Mahmoud Wf Yaish

List of Publications by Year
in descending order

56 papers	3,564 citations	159585 30 h-index	168389 53 g-index
56 all docs	56 docs citations	56 times ranked	4578 citing authors

#	Article	IF	Citations
1	Salt tolerance in plants: Using OMICS to assess the impact of plant growth-promoting bacteria (PGPB). , 2022, , 299-320.		3
2	Functional characterization and expression profiling of glyoxalase <scp>III</scp> genes in date palm grown under abiotic stresses. Physiologia Plantarum, 2021, 172, 780-794.	5.2	9
3	Genome analysis of a salinity adapted Achromobacter xylosoxidans rhizobacteria from the date palm. Rhizosphere, 2021, 19, 100401.	3.0	9
4	Isolation and functional characterization of a mVOC producing plant-growth-promoting bacterium isolated from the date palm rhizosphere. Rhizosphere, 2020, 16, 100267.	3.0	9
5	Functional characterization of the Glyoxalase-I (PdGLX1) gene family in date palm under abiotic stresses. Plant Signaling and Behavior, 2020, 15, 1811527.	2.4	10
6	Comparative Metabolic Profiling of Two Contrasting Date Palm Genotypes Under Salinity. Plant Molecular Biology Reporter, 2020, 39, 351.	1.8	9
7	A novel tonoplast Na+/H+ antiporter gene from date palm (PdNHX6) confers enhanced salt tolerance response in Arabidopsis. Plant Cell Reports, 2020, 39, 1079-1093.	5.6	33
8	Genome-wide identification and functional characterization of glutathione peroxidase genes in date palm (Phoenix dactylifera L.) under stress conditions. Plant Gene, 2020, 23, 100237.	2.3	9
9	Molecular Characterization of a Date Palm Vascular Highway 1-Interacting Kinase (PdVIK) under Abiotic Stresses. Genes, 2020, 11, 568.	2.4	6
10	Overexpression of a Metallothionein 2A Gene from Date Palm Confers Abiotic Stress Tolerance to Yeast and Arabidopsis thaliana. International Journal of Molecular Sciences, 2019, 20, 2871.	4.1	51
11	Metabolomic analysis of date palm seedlings exposed to salinity and silicon treatments. Plant Signaling and Behavior, 2019, 14, 1663112.	2.4	31
12	Antioxidant Response to Salinity in Salt-Tolerant and Salt-Susceptible Cultivars of Date Palm. Agriculture (Switzerland), 2019, 9, 8.	3.1	64
13	Functional Characterization of Date Palm Aquaporin Gene PdPIP1;2 Confers Drought and Salinity Tolerance to Yeast and Arabidopsis. Genes, 2019, 10, 390.	2.4	29
14	Comparative Water Relations of Two Contrasting Date Palm Genotypes under Salinity. International Journal of Agronomy, 2019, 2019, 1-16.	1.2	16
15	Identification of Candidate Genes Involved in the Salt Tolerance of Date Palm (<i>Phoenix) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.9	15
16	Neuropilin-1 promotes the oncogenic Tenascin-C/integrin Î²3 pathway and modulates chemoresistance in breast cancer cells. BMC Cancer, 2018, 18, 533.	2.6	42
17	Comparative transcriptome and translatome analysis in contrasting rice genotypes reveals differential mRNA translation in salt-tolerant Pokkali under salt stress. BMC Genomics, 2018, 19, 935.	2.8	66
18	Genome-wide DNA Methylation analysis in response to salinity in the model plant caliph medic (Medicago truncatula). BMC Genomics, 2018, 19, 78.	2.8	75

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19	Differential DNA methylation and transcription profiles in date palm roots exposed to salinity. PLoS ONE, 2018, 13, e0191492.	2.5	45
20	Genome-wide expression profiling in leaves and roots of date palm (Phoenix dactylifera L.) exposed to salinity. BMC Genomics, 2017, 18, 246.	2.8	80
21	Draft Genome Sequence of the Endophytic Bacillus aryabhattai Strain SQU-R12, Identified from Phoenix dactylifera L. Roots. Genome Announcements, 2017, 5, .	0.8	16
22	Detection of Differential DNA Methylation Under Stress Conditions Using Bisulfite Sequence Analysis. Methods in Molecular Biology, 2017, 1631, 121-137.	0.9	10
23	Genome Sequencing of Microbacterium sp. Yaish 1, a Bacterial Strain Isolated from the Rhizosphere of Date Palm Trees Affected by Salinity. Genome Announcements, 2017, 5, .	0.8	13
24	The Role of Na+ and K+ Transporters in Salt Stress Adaptation in Glycophytes. Frontiers in Physiology, 2017, 8, 509.	2.8	576
25	Editorial: Epigenetic Modifications Associated with Abiotic and Biotic Stresses in Plants: An Implication for Understanding Plant Evolution. Frontiers in Plant Science, 2017, 8, 1983.	3.6	33
26	Screening of Date Palm (Phoenix dactylifera L.) Cultivars for Salinity Tolerance. Forests, 2017, 8, 136.	2.1	42
27	Salt stress alters DNA methylation levels in alfalfa (Medicago spp). Genetics and Molecular Research, 2016, 15, 15018299.	0.2	45
28	Identification of Reference Genes for Quantitative Real-Time PCR in Date Palm (Phoenix dactylifera L.) Subjected to Drought and Salinity. PLoS ONE, 2016, 11, e0166216.	2.5	24
29	Draft Genome Sequence of Endophytic Bacterium Enterobacter asburiae PDA134, Isolated from Date Palm (Phoenix dactylifera L.) Roots. Genome Announcements, 2016, 4, .	0.8	22
30	Impact of Soil Salinity on the Structure of the Bacterial Endophytic Community Identified from the Roots of Caliph Medic (Medicago truncatula). PLoS ONE, 2016, 11, e0159007.	2.5	102
31	Diversity of Tetracycline Resistant Genes in Escherichia coli from Human and Environmental Sources. Open Biotechnology Journal, 2016, 10, 289-300.	1.2	11
32	The use of high throughput DNA sequence analysis to assess the endophytic microbiome of date palm roots grown under different levels of salt stress. International Microbiology, 2016, 19, 143-155.	2.4	41
33	Short Communication Proline accumulation is a general response to abiotic stress in the date palm tree (Phoenix dactylifera L.). Genetics and Molecular Research, 2015, 14, 9943-9950.	0.2	76
34	Salt tolerance research in date palm tree (Phoenix dactylifera L.), past, present, and future perspectives. Frontiers in Plant Science, 2015, 6, 348.	3.6	103
35	Overexpression of the CC-type glutaredoxin, OsGRX6 affects hormone and nitrogen status in rice plants. Frontiers in Plant Science, 2015, 6, 934.	3.6	44
36	A genome-wide identification of the miRNAome in response to salinity stress in date palm (Phoenix) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.6	54

