

Eve Syrkin Wurtele

List of Publications by Year in descending order

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99
papers

5,344
citations

101543

36
h-index

95266

68
g-index

109
all docs

109
docs citations

109
times ranked

6219
citing authors

#	ARTICLE	IF	CITATIONS
1	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. <i>Cell Reports Medicine</i> , 2022, 3, 100522.	6.5	24
2	Foster thy young: enhanced prediction of orphan genes in assembled genomes. <i>Nucleic Acids Research</i> , 2022, 50, e37-e37.	14.5	13
3	orfipy: a fast and flexible tool for extracting ORFs. <i>Bioinformatics</i> , 2021, 37, 3019-3020.	4.1	35
4	<tt>pyrpipe</tt>: a Python package for RNA-Seq workflows. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab049.	3.2	14
5	African Americans and European Americans exhibit distinct gene expression patterns across tissues and tumors associated with immunologic functions and environmental exposures. <i>Scientific Reports</i> , 2021, 11, 9905.	3.3	15
6	Landscape of the Dark Transcriptome Revealed Through Re-mining Massive RNA-Seq Data. <i>Frontiers in Genetics</i> , 2021, 12, 722981.	2.3	7
7	Role of miR-2392 in driving SARS-CoV-2 infection. <i>Cell Reports</i> , 2021, 37, 109839.	6.4	52
8	MetaOmGraph: a workbench for interactive exploratory data analysis of large expression datasets. <i>Nucleic Acids Research</i> , 2020, 48, e23-e23.	14.5	19
9	How new genes are born. <i>ELife</i> , 2020, 9, .	6.0	25
10	fagin: synteny-based phylostratigraphy and finer classification of young genes. <i>BMC Bioinformatics</i> , 2019, 20, 440.	2.6	16
11	<tt>phylostrat</tt>: a framework for phylostratigraphy. <i>Bioinformatics</i> , 2019, 35, 3617-3627.	4.1	32
12	Comprehensive transcriptome analyses correlated with untargeted metabolome reveal differentially expressed pathways in response to cell wall alterations. <i>Plant Molecular Biology</i> , 2018, 96, 509-529.	3.9	8
13	Raising orphans from a metadata morass: A researcher's guide to re-use of public â€™omics data. <i>Plant Science</i> , 2018, 267, 32-47.	3.6	18
14	Comparative Proteomics of Rubber Latex Revealed Multiple Protein Species of REF/SRPP Family Respond Diversely to Ethylene Stimulation among Different Rubber Tree Clones. <i>International Journal of Molecular Sciences</i> , 2017, 18, 958.	4.1	28
15	Differentially Expressed Genes in Hypericin-Containing <i>Hypericum perforatum</i> Leaf Tissues as Revealed by De Novo Assembly of RNA-Seq. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 1027-1041.	1.8	15
16	Identification and functional characterization of HbOsmotin from <i>Hevea brasiliensis</i> . <i>Plant Physiology and Biochemistry</i> , 2016, 109, 171-180.	5.8	14
17	A systems biology approach toward understanding seed composition in soybean. <i>BMC Genomics</i> , 2015, 16, S9.	2.8	39
18	The <i>QQS</i> orphan gene of <i>Arabidopsis</i> modulates carbon and nitrogen allocation in soybean. <i>Plant Biotechnology Journal</i> , 2015, 13, 177-187.	8.3	62

