

Hude Mao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3585458/publications.pdf>

Version: 2024-02-01

14
papers

920
citations

840776

11
h-index

1058476

14
g-index

21
all docs

21
docs citations

21
times ranked

965
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | A transposable element in a NAC gene is associated with drought tolerance in maize seedlings. <i>Nature Communications</i> , 2015, 6, 8326. | 12.8 | 392 |
| 2 | ZmNAC55, a maize stress-responsive NAC transcription factor, confers drought resistance in transgenic <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2016, 105, 55-66. | 5.8 | 85 |
| 3 | Genetic variation in <i>ZmTIP1</i> contributes to root hair elongation and drought tolerance in maize. <i>Plant Biotechnology Journal</i> , 2020, 18, 1271-1283. | 8.3 | 85 |
| 4 | Variation in cis-regulation of a NAC transcription factor contributes to drought tolerance in wheat. <i>Molecular Plant</i> , 2022, 15, 276-292. | 8.3 | 78 |
| 5 | Regulatory changes in <i>TaSNAC8A</i> are associated with drought tolerance in wheat seedlings. <i>Plant Biotechnology Journal</i> , 2020, 18, 1078-1092. | 8.3 | 73 |
| 6 | The wheat ABA receptor gene <i>TaPYL1B</i> contributes to drought tolerance and grain yield by increasing water-use efficiency. <i>Plant Biotechnology Journal</i> , 2022, 20, 846-861. | 8.3 | 55 |
| 7 | Molecular evolution and gene expression differences within the HD-Zip transcription factor family of <i>Zea mays</i> L.. <i>Genetica</i> , 2016, 144, 243-257. | 1.1 | 38 |
| 8 | Characterization of wheat homeodomain-leucine zipper family genes and functional analysis of <i>TaHDZ5-6A</i> in drought tolerance in transgenic <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2020, 20, 50. | 3.6 | 27 |
| 9 | Overexpression of the wheat NAC transcription factor <i>TaSNAC4-3A</i> gene confers drought tolerance in transgenic <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 160, 37-50. | 5.8 | 26 |
| 10 | Genome-wide analysis of trehalose-6-phosphate phosphatases (TPP) gene family in wheat indicates their roles in plant development and stress response. <i>BMC Plant Biology</i> , 2022, 22, 120. | 3.6 | 17 |
| 11 | A Deep Learning-Based Method for Automatic Assessment of Stomatal Index in Wheat Microscopic Images of Leaf Epidermis. <i>Frontiers in Plant Science</i> , 2021, 12, 716784. | 3.6 | 13 |
| 12 | The miR319/ <i>TaGAMYB3</i> module regulates plant architecture and improves grain yield in common wheat (<i>Triticum aestivum</i>). <i>New Phytologist</i> , 2022, 235, 1515-1530. | 7.3 | 12 |
| 13 | Genome-wide analysis of the AREB/ABF gene lineage in land plants and functional analysis of <i>TaABF3</i> in <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2020, 20, 558. | 3.6 | 11 |
| 14 | Genome-wide association study revealed <i>TaHXX3A</i> as a candidate gene controlling stomatal index in wheat seedlings. <i>Plant, Cell and Environment</i> , 2022, 45, 2306-2323. | 5.7 | 7 |