

Xiaohan Yang

List of Publications by Year in descending order

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114
papers

9,192
citations

71061

41
h-index

42364

92
g-index

121
all docs

121
docs citations

121
times ranked

11707
citing authors

#	ARTICLE	IF	CITATIONS
1	Diversity and conservation of plant small secreted proteins associated with arbuscular mycorrhizal symbiosis. <i>Horticulture Research</i> , 2022, 9, .	2.9	1
2	Editorial: Wood Development and Physiology in a Changing Climate. <i>Frontiers in Plant Science</i> , 2022, 13, 906736.	1.7	0
3	Reporter genes confer new-to-nature ornamental traits in plants. <i>Horticulture Research</i> , 2022, 9, .	2.9	7
4	Phylogeny and Expression Atlas of the NITRATE TRANSPORTER 1/PEPTIDE TRANSPORTER FAMILY in Agave. <i>Plants</i> , 2022, 11, 1434.	1.6	5
5	An Intein-Mediated Split-Cas9 System for Base Editing in Plants. <i>ACS Synthetic Biology</i> , 2022, 11, 2513-2517.	1.9	9
6	Transcriptome Sequencing of <i>Agave angustifolia</i> Reveals Conservation and Diversification in the Expression of Cinnamyl Alcohol Dehydrogenase Genes in Agave Species. <i>Agriculture (Switzerland)</i> , 2022, 12, 1003.	1.4	3
7	Precision genome editing in plants using gene targeting and prime editing: existing and emerging strategies. <i>Biotechnology Journal</i> , 2022, 17, .	1.8	2
8	Overexpression of an Agave Phosphoenolpyruvate Carboxylase Improves Plant Growth and Stress Tolerance. <i>Cells</i> , 2021, 10, 582.	1.8	24
9	Transcriptome and Degradome Profiling Reveals a Role of miR530 in the Circadian Regulation of Gene Expression in <i>Kalanchoë marnieriana</i> . <i>Cells</i> , 2021, 10, 1526.	1.8	5
10	Advances and perspectives in discovery and functional analysis of small secreted proteins in plants. <i>Horticulture Research</i> , 2021, 8, 130.	2.9	20
11	Construct design for CRISPR/Cas-based genome editing in plants. <i>Trends in Plant Science</i> , 2021, 26, 1133-1152.	4.3	76
12	Inference of Gene Regulatory Network Uncovers the Linkage between Circadian Clock and Crassulacean Acid Metabolism in <i>Kalanchoë fedtschenkoi</i> . <i>Cells</i> , 2021, 10, 2217.	1.8	2
13	Temporal dynamics of protein and post-translational modification abundances in <i>Populus</i> leaf across a diurnal period. <i>Proteomics</i> , 2021, 21, 2100127.	1.3	0
14	Expanding the application of a UV-visible reporter for transient gene expression and stable transformation in plants. <i>Horticulture Research</i> , 2021, 8, 234.	2.9	18
15	Biological Parts for Plant Biodesign to Enhance Land-Based Carbon Dioxide Removal. <i>Biodesign Research</i> , 2021, 2021, .	0.8	5
16	Plant-Based Biosensors for Detecting CRISPR-Mediated Genome Engineering. <i>ACS Synthetic Biology</i> , 2021, 10, 3600-3603.	1.9	7
17	Overexpression of a <i>Prefoldin Î²</i> subunit gene reduces biomass recalcitrance in the bioenergy crop <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 859-871.	4.1	17
18	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoë fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020, 9, .	3.3	11

