

Su-May Yu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1794326/publications.pdf>

Version: 2024-02-01

76
papers

5,673
citations

66336

42
h-index

79691

73
g-index

76
all docs

76
docs citations

76
times ranked

6289
citing authors

#	ARTICLE	IF	CITATIONS
1	A Novel Class of Gibberellin 2-Oxidases Control Semidwarfism, Tillering, and Root Development in Rice. <i>Plant Cell</i> , 2008, 20, 2603-2618.	6.6	410
2	Sourceâ€“Sink Communication: Regulated by Hormone, Nutrient, and Stress Cross-Signaling. <i>Trends in Plant Science</i> , 2015, 20, 844-857.	8.8	259
3	A Novel MYBS3-Dependent Pathway Confers Cold Tolerance in Rice Â Â. <i>Plant Physiology</i> , 2010, 153, 145-158.	4.8	254
4	Agrobacterium-mediated production of transgenic rice plants expressing a chimeric ?-amylase promoter/?-glucuronidase gene. <i>Plant Molecular Biology</i> , 1993, 22, 491-506.	3.9	230
5	Three Novel MYB Proteins with One DNA Binding Repeat Mediate Sugar and Hormone Regulation of Î±-Amylase Gene Expression. <i>Plant Cell</i> , 2002, 14, 1963-1980.	6.6	226
6	Coordinated Responses to Oxygen and Sugar Deficiency Allow Rice Seedlings to Tolerate Flooding. <i>Science Signaling</i> , 2009, 2, ra61.	3.6	215
7	The SnRK1A Protein Kinase Plays a Key Role in Sugar Signaling during Germination and Seedling Growth of Rice. <i>Plant Cell</i> , 2007, 19, 2484-2499.	6.6	207
8	A rice gene activation/knockout mutant resource for high throughput functional genomics. <i>Plant Molecular Biology</i> , 2007, 63, 351-364.	3.9	197
9	Cellular and Genetic Responses of Plants to Sugar Starvation. <i>Plant Physiology</i> , 1999, 121, 687-693.	4.8	183
10	Mutant Resources in Rice for Functional Genomics of the Grasses. <i>Plant Physiology</i> , 2009, 149, 165-170.	4.8	167
11	Title is missing!. <i>Transgenic Research</i> , 1998, 7, 213-222.	2.4	161
12	Sugar Response Sequence in the Promoter of a Rice Î±-Amylase Gene Serves as a Transcriptional Enhancer. <i>Journal of Biological Chemistry</i> , 1998, 273, 10120-10131.	3.4	160
13	Sugar Coordinately and Differentially Regulates Growth- and Stress-Related Gene Expression via a Complex Signal Transduction Network and Multiple Control Mechanisms. <i>Plant Physiology</i> , 2001, 125, 877-890.	4.8	153
14	Expression of alpha-amylases, carbohydrate metabolism, and autophagy in cultured rice cells is coordinately regulated by sugar nutrient. <i>Plant Journal</i> , 1994, 6, 625-636.	5.7	152
15	Cloning and Functional Characterization of a Constitutively Expressed Nitrate Transporter Gene, OsNRT1, from Rice. <i>Plant Physiology</i> , 2000, 122, 379-388.	4.8	151
16	Sugars act as signal molecules and osmotica to regulate the expression of ?-amylase genes and metabolic activities in germinating cereal grains. <i>Plant Molecular Biology</i> , 1996, 30, 1277-1289.	3.9	122
17	<scp>ALFIN</scp>â€“<scp>LIKE</scp> 6 is involved in root hair elongation during phosphate deficiency in Arabidopsis. <i>New Phytologist</i> , 2013, 198, 709-720.	7.3	109
18	Signal Peptide-Dependent Targeting of a Rice Î±-Amylase and Cargo Proteins to Plastids and Extracellular Compartments of Plant Cells. <i>Plant Physiology</i> , 2004, 135, 1367-1377.	4.8	104

