Sean May

List of Publications by Year in descending order

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SEAN ΜΑΥ

#	Article	IF	CITATIONS
1	Arabidopsis AUX1 Gene: A Permease-Like Regulator of Root Gravitropism. Science, 1996, 273, 948-950.	12.6	955
2	The auxin influx carrier LAX3 promotes lateral root emergence. Nature Cell Biology, 2008, 10, 946-954.	10.3	715
3	AUX1 regulates root gravitropism in Arabidopsis by facilitating auxin uptake within root apical tissues. EMBO Journal, 1999, 18, 2066-2073.	7.8	541
4	Changes in Gene Expression in Arabidopsis Shoots during Phosphate Starvation and the Potential for Developing Smart Plants. Plant Physiology, 2003, 132, 578-596.	4.8	393
5	NASCArrays: a repository for microarray data generated by NASC's transcriptomics service. Nucleic Acids Research, 2004, 32, 575D-577.	14.5	346
6	Structure-Function Analysis of the Presumptive Arabidopsis Auxin Permease AUX1[W]. Plant Cell, 2004, 16, 3069-3083.	6.6	308
7	Cytokinin Regulation of Auxin Synthesis in <i>Arabidopsis</i> Involves a Homeostatic Feedback Loop Regulated via Auxin and Cytokinin Signal Transduction Â. Plant Cell, 2010, 22, 2956-2969.	6.6	247
8	Seed and Molecular Resources for Arabidopsis. Plant Physiology, 2000, 124, 1477-1480.	4.8	244
9	Loss of the AKT2/3 potassium channel affects sugar loading into the phloem of Arabidopsis. Planta, 2002, 216, 334-344.	3.2	226
10	Polar auxin transport in the wood-forming tissues of hybrid aspen is under simultaneous control of developmental and environmental signals. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10096-10101.	7.1	225
11	A comparison of the Thlaspi caerulescens and Thlaspi arvense shoot transcriptomes. New Phytologist, 2006, 170, 239-260.	7.3	213
12	Adenosine Methylation in Arabidopsis mRNA is Associated with the 3′ End and Reduced Levels Cause Developmental Defects. Frontiers in Plant Science, 2012, 3, 48.	3.6	213
13	<i>Medicago truncatula</i> CYP716A12 Is a Multifunctional Oxidase Involved in the Biosynthesis of Hemolytic Saponins. Plant Cell, 2011, 23, 3070-3081.	6.6	190
14	Brassinosteroids participate in the control of basal and acquired freezing tolerance of plants. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5982-E5991.	7.1	162
15	Expression Studies on AUX1-like Genes in Medicago truncatula Suggest That Auxin Is Required at Two Steps in Early Nodule Development. Molecular Plant-Microbe Interactions, 2001, 14, 267-277.	2.6	140
16	Probing the Reproducibility of Leaf Growth and Molecular Phenotypes: A Comparison of Three Arabidopsis Accessions Cultivated in Ten Laboratories Â. Plant Physiology, 2010, 152, 2142-2157.	4.8	137
17	How to decide? Different methods of calculating gene expression from short oligonucleotide array data will give different results. BMC Bioinformatics, 2006, 7, 137.	2.6	124
18	Quick on the Uptake: Characterization of a Family of Plant Auxin Influx Carriers. Journal of Plant Growth Regulation, 2001, 20, 217-225.	5.1	101

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19	Flexible Tools for Gene Expression and Silencing in Tomato Â. Plant Physiology, 2009, 151, 1729-1740.	4.8	100
20	Benchmarking the CATMA Microarray. A Novel Tool forArabidopsis Transcriptome Analysis. Plant Physiology, 2005, 137, 588-601.	4.8	91
21	Yeast m6A Methylated mRNAs Are Enriched on Translating Ribosomes during Meiosis, and under Rapamycin Treatment. PLoS ONE, 2015, 10, e0132090.	2.5	78
22	Using genomic DNA-based probe-selection to improve the sensitivity of high-density oligonucleotide arrays when applied to heterologous species. Plant Methods, 2005, 1, 10.	4.3	73
23	Authentication of Coffee by Means of PCR-RFLP Analysis and Lab-on-a-Chip Capillary Electrophoresis. Journal of Agricultural and Food Chemistry, 2006, 54, 7466-7470.	5.2	72
24	Going the distance with auxin: unravelling the molecular basis of auxin transport. Philosophical Transactions of the Royal Society B: Biological Sciences, 1998, 353, 1511-1515.	4.0	62
25	MIAME/Plant - adding value to plant microarrray experiments. Plant Methods, 2006, 2, 1.	4.3	61
26	Cellular colocalization of diuretic peptides in locusts: A potent control mechanism. Peptides, 1995, 16, 95-104.	2.4	60
27	Heterologous oligonucleotide microarrays for transcriptomics in a non-model species; a proof-of-concept study of drought stress in Musa. BMC Genomics, 2009, 10, 436.	2.8	56
28	Identification of Gene Modules Associated with Low Temperatures Response in Bambara Groundnut by Network-Based Analysis. PLoS ONE, 2016, 11, e0148771.	2.5	44
29	Analysis of ripening-related gene expression in papaya using an Arabidopsis-based microarray. BMC Plant Biology, 2012, 12, 242.	3.6	41
30	Cell marking inArabidopsis thaliana andits application to patch-clamp studies. Plant Journal, 1998, 15, 843-851.	5.7	40
31	Taking the Next Step: Building an Arabidopsis Information Portal. Plant Cell, 2012, 24, 2248-2256.	6.6	38
32	The vasopressin-like immunoreactive (VPLI) neurons of the locust, Locusta migratoria. I. Anatomy. Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology, 1991, 168, 605-617.	1.6	37
33	Evidence of neutral transcriptome evolution in plants. New Phytologist, 2008, 180, 587-593.	7.3	30
34	Functional Characterization of PaLAX1, a Putative Auxin Permease, in Heterologous Plant Systems Â. Plant Physiology, 2008, 146, 1128-1141.	4.8	29
35	The study of progesterone action in human myometrial explants. Molecular Human Reproduction, 2016, 22, 877-889.	2.8	28
36	A Brassica Exon Array for Whole-Transcript Gene Expression Profiling. PLoS ONE, 2010, 5, e12812.	2.5	27

