

Richard O Magwanga

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

1,169
citations

430754

18
h-index

414303

32
g-index

57
all docs

57
docs citations

57
times ranked

1080
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of the late embryogenesis abundant (LEA) proteins family and their role in drought stress tolerance in upland cotton. <i>BMC Genetics</i> , 2018, 19, 6.	2.7	216
2	Overexpression of Cotton a DTX/MATE Gene Enhances Drought, Salt, and Cold Stress Tolerance in Transgenic Arabidopsis. <i>Frontiers in Plant Science</i> , 2019, 10, 299.	1.7	68
3	Genome wide identification of the trihelix transcription factors and overexpression of Gh_A05G2067 (GhATE2), a novel gene contributing to increased drought and salt stresses tolerance in cotton. <i>Physiologia Plantarum</i> , 2019, 167, 447-464.	2.6	57
4	Genome-Wide Analysis of Multidrug and Toxic Compound Extrusion (MATE) Family in <i>Gossypium raimondii</i> and <i>Gossypium arboreum</i> and Its Expression Analysis Under Salt, Cadmium, and Drought Stress. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2483-2500.	0.8	56
5	Knockdown of Cytochrome P450 Genes Gh_D07G1197 and Gh_A13G2057 on Chromosomes D07 and A13 Reveals Their Putative Role in Enhancing Drought and Salt Stress Tolerance in <i>Gossypium hirsutum</i> . <i>Genes</i> , 2019, 10, 226.	1.0	52
6	Whole Genome Analysis of Cyclin Dependent Kinase (CDK) Gene Family in Cotton and Functional Evaluation of the Role of CDK4 Gene in Drought and Salt Stress Tolerance in Plants. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2625.	1.8	51
7	Cotton Late Embryogenesis Abundant (LEA2) Genes Promote Root Growth and Confer Drought Stress Tolerance in Transgenic <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2781-2803.	0.8	51
8	A Novel G-Protein-Coupled Receptors Gene from Upland Cotton Enhances Salt Stress Tolerance in Transgenic Arabidopsis. <i>Genes</i> , 2018, 9, 209.	1.0	50
9	High-Density Linkage Map Construction and Mapping of Salt-Tolerant QTLs at Seedling Stage in Upland Cotton Using Genotyping by Sequencing (GBS). <i>International Journal of Molecular Sciences</i> , 2017, 18, 2622.	1.8	42
10	GBS Mapping and Analysis of Genes Conserved between <i>Gossypium tomentosum</i> and <i>Gossypium hirsutum</i> Cotton Cultivars that Respond to Drought Stress at the Seedling Stage of the BC2F2 Generation. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1614.	1.8	39
11	Functional characterization of Gh_A08G1120 (GH3.5) gene reveal their significant role in enhancing drought and salt stress tolerance in cotton. <i>BMC Genetics</i> , 2019, 20, 62.	2.7	39
12	QTL Mapping of Fiber Quality and Yield-Related Traits in an Intra-Specific Upland Cotton Using Genotype by Sequencing (GBS). <i>International Journal of Molecular Sciences</i> , 2018, 19, 441.	1.8	37
13	Genetic regulatory networks for salt-alkali stress in <i>Gossypium hirsutum</i> with differing morphological characteristics. <i>BMC Genomics</i> , 2020, 21, 15.	1.2	33
14	Simple Sequence Repeat (SSR) Genetic Linkage Map of D Genome Diploid Cotton Derived from an Interspecific Cross between <i>Gossypium davidsonii</i> and <i>Gossypium klotzschianum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 204.	1.8	31
15	RNA-Sequencing, Physiological and RNAi Analyses Provide Insights into the Response Mechanism of the ABC-Mediated Resistance to <i>Verticillium dahliae</i> Infection in Cotton. <i>Genes</i> , 2019, 10, 110.	1.0	31
16	Deep Transcriptome Analysis Reveals Reactive Oxygen Species (ROS) Network Evolution, Response to Abiotic Stress, and Regulation of Fiber Development in Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1863.	1.8	29
17	Comparative transcriptome, physiological and biochemical analyses reveal response mechanism mediated by CBF4 and ICE2 in enhancing cold stress tolerance in <i>Gossypium thurberi</i> . <i>AoB PLANTS</i> , 2019, 11, plz045.	1.2	27
18	Genome-wide analysis of the cotton G-coupled receptor proteins (GPCR) and functional analysis of GTOM1, a novel cotton GPCR gene under drought and cold stress. <i>BMC Genomics</i> , 2019, 20, 651.	1.2	21