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19	Modifications of membrane lipids in response to wounding of <i>Arabidopsis thaliana</i> leaves. <i>Plant Signaling and Behavior</i> , 2015, 10, e1056422.	2.4	20
20	ArcA Controls Metabolism, Chemotaxis, and Motility Contributing to the Pathogenicity of Avian Pathogenic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2015, 83, 3545-3554.	2.2	41
21	<i>QQS</i> orphan gene regulates carbon and nitrogen partitioning across species via NF-YC interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14734-14739.	7.1	109
22	Coming of age: orphan genes in plants. <i>Trends in Plant Science</i> , 2014, 19, 698-708.	8.8	158
23	Metabolomic Characterization of Knockout Mutants in <i>Arabidopsis</i> : Development of a Metabolite Profiling Database for Knockout Mutants in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2014, 165, 948-961.	4.8	49
24	Identification and biosynthesis of acylphloroglucinols in <i>Hypericum gentianoides</i> . <i>Physiologia Plantarum</i> , 2013, 148, 354-370.	5.2	28
25	Automatic extraction of biomolecular interactions: an empirical approach. <i>BMC Bioinformatics</i> , 2013, 14, 234.	2.6	4
26	Use of Metabolomics and Transcriptomics to Gain Insights into the Regulation and Biosynthesis of Medicinal Compounds: <i>Hypericum</i> as a Model. , 2013, , 395-411.		3
27	A global approach to analysis and interpretation of metabolic data for plant natural product discovery. <i>Natural Product Reports</i> , 2013, 30, 565.	10.3	104
28	Functional Identification of Valerena-1,10-diene Synthase, a Terpene Synthase Catalyzing a Unique Chemical Cascade in the Biosynthesis of Biologically Active Sesquiterpenes in <i>Valeriana officinalis</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 3163-3173.	3.4	39
29	Holocarboxylase Synthetase 1 Physically Interacts with Histone H3 in <i>Arabidopsis</i> . <i>Scientifica</i> , 2013, 2013, 1-9.	1.7	10
30	Comprehensive analysis of correlation coefficients estimated from pooling heterogeneous microarray data. <i>BMC Bioinformatics</i> , 2013, 14, 214.	2.6	14
31	MetaBlast computer game: a pipeline from science to 3D art to education. , 2012, , .		3
32	MetNet Online: a novel integrated resource for plant systems biology. <i>BMC Bioinformatics</i> , 2012, 13, 267.	2.6	17
33	Medicinal Plants: A Public Resource for Metabolomics and Hypothesis Development. <i>Metabolites</i> , 2012, 2, 1031-1059.	2.9	32
34	Evolution of the chalcone-isomerase fold from fatty-acid binding to stereospecific catalysis. <i>Nature</i> , 2012, 485, 530-533.	27.8	191
35	BirdsEyeView (BEV): graphical overviews of experimental data. <i>BMC Bioinformatics</i> , 2012, 13, S11.	2.6	1
36	Massive Human Co-expression Network and Its Medical Applications. <i>Chemistry and Biodiversity</i> , 2012, 9, 868-887.	2.1	15

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37	AtRabD2b and AtRabD2c have overlapping functions in pollen development and pollen tube growth. <i>BMC Plant Biology</i> , 2011, 11, 25.	3.6	44
38	Reverse-Genetic Analysis of the Two Biotin-Containing Subunit Genes of the Heteromeric Acetyl-Coenzyme A Carboxylase in Arabidopsis Indicates a Unidirectional Functional Redundancy. <i>Plant Physiology</i> , 2011, 155, 293-314.	4.8	62
39	Echinacea-induced cytosolic Ca ²⁺ elevation in HEK293. <i>BMC Complementary and Alternative Medicine</i> , 2010, 10, 72.	3.7	1
40	MetNetAPI: A flexible method to access and manipulate biological network data from MetNet. <i>BMC Research Notes</i> , 2010, 3, 312.	1.4	4
41	PlantMetabolomics.org: A Web Portal for Plant Metabolomics Experiments. <i>Plant Physiology</i> , 2010, 152, 1807-1816.	4.8	93
42	Visualizing Multivariate Hierarchic Data Using Enhanced Radial Space-Filling Layout. <i>Lecture Notes in Computer Science</i> , 2010, , 350-360.	1.3	2
43	Metabolic Profiling of Echinacea Genotypes and a Test of Alternative Taxonomic Treatments. <i>Planta Medica</i> , 2009, 75, 178-183.	1.3	19
44	PathBinder – text empirics and automatic extraction of biomolecular interactions. <i>BMC Bioinformatics</i> , 2009, 10, S18.	2.6	10
45	Identification of the novel protein QOS as a component of the starch metabolic network in Arabidopsis leaves. <i>Plant Journal</i> , 2009, 58, 485-498.	5.7	118
46	Quantitative analysis of short-chain acyl-coenzymeAs in plant tissues by LC-MS/MS electrospray ionization method. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 482-488.	2.3	36
47	Acetyl-CoA – Life at the metabolic nexus. <i>Plant Science</i> , 2009, 176, 597-601.	3.6	102
48	MetNetGE: Visualizing biological networks in hierarchical views and 3D tiered layouts. , 2009, , .		4
49	Direct profiling and imaging of plant metabolites in intact tissues by using colloidal graphite-assisted laser desorption ionization mass spectrometry. <i>Plant Journal</i> , 2008, 55, 348-360.	5.7	138
50	Articulation of three core metabolic processes in Arabidopsis: Fatty acid biosynthesis, leucine catabolism and starch metabolism. <i>BMC Plant Biology</i> , 2008, 8, 76.	3.6	83
51	Regulon organization of Arabidopsis. <i>BMC Plant Biology</i> , 2008, 8, 99.	3.6	90
52	Characterizing the Metabolic Fingerprint and Anti-inflammatory Activity of Hypericum gentianoides. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 4359-4366.	5.2	19
53	Genome wide co-expression among the starch debranching enzyme genes AtISA1, AtISA2, and AtISA3 in Arabidopsis thaliana. <i>Journal of Experimental Botany</i> , 2007, 58, 3323-3342.	4.8	32
54	MetNet: Systems Biology Tools for Arabidopsis. , 2007, , 145-157.		24

