

Xiaohan Yang

List of Publications by Year in descending order

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114
papers

9,192
citations

71102

41
h-index

42399

92
g-index

121
all docs

121
docs citations

121
times ranked

11707
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	27.8	1,685
2	The role of root exudates and allelochemicals in the rhizosphere. <i>Plant and Soil</i> , 2003, 256, 67-83.	3.7	1,019
3	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	17.5	864
4	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725
5	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	21.4	472
6	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.	7.3	211
7	Engineering crassulacean acid metabolism to improve water-use efficiency. <i>Trends in Plant Science</i> , 2014, 19, 327-338.	8.8	206
8	Comparative genome analysis of lignin biosynthesis gene families across the plant kingdom. <i>BMC Bioinformatics</i> , 2009, 10, S3.	2.6	190
9	Divergence of the Dof Gene Families in Poplar, Arabidopsis, and Rice Suggests Multiple Modes of Gene Evolution after Duplication. <i>Plant Physiology</i> , 2006, 142, 820-830.	4.8	184
10	The <i>Kalanchoë</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	12.8	159
11	Transcript, protein and metabolite temporal dynamics in the CAM plant <i>Agave</i> . <i>Nature Plants</i> , 2016, 2, 16178.	9.3	158
12	Sugar release and growth of biofuel crops are improved by downregulation of pectin biosynthesis. <i>Nature Biotechnology</i> , 2018, 36, 249-257.	17.5	136
13	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
14	The F-Box Gene Family Is Expanded in Herbaceous Annual Plants Relative to Woody Perennial Plants. <i>Plant Physiology</i> , 2008, 148, 1189-1200.	4.8	125
15	Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. <i>Genome Research</i> , 2011, 21, 634-641.	5.5	105
16	<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.	2.6	100
17	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.	7.1	94
18	Development and use of bioenergy feedstocks for semi-arid and arid lands. <i>Journal of Experimental Botany</i> , 2015, 66, 4177-4193.	4.8	88

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19	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.	7.3	85
20	Abscisic Acid Receptors: Past, Present and Future. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 469-479.	8.5	82
21	Construct design for CRISPR/Cas-based genome editing in plants. <i>Trends in Plant Science</i> , 2021, 26, 1133-1152.	8.8	76
22	Genome-wide analysis of lectin receptor-like kinases in <i>Populus</i> . <i>BMC Genomics</i> , 2016, 17, 699.	2.8	72
23	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.	5.7	71
24	Transcriptome Analysis in Sheepgrass (<i>Leymus chinensis</i>): A Dominant Perennial Grass of the Eurasian Steppe. <i>PLoS ONE</i> , 2013, 8, e67974.	2.5	68
25	A host plant genome (<i>Zizania latifolia</i>) after a century-long endophyte infection. <i>Plant Journal</i> , 2015, 83, 600-609.	5.7	67
26	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.	8.3	64
27	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.	2.8	64
28	New technologies accelerate the exploration of non-coding RNAs in horticultural plants. <i>Horticulture Research</i> , 2017, 4, 17031.	6.3	61
29	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.	5.7	59
30	Mitigating climate change through managing constructed-microbial communities in agriculture. <i>Agriculture, Ecosystems and Environment</i> , 2016, 216, 304-308.	5.3	56
31	Annotation and comparative analysis of the glycoside hydrolase genes in <i>Brachypodium distachyon</i> . <i>BMC Genomics</i> , 2010, 11, 600.	2.8	53
32	Genome-wide identification of lineage-specific genes in <i>Arabidopsis</i> , <i>Oryza</i> and <i>Populus</i> . <i>Genomics</i> , 2009, 93, 473-480.	2.9	50
33	Synthetic biology as it relates to CAM photosynthesis: challenges and opportunities. <i>Journal of Experimental Botany</i> , 2014, 65, 3381-3393.	4.8	49
34	Orchestration of carbohydrate processing for crassulacean acid metabolism. <i>Current Opinion in Plant Biology</i> , 2016, 31, 118-124.	7.1	49
35	The Endo- β -Mannanase gene families in <i>Arabidopsis</i> , rice, and poplar. <i>Functional and Integrative Genomics</i> , 2006, 7, 1-16.	3.5	47
36	Manipulation of Root Hair Development and Sorgoleone Production in <i>Sorghum</i> Seedlings. <i>Journal of Chemical Ecology</i> , 2004, 30, 199-213.	1.8	46

