

# Ghulam Qanmber

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6902507/publications.pdf>

Version: 2024-02-01

29  
papers

832  
citations

471509

17  
h-index

526287

27  
g-index

34  
all docs

34  
docs citations

34  
times ranked

508  
citing authors

#	ARTICLE	IF	CITATIONS
1	Updated role of ABA in seed maturation, dormancy, and germination. <i>Journal of Advanced Research</i> , 2022, 35, 199-214.	9.5	104
2	Gossypium Genomics: Trends, Scope, and Utilization for Cotton Improvement. <i>Trends in Plant Science</i> , 2020, 25, 488-500.	8.8	87
3	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
4	Genome-wide identification and expression analysis of <i>Gossypium</i> RING-H2 finger E3 ligase genes revealed their roles in fiber development, and phytohormone and abiotic stress responses. <i>Journal of Cotton Research</i> , 2018, 1, .	2.5	50
5	Genome-wide analysis of cotton GH3 subfamily II reveals functional divergence in fiber development, hormone response and plant architecture. <i>BMC Plant Biology</i> , 2018, 18, 350.	3.6	48
6	The abiotic stress-responsive NAC transcription factor SINAC11 is involved in drought and salt response in tomato ( <i>Solanum lycopersicum</i> L.). <i>Plant Cell, Tissue and Organ Culture</i> , 2017, 129, 161-174.	2.3	43
7	Genome-wide analysis of BES1 genes in <i>Gossypium</i> revealed their evolutionary conserved roles in brassinosteroid signaling. <i>Science China Life Sciences</i> , 2018, 61, 1566-1582.	4.9	43
8	Genome-wide identification of GhAAI genes reveals that GhAAI66 triggers a phase transition to induce early flowering. <i>Journal of Experimental Botany</i> , 2019, 70, 4721-4736.	4.8	43
9	Genome-Wide Identification and Characterization of the PERK Gene Family in <i>Gossypium hirsutum</i> Reveals Gene Duplication and Functional Divergence. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1750.	4.1	41
10	Genome-wide characterization and phylogenetic analysis of GSK gene family in three species of cotton: evidence for a role of some GSKs in fiber development and responses to stress. <i>BMC Plant Biology</i> , 2018, 18, 330.	3.6	34
11	Identification of Histone H3 (HH3) Genes in <i>Gossypium hirsutum</i> Revealed Diverse Expression During Ovule Development and Stress Responses. <i>Genes</i> , 2019, 10, 355.	2.4	29
12	GhKLCR1, a kinesin light chain-related gene, induces drought-stress sensitivity in <i>Arabidopsis</i> . <i>Science China Life Sciences</i> , 2019, 62, 63-75.	4.9	26
13	Genome-wide characterization and expression analysis of geranylgeranyl diphosphate synthase genes in cotton ( <i>Gossypium</i> spp.) in plant development and abiotic stresses. <i>BMC Genomics</i> , 2020, 21, 561.	2.8	24
14	The bHLH transcription factor GhPAS1 mediates BR signaling to regulate plant development and architecture in cotton. <i>Crop Journal</i> , 2021, 9, 1049-1059.	5.2	23
15	Hypocotyl Elongation Inhibition of Melatonin Is Involved in Repressing Brassinosteroid Biosynthesis in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1082.	3.6	22
16	Response of phytohormone mediated plant homeodomain (PHD) family to abiotic stress in upland cotton ( <i>Gossypium hirsutum</i> spp.). <i>BMC Plant Biology</i> , 2021, 21, 13.	3.6	22
17	Photomorphogenesis in plants: The central role of phytochrome interacting factors (PIFs). <i>Environmental and Experimental Botany</i> , 2022, 194, 104704.	4.2	22
18	Genome-Wide Study of the GATL Gene Family in <i>Gossypium hirsutum</i> L. Reveals that GhGATL Genes Act on Pectin Synthesis to Regulate Plant Growth and Fiber Elongation. <i>Genes</i> , 2020, 11, 64.	2.4	19

#	ARTICLE	IF	CITATIONS
19	Identification of GhLOG gene family revealed that GhLOG3 is involved in regulating salinity tolerance in cotton ( <i>Gossypium hirsutum</i> L.). <i>Plant Physiology and Biochemistry</i> , 2021, 166, 328-340.	5.8	17
20	Genome-wide identification of <i>Gossypium</i> INDETERMINATE DOMAIN genes and their expression profiles in ovule development and abiotic stress responses. <i>Journal of Cotton Research</i> , 2019, 2, .	2.5	15
21	Characterization of Vascular plant One-Zinc finger (VOZ) in soybean ( <i>Glycine max</i> and <i>Glycine soja</i> ) and their expression analyses under drought condition. <i>PLoS ONE</i> , 2021, 16, e0253836.	2.5	12
22	Identification and Characterization of the ERF Subfamily B3 Group Revealed GhERF13.12 Improves Salt Tolerance in Upland Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 705883.	3.6	12
23	Systematic Characterization of TCP Gene Family in Four Cotton Species Revealed That GhTCP62 Regulates Branching in Arabidopsis. <i>Biology</i> , 2021, 10, 1104.	2.8	11
24	Identification, evolutionary analysis and functional diversification of RAV gene family in cotton ( <i>G.</i> ) <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	3.2	10
25	Identification of BR biosynthesis genes in cotton reveals that GhCPD-3 restores BR biosynthesis and mediates plant growth and development. <i>Planta</i> , 2021, 254, 75.	3.2	8
26	Genome-wide analysis of ZAT gene family revealed GhZAT6 regulates salt stress tolerance in <i>G. hirsutum</i> . <i>Plant Science</i> , 2021, 312, 111055.	3.6	5
27	Identification and Analysis of GhEXO Gene Family Indicated That GhEXO7_At Promotes Plant Growth and Development Through Brassinosteroid Signaling in Cotton ( <i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 719889.	3.6	4
28	RAD gene family analysis in cotton provides some key genes for flowering and stress tolerance in upland cotton <i>G. hirsutum</i> . <i>BMC Genomics</i> , 2022, 23, 40.	2.8	4
29	THE FULL-LENGTH TRANSCRIPTOME BY THE SINGLEMOLECULE LONG-READ SEQUENCING REVEALS A HEATRESISTANT MECHANISM IN CAPER BUSH ( <i>CAPPARIS SPINOSA</i> L.). <i>Applied Ecology and Environmental Research</i> , 2022, 20, 601-617.	0.5	0