plant Striga hermonthica. Plant Physiology, 2022, 189, 2281-2297.	2.3	7
3	Mechanisms of stress response in the root stem cell niche. Journal of Experimental Botany, 2021, 72, 6746-6754.	2.4	10
4	Transcriptional regulation in plants: Using omics data to crack the cis-regulatory code. Current Opinion in Plant Biology, 2021, 63, 102058.	3.5	9
5	Tissue-specific transcriptome profiling of the Arabidopsis inflorescence stem reveals local cellular signatures. Plant Cell, 2021, 33, 200-223.	3.1	48
6	Cell Dynamics in WOX5-Overexpressing Root Tips: The Impact of Local Auxin Biosynthesis. Frontiers in Plant Science, 2020, 11, 560169.	1.7	26
7	Architecture of DNA elements mediating ARF transcription factor binding and auxin-responsive gene expression in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24557-24566.	3.3	53
8	Meta-Analysis of Transcriptome Data Detected New Potential Players in Response to Dioxin Exposure in Humans. International Journal of Molecular Sciences, 2020, 21, 7858.	1.8	4
9	metaRE R Package for Meta-Analysis of Transcriptome Data to Identify the cis-Regulatory Code behind the Transcriptional Reprogramming. Genes, 2020, 11, 634.	1.0	8
10	Specification and regulation of vascular tissue identity in the Arabidopsis embryo. Development (Cambridge), 2020, 147, .	1.2	24
11	Rocks in the auxin stream: Wound-induced auxin accumulation and ERF115 expression synergistically drive stem cell regeneration. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16667-16677.	3.3	63
12	Fold-Change-Specific Enrichment Analysis (FSEA): Quantification of Transcriptional Response Magnitude for Functional Gene Groups. Genes, 2020, 11, 434.	1.0	7
13	3D Analysis of Mitosis Distribution Pattern in the Plant Root Tip with iRoCS Toolbox. Methods in Molecular Biology, 2020, 2094, 119-125.	0.4	16
14	PlantLayout pipeline to model tissue patterning. Vavilovskii Zhurnal Genetiki I Selektsii, 2020, 24, 102-107.	0.4	1
15	A single-cell view of tissue regeneration in plants. Current Opinion in Plant Biology, 2019, 52, 149-154.	3.5	24
16	Capturing Auxin Response Factors Syntax Using DNA Binding Models. Molecular Plant, 2019, 12, 822-832.	3.9	38
17	Salicylic Acid Affects Root Meristem Patterning via Auxin Distribution in a Concentration-Dependent Manner. Plant Physiology, 2019, 180, 1725-1739.	2.3	114
18	A single ChIP-seq dataset is sufficient for comprehensive analysis of motifs co-occurrence with MCOT package. Nucleic Acids Research, 2019, 47, e139-e139.	6.5	28

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19	Diversity of cis-regulatory elements associated with auxin response in Arabidopsis thaliana. Journal of Experimental Botany, 2018, 69, 329-339.	2.4	45
20	Deciphering Auxin-Ethylene Crosstalk at a Systems Level. International Journal of Molecular Sciences, 2018, 19, 4060.	1.8	34
21	The Systems Biology of Auxin in Developing Embryos. Trends in Plant Science, 2017, 22, 225-235.	4.3	37
22	Mechanisms regulating ethylene signal transduction in plants. Russian Journal of Genetics: Applied Research, 2017, 7, 335-344.	0.4	3
23	A Sacrifice-for-Survival Mechanism Protects Root Stem Cell Niche from Chilling Stress. Cell, 2017, 170, 102-113.e14.	13.5	139
24	3D analysis of mitosis distribution highlights the longitudinal zonation and diarch symmetry in proliferation activity of the Arabidopsis thaliana root meristem. Plant Journal, 2017, 92, 834-845.	2.8	32
25	Auxin regulates functional gene groups in a fold-change-specific manner in Arabidopsis thaliana roots. Scientific Reports, 2017, 7, 2489.	1.6	42