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37	MicroSyn: A user friendly tool for detection of microsynteny in a gene family. BMC Bioinformatics, 2011, 12, 79.	2.6	46
38	Systems and synthetic biology approaches to alter plant cell walls and reduce biomass recalcitrance. Plant Biotechnology Journal, 2014, 12, 1207-1216.	8.3	46
39	Genomic aspects of research involving polyploid plants. Plant Cell, Tissue and Organ Culture, 2011, 104, 387-397.	2.3	45
40	The nature of the progression of drought stress drives differential metabolomic responses in <i>Populus deltoides</i> . Annals of Botany, 2019, 124, 617-626.	2.9	45
41	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. Plant Science, 2011, 181, 675-687.	3.6	44
42	SOR1, a gene associated with bioherbicide production in sorghum root hairs. Journal of Experimental Botany, 2004, 55, 2251-2259.	4.8	43
43	Poplar Genomics: State of the Science. Critical Reviews in Plant Sciences, 2009, 28, 285-308.	5.7	42
44	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. Nature Plants, 2019, 5, 676-680.	9.3	42
45	A <i>Vitis vinifera</i> basic helix-loop-helix transcription factor enhances plant cell size, vegetative biomass and reproductive yield. Plant Biotechnology Journal, 2018, 16, 1595-1615.	8.3	39
46	Efficient Purging of Deleterious Mutations in Plants with Haploid Selfing. Genome Biology and Evolution, 2014, 6, 1238-1252.	2.5	38
47	Development of <i>Agave</i> as a dedicated biomass source: production of biofuels from whole plants. Biotechnology for Biofuels, 2015, 8, 79.	6.2	38
48	<i>Populus trichocarpa</i> encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. Scientific Reports, 2017, 7, 382.	3.3	36
49	Comparative analysis of cation/proton antiporter superfamily in plants. Gene, 2013, 521, 245-251.	2.2	34
50	Prime Editing Technology and Its Prospects for Future Applications in Plant Biology Research. Biodesign Research, 2020, 2020, .	1.9	34
51	CRISPR/Cas9-mediated targeted mutagenesis for functional genomics research of crassulacean acid metabolism plants. Journal of Experimental Botany, 2019, 70, 6621-6629.	4.8	33
52	Working towards recalcitrance mechanisms: increased xylan and homogalacturonan production by overexpression of GALactUronosylTransferase12 (GAUT12) causes increased recalcitrance and decreased growth in <i>Populus</i> . Biotechnology for Biofuels, 2018, 11, 9.	6.2	31
53	A New Calmodulin-Binding Protein Expresses in the Context of Secondary Cell Wall Biosynthesis and Impacts Biomass Properties in <i>Populus</i> . Frontiers in Plant Science, 2018, 9, 1669.	3.6	31
54	Functional Anatomical Traits of the Photosynthetic Organs of Plants with Crassulacean Acid Metabolism. Advances in Photosynthesis and Respiration, 2018, , 281-305.	1.0	30