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19	Genome-wide identification of OSCA gene family and their potential function in the regulation of dehydration and salt stress in <i>Gossypium hirsutum</i> . <i>Journal of Cotton Research</i> , 2019, 2, .	1.0	21
20	Late embryogenesis abundant gene LEA3 (Gh_A08G0694) enhances drought and salt stress tolerance in cotton. <i>International Journal of Biological Macromolecules</i> , 2022, 207, 700-714.	3.6	20
21	Knockdown of Gh_A05G1554 (GhDHN_03) and Gh_D05G1729 (GhDHN_04) Dehydrin genes, Reveals their potential role in enhancing osmotic and salt tolerance in cotton. <i>Genomics</i> , 2020, 112, 1902-1915.	1.3	19
22	Long non-coding RNAs and their potential functions in Ligon-lintless-1 mutant cotton during fiber development. <i>BMC Genomics</i> , 2019, 20, 661.	1.2	18
23	Knockdown of GhIQD31 and GhIQD32 increases drought and salt stress sensitivity in <i>Gossypium hirsutum</i> . <i>Plant Physiology and Biochemistry</i> , 2019, 144, 166-177.	2.8	16
24	Identification of QTLs and candidate genes for physiological traits associated with drought tolerance in cotton. <i>Journal of Cotton Research</i> , 2020, 3, .	1.0	16
25	Comparisons of photosynthetic and anatomical traits between wild and domesticated cotton. <i>Journal of Experimental Botany</i> , 2022, 73, 873-885.	2.4	15
26	Functional Characterization of GhACX3 Gene Reveals Its Significant Role in Enhancing Drought and Salt Stress Tolerance in Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 658755.	1.7	15
27	Identification and functional characterization of Gh_D01G0514 (GhNAC072) transcription factor in response to drought stress tolerance in cotton. <i>Plant Physiology and Biochemistry</i> , 2021, 166, 361-375.	2.8	15
28	Knockdown of 60S ribosomal protein L14-2 reveals their potential regulatory roles to enhance drought and salt tolerance in cotton. <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	13
29	Map-Based Functional Analysis of the GhNLP Genes Reveals Their Roles in Enhancing Tolerance to N-Deficiency in Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4953.	1.8	11
30	Transcriptomic and proteomic analyses of a new cytoplasmic male sterile line with a wild <i>Gossypium bickii</i> genetic background. <i>BMC Genomics</i> , 2020, 21, 859.	1.2	11
31	Functional Characterization of Cotton C-Repeat Binding Factor Genes Reveal Their Potential Role in Cold Stress Tolerance. <i>Frontiers in Plant Science</i> , 2021, 12, 766130.	1.7	10
32	Genome wide identification and characterization of light-harvesting Chloro a/b binding (LHC) genes reveals their potential role in enhancing drought tolerance in <i>Gossypium hirsutum</i> . <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	8
33	A Comparison of Nitrogen Transfer and Transformation in Traditional Farming and the Riceâ€™Duck Farming System by ¹⁵ N Tracer Method. <i>Agronomy</i> , 2018, 8, 289.	1.3	7
34	SSR-Linkage map of interspecific populations derived from <i>Gossypium trilobum</i> and <i>Gossypium thurberi</i> and determination of genes harbored within the segregating distortion regions. <i>PLoS ONE</i> , 2018, 13, e0207271.	1.1	6
35	Knockdown of ghAlba_4 and ghAlba_5 Proteins in Cotton Inhibits Root Growth and Increases Sensitivity to Drought and Salt Stresses. <i>Frontiers in Plant Science</i> , 2019, 10, 1292.	1.7	6
36	Comparative transcriptome analysis reveals evolutionary divergence and shared network of cold and salt stress response in diploid D-genome cotton. <i>BMC Plant Biology</i> , 2020, 20, 518.	1.6	6

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37	Identification of a genome-specific repetitive element in the <i>Gossypium</i> D genome. PeerJ, 2020, 8, e8344.	0.9	2
38	Genetic map construction and functional characterization of genes within the segregation distortion regions (SDRs) in the F2:3 populations derived from wild cotton species of the D genome. Journal of Cotton Research, 2020, 3, .	1.0	0
39	Physiological and Developmental Response of Selected Upland Rice Genotypes to Water and Nutrient Stress Condition. , 0, , 22-39.		0