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37	On the causes of outliers in Affymetrix GeneChip data. Briefings in Functional Genomics & Proteomics, 2009, 8, 199-212.	3.8	24
38	An International Bioinformatics Infrastructure to Underpin the <i>Arabidopsis</i> Community. Plant Cell, 2010, 22, 2530-2536.	6.6	23
39	The Mediator complex subunits MED25/PFT1 and MED8 are required for transcriptional responses to changes in cell wall arabinose composition and glucose treatment in Arabidopsis thaliana. BMC Plant Biology, 2015, 15, 215.	3.6	21
40	Gene pathway development in human epicardial adipose tissue during early life. JCI Insight, 2016, 1, e87460.	5.0	20
41	Transcriptional analysis of adipose tissue during development reveals depot-specific responsiveness to maternal dietary supplementation. Scientific Reports, 2018, 8, 9628.	3.3	20
42	A Cross-Species Gene Expression Marker-Based Genetic Map and QTL Analysis in Bambara Groundnut. Genes, 2017, 8, 84.	2.4	19
43	Metallome of cerebrovascular endothelial cells infected with <i>Toxoplasma gondii</i> using μ-XRF imaging and inductively coupled plasma mass spectrometry. Metallomics, 2018, 10, 1401-1414.	2.4	19
44	Integrating genetic information into plant breeding programmes: how will we produce varieties from molecular variation, using bioinformatics?. Annals of Applied Biology, 2005, 146, 223-237.	2.5	17
45	UK CropNet: a collection of databases and bioinformatics resources for crop plant genomics. Nucleic Acids Research, 2000, 28, 104-107.	14.5	16
46	Repurposing Antibacterial AM404 As a Potential Anticancer Drug for Targeting Colorectal Cancer Stem-Like Cells. Cancers, 2020, 12, 106.	3.7	15
47	Brevicoryne brassicae aphids interfere with transcriptome responses of Arabidopsis thaliana to feeding by Plutella xylostella caterpillars in a density-dependent manner. Oecologia, 2017, 183, 107-120.	2.0	14
48	Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. Plant Direct, 2019, 3, e00109.	1.9	14
49	Current status of the multinational Arabidopsis community. Plant Direct, 2020, 4, e00248.	1.9	13
50	A molecular signature of dormancy in CD34+CD38- acute myeloid leukaemia cells. Oncotarget, 2017, 8, 111405-111418.	1.8	13
51	Lowâ€intensity microwave irradiation does not substantially alter gene expression in late larval and adult <i>Caenorhabditis elegans</i> . Bioelectromagnetics, 2009, 30, 602-612.	1.6	12
52	MicroRNA-495/TGF-β/FOXC1 axis regulates multidrug resistance in metaplastic breast cancer cells. Biochemical Pharmacology, 2021, 192, 114692.	4.4	12
53	Effects of Alzheimer's peptide and α1-antichymotrypsin on astrocyte gene expression. Neurobiology of Aging, 2007, 28, 51-61.	3.1	11
54	Optimising the analysis of transcript data using high density oligonucleotide arrays and genomic DNA-based probe selection. BMC Genomics, 2007, 8, 344.	2.8	11