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19	Editorial: Systems Biology and Synthetic Biology in Relation to Drought Tolerance or Avoidance in Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 394.	1.7	13
20	The Role of Synthetic Biology in Atmospheric Greenhouse Gas Reduction: Prospects and Challenges. <i>Biodesign Research</i> , 2020, 2020, .	0.8	24
21	Biosystems Design to Accelerate C ₃ -to-CAM Progression. <i>Biodesign Research</i> , 2020, 2020, .	0.8	16
22	Plant Biosystems Design for a Carbon-Neutral Bioeconomy. <i>Biodesign Research</i> , 2020, 2020, .	0.8	5
23	Plant Biosystems Design Research Roadmap 1.0. <i>Biodesign Research</i> , 2020, 2020, .	0.8	16
24	Reconfiguring Plant Metabolism for Biodegradable Plastic Production. <i>Biodesign Research</i> , 2020, 2020, .	0.8	7
25	Prime Editing Technology and Its Prospects for Future Applications in Plant Biology Research. <i>Biodesign Research</i> , 2020, 2020, .	0.8	34
26	<i>Agrobacterium</i> -mediated Transformation of <i>Kalanchoe laxiflora</i> . <i>Horticultural Plant Journal</i> , 2019, 5, 221-228.	2.3	7
27	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680.	4.7	42
28	A Suggestion of Converting Protein Intrinsic Disorder to Structural Entropy Using Shannon's Information Theory. <i>Entropy</i> , 2019, 21, 591.	1.1	2
29	Comparative genomics can provide new insights into the evolutionary mechanisms and gene function in CAM plants. <i>Journal of Experimental Botany</i> , 2019, 70, 6539-6547.	2.4	21
30	CRISPR/Cas9-mediated targeted mutagenesis for functional genomics research of crassulacean acid metabolism plants. <i>Journal of Experimental Botany</i> , 2019, 70, 6621-6629.	2.4	33
31	Overexpression of a serine hydroxymethyltransferase increases biomass production and reduces recalcitrance in the bioenergy crop <i>Populus</i> . <i>Sustainable Energy and Fuels</i> , 2019, 3, 195-207.	2.5	27
32	Comparative Genomics Analysis Provides New Insight Into Molecular Basis of Stomatal Movement in <i>Kalanchoe fedtschenkoi</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 292.	1.7	8
33	Multitrait genome-wide association analysis of <i>Populus trichocarpa</i> identifies key polymorphisms controlling morphological and physiological traits. <i>New Phytologist</i> , 2019, 223, 293-309.	3.5	85
34	Identification of <i>Populus</i> Small RNAs Responsive to Mutualistic Interactions With Mycorrhizal Fungi, <i>Laccaria bicolor</i> and <i>Rhizophagus irregularis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 515.	1.5	17
35	The nature of the progression of drought stress drives differential metabolomic responses in <i>Populus deltoides</i> . <i>Annals of Botany</i> , 2019, 124, 617-626.	1.4	45
36	PdWND3A, a wood-associated NAC domain-containing protein, affects lignin biosynthesis and composition in <i>Populus</i> . <i>BMC Plant Biology</i> , 2019, 19, 486.	1.6	28