#	ARTICLE	IF	CITATIONS
19	Interaction between Rice MYBGA and the Gibberellin Response Element Controls Tissue-Specific Sugar Sensitivity of α -Amylase Genes. <i>Plant Cell</i> , 2006, 18, 2326-2340.	6.6	98
20	Ectopic expression of specific <i>GA</i> 2 oxidase mutants promotes yield and stress tolerance in rice. <i>Plant Biotechnology Journal</i> , 2017, 15, 850-864.	8.3	97
21	High-level production of a thermoacidophilic α -glucosidase from <i>Penicillium citrinum</i> YS40-5 by solid-state fermentation with rice bran. <i>Bioresource Technology</i> , 2010, 101, 1310-1317.	9.6	90
22	SnRK1A-Interacting Negative Regulators Modulate the Nutrient Starvation Signaling Sensor SnRK1 in Source-Sink Communication in Cereal Seedlings under Abiotic Stress. <i>Plant Cell</i> , 2014, 26, 808-827.	6.6	86
23	Carbohydrate Starvation Stimulates Differential Expression of Rice α -Amylase Genes That Is Modulated through Complicated Transcriptional and Posttranscriptional Processes. <i>Journal of Biological Chemistry</i> , 1996, 271, 26998-27004.	3.4	84
24	Production of two Highly Active Bacterial Phytases with Broad pH Optima in Germinated Transgenic Rice Seeds. <i>Transgenic Research</i> , 2004, 13, 29-39.	2.4	84
25	Sugar starvation- and GA-inducible calcium-dependent protein kinase 1 feedback regulates GA biosynthesis and activates a 14-3-3 protein to confer drought tolerance in rice seedlings. <i>Plant Molecular Biology</i> , 2013, 81, 347-361.	3.9	83
26	Production of human serum albumin by sugar starvation induced promoter and rice cell culture. <i>Transgenic Research</i> , 2005, 14, 569-581.	2.4	75
27	Control of transcription and mRNA turnover as mechanisms of metabolic repression of alpha-amylase gene expression. <i>Plant Journal</i> , 1994, 5, 655-664.	5.7	70
28	A late embryogenesis abundant protein <i>HVA</i> 1 regulated by an inducible promoter enhances root growth and abiotic stress tolerance in rice without yield penalty. <i>Plant Biotechnology Journal</i> , 2015, 13, 105-116.	8.3	69
29	A novel endo-glucanase from the thermophilic bacterium <i>Geobacillus</i> sp. 70PC53 with high activity and stability over a broad range of temperatures. <i>Extremophiles</i> , 2009, 13, 425-435.	2.3	68
30	Sugar starvation-regulated MYBS2 and 14-3-3 protein interactions enhance plant growth, stress tolerance, and grain weight in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21925-21935.	7.1	68
31	Convergent Starvation Signals and Hormone Crosstalk in Regulating Nutrient Mobilization upon Germination in Cereals. <i>Plant Cell</i> , 2012, 24, 2857-2873.	6.6	66
32	Construction of Chromosomally Located T7 Expression System for Production of Heterologous Secreted Proteins in <i>Bacillus subtilis</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 5392-5399.	5.2	56
33	Serotonin accumulation in transgenic rice by over-expressing tryptophan decarboxylase results in a dark brown phenotype and stunted growth. <i>Plant Molecular Biology</i> , 2012, 78, 525-543.	3.9	56
34	Rice α -Amylase Transcriptional Enhancers Direct Multiple Mode Regulation of Promoters in Transgenic Rice. <i>Journal of Biological Chemistry</i> , 2002, 277, 13641-13649.	3.4	55
35	Metabolic adaptation to sugar/ <i>O</i> ₂ deficiency for anaerobic germination and seedling growth in rice. <i>Plant, Cell and Environment</i> , 2014, 37, 2234-2244.	5.7	54
36	Multiple Mode Regulation of a Cysteine Proteinase Gene Expression in Rice. <i>Plant Physiology</i> , 2000, 122, 57-66.	4.8	53