26	Meta-analysis of transcriptome data identified TGTCNN motif variants associated with the response to plant hormone auxin in Arabidopsis thaliana L.. Journal of Bioinformatics and Computational Biology, 2016, 14, 1641009.	0.3	31
27	A detailed expression map of the PIN1 auxin transporter in Arabidopsis thaliana root. BMC Plant Biology, 2016, 16, 5.	1.6	111
28	The Interplay of Chromatin Landscape and DNA-Binding Context Suggests Distinct Modes of EIN3 Regulation in Arabidopsis thaliana. Frontiers in Plant Science, 2016, 7, 2044.	1.7	6
29	RNA-Seq Data Analysis for Studying Abiotic Stress in Horticultural Plants. , 2015, , 197-220.		6
30	On the distribution of auxin concentrations in root horizontal layer cells. Russian Journal of Genetics: Applied Research, 2015, 5, 293-299.	0.4	0
31	The key role of PIN proteins in auxin transport in Arabidopsis thaliana Roots. Russian Journal of Genetics: Applied Research, 2015, 5, 279-285.	0.4	2
32	Computational analysis of auxin responsive elements in the Arabidopsis thaliana L. genome. BMC Genomics, 2014, 15, S4.	1.2	54
33	Mathematical modeling of matter distribution in a circular cell ensemble. Numerical Analysis and Applications, 2013, 6, 151-162.	0.2	0
34	HOW MULTIPLE AUXIN RESPONSIVE ELEMENTS MAY INTERACT IN PLANT PROMOTERS: A REVERSE PROBLEM SOLUTION. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340011.	0.3	11
35	Deformable Cell Model and its Application to Growth of Plant Meristem. Mathematical Modelling of Natural Phenomena, 2013, 8, 62-79.	0.9	3
36	MATHEMATICAL MODELING OF AUXIN TRANSPORT IN PROTOXYLEM AND PROTOPHLOEM OF ARABIDOPSIS THALIANA ROOT TIPS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340010.	0.3	9

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37	Combined in silico/in vivo analysis of mechanisms providing for root apical meristem self-organization and maintenance. Annals of Botany, 2012, 110, 349-360.	1.4	55
38	From Published Expression and Phenotype Data to Structured Knowledge: The Arabidopsis Gene Net Supplementary Database and Its Applications. Lecture Notes in Computer Science, 2011, , 101-120.	1.0	0
39	Specific/nonspecific binding of TBP to promoter DNA of the auxin response factor genes in plants correlated with ARFs function on gene transcription (activator/repressor). Doklady Biochemistry and Biophysics, 2010, 433, 191-196.	0.3	10
40	A plausible mechanism for auxin patterning along the developing root. BMC Systems Biology, 2010, 4, 98.	3.0	82
41	Plant developmental genetics: Integrating data from different experiments in databases. Russian Journal of Genetics, 2009, 45, 1302-1316.	0.2	0
42	Mathematical modeling of plant morphogenesis. Numerical Analysis and Applications, 2008, 1, 123-134.	0.2	5
43	A CELLULAR AUTOMATON TO MODEL THE DEVELOPMENT OF PRIMARY SHOOT MERISTEMS OF ARABIDOPSIS THALIANA. Journal of Bioinformatics and Computational Biology, 2007, 05, 641-650.	0.3	4
44	Mathematical model of auxin distribution in the plant root. Russian Journal of Developmental Biology, 2007, 38, 374-382.	0.1	8
45	A systems approach to morphogenesis in Arabidopsis thaliana: I. AGNS database. Biophysics (Russian) Tj ETQq1 1 0.784314 rgBT /Ove	0.2	1
46	A systems approach to morphogenesis in Arabidopsis thaliana: II. Modeling the regulation of shoot apical meristem structure. Biophysics (Russian Federation), 2006, 51, 83-90.	0.2	1
47	A cellular automaton model of morphogenesis in Arabidopsis thaliana. Biophysics (Russian) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.2	0