Karen A Schlauch

List of Publications by Year
in descending order

63 papers	5,961 citations	147801 31 h-index	144013 57 g-index
64 all docs	64 docs citations	64 times ranked	8379 citing authors

#	Article	IF	Citations
1	The Plant NADPH Oxidase RBOHD Mediates Rapid Systemic Signaling in Response to Diverse Stimuli. Science Signaling, 2009, 2, ra45.	3.6	897
2	Cytosolic Ascorbate Peroxidase 1 Is a Central Component of the Reactive Oxygen Gene Network of Arabidopsis. Plant Cell, 2005, 17, 268-281.	6.6	858
3	The Zinc-Finger Protein Zat12 Plays a Central Role in Reactive Oxygen and Abiotic Stress Signaling in Arabidopsis Â. Plant Physiology, 2005, 139, 847-856.	4.8	601
4	Water and salinity stress in grapevines: early and late changes in transcript and metabolite profiles. Functional and Integrative Genomics, 2007, 7, 111-134.	3.5	474
5	Temporal-Spatial Interaction between Reactive Oxygen Species and Abscisic Acid Regulates Rapid Systemic Acclimation in Plants Â. Plant Cell, 2013, 25, 3553-3569.	6.6	316
6	A roadmap for research on crassulacean acid metabolism (<scp>CAM</scp>) to enhance sustainable food and bioenergy production in a hotter, drier world. New Phytologist, 2015, 207, 491-504.	7.3	211
7	A genomic and proteomic study of the spectrum of nonalcoholic fatty liver disease. Hepatology, 2005, 42, 665-674.	7.3	209
8	Engineering crassulacean acid metabolism to improve water-use efficiency. Trends in Plant Science, 2014, 19, 327-338.	8.8	206
9	Proteomic analysis reveals differences between Vitis vinifera L. cv. Chardonnay and cv. Cabernet Sauvignon and their responses to water deficit and salinity. Journal of Experimental Botany, 2007, 58, 1873-1892.	4.8	181
10	Identification of the MBF1 heat‐response regulon of <i>Arabidopsis thaliana</i>. Plant Journal, 2011, 66, 844-851.	5.7	148
11	MicroRNA Expression in Human Airway Smooth Muscle Cells. American Journal of Respiratory Cell and Molecular Biology, 2010, 42, 506-513.	2.9	137
12	Large-scale mRNA expression profiling in the common ice plant, Mesembryanthemum crystallinum, performing C3 photosynthesis and Crassulacean acid metabolism (CAM). Journal of Experimental Botany, 2008, 59, 1875-1894.	4.8	128
13	Population genetic screening efficiently identifies carriers of autosomal dominant diseases. Nature Medicine, 2020, 26, 1235-1239.	30.7	121
14	Transcript abundance profiles reveal larger and more complex responses of grapevine to chilling compared to osmotic and salinity stress. Functional and Integrative Genomics, 2007, 7, 317-333.	3.5	120
15	Transcriptomic analysis of the late stages of grapevine (Vitis vinifera cv. Cabernet Sauvignon) berry ripening reveals significant induction of ethylene signaling and flavor pathways in the skin. BMC Plant Biology, 2014, 14, 370.	3.6	105
16	Hepatic gene expression in patients with obesity-related non-alcoholic steatohepatitis. Liver International, 2005, 25, 760-771.	3.9	100
17	Gene Expression of Leptin, Resistin, and Adiponectin in the White Adipose Tissue of Obese Patients with Non-Alcoholic Fatty Liver Disease and Insulin Resistance. Obesity Surgery, 2006, 16, 1118-1125.	2.1	98
18	The <i>Vitis vinifera</i> C‐repeat binding protein 4 (<i>VvCBF4</i>) transcriptional factor enhances freezing tolerance in wine grape. Plant Biotechnology Journal, 2012, 10, 105-124.	8.3	83

