

M Shahid Mukhtar

List of Publications by Year in descending order

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Version: 2024-02-01

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	Epigenetic regulation in the pathogenesis of non-melanoma skin cancer. <i>Seminars in Cancer Biology</i> , 2022, 83, 36-56.	9.6	24
2	Advances in molecular pathogenesis of hidradenitis suppurativa: Dysregulated keratins and ECM signaling. <i>Seminars in Cell and Developmental Biology</i> , 2022, 128, 120-129.	5.0	5
3	A TIReless battle: TIR domains in plantâ€“pathogen interactions. <i>Trends in Plant Science</i> , 2022, 27, 426-429.	8.8	4
4	Ex Vivo Culture Models of Hidradenitis Suppurativa for Defining Molecular Pathogenesis and Treatment Efficacy of Novel Drugs. <i>Inflammation</i> , 2022, 45, 1388-1401.	3.8	2
5	Genome wide study of cysteine rich receptor like proteins in <i>Gossypium sp.</i> . <i>Scientific Reports</i> , 2022, 12, 4885.	3.3	12
6	A rice protein interaction network reveals high centrality nodes and candidate pathogen effector targets. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2001-2012.	4.1	12
7	Combined inhibition of BET bromodomain and mTORC1/2 provides therapeutic advantage for rhabdomyosarcoma by switching cell death mechanism. <i>Molecular Carcinogenesis</i> , 2022, 61, 737-751.	2.7	6
8	Cover Image, Volume 61, Issue 8. <i>Molecular Carcinogenesis</i> , 2022, 61, .	2.7	0
9	5â€“Capâ€“Dependent Translation as a Potent Therapeutic Target for Lethal Human Squamous Cell Carcinoma. <i>Journal of Investigative Dermatology</i> , 2021, 141, 742-753.e10.	0.7	7
10	Molecular pathology associated with altered synaptic transcriptome in the dorsolateral prefrontal cortex of depressed subjects. <i>Translational Psychiatry</i> , 2021, 11, 73.	4.8	16
11	Inference of Gene Regulatory Network from Single-Cell Transcriptomic Data Using pySCENIC. <i>Methods in Molecular Biology</i> , 2021, 2328, 171-182.	0.9	25
12	Transcriptional circuitry atlas of genetic diverse unstimulated murine and human macrophages define disparity in population-wide innate immunity. <i>Scientific Reports</i> , 2021, 11, 7373.	3.3	7
13	High Fructose Corn Syrup-Moderate Fat Diet Potentiates Anxio-Depressive Behavior and Alters Ventral Striatal Neuronal Signaling. <i>Frontiers in Neuroscience</i> , 2021, 15, 669410.	2.8	11
14	Network biology to uncover functional and structural properties of the plant immune system. <i>Current Opinion in Plant Biology</i> , 2021, 62, 102057.	7.1	26
15	Dynamic Regulation of the Nexus Between Stress Granules, Roquin, and Regnase-1 Underlies the Molecular Pathogenesis of Warfare Vesicants. <i>Frontiers in Immunology</i> , 2021, 12, 809365.	4.8	5
16	Molecular insight into cotton leaf curl geminivirus disease resistance in cultivated cotton (<i>Gossypium hirsutum</i>). <i>Plant Biotechnology Journal</i> , 2020, 18, 691-706.	8.3	44
17	Integrative Network Biology Framework Elucidates Molecular Mechanisms of SARS-CoV-2 Pathogenesis. <i>IScience</i> , 2020, 23, 101526.	4.1	52
18	Genome-wide identification and classification of resistance genes predicted several decoy domains in <i>Gossypium sp.</i> . <i>Plant Gene</i> , 2020, 24, 100250.	2.3	7

