

Ying-Peng Hua

List of Publications by Year in descending order

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Version: 2024-02-01

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papers

529
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687363

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#	ARTICLE	IF	CITATIONS
1	Increased nitrogen use efficiency via amino acid remobilization from source to sink organs in <i>Brassica napus</i> . <i>Crop Journal</i> , 2023, 11, 119-131.	5.2	13
2	Transcriptomic Dissection of Allotetraploid Rapeseed (<i>Brassica napus</i> L.) in Responses to Nitrate and Ammonium Regimes and Functional Analysis of <i>BnaA2.Gln1;4</i> in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2022, 63, 755-769.	3.1	1
3	Multimiomics reveal pivotal roles of sodium translocation and compartmentation in regulating salinity resistance in allotetraploid rapeseed. <i>Journal of Experimental Botany</i> , 2021, 72, 5687-5708.	4.8	7
4	Genome-wide identification of Brassicaceae B-BOX genes and molecular characterization of their transcriptional responses to various nutrient stresses in allotetraploid rapeseed. <i>BMC Plant Biology</i> , 2021, 21, 288.	3.6	5
5	Genomic identification of nitrogen assimilation-related genes and transcriptional characterization of their responses to nitrogen in allotetraploid rapeseed. <i>Molecular Biology Reports</i> , 2021, 48, 5977-5992.	2.3	1
6	Integrated ionic and transcriptomic dissection reveals the core transporter genes responsive to varying cadmium abundances in allotetraploid rapeseed. <i>BMC Plant Biology</i> , 2021, 21, 372.	3.6	3
7	Comparative physiological and transcriptomic analyses reveal ascorbate and glutathione coregulation of cadmium toxicity resistance in wheat genotypes. <i>BMC Plant Biology</i> , 2021, 21, 459.	3.6	14
8	Comprehensive dissection into morpho-physiologic responses, ionic homeostasis, and transcriptomic profiling reveals the systematic resistance of allotetraploid rapeseed to salinity. <i>BMC Plant Biology</i> , 2020, 20, 534.	3.6	12
9	Genome-Wide Differential DNA Methylation and miRNA Expression Profiling Reveals Epigenetic Regulatory Mechanisms Underlying Nitrogen-Limitation-Triggered Adaptation and Use Efficiency Enhancement in Allotetraploid Rapeseed. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8453.	4.1	10
10	Global Landscapes of the Na ⁺ /H ⁺ Antiporter (NHX) Family Members Uncover their Potential Roles in Regulating the Rapeseed Resistance to Salt Stress. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3429.	4.1	23
11	Integrated Transcriptional and Proteomic Profiling Reveals Potential Amino Acid Transporters Targeted by Nitrogen Limitation Adaptation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2171.	4.1	4
12	Genome-wide identification of the amino acid permease genes and molecular characterization of their transcriptional responses to various nutrient stresses in allotetraploid rapeseed. <i>BMC Plant Biology</i> , 2020, 20, 151.	3.6	22
13	A multiomics approach reveals the pivotal role of subcellular reallocation in determining rapeseed resistance to cadmium toxicity. <i>Journal of Experimental Botany</i> , 2019, 70, 5437-5455.	4.8	64
14	Integrated genomic and transcriptomic insights into the two-component high-affinity nitrate transporters in allotetraploid rapeseed. <i>Plant and Soil</i> , 2018, 427, 245-268.	3.7	13
15	Integrated physiologic, genomic and transcriptomic strategies involving the adaptation of allotetraploid rapeseed to nitrogen limitation. <i>BMC Plant Biology</i> , 2018, 18, 322.	3.6	19
16	Genomics-Assisted Identification and Characterization of the Genetic Variants Underlying Differential Nitrogen Use Efficiencies in Allotetraploid Rapeseed Genotypes. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2757-2771.	1.8	16
17	Genome-scale mRNA transcriptomic insights into the responses of oilseed rape (<i>Brassica napus</i> L.) to varying boron availabilities. <i>Plant and Soil</i> , 2017, 416, 205-225.	3.7	25
18	Low-Boron Tolerance Strategies Involving Pectin-Mediated Cell Wall Mechanical Properties in <i>Brassica napus</i> . <i>Plant and Cell Physiology</i> , 2017, 58, 1991-2005.	3.1	18

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19	Genome-Wide Identification and Characterization of the Aquaporin Gene Family and Transcriptional Responses to Boron Deficiency in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1336.	3.6	54
20	Physiological and Transcriptional Analyses Reveal Differential Phytohormone Responses to Boron Deficiency in <i>Brassica napus</i> Genotypes. <i>Frontiers in Plant Science</i> , 2016, 7, 221.	3.6	36
21	Transcriptomics-assisted quantitative trait locus fine mapping for the rapid identification of a nodulin 26-like intrinsic protein gene regulating boron efficiency in allotetraploid rapeseed. <i>Plant, Cell and Environment</i> , 2016, 39, 1601-1618.	5.7	71
22	Physiological, genomic and transcriptional diversity in responses to boron deficiency in rapeseed genotypes. <i>Journal of Experimental Botany</i> , 2016, 67, 5769-5784.	4.8	38
23	A High-Density Genetic Map Identifies a Novel Major QTL for Boron Efficiency in Oilseed Rape (<i>Brassica</i>) Tj ETQq1	1.0, 2.5	784314, 66