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55	Comparative analysis of GT14/GT14-like gene family in Arabidopsis, Oryza, Populus, Sorghum and Vitis. <i>Plant Science</i> , 2011, 181, 688-695.	3.6	29
56	PdWND3A, a wood-associated NAC domain-containing protein, affects lignin biosynthesis and composition in Populus. <i>BMC Plant Biology</i> , 2019, 19, 486.	3.6	28
57	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.	4.9	27
58	Overexpression of a Domain of Unknown Function 231-containing protein increases O-xylan acetylation and cellulose biosynthesis in Populus. <i>Biotechnology for Biofuels</i> , 2017, 10, 311.	6.2	26
59	Bioinformatics-Based Identification of Candidate Genes from QTLs Associated with Cell Wall Traits in Populus. <i>Bioenergy Research</i> , 2010, 3, 172-182.	3.9	25
60	Initial characterization of shade avoidance response suggests functional diversity between <i>Populus</i> phytochrome B genes. <i>New Phytologist</i> , 2012, 196, 726-737.	7.3	25
61	Functional Genomics of Drought Tolerance in Bioenergy Crops. <i>Critical Reviews in Plant Sciences</i> , 2014, 33, 205-224.	5.7	25
62	Overexpression of an Agave Phosphoenolpyruvate Carboxylase Improves Plant Growth and Stress Tolerance. <i>Cells</i> , 2021, 10, 582.	4.1	24
63	The Role of Synthetic Biology in Atmospheric Greenhouse Gas Reduction: Prospects and Challenges. <i>Biodesign Research</i> , 2020, 2020, .	1.9	24
64	Conservation and Diversification of Circadian Rhythmicity Between a Model Crassulacean Acid Metabolism Plant <i>Kalanchoe fedtschenkoi</i> and a Model C3 Photosynthesis Plant <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1757.	3.6	23
65	Phytobiome and Transcriptional Adaptation of <i>Populus deltoides</i> to Acute Progressive Drought and Cyclic Drought. <i>Phytobiomes Journal</i> , 2018, 2, 249-260.	2.7	23
66	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 Populus. <i>Biotechnology for Biofuels</i> , 2017, 10, 74.	6.2	22
67	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.	4.8	21
68	An innovative platform for quick and flexible joining of assorted DNA fragments. <i>Scientific Reports</i> , 2016, 6, 19278.	3.3	20
69	Advances and perspectives in discovery and functional analysis of small secreted proteins in plants. <i>Horticulture Research</i> , 2021, 8, 130.	6.3	20
70	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.	2.5	19
71	Perspectives on the basic and applied aspects of crassulacean acid metabolism (CAM) research. <i>Plant Science</i> , 2018, 274, 394-401.	3.6	18
72	Expanding the application of a UV-visible reporter for transient gene expression and stable transformation in plants. <i>Horticulture Research</i> , 2021, 8, 234.	6.3	18

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73	Quantitative proteome profile of water deficit stress responses in eastern cottonwood (<i>Populus</i>) TJ ETQq1 1 0.784314 rgBT /Overlock	2.5	17
74	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.	3.5	17
75	Overexpression of a <i>Prefoldin 1</i> subunit gene reduces biomass recalcitrance in the bioenergy crop <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 859-871.	8.3	17
76	Biosystems Design to Accelerate C ₃ -to-CAM Progression. <i>Biodesign Research</i> , 2020, 2020, .	1.9	16
77	Plant Biosystems Design Research Roadmap 1.0. <i>Biodesign Research</i> , 2020, 2020, .	1.9	16
78	CURCUMA ALISMATIFOLIA. I. PLANT MORPHOLOGY AND THE EFFECT OF TUBEROUS ROOT NUMBER ON FLOWERING DATE AND YIELD OF INFLORESCENCES. <i>Acta Horticulturae</i> , 1997, , 747-754.	0.2	14
79	Eukaryotic initiation factor 6, an evolutionarily conserved regulator of ribosome biogenesis and protein translation. <i>Plant Signaling and Behavior</i> , 2011, 6, 766-771.	2.4	14
80	Informing the improvement and biodesign of crassulacean acid metabolism via system dynamics modelling. <i>New Phytologist</i> , 2013, 200, 946-949.	7.3	14
81	Editorial: Systems Biology and Synthetic Biology in Relation to Drought Tolerance or Avoidance in Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 394.	3.6	13
82	CURCUMA ALISMATIFOLIA. II. EFFECTS OF TEMPERATURE AND DAYLENGTH ON THE DEVELOPMENT OF FLOWERS AND PROPAGULES. <i>Acta Horticulturae</i> , 1997, , 755-761.	0.2	12
83	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.	5.4	12
84	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.	4.3	12
85	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoe fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020, 9, .	6.4	11
86	Recent developments in primer design for DNA polymorphism and mRNA profiling in higher plants. <i>Plant Methods</i> , 2006, 2, 4.	4.3	9
87	An Intein-Mediated Split-Cas9 System for Base Editing in Plants. <i>ACS Synthetic Biology</i> , 2022, 11, 2513-2517.	3.8	9
88	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.	3.6	8
89	Evolutionary analyses of non-family genes in plants. <i>Plant Journal</i> , 2013, 73, 788-797.	5.7	7
90	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.	5.7	7