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19	EffectorK, a comprehensive resource to mine for <i>Ralstonia</i> , <i>Xanthomonas</i> , and other published effector interactors in the <i>Arabidopsis</i> proteome. <i>Molecular Plant Pathology</i> , 2020, 21, 1257-1270.	4.2	38
20	Integrative Network Biology Framework Elucidates Molecular Mechanisms of SARS-CoV-2 Pathogenesis. <i>SSRN Electronic Journal</i> , 2020, , 3581857.	0.4	4
21	Transcriptomic analysis of cultivated cotton <i>Gossypium hirsutum</i> provides insights into host responses upon whitefly-mediated transmission of cotton leaf curl disease. <i>PLoS ONE</i> , 2019, 14, e0210011.	2.5	28
22	Systems Biology and Machine Learning in Plant-Pathogen Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 45-55.	2.6	68
23	Direct Regulation of the EFR-Dependent Immune Response by Arabidopsis TCP Transcription Factors. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 540-549.	2.6	19
24	Map of physical interactions between extracellular domains of Arabidopsis leucine-rich repeat receptor kinases. <i>Scientific Data</i> , 2019, 6, 190025.	5.3	17
25	An extracellular network of Arabidopsis leucine-rich repeat receptor kinases. <i>Nature</i> , 2018, 553, 342-346.	27.8	241
26	Elucidating the role of WRKY27 in male sterility in Arabidopsis. <i>Plant Signaling and Behavior</i> , 2018, 13, e1363945.	2.4	23
27	Dynamic modeling of transcriptional gene regulatory network uncovers distinct pathways during the onset of Arabidopsis leaf senescence. <i>Npj Systems Biology and Applications</i> , 2018, 4, 35.	3.0	22
28	Genome Editing: Targeting Susceptibility Genes for Plant Disease Resistance. <i>Trends in Biotechnology</i> , 2018, 36, 898-906.	9.3	215
29	NPR1 in JazzSet with Pathogen Effectors. <i>Trends in Plant Science</i> , 2018, 23, 469-472.	8.8	25
30	Network biology discovers pathogen contact points in host protein-protein interactomes. <i>Nature Communications</i> , 2018, 9, 2312.	12.8	101
31	Mapping Protein-Protein Interaction Using High-Throughput Yeast 2-Hybrid. <i>Methods in Molecular Biology</i> , 2017, 1610, 217-230.	0.9	22
32	Global temporal dynamic landscape of pathogen-mediated subversion of Arabidopsis innate immunity. <i>Scientific Reports</i> , 2017, 7, 7849.	3.3	32
33	Transcriptomics reveals multiple resistance mechanisms against cotton leaf curl disease in a naturally immune cotton species, <i>Gossypium arboreum</i> . <i>Scientific Reports</i> , 2017, 7, 15880.	3.3	61
34	The Roles of Aquaporins in Plant Stress Responses. <i>Journal of Developmental Biology</i> , 2016, 4, 9.	1.7	249
35	Cytokinin Response Factor 6 Represses Cytokinin-Associated Genes during Oxidative Stress. <i>Plant Physiology</i> , 2016, 172, pp.00415.2016.	4.8	85
36	Pathogen Tactics to Manipulate Plant Cell Death. <i>Current Biology</i> , 2016, 26, R608-R619.	3.9	81

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37	<i>Pseudomonas syringae</i> 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
38	Making the right connections: Network biology and plant immune system dynamics. Current Plant Biology, 2016, 5, 2-12.	4.7	34
39	Heterotrimeric G-proteins in <i>Picea abies</i> and their regulation in response to <i>Heterobasidion annosum</i> s.l. infection. BMC Plant Biology, 2015, 15, 287.	3.6	2
40	TCP three-way handshake: linking developmental processes with plant immunity. Trends in Plant Science, 2015, 20, 238-245.	8.8	90
41	The Top 10 oomycete pathogens in molecular plant pathology. Molecular Plant Pathology, 2015, 16, 413-434.	4.2	695
42	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
43	Expression-based network biology identifies immune-related functional modules involved in plant defense. BMC Genomics, 2014, 15, 421.	2.8	36
44	Engineering NLR immune receptors for broad-spectrum disease resistance. Trends in Plant Science, 2013, 18, 469-472.	8.8	21
45	Tell me more: roles of NPRs in plant immunity. Trends in Plant Science, 2013, 18, 402-411.	8.8	169
46	The Molecular Basis of Host Specialization in Bean Pathovars of <i>Pseudomonas syringae</i> . Molecular Plant-Microbe Interactions, 2012, 25, 877-888.	2.6	83
47	IRE1/bZIP60-Mediated Unfolded Protein Response Plays Distinct Roles in Plant Immunity and Abiotic Stress Responses. PLoS ONE, 2012, 7, e31944.	2.5	200
48	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. Science, 2011, 333, 601-607.	12.6	838
49	<i>Arabidopsis</i> G-protein interactome reveals connections to cell wall carbohydrates and morphogenesis. Molecular Systems Biology, 2011, 7, 532.	7.2	191
50	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. Science, 2011, 333, 596-601.	12.6	776
51	Dynamic Evolution of Pathogenicity Revealed by Sequencing and Comparative Genomics of 19 <i>Pseudomonas syringae</i> Isolates. PLoS Pathogens, 2011, 7, e1002132.	4.7	413
52	NPR1 in Plant Defense: It's Not over 'til It's Turned over. Cell, 2009, 137, 804-806.	28.9	66
53	Natural variation of potato allene oxide synthase 2 causes differential levels of jasmonates and pathogen resistance in <i>Arabidopsis</i> . Planta, 2008, 228, 293-306.	3.2	48
54	The <i>Arabidopsis</i> transcription factor WRKY27 influences wilt disease symptom development caused by <i>Ralstonia solanacearum</i> . Plant Journal, 2008, 56, 935-947.	5.7	101

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55	The WRKY70 transcription factor of Arabidopsis influences both the plant senescence and defense signaling pathways. <i>Planta</i> , 2007, 226, 125-137.	3.2	243