M Shahid Mukhtar

List of Publications by Year
in descending order

55 papers	6,054 citations	186265 28 h-index	155660 55 g-index
68 all docs	68 docs citations	68 times ranked	7862 citing authors

#	Article	IF	Citations
1	Evidence for Network Evolution in an Arabidopsis Interactome Map. Science, 2011, 333, 601-607.	12.6	838
2	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. Science, 2011, 333, 596-601.	12.6	776
3	The Top 10 oomycete pathogens in molecular plant pathology. Molecular Plant Pathology, 2015, 16, 413-434.	4.2	695
4	Dynamic Evolution of Pathogenicity Revealed by Sequencing and Comparative Genomics of 19 Pseudomonas syringae Isolates. PLoS Pathogens, 2011, 7, e1002132.	4.7	413
5	Convergent Targeting of a Common Host Protein-Network by Pathogen Effectors from Three Kingdoms of Life. Cell Host and Microbe, 2014, 16, 364-375.	11.0	367
6	The Roles of Aquaporins in Plant Stress Responses. Journal of Developmental Biology, 2016, 4, 9.	1.7	249
7	The WRKY70 transcription factor of Arabidopsis influences both the plant senescence and defense signaling pathways. Planta, 2007, 226, 125-137.	3.2	243
8	An extracellular network of Arabidopsis leucine-rich repeat receptor kinases. Nature, 2018, 553, 342-346.	27.8	241
9	Genome Editing: Targeting Susceptibility Genes for Plant Disease Resistance. Trends in Biotechnology, 2018, 36, 898-906.	9.3	215
10	IRE1/bZIP60-Mediated Unfolded Protein Response Plays Distinct Roles in Plant Immunity and Abiotic Stress Responses. PLoS ONE, 2012, 7, e31944.	2.5	200
11	Arabidopsis Gâ€protein interactome reveals connections to cell wall carbohydrates and morphogenesis. Molecular Systems Biology, 2011, 7, 532.	7.2	191
12	Tell me more: roles of NPRs in plant immunity. Trends in Plant Science, 2013, 18, 402-411.	8.8	169
13	The Arabidopsis transcription factor WRKY27 influences wilt disease symptom development caused by Ralstonia solanacearum. Plant Journal, 2008, 56, 935-947.	5.7	101
14	Network biology discovers pathogen contact points in host protein-protein interactomes. Nature Communications, 2018, 9, 2312.	12.8	101
15	TCP three-way handshake: linking developmental processes with plant immunity. Trends in Plant Science, 2015, 20, 238-245.	8.8	90
16	Cytokinin Response Factor 6 Represses Cytokinin-Associated Genes during Oxidative Stress. Plant Physiology, 2016, 172, pp.00415.2016.	4.8	85
17	The Molecular Basis of Host Specialization in Bean Pathovars of Pseudomonas syringae. Molecular Plant-Microbe Interactions, 2012, 25, 877-888.	2.6	83
18	Pathogen Tactics to Manipulate Plant Cell Death. Current Biology, 2016, 26, R608-R619.	3.9	81

#	Article	IF	Citations
19	Systems Biology and Machine Learning in Plantâ€“Pathogen Interactions. Molecular Plant-Microbe Interactions, 2019, 32, 45-55.	2.6	68
20	NPR1 in Plant Defense: It's Not over 'til It's Turned over. Cell, 2009, 137, 804-806.	28.9	66
21	Pseudomonas syringae type III effector HopAF1 suppresses plant immunity by targeting methionine recycling to block ethylene induction. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3577-86.	7.1	66
22	Transcriptomics reveals multiple resistance mechanisms against cotton leaf curl disease in a naturally immune cotton species, Gossypium arboreum. Scientific Reports, 2017, 7, 15880.	3.3	61
23	Integrative Network Biology Framework Elucidates Molecular Mechanisms of SARS-CoV-2 Pathogenesis. IScience, 2020, 23, 101526.	4.1	52
24	Natural variation of potato allene oxide synthase 2 causes differential levels of jasmonates and pathogen resistance in Arabidopsis. Planta, 2008, 228, 293-306.	3.2	48
25	Molecular insight into cotton leaf curl geminivirus disease resistance in cultivated cotton (Gossypium hirsutum). Plant Biotechnology Journal, 2020, 18, 691-706.	8.3	44
26	EffectorK, a comprehensive resource to mine for Ralstonia, Xanthomonas, and other published effector interactors in the Arabidopsis proteome. Molecular Plant Pathology, 2020, 21, 1257-1270.	4.2	38
27	Expression-based network biology identifies immune-related functional modules involved in plant defense. BMC Genomics, 2014, 15, 421.	2.8	36
28	Making the right connections: Network biology and plant immune system dynamics. Current Plant Biology, 2016, 5, 2-12.	4.7	34
29	Global temporal dynamic landscape of pathogen-mediated subversion of Arabidopsis innate immunity. Scientific Reports, 2017, 7, 7849.	3.3	32
30	Transcriptomic analysis of cultivated cotton Gossypium hirsutum provides insights into host responses upon whitefly-mediated transmission of cotton leaf curl disease. PLoS ONE, 2019, 14, e0210011.	2.5	28
31	Network biology to uncover functional and structural properties of the plant immune system. Current Opinion in Plant Biology, 2021, 62, 102057.	7.1	26
32	NPR1 in JazzSet with Pathogen Effectors. Trends in Plant Science, 2018, 23, 469-472.	8.8	25
33	Inference of Gene Regulatory Network from Single-Cell Transcriptomic Data Using pySCENIC. Methods in Molecular Biology, 2021, 2328, 171-182.	0.9	25
34	Epigenetic regulation in the pathogenesis of non-melanoma skin cancer. Seminars in Cancer Biology, 2022, 83, 36-56.	9.6	24
35	Elucidating the role of WRKY27 in male sterility in Arabidopsis. Plant Signaling and Behavior, 2018, 13, e1363945.	2.4	23
36	Mapping Protein-Protein Interaction Using High-Throughput Yeast 2-Hybrid. Methods in Molecular Biology, 2017, 1610, 217-230.	0.9	22