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55	Year-and-a-Half Old, Dried Echinacea Roots Retain Cytokine-Modulating Capabilities in an in vitro Human Older Adult Model of Influenza Vaccination. <i>Planta Medica</i> , 2006, 72, 1207-1215.	1.3	30
56	PubMed Assistant: a biologist-friendly interface for enhanced PubMed search. <i>Bioinformatics</i> , 2006, 22, 378-380.	4.1	17
57	Hierarchical visualization of metabolic networks using virtual reality. , 2006, , .		10
58	Creating, Modeling, and Visualizing Metabolic Networks. , 2005, , 491-518.		5
59	Integration of metabolic networks and gene expression in virtual reality. <i>Bioinformatics</i> , 2005, 21, 3645-3650.	4.1	39
60	Modeling Gene Expression Networks Using Fuzzy Logic. <i>IEEE Transactions on Systems, Man, and Cybernetics</i> , 2005, 35, 1351-1359.	5.0	57
61	Reverse Genetic Characterization of Cytosolic Acetyl-CoA Generation by ATP-Citrate Lyase in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2005, 17, 182-203.	6.6	185
62	A proposed framework for the description of plant metabolomics experiments and their results. <i>Nature Biotechnology</i> , 2004, 22, 1601-1606.	17.5	283
63	Diacetylenic isobutylamides of Echinacea: synthesis and natural distribution. <i>Phytochemistry</i> , 2004, 65, 2477-2484.	2.9	32
64	Potential of metabolomics as a functional genomics tool. <i>Trends in Plant Science</i> , 2004, 9, 418-425.	8.8	685
65	MetNet: Software to Build and Model the Biogenetic Lattice of <i>Arabidopsis</i> . <i>Comparative and Functional Genomics</i> , 2003, 4, 239-245.	2.0	57
66	Plant biotin-containing carboxylases. <i>Archives of Biochemistry and Biophysics</i> , 2003, 414, 211-222.	3.0	208
67	The Role of Biotin in Regulating 3-Methylcrotonyl-Coenzyme A Carboxylase Expression in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2003, 131, 1479-1486.	4.8	29
68	Metabolic and Environmental Regulation of 3-Methylcrotonyl-Coenzyme A Carboxylase Expression in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2002, 129, 625-637.	4.8	49
69	Molecular Characterization of a Heteromeric ATP-Citrate Lyase That Generates Cytosolic Acetyl-Coenzyme A in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2002, 130, 740-756.	4.8	183
70	Functional Genomics: High-Throughput mRNA, Protein, and Metabolite Analyses. <i>Metabolic Engineering</i> , 2002, 4, 98-106.	7.0	97
71	Characterization of 3-Methylcrotonyl-CoA Carboxylase from Plants. <i>Methods in Enzymology</i> , 2000, 324, 280-292.	1.0	9
72	The Role of Pyruvate Dehydrogenase and Acetyl-Coenzyme A Synthetase in Fatty Acid Synthesis in Developing <i>Arabidopsis</i> Seeds. <i>Plant Physiology</i> , 2000, 123, 497-508.	4.8	147