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55	Use of the Affymetrix Human GeneChip array and genomic DNA hybridisation probe selection to study ovine transcriptomes. Animal, 2011, 5, 861-866.	3.3	11
56	Mast-Cell Tryptase Release Contributes to Disease Progression in Lymphangioleiomyomatosis. American Journal of Respiratory and Critical Care Medicine, 2021, 204, 431-444.	5.6	11
57	GARNet, the Genomic Arabidopsis Resource Network. Trends in Plant Science, 2002, 7, 145-147.	8.8	10
58	Integrated BioBank of Luxembourg–University of Luxembourg: University Biobanking Certificate. Biopreservation and Biobanking, 2020, 18, 7-9.	1.0	10
59	Improved nucleic acid extraction protocols for Ganoderma boninense, G. miniatocinctum and G. tornatum. Biotechnology Letters, 2018, 40, 1541-1550.	2.2	9
60	Genome-Wide Expression and Anti-Proliferative Effects of Electric Field Therapy on Pediatric and Adult Brain Tumors. International Journal of Molecular Sciences, 2022, 23, 1982.	4.1	8
61	Data management challenges for artificial intelligence in plant and agricultural research. F1000Research, 0, 10, 324.	1.6	7
62	Differential Yeast Gene Transcription during Brewery Propagation. Journal of the American Society of Brewing Chemists, 2010, 68, 21-29.	1.1	6
63	A Genetic Analysis of Tumor Progression in Drosophila Identifies the Cohesin Complex as a Suppressor of Individual and Collective Cell Invasion. IScience, 2020, 23, 101237.	4.1	6
64	Transcriptomeâ€based screening of ion channels and transporters in a migratory chondroprogenitor cell line isolated from lateâ€stage osteoarthritic cartilage. Journal of Cellular Physiology, 2021, 236, 7421-7439.	4.1	6
65	AtEnsEMBL. , 2005, 406, 213-227.		5
66	Equine transcriptome quantification using human GeneChip arrays can be improved using genomic DNA hybridisation and probe selection. Veterinary Journal, 2010, 186, 323-327.	1.7	5
67	Pigeons: A Novel GUI Software for Analysing and Parsing High Density Heterologous Oligonucleotide Microarray Probe Level Data. Microarrays (Basel, Switzerland), 2014, 3, 1-23.	1.4	5
68	The small molecule hyperphyllin enhances leaf formation rate and mimics shoot meristem integrity defects associated with AMP1 deficiency. Plant Physiology, 2016, 171, pp.01633.2015.	4.8	5
69	Finding Your Knockout: Reverse Genetics Techniques for Plants. Molecular Biotechnology, 2002, 20, 209-222.	2.4	4
70	Agronomic and molecular analysis of heterosis in alfalfa. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 288-290.	0.8	3
71	Molecular Characterization of Adipose Tissue in the African Elephant (Loxodonta africana). PLoS ONE, 2014, 9, e91717.	2.5	3
72	Increased expression of serine biosynthetic pathway genes is associated with skeletal muscle hypertrophy in sheep. Proceedings of the Nutrition Society, 2015, 74, .	1.0	2

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73	Suboptimal mid-luteal progesterone concentrations are associated with aberrant endometrial gene expression, potentially resulting in implantation failure. Reproductive BioMedicine Online, 2021, 42, 595-608.	2.4	2
74	Integrated Metabolomics and Transcriptomics Using an Optimised Dual Extraction Process to Study Human Brain Cancer Cells and Tissues. Metabolites, 2021, 11, 240.	2.9	2
75	Evaluating the influence of progesterone concentration and time of exposure on in vitro endometrial decidualisation. Molecular and Cellular Endocrinology, 2021, 528, 111242.	3.2	2
76	Teaching Data Science and Cloud Computing in Low and Middle Income Countries. Advanced Techniques in Biology & Medicine, 2015, 03, .	0.1	1
77	Proteasome Inhibition in Brassica napus Roots Increases Amino Acid Synthesis to Offset Reduced Proteolysis. Plant and Cell Physiology, 2020, 61, 1028-1040.	3.1	1
78	CG7379 and ING1 suppress cancer cell invasion by maintaining cell–cell junction integrity. Open Biology, 2021, 11, 210077.	3.6	1
79	The UK Crop Plant Bioinformatics Network (UK CropNet). Yeast, 2000, 1, 335-338.	1.7	0
80	Reverse Genetics: Screening Plant Populations for Gene Knockouts. , 2000, 141, 175-195.		0
81	P4-043 Gene expression profiles of primary human astrocytes exposed to Abeta and ACT/ABETA complexes assessed using a global DNA microarray. Neurobiology of Aging, 2004, 25, S485.	3.1	0
82	A GBM invasive region expression profile identified through a multi-region sampling approach. Neuro-Oncology, 2018, 20, i16-i17.	1.2	0
83	How to build an effective research network: lessons from two decades of the GARNet plant science community. Journal of Experimental Botany, 2020, 71, 6881-6889.	4.8	0
84	Molecular Signature of Dormancy in CD34+CD38- Acute Myeloid Leukaemia Cells. Blood, 2016, 128, 1660-1660.	1.4	0