

# Hua Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2219817/publications.pdf>

Version: 2024-02-01

14  
papers

2,054  
citations

840776

11  
h-index

996975

15  
g-index

15  
all docs

15  
docs citations

15  
times ranked

1849  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Transcriptome Analysis Reveals Genes Respond to Chlorophyll Deficiency in Green and Yellow Leaves of <i>Chrysanthemum morifolium</i> Ramat. <i>Horticulturae</i> , 2022, 8, 14.  | 2.8  | 2         |
| 2  | Genome-wide characterization of the UDP-glycosyltransferase gene family in upland cotton. <i>Biotech</i> , 2019, 9, 453.   | 2.2  | 17        |
| 3  | Validation of reference genes for accurate normalization of gene expression with quantitative real-time PCR in <i>Haloxylon ammodendron</i> under different abiotic stresses. <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 455-463. | 3.1  | 14        |
| 4  | Genetics and evolution of <i>MIXTA</i> genes regulating cotton lint fiber development. <i>New Phytologist</i> , 2018, 217, 883-895.  | 7.3  | 112       |
| 5  | A cupin domain is involved in $\alpha$ -amylase inhibitory activity. <i>Plant Science</i> , 2018, 277, 285-295.  | 3.6  | 10        |
| 6  | Genome-Wide Identification of the MIKC-Type MADS-Box Gene Family in <i>Gossypium hirsutum</i> L. Unravels Their Roles in Flowering. <i>Frontiers in Plant Science</i> , 2017, 8, 384.  | 3.6  | 54        |
| 7  | Small interfering RNAs from bidirectional transcripts of <i>GhMML3_A12</i> regulate cotton fiber development. <i>New Phytologist</i> , 2016, 210, 1298-1310.   | 7.3  | 124       |
| 8  | Sequencing of allotetraploid cotton ( <i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.  | 17.5 | 1,560     |
| 9  | Genome-Wide Transcriptome Profiling Revealed Cotton Fuzz Fiber Development Having a Similar Molecular Model as <i>Arabidopsis Trichome</i> . <i>PLoS ONE</i> , 2014, 9, e97313.  | 2.5  | 54        |
| 10 | CarNAC2, a novel NAC transcription factor in chickpea ( <i>Cicer arietinum</i> L.), is associated with drought-response and various developmental processes in transgenic arabidopsis. <i>Journal of Plant Biology</i> , 2014, 57, 55-66.            | 2.1  | 24        |
| 11 | Genome-Wide Analysis of Small RNA and Novel MicroRNA Discovery during Fiber and Seed Initial Development in <i>Gossypium hirsutum</i> L. <i>PLoS ONE</i> , 2013, 8, e69743.  | 2.5  | 17        |
| 12 | Effect of high desert surface layer temperature stress on <i>Haloxylon ammodendron</i> (C.A. Mey.) Bunge. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2012, 207, 572-580.   | 1.2  | 12        |
| 13 | Molecular cloning and characterization of an F-box family gene CarF-box1 from chickpea ( <i>Cicer</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock  | 2.3  | 36        |
| 14 | Identification and characterization of a LEA family gene CarLEA4 from chickpea ( <i>Cicer arietinum</i> L.). <i>Molecular Biology Reports</i> , 2012, 39, 3565-3572.   | 2.3  | 17        |