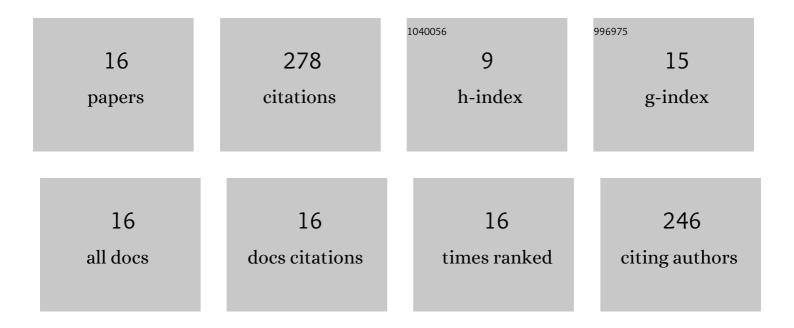
Delong Wang

List of Publications by Year in descending order

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| # | Article | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Molecular structures and functional exploration of NDA family genes respond tolerant to alkaline stress in Gossypium hirsutum L Biological Research, 2022, 55, 4. | 3.4 | 4 |
| 2 | Identification and Structure Analysis of KCS Family Genes Suggest Their Reponding to Regulate Fiber Development in Long-Staple Cotton Under Salt-Alkaline Stress. Frontiers in Genetics, 2022, 13, 812449. | 2.3 | 11 |
| 3 | Identification of SNAT Family Genes Suggests GhSNAT3D Functional Reponse to Melatonin Synthesis Under Salinity Stress in Cotton. Frontiers in Molecular Biosciences, 2022, 9, 843814. | 3.5 | 12 |
| 4 | A high-quality assembled genome and its comparative analysis decode the adaptive molecular mechanism of the number one Chinese cotton variety CRI-12. GigaScience, 2022, 11, . | 6.4 | 6 |
| 5 | Genome-wide expression analysis of carboxylesterase (CXE) gene family implies GBCXE49 functional responding to alkaline stress in cotton. BMC Plant Biology, 2022, 22, 194. | 3.6 | 8 |
| 6 | Cotton transcriptome analysis reveals novel biological pathways that eliminate reactive oxygen species (ROS) under sodium bicarbonate (NaHCO3) alkaline stress. Genomics, 2021, 113, 1157-1169. | 2.9 | 27 |
| 7 | Melatonin Improves Cotton Salt Tolerance by Regulating ROS Scavenging System and Ca2 + Signal Transduction. Frontiers in Plant Science, 2021, 12, 693690. | 3.6 | 44 |
| 8 | Genome-wide identification of CK gene family suggests functional expression pattern against Cd2+ stress in Gossypium hirsutum L International Journal of Biological Macromolecules, 2021, 188, 272-282. | 7.5 | 15 |
| 9 | A novel raffinose biological pathway is observed by symbionts of cotton≡ <i>Verticillium dahliae</i> to improve salt tolerance genetically on cotton. Journal of Agronomy and Crop Science, 2021, 207, 956-969. | 3.5 | 14 |
| 10 | Genome-wide expression analysis of phospholipase A1 (PLA1) gene family suggests phospholipase A1-32 gene responding to abiotic stresses in cotton. International Journal of Biological Macromolecules, 2021, 192, 1058-1074. | 7.5 | 13 |
| 11 | Genome-wide identification and characteristic analysis of the downstream melatonin metabolism gene GhM2H in Gossypium hirsutum L Biological Research, 2021, 54, 36. | 3.4 | 8 |
| 12 | Insight Between the Epigenetics and Transcription Responding of Cotton Hypocotyl Cellular Elongation Under Salt-Alkaline Stress. Frontiers in Plant Science, 2021, 12, 772123. | 3.6 | 0 |
| 13 | Genome-wide identification and expression analysis of PUB genes in cotton. BMC Genomics, 2020, 21, 213. | 2.8 | 26 |
| 14 | Resequencing of <i>cv</i> CRIâ€12 family reveals haplotype block inheritance and recombination of agronomically important genes in artificial selection. Plant Biotechnology Journal, 2019, 17, 945-955. | 8.3 | 20 |
| 15 | Identification and function analysis of drought-specific small RNAs in Gossypium hirsutum L Plant Science, 2019, 280, 187-196. | 3.6 | 12 |
| 16 | Single-base resolution methylomes of upland cotton (Gossypium hirsutum L.) reveal epigenome modifications in response to drought stress. BMC Genomics, 2017, 18, 297. | 2.8 | 58 |