#	Article	IF	Citations
37	Dynamic modeling of transcriptional gene regulatory network uncovers distinct pathways during the onset of Arabidopsis leaf senescence. Npj Systems Biology and Applications, 2018, 4, 35.	3.0	22
38	Engineering NLR immune receptors for broad-spectrum disease resistance. Trends in Plant Science, 2013, 18, 469-472.	8.8	21
39	Direct Regulation of the EFR-Dependent Immune Response by Arabidopsis TCP Transcription Factors. Molecular Plant-Microbe Interactions, 2019, 32, 540-549.	2.6	19
40	Map of physical interactions between extracellular domains of Arabidopsis leucine-rich repeat receptor kinases. Scientific Data, 2019, 6, 190025.	5.3	17
41	Molecular pathology associated with altered synaptic transcriptome in the dorsolateral prefrontal cortex of depressed subjects. Translational Psychiatry, 2021, 11, 73.	4.8	16
42	Genome wide study of cysteine rich receptor like proteins in Gossypium sp.. Scientific Reports, 2022, 12, 4885.	3.3	12
43	A rice protein interaction network reveals high centrality nodes and candidate pathogen effector targets. Computational and Structural Biotechnology Journal, 2022, 20, 2001-2012.	4.1	12
44	High Fructose Corn Syrup-Moderate Fat Diet Potentiates Anxio-Depressive Behavior and Alters Ventral Striatal Neuronal Signaling. Frontiers in Neuroscience, 2021, 15, 669410.	2.8	11
45	Genome-wide identification and classification of resistance genes predicted several decoy domains in Gossypium sp.. Plant Gene, 2020, 24, 100250.	2.3	7
46	5â€²-Capâ€'Dependent Translation as a Potent Therapeutic Target for Lethal Human Squamous Cell Carcinoma. Journal of Investigative Dermatology, 2021, 141, 742-753.e10.	0.7	7
47	Transcriptional circuitry atlas of genetic diverse unstimulated murine and human macrophages define disparity in population-wide innate immunity. Scientific Reports, 2021, 11, 7373.	3.3	7
48	Combined inhibition of BET bromodomain and mTORC1/2 provides therapeutic advantage for rhabdomyosarcoma by switching cell death mechanism. Molecular Carcinogenesis, 2022, 61, 737-751.	2.7	6
49	Dynamic Regulation of the Nexus Between Stress Granules, Roquin, and Regnase-1 Underlies the Molecular Pathogenesis of Warfare Vesicants. Frontiers in Immunology, 2021, 12, 809365.	4.8	5
50	Advances in molecular pathogenesis of hidradenitis suppurativa: Dysregulated keratins and ECM signaling. Seminars in Cell and Developmental Biology, 2022, 128, 120-129.	5.0	5
51	Integrative Network Biology Framework Elucidates Molecular Mechanisms of SARS-CoV-2 Pathogenesis. SSRN Electronic Journal, 2020, , 3581857.	0.4	4
52	A TIReless battle: TIR domains in plantâ€“pathogen interactions. Trends in Plant Science, 2022, 27, 426-429.	8.8	4
53	Heterotrimeric Gâ€“proteins in Picea abies and their regulation in response to Heterobasidion annosum s.l. infection. BMC Plant Biology, 2015, 15, 287.	3.6	2
54	Ex Vivo Culture Models of Hidradenitis Suppurativa for Defining Molecular Pathogenesis and Treatment Efficacy of Novel Drugs. Inflammation, 2022, 45, 1388-1401.	3.8	2

#	Article	IF	Citations
55	Cover Image, Volume 61, Issue 8. Molecular Carcinogenesis, 2022, 61, .	2.7	0