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37	Biodesign Research to Advance the Principles and Applications of Biosystems Design. <i>Biodesign Research</i> , 2019, 2019, .	0.8	3
38	A <i>Vitis vinifera</i> basic helix-loop-helix transcription factor enhances plant cell size, vegetative biomass and reproductive yield. <i>Plant Biotechnology Journal</i> , 2018, 16, 1595-1615.	4.1	39
39	Working towards recalcitrance mechanisms: increased xylan and homogalacturonan production by overexpression of GALactUronosylTransferase12 (GAUT12) causes increased recalcitrance and decreased growth in <i>Populus</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 9.	6.2	31
40	Sugar release and growth of biofuel crops are improved by downregulation of pectin biosynthesis. <i>Nature Biotechnology</i> , 2018, 36, 249-257.	9.4	136
41	Conservation and Diversification of Circadian Rhythmicity Between a Model Crassulacean Acid Metabolism Plant <i>Kalanchoë fedtschenkoi</i> and a Model C3 Photosynthesis Plant <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1757.	1.7	23
42	Phytobiome and Transcriptional Adaptation of <i>Populus deltoides</i> to Acute Progressive Drought and Cyclic Drought. <i>Phytobiomes Journal</i> , 2018, 2, 249-260.	1.4	23
43	A New Calmodulin-Binding Protein Expresses in the Context of Secondary Cell Wall Biosynthesis and Impacts Biomass Properties in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1669.	1.7	31
44	Functional Anatomical Traits of the Photosynthetic Organs of Plants with Crassulacean Acid Metabolism. <i>Advances in Photosynthesis and Respiration</i> , 2018, , 281-305.	1.0	30
45	Classification of Complete Proteomes of Different Organisms and Protein Sets Based on Their Protein Distributions in Terms of Some Key Attributes of Proteins. <i>International Journal of Genomics</i> , 2018, 2018, 1-12.	0.8	3
46	Perspectives on the basic and applied aspects of crassulacean acid metabolism (CAM) research. <i>Plant Science</i> , 2018, 274, 394-401.	1.7	18
47	Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in <i>Agave</i> . <i>BMC Genomics</i> , 2018, 19, 588.	1.2	64
48	Quantitative proteome profile of water deficit stress responses in eastern cottonwood (<i>Populus</i>)	1.1	17
49	Overexpression of a Domain of Unknown Function 266-containing protein results in high cellulose content, reduced recalcitrance, and enhanced plant growth in the bioenergy crop <i>Populus</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 74.	6.2	22
50	<i>Populus trichocarpa</i> encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. <i>Scientific Reports</i> , 2017, 7, 382.	1.6	36
51	Disposition and bioavailability of inulin and free sugar in untreated and dilute acid pretreated <i>Agave tequilana</i> leaves. <i>Biomass and Bioenergy</i> , 2017, 106, 176-181.	2.9	7
52	The <i>Kalanchoë</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	5.8	159
53	New technologies accelerate the exploration of non-coding RNAs in horticultural plants. <i>Horticulture Research</i> , 2017, 4, 17031.	2.9	61
54	Overexpression of a Domain of Unknown Function 231-containing protein increases O-xylan acetylation and cellulose biosynthesis in <i>Populus</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 311.	6.2	26

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55	Orchestration of carbohydrate processing for crassulacean acid metabolism. <i>Current Opinion in Plant Biology</i> , 2016, 31, 118-124.	3.5	49
56	Knockdown of a laccase in <i>Populus deltoides</i> confers altered cell wall chemistry and increased sugar release. <i>Plant Biotechnology Journal</i> , 2016, 14, 2010-2020.	4.1	64
57	Understanding the Catalytic Mechanism of Xanthosine Methyltransferase in Caffeine Biosynthesis from QM/MM Molecular Dynamics and Free Energy Simulations. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1755-1761.	2.5	12
58	Transcript, protein and metabolite temporal dynamics in the CAM plant Agave. <i>Nature Plants</i> , 2016, 2, 16178.	4.7	158
59	Genome-wide analysis of lectin receptor-like kinases in <i>Populus</i> . <i>BMC Genomics</i> , 2016, 17, 699.	1.2	72
60	An innovative platform for quick and flexible joining of assorted DNA fragments. <i>Scientific Reports</i> , 2016, 6, 19278.	1.6	20
61	Simultaneous knockdown of six non-family genes using a single synthetic RNAi fragment in <i>Arabidopsis thaliana</i> . <i>Plant Methods</i> , 2016, 12, 16.	1.9	12
62	Advances and perspectives on the use of CRISPR/Cas9 systems in plant genomics research. <i>Current Opinion in Plant Biology</i> , 2016, 30, 70-77.	3.5	94
63	Mitigating climate change through managing constructed-microbial communities in agriculture. <i>Agriculture, Ecosystems and Environment</i> , 2016, 216, 304-308.	2.5	56
64	A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. <i>New Phytologist</i> , 2015, 207, 491-504.	3.5	211
65	Development of Agave as a dedicated biomass source: production of biofuels from whole plants. <i>Biotechnology for Biofuels</i> , 2015, 8, 79.	6.2	38
66	A host plant genome (<i>Zizania latifolia</i>) after a century-long endophyte infection. <i>Plant Journal</i> , 2015, 83, 600-609.	2.8	67
67	PPCM: Combing Multiple Classifiers to Improve Protein-Protein Interaction Prediction. <i>International Journal of Genomics</i> , 2015, 2015, 1-7.	0.8	4
68	Plant Comparative and Functional Genomics. <i>International Journal of Genomics</i> , 2015, 2015, 1-2.	0.8	0
69	Development and use of bioenergy feedstocks for semi-arid and arid lands. <i>Journal of Experimental Botany</i> , 2015, 66, 4177-4193.	2.4	88
70	Downregulation of GAUT12 in <i>Populus deltoides</i> by RNA silencing results in reduced recalcitrance, increased growth and reduced xylan and pectin in a woody biofuel feedstock. <i>Biotechnology for Biofuels</i> , 2015, 8, 41.	6.2	133
71	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
72	Substrate-Assisted Catalysis in the Reaction Catalyzed by Salicylic Acid Binding Protein 2 (SABP2), a Potential Mechanism of Substrate Discrimination for Some Promiscuous Enzymes. <i>Biochemistry</i> , 2015, 54, 5366-5375.	1.2	19