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91	Agrobacterium-mediated Transformation of Kalanchoe laxiflora. Horticultural Plant Journal, 2019, 5, 221-228.	5.0	7
92	Reconfiguring Plant Metabolism for Biodegradable Plastic Production. Biodesign Research, 2020, 2020, .	1.9	7
93	Plant-Based Biosensors for Detecting CRISPR-Mediated Genome Engineering. ACS Synthetic Biology, 2021, 10, 3600-3603.	3.8	7
94	Reporter genes confer new-to-nature ornamental traits in plants. Horticulture Research, 2022, 9, .	6.3	7
95	Transcriptome and Degradome Profiling Reveals a Role of miR530 in the Circadian Regulation of Gene Expression in Kalanchoe marnieriana. Cells, 2021, 10, 1526.	4.1	5
96	Plant Biosystems Design for a Carbon-Neutral Bioeconomy. Biodesign Research, 2020, 2020, .	1.9	5
97	Micropropagation of Japanese Honeysuckle (Lonicera japonica) and Amur Honeysuckle (L. maackii) by Shoot Tip Culture. Journal of Environmental Horticulture, 2009, 27, 195-199.	0.5	5
98	Biological Parts for Plant Biodesign to Enhance Land-Based Carbon Dioxide Removal. Biodesign Research, 2021, 2021, .	1.9	5
99	Phylogeny and Expression Atlas of the NITRATE TRANSPORTER 1/PEPTIDE TRANSPORTER FAMILY in Agave. Plants, 2022, 11, 1434.	3.5	5
100	PPCM: Combing Multiple Classifiers to Improve Protein-Protein Interaction Prediction. International Journal of Genomics, 2015, 2015, 1-7.	1.6	4
101	Third-codon transversion rate-based Nymphaea basal angiosperm phylogeny – concordance with developmental evidence. Nature Precedings, 0, , .	0.1	3
102	Classification of Complete Proteomes of Different Organisms and Protein Sets Based on Their Protein Distributions in Terms of Some Key Attributes of Proteins. International Journal of Genomics, 2018, 2018, 1-12.	1.6	3
103	Biodesign Research to Advance the Principles and Applications of Biosystems Design. Biodesign Research, 2019, 2019, .	1.9	3
104	Transcriptome Sequencing of Agave angustifolia Reveals Conservation and Diversification in the Expression of Cinnamyl Alcohol Dehydrogenase Genes in Agave Species. Agriculture (Switzerland), 2022, 12, 1003.	3.1	3
105	A Suggestion of Converting Protein Intrinsic Disorder to Structural Entropy Using Shannon's Information Theory. Entropy, 2019, 21, 591.	2.2	2
106	Inference of Gene Regulatory Network Uncovers the Linkage between Circadian Clock and Crassulacean Acid Metabolism in Kalanchoe fedtschenkoi. Cells, 2021, 10, 2217.	4.1	2
107	Precision genome editing in plants using gene targeting and prime editing: existing and emerging strategies. Biotechnology Journal, 2022, 17, .	3.5	2
108	Innovative Biological Solutions to Challenges in Sustainable Biofuels Production. , 0, , .		1

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109	Diversity and conservation of plant small secreted proteins associated with arbuscular mycorrhizal symbiosis. Horticulture Research, 2022, 9, .	6.3	1
110	Plant Comparative and Functional Genomics. International Journal of Genomics, 2015, 2015, 1-2.	1.6	0
111	Temporal dynamics of protein and post-translational modification abundances in Populus leaf across a diurnal period. Proteomics, 2021, 21, 2100127.	2.2	0
112	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.	1.0	0
113	The Populus Genome Sequence. , 2011, , 85-111.		0
114	Editorial: Wood Development and Physiology in a Changing Climate. Frontiers in Plant Science, 2022, 13, 906736.	3.6	0