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73	Coordinate Regulation of the Nuclear and Plastidic Genes Coding for the Subunits of the Heteromeric Acetyl-Coenzyme A Carboxylase. <i>Plant Physiology</i> , 2000, 122, 1057-1072.	4.8	99
74	Molecular Characterization of the Non-biotin-containing Subunit of 3-Methylcrotonyl-CoA Carboxylase. <i>Journal of Biological Chemistry</i> , 2000, 275, 5582-5590.	3.4	29
75	Geranyl-CoA Carboxylase: A Novel Biotin-Containing Enzyme in Plants. <i>Archives of Biochemistry and Biophysics</i> , 1999, 362, 12-21.	3.0	30
76	Tissue distribution of acetyl-CoA carboxylase in leaves of leek (<i>Allium porrum</i> L.). <i>Journal of Plant Physiology</i> , 1998, 153, 265-269.	3.5	3
77	3-Methylcrotonyl-Coenzyme A Carboxylase Is a Component of the Mitochondrial Leucine Catabolic Pathway in Plants. <i>Plant Physiology</i> , 1998, 118, 1127-1138.	4.8	99
78	Zrp2: a novel maize gene whose mRNA accumulates in the root cortex and mature stems. <i>Plant Molecular Biology</i> , 1997, 35, 367-375.	3.9	10
79	Genomic Organization of 251 kDa Acetyl-CoA Carboxylase Genes in Arabidopsis: Tandem Gene Duplication has Made Two Differentially Expressed Isozymes. <i>Plant and Cell Physiology</i> , 1995, 36, 779-787.	3.1	59
80	Accumulation of the ZRP3 mRNA in the root and coleorhiza of germinating maize (<i>Zea mays</i> , Poaceae). <i>American Journal of Botany</i> , 1995, 82, 1083-1088.	1.7	2
81	Accumulation of the ZRP3 mRNA in the Root and Coleorhiza of Germinating Maize (<i>Zea mays</i> , Poaceae). <i>American Journal of Botany</i> , 1995, 82, 1083.	1.7	1
82	Biochemical and Molecular Biological Characterization of Biotinylated Proteins of Plants. , 1995, , 49-51.		0
83	Biochemical and Molecular Biological Characterization of Acetyl-CoA Carboxylases. , 1995, , 39-42.		0
84	Abscisic acid is present in liverworts. <i>Phytochemistry</i> , 1994, 37, 625-627.	2.9	27
85	Accumulation of petroselinic acid in developing somatic carrot embryos. <i>Phytochemistry</i> , 1994, 37, 749-753.	2.9	11
86	Differential Accumulation of Biotin Enzymes during Carrot Somatic Embryogenesis. <i>Plant Physiology</i> , 1992, 99, 1699-1703.	4.8	37
87	An mRNA that specifically accumulates in maize roots delineates a novel subset of developing cortical cells. <i>Plant Molecular Biology</i> , 1992, 20, 821-831.	3.9	43
88	Plants contain multiple biotin enzymes: Discovery of 3-methylcrotonyl-CoA carboxylase, propionyl-CoA carboxylase and pyruvate carboxylase in the plant kingdom. <i>Archives of Biochemistry and Biophysics</i> , 1990, 278, 179-186.	3.0	99
89	A simple, efficient method for the <i>Agrobacterium</i> -mediated transformation of carrot callus cells. <i>Plant Science</i> , 1989, 61, 253-262.	3.6	36
90	Isolation and characterization of a tomato cDNA clone which codes for a salt-induced protein. <i>Plant Molecular Biology</i> , 1988, 10, 401-412.	3.9	136

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91	Quantitation of Starch and ADP-Glucose Pyrophosphorylase in non-Embryogenic Cells and Embryogenic Cell Clusters from Carrot Suspension Cultures. <i>Journal of Plant Physiology</i> , 1988, 132, 683-689.	3.5	20
92	Comparison of Starch and ADP-Glucose Pyrophosphorylase Levels in Nonembryogenic Cells and Developing Embryos from Induced Carrot Cultures. <i>Plant Physiology</i> , 1988, 86, 451-456.	4.8	18
93	Propagation of an elite high biomass-producing genotype of <i>Atriplex canescens</i> by axillary enhancement. <i>Bioresource Technology</i> , 1987, 12, 281-291.	0.3	7
94	Use of streptavidin to detect biotin-containing proteins in plants. <i>Analytical Biochemistry</i> , 1985, 149, 448-453.	2.4	64
95	Subcellular and Developmental Distribution of $\hat{1}^2$ -Cyanoalanine Synthase in Barley Leaves. <i>Plant Physiology</i> , 1985, 78, 285-290.	4.8	55
96	Tissue Distribution of Acetyl-Coenzyme A Carboxylase in Leaves. <i>Plant Physiology</i> , 1984, 75, 895-901.	4.8	51
97	Tissue Distribution of $\hat{1}^2$ -Cyanoalanine Synthase in Leaves. <i>Plant Physiology</i> , 1984, 75, 979-982.	4.8	35
98	Subcellular distribution of acetyl-coenzyme A carboxylase in mesophyll cells of barley and sorghum leaves. <i>Archives of Biochemistry and Biophysics</i> , 1984, 235, 555-561.	3.0	16
99	Subcellular Localization of a UDP-Glucose:Aldehyde Cyanohydrin $\hat{1}^2$ -Glucosyl Transferase in Epidermal Plastids of <i>Sorghum</i> Leaf Blades. <i>Plant Physiology</i> , 1982, 70, 1732-1737.	4.8	22