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73	Climate-resilient agroforestry: physiological responses to climate change and engineering of crassulacean acid metabolism (CAM) as a mitigation strategy. <i>Plant, Cell and Environment</i> , 2015, 38, 1833-1849.	2.8	59
74	Systems and synthetic biology approaches to alter plant cell walls and reduce biomass recalcitrance. <i>Plant Biotechnology Journal</i> , 2014, 12, 1207-1216.	4.1	46
75	Engineering crassulacean acid metabolism to improve water-use efficiency. <i>Trends in Plant Science</i> , 2014, 19, 327-338.	4.3	206
76	Synthetic biology as it relates to CAM photosynthesis: challenges and opportunities. <i>Journal of Experimental Botany</i> , 2014, 65, 3381-3393.	2.4	49
77	Efficient Purging of Deleterious Mutations in Plants with Haploid Selfing. <i>Genome Biology and Evolution</i> , 2014, 6, 1238-1252.	1.1	38
78	Functional Genomics of Drought Tolerance in Bioenergy Crops. <i>Critical Reviews in Plant Sciences</i> , 2014, 33, 205-224.	2.7	25
79	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	13.7	725
80	Informing the improvement and biodesign of crassulacean acid metabolism via system dynamics modelling. <i>New Phytologist</i> , 2013, 200, 946-949.	3.5	14
81	Comparative analysis of cation/proton antiporter superfamily in plants. <i>Gene</i> , 2013, 521, 245-251.	1.0	34
82	Evolutionary analyses of non-CF family genes in plants. <i>Plant Journal</i> , 2013, 73, 788-797.	2.8	7
83	Transcriptome Analysis in Sheepgrass (<i>Leymus chinensis</i>): A Dominant Perennial Grass of the Eurasian Steppe. <i>PLoS ONE</i> , 2013, 8, e67974.	1.1	68
84	Initial characterization of shade avoidance response suggests functional diversity between <i>Populus</i> phytochrome B genes. <i>New Phytologist</i> , 2012, 196, 726-737.	3.5	25
85	<i>Pseudomonas fluorescens</i> Induces Strain-Dependent and Strain-Independent Host Plant Responses in Defense Networks, Primary Metabolism, Photosynthesis, and Fitness. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 765-778.	1.4	100
86	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	9.4	864
87	Identification of candidate genes in <i>Arabidopsis</i> and <i>Populus</i> cell wall biosynthesis using text-mining, co-expression network analysis and comparative genomics. <i>Plant Science</i> , 2011, 181, 675-687.	1.7	44
88	Comparative analysis of GT14/GT14-like gene family in <i>Arabidopsis</i> , <i>Oryza</i> , <i>Populus</i> , <i>Sorghum</i> and <i>Vitis</i> . <i>Plant Science</i> , 2011, 181, 688-695.	1.7	29
89	Comparative physiology and transcriptional networks underlying the heat shock response in <i>Populus trichocarpa</i> , <i>Arabidopsis thaliana</i> and <i>Glycine max</i> . <i>Plant, Cell and Environment</i> , 2011, 34, 1488-1506.	2.8	71
90	Abscisic Acid Receptors: Past, Present and Future. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 469-479.	4.1	82