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19	Obesity-related Differential Gene Expression in the Visceral Adipose Tissue. Obesity Surgery, 2005, 15, 758-765.	2.1	67
20	Transcriptomic network analyses of leaf dehydration responses identify highly connected ABA and ethylene signaling hubs in three grapevine species differing in drought tolerance. BMC Plant Biology, 2016, 16, 118.	3.6	62
21	Genome-wide association analysis identifies genetic variations in subjects with myalgic encephalomyelitis/chronic fatigue syndrome. Translational Psychiatry, 2016, 6, e730-e730.	4.8	56
22	Gene expression of the liver in response to chronic hypoxia. Physiological Genomics, 2010, 41, 275-288.	2.3	51
23	Gene Expression Patterns in Hepatic Tissue and Visceral Adipose Tissue of Patients with Non-Alcoholic Fatty Liver Disease. Obesity Surgery, 2007, 17, 1111-1118.	2.1	50
24	Differential floral development and gene expression in grapevines during long and short photoperiods suggests a role for floral genes in dormancy transitioning. Plant Molecular Biology, 2010, 73, 191-205.	3.9	49
25	Short day transcriptomic programming during induction of dormancy in grapevine. Frontiers in Plant Science, 2015, 6, 834.	3.6	48
26	Frax Prediction without BMD for Assessment of Osteoporotic Fracture Risk. Endocrine Practice, 2013, 19, 780-784.	2.1	47
27	Abscisic acid transcriptomic signaling varies with grapevine organ. BMC Plant Biology, 2016, 16, 72.	3.6	45
28	The common transcriptional subnetworks of the grape berry skin in the late stages of ripening. BMC Plant Biology, 2017, 17, 94.	3.6	42
29	Five omic technologies are concordant in differentiating the biochemical characteristics of the berries of five grapevine (Vitis vinifera L.) cultivars. BMC Genomics, 2015, 16, 946.	2.8	41
30	A comparison of heat-stress transcriptome changes between wild-type Arabidopsis pollen and a heat-sensitive mutant harboring a knockout of cyclic nucleotide-gated cation channel 16 (cngc16). BMC Genomics, 2018, 19, 549.	2.8	37
31	Distinct organization of the candidate tumor suppressor gene RFP2 in human and mouse: multiple mRNA isoforms in both species- and human-specific antisense transcript RFP2OS. Gene, 2003, 321, 103-112.	2.2	35
32	The CHADS Score Role in Managing Anticoagulation After Surgical Ablation for Atrial Fibrillation. Annals of Thoracic Surgery, 2010, 90, 1257-1262.	1.3	34
33	Cardiac mitochondrial metabolism may contribute to differences in thermal tolerance of red- and white-blooded Antarctic notothenioid fishes. Journal of Experimental Biology, 2018, 221, .	1.7	31
34	Obesity-mediated regulation of cardiac protein acetylation: parallel analysis of total and acetylated proteins via TMT-tagged mass spectrometry. Bioscience Reports, 2018, 38, .	2.4	26
35	A Comprehensive Genome-Wide and Phenome-Wide Examination of BMI and Obesity in a Northern Nevadan Cohort. G3: Genes, Genomes, Genetics, 2020, 10, 645-664.	1.8	25
36	Drought tolerance of the grapevine, Vitis champinii cv. Ramsey, is associated with higher photosynthesis and greater transcriptomic responsiveness of abscisic acid biosynthesis and signaling. BMC Plant Biology, 2020, 20, 55.	3.6	25