#	ARTICLE	IF	CITATIONS
37	A rice phenomics studyâ€”phenotype scoring and seed propagation of a T-DNA insertion-induced rice mutant population. <i>Plant Molecular Biology</i> , 2007, 65, 427-438.	3.9	52
38	Abscisic Acid- and Stress-Induced Highly Proline-Rich Glycoproteins Regulate Root Growth in Rice. <i>Plant Physiology</i> , 2013, 163, 118-134.	4.8	52
39	The 3â€² untranslated region of a rice Î±-amylase gene mediates sugar-dependent abundance of mRNA. <i>Plant Journal</i> , 1998, 15, 685-695.	5.7	50
40	Transcriptomic adaptations in rice suspension cells under sucrose starvation. <i>Plant Molecular Biology</i> , 2007, 63, 441-463.	3.9	49
41	Dynamic synergistic effect on <i>Trichoderma reesei</i> cellulases by novel Î²-glucosidases from Taiwanese fungi. <i>Bioresource Technology</i> , 2011, 102, 6073-6081.	9.6	47
42	Expression of a bi-functional and thermostable amylopullulanase in transgenic rice seeds leads to autohydrolysis and altered composition of starch. <i>Molecular Breeding</i> , 2005, 15, 125-143.	2.1	46
43	The sweet potato sporamin promoter confers high-level phytase expression and improves organic phosphorus acquisition and tuber yield of transgenic potato. <i>Plant Molecular Biology</i> , 2008, 67, 347-361.	3.9	42
44	A metagenomic approach for the identification and cloning of an endoglucanase from rice straw compost. <i>Gene</i> , 2013, 519, 360-366.	2.2	42
45	Genetic resources offer efficient tools for rice functional genomics research. <i>Plant, Cell and Environment</i> , 2016, 39, 998-1013.	5.7	42
46	Increasing Leaf Vein Density by Mutagenesis: Laying the Foundations for C4 Rice. <i>PLoS ONE</i> , 2014, 9, e94947.	2.5	36
47	Enhancement of laccase activity by pre-incubation with organic solvents. <i>Scientific Reports</i> , 2019, 9, 9754.	3.3	35
48	Somaclonal variation does not preclude the use of rice transformants for genetic screening. <i>Plant Journal</i> , 2016, 85, 648-659.	5.7	34
49	Exploring the Mechanism Responsible for Cellulase Thermostability by Structure-Guided Recombination. <i>PLoS ONE</i> , 2016, 11, e0147485.	2.5	32
50	Production of mouse granulocyteâ€”macrophage colonyâ€”stimulating factor by gateway technology and transgenic rice cell culture. <i>Biotechnology and Bioengineering</i> , 2012, 109, 1239-1247.	3.3	29
51	A novel exo-cellulase from white spotted longhorn beetle (<i>Anoplophora malasiaca</i>). <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 629-636.	2.7	26
52	<i>Rice Big Grain 1</i> promotes cell division to enhance organ development, stress tolerance and grain yield. <i>Plant Biotechnology Journal</i> , 2020, 18, 1969-1983.	8.3	25
53	How does rice cope with too little oxygen during its early life?. <i>New Phytologist</i> , 2021, 229, 36-41.	7.3	25
54	T-DNA Activation Tagging as a Tool to Isolate <i>Salvia miltiorrhiza</i> Transgenic Lines for Higher Yields of Tanshinones. <i>Planta Medica</i> , 2008, 74, 780-786.	1.3	24