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37	Isolation and characterization of endophytic plant growth-promoting bacteria from date palm tree (Phoenix dactylifera L.) and their potential role in salinity tolerance. Antonie Van Leeuwenhoek, 2015, 107, 1519-1532.	1.7	161
38	Freezing tolerance in Norway spruce, the potential role of pathogenesis-related proteins. Acta Physiologiae Plantarum, 2015, 37, 1.	2.1	3
39	Global DNA Methylation Analysis Using Methyl-Sensitive Amplification Polymorphism (MSAP). Methods in Molecular Biology, 2014, 1062, 285-298.	0.9	37
40	Functional Characterization of the Rice UDP-glucose 4-epimerase 1, OsUGE1: A Potential Role in Cell Wall Carbohydrate Partitioning during Limiting Nitrogen Conditions. PLoS ONE, 2014, 9, e96158.	2.5	33
41	DNA Methylation-Associated Epigenetic Changes in Stress Tolerance of Plants. , 2013, , 427-440.		17
42	The role of epigenetic processes in controlling flowering time in plants exposed to stress. Journal of Experimental Botany, 2011, 62, 3727-3735.	4.8	172
43	GNC and CGA1 Modulate Chlorophyll Biosynthesis and Glutamate Synthase (GLU1/Fd-GOGAT) Expression in Arabidopsis. PLoS ONE, 2011, 6, e26765.	2.5	121
44	Zinc induces disorder-to-order transitions in free and membrane-associated Thellungiella salsuginea dehydrins TsDHN-1 and TsDHN-2: a solution CD and solid-state ATR-FTIR study. Amino Acids, 2011, 40, 1485-1502.	2.7	21
45	The APETALA-2-Like Transcription Factor OsAP2-39 Controls Key Interactions between Abscisic Acid and Gibberellin in Rice. PLoS Genetics, 2010, 6, e1001098.	3.5	161
46	Axillary Shoot Branching in Plants. , 2010, , 37-52.		7
47	Interactions of intrinsically disordered Thellungiella salsuginea dehydrins TsDHN-1 and TsDHN-2 with membranesÂâ€" synergistic effects of lipid composition and temperature on secondary structure. Biochemistry and Cell Biology, 2010, 88, 791-807.	2.0	58
48	AtMBD9 modulates Arabidopsis development through the dual epigenetic pathways of DNA methylation and histone acetylation. Plant Journal, 2009, 59, 123-135.	5.7	55
49	Functional Divergence in the Arabidopsis Â-1,3-Glucanase Gene Family Inferred by Phylogenetic Reconstruction of Expression States. Molecular Biology and Evolution, 2007, 24, 1045-1055.	8.9	148
50	Ordered surface carbons distinguish antifreeze proteins and their ice-binding regions. Nature Biotechnology, 2006, 24, 852-855.	17.5	68
51	Genetic mapping of quantitative resistance to race 5 of Pseudomonas syringae pv. phaseolicola in common bean. Euphytica, 2006, 152, 397-404.	1.2	8
52	Cold-Active Winter Rye Glucanases with Ice-Binding Capacity. Plant Physiology, 2006, 141, 1459-1472.	4.8	62
53	Cloning and Expression of afpA, a Gene Encoding an Antifreeze Protein from the Arctic Plant Growth-Promoting Rhizobacterium Pseudomonas putida GR12-2. Journal of Bacteriology, 2004, 186, 5661-5671.	2.2	82
54	Isolation of a family of resistance gene analogue sequences of the nucleotide binding site (NBS) type fromLensspecies. Genome, 2004, 47, 650-659.	2.0	46

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55	Antifreeze proteins in overwintering plants: a tale of two activities. Trends in Plant Science, 2004, 9, 399-405.	8.8	454
56	Isolation of (GA)n microsatellite sequences and description of a predicted MADS-box sequence isolated from common bean (Phaseolus vulgaris L.). Genetics and Molecular Biology, 2003, 26, 337-342.	1.3	27