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37	Humoral Immunity Profiling of Subjects with Myalgic Encephalomyelitis Using a Random Peptide Microarray Differentiates Cases from Controls with High Specificity and Sensitivity. Molecular Neurobiology, 2018, 55, 633-641.	4.0	19
38	Health-related quality of life after coronary artery bypass grafting surgery and the role of gender. Cardiovascular Revascularization Medicine, 2012, 13, 321-327.	0.8	18
39	Microarray technology in the study of obesity and non-alcoholic fatty liver disease. Liver International, 2005, 25, 1091-1096.	3.9	15
40	Adding Confidence to Gene Expression Clustering. Genetics, 2005, 170, 2003-2011.	2.9	14
41	Transcriptional Analysis of Blood Lymphocytes and Skin Fibroblasts, Keratinocytes, and Endothelial Cells asÂaÂPotential Biomarker for Alzheimer's Disease. Journal of Alzheimer's Disease, 2016, 54, 1373-1383.	2.6	14
42	GWAS and PheWAS of red blood cell components in a Northern Nevadan cohort. PLoS ONE, 2019, 14, e0218078.	2.5	13
43	Single-nucleotide polymorphisms in a cohort of significantly obese women without cardiometabolic diseases. International Journal of Obesity, 2019, 43, 253-262.	3.4	12
44	Characterization of novel pollen-expressed transcripts reveals their potential roles in pollen heat stress response in Arabidopsis thaliana. Plant Reproduction, 2021, 34, 61-78.	2.2	11
45	EphB2 isolates a human marrow stromal cell subpopulation with enhanced ability to contribute to the resident intestinal cellular pool. FASEB Journal, 2013, 27, 2111-2121.	0.5	9
46	The Impact of ACEs on BMI: An Investigation of the Genotype-Environment Effects of BMI. Frontiers in Genetics, 2022, 13, 816660.	2.3	9
47	GeneX Va: VBC open source microarray database and analysis software. BioTechniques, 2004, 36, 634-642.	1.8	8
48	Open-access database of candidate associations from a genome-wide SNP scan of the Framingham Heart Study. Nature Genetics, 2007, 39, 135-136.	21.4	8
49	MULTBLAST: A web application for multiple BLAST searches. Bioinformation, 2010, 5, 224-226.	0.5	8
50	Genome-Wide Identification of Rare and Common Variants Driving Triglyceride Levels in a Nevada Population. Frontiers in Genetics, 2021, 12, 639418.	2.3	7
51	The road not taken: Evolution of tetrodotoxin resistance in the Sierra garter snake (<i>Thamnophis) Tj ETQq1 1 0.784314 rgBT /Overl	3.9	7
52	Mechanical strain induced phospho-proteomic signaling in uterine smooth muscle cells. Journal of Biomechanics, 2018, 73, 99-107.	2.1	5
53	RNA-Seq used to identify ipsdienone reductase (IDONER): A novel monoterpene carbon-carbon double bond reductase central to Ips confusus pheromone production. Insect Biochemistry and Molecular Biology, 2021, 129, 103513.	2.7	5
54	Proteomic network analysis of human uterine smooth muscle in pregnancy, labor, and preterm labor. Integrative Molecular Medicine, 2015, 2, 261-269.	0.3	5

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55	An Algorithm for the Quillen–Suslin Theorem for Quotients of Polynomial Rings by Monomial Ideals. Journal of Symbolic Computation, 2000, 30, 555-571.	0.8	4
56	Biomass Production, Nutritional and Mineral Content of Desiccation-Sensitive and Desiccation-Tolerant Species of Sporobolus under Multiple Irrigation Regimes. Journal of Agronomy and Crop Science, 2013, 199, 309-320.	3.5	4
57	Mixing patterns in a global influenza a virus network using whole genome comparisons. , 2010, , .		1
58	Outcomes of Less Intensive Glycemic Target for a Subcutaneous Insulin Protocol in Hospitalized Patients. American Journal of the Medical Sciences, 2015, 350, 442-446.	1.1	1
59	Computational Energetic Analysis of Intrafacial Binding Energies in Interpolated Myosin States. Biophysical Journal, 2009, 96, 491a-492a.	0.5	0
60	Evaluation of 578,000 Patients From the National Inpatient Database on Changing Patient Clinical Profiles and Mortality After Coronary Artery Bypass Grafting Surgery Over a 10-Year Period. Chest, 2010, 138, 496A.	0.8	0
61	LC/MS/MS data analysis of the human uterine smooth muscle S-nitrosoproteome fingerprint in pregnancy, labor, and preterm labor. Data in Brief, 2015, 4, 591-594.	1.0	0
62	Phenome-wide association study of the FIB-4 index in a large, populational-based study in the United States. Journal of Hepatology, 2020, 73, S418.	3.7	0
63	Obesity–Mediated Regulation of the Cardiac Acetylome. FASEB Journal, 2017, 31, 602.14.	0.5	0