

# Fafu Shen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3436992/publications.pdf>

Version: 2024-02-01

22  
papers

1,673  
citations

430754

18  
h-index

642610

23  
g-index

23  
all docs

23  
docs citations

23  
times ranked

2007  
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 conserved microRNAs and their target genes in tomato ( <i>Lycopersicon esculentum</i> ). Gene, 2008, 414, 60-66.   | 1.0 | 154       |
| 3  | Identification of <i>Gossypium hirsutum</i> long non-coding RNAs (lncRNAs) under salt stress. BMC Plant Biology, 2018, 18, 23.   | 1.6 | 142       |
| 4  | Genome-Wide Profiling of miRNAs and Other Small Non-Coding RNAs in the <i>Verticillium dahliae</i> -Inoculated Cotton Roots. PLoS ONE, 2012, 7, e35765.  | 1.1 | 115       |
| 5  | Genome-wide characterization and expression analyses of superoxide dismutase (SOD) genes in <i>Gossypium hirsutum</i> . BMC Genomics, 2017, 18, 376.   | 1.2 | 101       |
| 6  | Difference in miRNA expression profiles between two cotton cultivars with distinct salt sensitivity. Molecular Biology Reports, 2012, 39, 4961-4970.   | 1.0 | 77        |
| 7  | Role of plant respiratory burst oxidase homologs in stress responses. Free Radical Research, 2018, 52, 826-839.  | 1.5 | 76        |
| 8  | The long non-coding RNA lncRNA973 is involved in cotton response to salt stress. BMC Plant Biology, 2019, 19, 459.   | 1.6 | 70        |
| 9  | The Catalase Gene Family in Cotton: Genome-Wide Characterization and Bioinformatics Analysis. Cells, 2019, 8, 86.  | 1.8 | 57        |
| 10 | Plant MicroRNAs in Cross-Kingdom Regulation of Gene Expression. International Journal of Molecular Sciences, 2018, 19, 2007.   | 1.8 | 53        |
| 11 | Data set for phylogenetic tree and RAMPAGE Ramachandran plot analysis of SODs in <i>Gossypium raimondii</i> and <i>G. arboreum</i> . Data in Brief, 2016, 9, 345-348.  | 0.5 | 49        |
| 12 | Identification of miRNAs and Their Targets in Cotton Inoculated with <i>Verticillium dahliae</i> by High-Throughput Sequencing and Degradome Analysis. International Journal of Molecular Sciences, 2015, 16, 14749-14768.   | 1.8 | 46        |
| 13 | Long noncoding <i>lncRNA354</i> functions as a competing endogenous <i>RNA</i> of <i>miR160b</i> to regulate <i>ARF</i> genes in response to salt stress in upland cotton. Plant, Cell and Environment, 2021, 44, 3302-3321. | 2.8 | 46        |
| 14 | Genome-wide analysis of superoxide dismutase gene family in <i>Gossypium raimondii</i> and <i>G. arboreum</i> . Plant Gene, 2016, 6, 18-29.  | 1.4 | 43        |
| 15 | MicroRNA414c affects salt tolerance of cotton by regulating reactive oxygen species metabolism under salinity stress. RNA Biology, 2019, 16, 362-375.  | 1.5 | 43        |
| 16 | Genome-Wide Analysis of the RNA Helicase Gene Family in <i>Gossypium raimondii</i> . International Journal of Molecular Sciences, 2014, 15, 4635-4656.   | 1.8 | 24        |
| 17 | Overexpression of an <i>Apocynum venetum</i> DEAD-Box Helicase Gene ( <i>AvDH1</i> ) in Cotton Confers Salinity Tolerance and Increases Yield in a Saline Field. Frontiers in Plant Science, 2015, 6, 1227.                  | 1.7 | 22        |
| 18 | Comprehensive analysis of the <i>Gossypium hirsutum</i> L. respiratory burst oxidase homolog ( <i>Chrbh</i> ) gene family. BMC Genomics, 2020, 21, 91.   | 1.2 | 22        |

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|----|--|-----|-----------|
| 19 | Mitigation of salt stress response in upland cotton ( <i>Gossypium hirsutum</i> ) by exogenous melatonin. <i>Journal of Plant Research</i> , 2021, 134, 857-871.                           | 1.2 | 19        |
| 20 | Transcriptome Analysis of Early Anther Development of Cotton Revealed Male Sterility Genes for Major Metabolic Pathways. <i>Journal of Plant Growth Regulation</i> , 2015, 34, 223-232.    | 2.8 | 14        |
| 21 | Identification of genes associated with cotyledon senescence in upland cotton. <i>Science Bulletin</i> , 2006, 51, 1085-1094.  | 1.7 | 4         |
| 22 | Differential Expression of MicroRNAs Between 21A Genetic Male Sterile Line and Its Maintainer Line in Cotton ( <i>Gossypium hirsutum</i> L.). <i>Journal of Plant Studies</i> , 2013, 3, . | 0.3 | 1         |