## Wei Wang

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5126996/publications.pdf

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| 15<br>papers | 1,284<br>citations | 15<br>h-index | 996849<br>15<br>g-index |
|--------------|--------------------|---------------|-------------------------|
| 15           | 15                 | 15            | 1499                    |
| all docs     | docs citations     | times ranked  | citing authors          |

| #  | Article   | IF  | Citations |
|----|---|-----|-----------|
| 1  | Mechanisms and Functions of Long Non-Coding RNAs at Multiple Regulatory Levels. International Journal of Molecular Sciences, 2019, 20, 5573.  | 1.8 | 493       |
| 2  | Identification of Gossypium hirsutum long non-coding RNAs (IncRNAs) under salt stress. BMC Plant Biology, 2018, 18, 23.   | 1.6 | 142       |
| 3  | Genome-wide characterization and expression analyses of superoxide dismutase (SOD) genes in Gossypium hirsutum. BMC Genomics, 2017, 18, 376.  | 1.2 | 101       |
| 4  | Role of plant respiratory burst oxidase homologs in stress responses. Free Radical Research, 2018, 52, 826-839.   | 1.5 | 76        |
| 5  | The long non-coding RNA lncRNA973 is involved in cotton response to salt stress. BMC Plant Biology, 2019, 19, 459.  | 1.6 | 70        |
| 6  | The Catalase Gene Family in Cotton: Genome-Wide Characterization and Bioinformatics Analysis. Cells, 2019, 8, 86.   | 1.8 | 57        |
| 7  | Plant MicroRNAs in Cross-Kingdom Regulation of Gene Expression. International Journal of Molecular Sciences, 2018, 19, 2007.  | 1.8 | 53        |
| 8  | Data set for phylogenetic tree and RAMPAGE Ramachandran plot analysis of SODs in Gossypium raimondii and G. arboreum. Data in Brief, 2016, 9, 345-348.  | 0.5 | 49        |
| 9  | Identification of miRNAs and Their Targets in Cotton Inoculated with Verticillium dahliae by High-Throughput Sequencing and Degradome Analysis. International Journal of Molecular Sciences, 2015, 16, 14749-14768.                                     | 1.8 | 46        |
| 10 | Long noncoding <scp>RNA lncRNA354</scp> functions as a competing endogenous <scp>RNA</scp> of <scp>miR160b</scp> to regulate <scp><i>ARF</i></scp> genes in response to salt stress in upland cotton. Plant, Cell and Environment, 2021, 44, 3302-3321. | 2.8 | 46        |
| 11 | Genome-wide analysis of superoxide dismutase gene family in Gossypium raimondii and G. arboreum.<br>Plant Gene, 2016, 6, 18-29.   | 1.4 | 43        |
| 12 | MicroRNA414c affects salt tolerance of cotton by regulating reactive oxygen species metabolism under salinity stress. RNA Biology, 2019, 16, 362-375.   | 1.5 | 43        |
| 13 | Genome-Wide Analysis of the RNA Helicase Gene Family in Gossypium raimondii. International Journal of Molecular Sciences, 2014, 15, 4635-4656.  | 1.8 | 24        |
| 14 | Comprehensive analysis of the Gossypium hirsutum L. respiratory burst oxidase homolog (Ghrboh) gene family. BMC Genomics, 2020, 21, 91.   | 1.2 | 22        |
| 15 | Mitigation of salt stress response in upland cotton (Gossypium hirsutum) by exogenous melatonin.<br>Journal of Plant Research, 2021, 134, 857-871.  | 1.2 | 19        |