#	ARTICLE	IF	CITATIONS
55	Characterization of an immunomodulatory Der p 2-FIP-fve fusion protein produced in transformed rice suspension cell culture. <i>Transgenic Research</i> , 2012, 21, 177-192.	2.4	21
56	Kinetic analysis and structural studies of a high efficiency laccase from <i>Cerrena</i> sp. <scp>RSD</scp>1. <i>FEBS Open Bio</i> , 2018, 8, 1230-1246.	2.3	20
57	<i>Chaetomella raphigera</i> β -glucosidase D2-BGL has intriguing structural features and a high substrate affinity that renders it an efficient cellulase supplement for lignocellulosic biomass hydrolysis. <i>Biotechnology for Biofuels</i> , 2019, 12, 258.	6.2	19
58	Candidate regulators of Early Leaf Development in Maize Perturb Hormone Signalling and Secondary Cell Wall Formation When Constitutively Expressed in Rice. <i>Scientific Reports</i> , 2017, 7, 4535.	3.3	18
59	Improvements of the productivity and saccharification efficiency of the cellulolytic β -glucosidase D2-BGL in <i>Pichia pastoris</i> via directed evolution. <i>Biotechnology for Biofuels</i> , 2021, 14, 126.	6.2	16
60	Large-scale phenomics analysis of a T-DNA tagged mutant population. <i>GigaScience</i> , 2017, 6, 1-7.	6.4	15
61	Global functional analyses of rice promoters by genomics approaches. <i>Plant Molecular Biology</i> , 2007, 65, 417-425.	3.9	14
62	A rice DEAD-box protein, OsRH36, can complement an <i>Arabidopsis</i> <i>atrh36</i> mutant, but cannot functionally replace its yeast homolog <i>Dbp8p</i> . <i>Plant Molecular Biology</i> , 2010, 74, 119-128.	3.9	13
63	The modified rice β -Amy8 promoter confers high-level foreign gene expression in a novel hypoxia-inducible expression system in transgenic rice seedlings. <i>Plant Molecular Biology</i> , 2014, 85, 147-161.	3.9	11
64	T-DNA Insertion Mutants as a Resource for Rice Functional Genomics. , 2007, , 181-221.		10
65	An ABA-responsive bZIP protein, OsBZ8, mediates sugar repression of β -amylase gene expression. <i>Physiologia Plantarum</i> , 2003, 119, 78-86.	5.2	8
66	Glycosylation Variants of a β -Glucosidase Secreted by a Taiwanese Fungus, <i>Chaetomella raphigera</i> , Exhibit Variant-Specific Catalytic and Biochemical Properties. <i>PLoS ONE</i> , 2014, 9, e106306.	2.5	8
67	Molecular cloning and characterization of a novel starvation inducible MAP kinase gene in rice. <i>Plant Physiology and Biochemistry</i> , 2003, 41, 207-213.	5.8	7
68	Lack of Genotype and Phenotype Correlation in a Rice T-DNA Tagged Line Is Likely Caused by Introgression in the Seed Source. <i>PLoS ONE</i> , 2016, 11, e0155768.	2.5	7
69	The Nucleotide-Dependent Interactome of Rice Heterotrimeric G-Protein β Subunit. <i>Proteomics</i> , 2019, 19, 1800385.	2.2	6
70	Knockdown expression of a MYB-related transcription factor gene, OsMYBS2, enhances production of recombinant proteins in rice suspension cells. <i>Plant Methods</i> , 2021, 17, 99.	4.3	5
71	Methods for Rice Phenomics Studies. <i>Methods in Molecular Biology</i> , 2011, 678, 129-138.	0.9	5
72	Activation Tagging Systems in Rice. , 2007, , 333-353.		3

#	ARTICLE	IF	CITATIONS
73	Ectopic Expression of WINDING 1 Leads to Asymmetrical Distribution of Auxin and a Spiral Phenotype in Rice. <i>Plant and Cell Physiology</i> , 2017, 58, 1494-1506.	3.1	3
74	From simple and specific zymographic detections to the annotation of a fungus <i>Daldinia caldariorum</i> D263 that encodes a wide range of highly bioactive cellulolytic enzymes. <i>Biotechnology for Biofuels</i> , 2021, 14, 120.	6.2	2
75	TTRSIS: A Cloud Computing Platform for Rice Functional Genomics Research through a Reverse Genetics Approach. , 2011, , .		1
76	A unique self-truncation of bacterial GH5 endoglucanases leads to enhanced activity and thermostability. <i>BMC Biology</i> , 2022, 20, .	3.8	1