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91	MicroSyn: A user friendly tool for detection of microsynteny in a gene family. BMC Bioinformatics, 2011, 12, 79.	1.2	46
92	Genomic aspects of research involving polyploid plants. Plant Cell, Tissue and Organ Culture, 2011, 104, 387-397.	1.2	45
93	Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. Genome Research, 2011, 21, 634-641.	2.4	105
94	Eukaryotic initiation factor 6, an evolutionarily conserved regulator of ribosome biogenesis and protein translation. Plant Signaling and Behavior, 2011, 6, 766-771.	1.2	14
95	The Populus Genome Sequence. , 2011, , 85-111.		0
96	Bioinformatics-Based Identification of Candidate Genes from QTLs Associated with Cell Wall Traits in Populus. Bioenergy Research, 2010, 3, 172-182.	2.2	25
97	Annotation and comparative analysis of the glycoside hydrolase genes in Brachypodium distachyon. BMC Genomics, 2010, 11, 600.	1.2	53
98	Genome sequencing and analysis of the model grass Brachypodium distachyon. Nature, 2010, 463, 763-768.	13.7	1,685
99	Comparative genome analysis of lignin biosynthesis gene families across the plant kingdom. BMC Bioinformatics, 2009, 10, S3.	1.2	190
100	Genome-wide identification of lineage-specific genes in Arabidopsis, Oryza and Populus. Genomics, 2009, 93, 473-480.	1.3	50
101	Poplar Genomics: State of the Science. Critical Reviews in Plant Sciences, 2009, 28, 285-308.	2.7	42
102	Micropropagation of Japanese Honeysuckle (<i>Lonicera japonica</i>) and Amur Honeysuckle (<i>L. maackii</i>) by Shoot Tip Culture. Journal of Environmental Horticulture, 2009, 27, 195-199.	0.3	5
103	The F-Box Gene Family Is Expanded in Herbaceous Annual Plants Relative to Woody Perennial Plants. Plant Physiology, 2008, 148, 1189-1200.	2.3	125
104	Recent developments in primer design for DNA polymorphism and mRNA profiling in higher plants. Plant Methods, 2006, 2, 4.	1.9	9
105	The Endo- β -Mannanase gene families in Arabidopsis, rice, and poplar. Functional and Integrative Genomics, 2006, 7, 1-16.	1.4	47
106	Divergence of the Dof Gene Families in Poplar, Arabidopsis, and Rice Suggests Multiple Modes of Gene Evolution after Duplication. Plant Physiology, 2006, 142, 820-830.	2.3	184
107	Recent Developments in Primer Design for DNA Markers in Higher Plants. Hortscience: A Publication of the American Society for Horticultural Science, 2006, 41, 1006C-1006.	0.5	0
108	SOR1, a gene associated with bioherbicide production in sorghum root hairs. Journal of Experimental Botany, 2004, 55, 2251-2259.	2.4	43

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109	Manipulation of Root Hair Development and Sorgoleone Production in Sorghum Seedlings. Journal of Chemical Ecology, 2004, 30, 199-213.	0.9	46
110	The role of root exudates and allelochemicals in the rhizosphere. Plant and Soil, 2003, 256, 67-83.	1.8	1,019
111	CURCUMA ALISMATIFOLIA. I. PLANT MORPHOLOGY AND THE EFFECT OF TUBEROLUS ROOT NUMBER ON FLOWERING DATE AND YIELD OF INFLORESCENCES. Acta Horticulturae, 1997, , 747-754.	0.1	14
112	CURCUMA ALISMATIFOLIA. II. EFFECTS OF TEMPERATURE AND DAYLENGTH ON THE DEVELOPMENT OF FLOWERS AND PROPAGULES. Acta Horticulturae, 1997, , 755-761.	0.1	12
113	Third-codon transversion rate-based Nymphaea basal angiosperm phylogeny -- concordance with developmental evidence. Nature Precedings, 0, , .	0.1	3
114	Innovative Biological Solutions to Challenges in Sustainable Biofuels Production. , 0, , .		1