

Angela Mehta

List of Publications by Year in descending order

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65
papers

1,234
citations

361413

20
h-index

414414

32
g-index

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65
docs citations

65
times ranked

1701
citing authors

#	ARTICLE	IF	CITATIONS
1	Host induced gene silencing of <i>Sclerotinia sclerotiorum</i> effector genes for the control of white mold. <i>Biocatalysis and Agricultural Biotechnology</i> , 2022, 40, 102302.	3.1	4
2	Priming of defense-related genes in <i>Brassica oleracea</i> var. <i>capitata</i> using concentrated metabolites produced by <i>Rhizobium tropici</i> CIAT 899. <i>Brazilian Journal of Microbiology</i> , 2022, , 1.	2.0	0
3	NBS-LRR-WRKY genes and protease inhibitors (PIs) seem essential for cowpea resistance to root-knot nematode. <i>Journal of Proteomics</i> , 2022, 261, 104575.	2.4	4
4	Proteome dataset of <i>Hemileia vastatrix</i> by LC-MS/MS label-free identification. <i>Data in Brief</i> , 2022, 43, 108433.	1.0	0
5	Proteome responses of <i>Rhizobium tropici</i> CIAT 899 upon apigenin and salt stress induction. <i>Applied Soil Ecology</i> , 2021, 159, 103815.	4.3	6
6	Proteomic screening for the identification of proteins involved in resistance to <i>Xanthomonas campestris</i> pv. <i>malvacearum</i> in cotton. <i>Physiological and Molecular Plant Pathology</i> , 2021, 113, 101562.	2.5	2
7	Seasonal differences in seminal plasma proteins from two bovine breeds adapted to a subtropical climate. <i>Tropical Animal Health and Production</i> , 2021, 53, 61.	1.4	1
8	Shotgun proteomics coupled to transient-inducible gene silencing reveal rice susceptibility genes as new sources for blast disease resistance. <i>Journal of Proteomics</i> , 2021, 241, 104223.	2.4	5
9	CRISPR Genome Editing Technology: A Powerful Tool Applied to Developing Agribusiness. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 6379-6395.	5.2	10
10	MALDI TOF MS-profiling: Applications for bacterial and plant sample differentiation and biological variability assessment. <i>Journal of Proteomics</i> , 2020, 213, 103619.	2.4	6
11	Capacity for somatic embryogenesis of adult oil palm genitors (<i>Elaeis guineensis</i> , var. <i>Pisifera</i>) from immature leaf tissues. <i>South African Journal of Botany</i> , 2020, 131, 229-239.	2.5	8
12	Proteomics unravels new candidate genes for <i>Meloidogyne</i> resistance in wild <i>Arachis</i> . <i>Journal of Proteomics</i> , 2020, 217, 103690.	2.4	12
13	Pan Proteome of <i>Xanthomonas campestris</i> pv. <i>campestris</i> Isolates Contrasting in Virulence. <i>Proteomics</i> , 2019, 19, e1900082.	2.2	4
14	Proteomic Analysis and Functional Validation of a <i>Brassica oleracea</i> Endochitinase Involved in Resistance to <i>Xanthomonas campestris</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 414.	3.6	13
15	Quantitative expression of microRNAs in <i>Brassica oleracea</i> infected with <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Molecular Biology Reports</i> , 2019, 46, 3523-3529.	2.3	10
16	Stress and cell cycle regulation during somatic embryogenesis plays a key role in oil palm callus development. <i>Journal of Proteomics</i> , 2019, 192, 137-146.	2.4	15
17	Differential protein profiles in interspecific hybrids between <i>Elaeis oleifera</i> and <i>E. guineensis</i> with contrasting responses to somatic embryogenesis competence acquisition. <i>Plant Cell, Tissue and Organ Culture</i> , 2019, 137, 11-21.	2.3	8
18	Comparative proteomics and gene expression analysis in <i>Arachis duranensis</i> reveal stress response proteins associated to drought tolerance. <i>Journal of Proteomics</i> , 2019, 192, 299-310.	2.4	39

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19	Genotype-dependent changes of gene expression during somatic embryogenesis in oil palm hybrids (<i>Elaeis oleifera</i> x <i>E. guineensis</i>). PLoS ONE, 2018, 13, e0209445.	2.5	16
20	Chloroplast Proteome of <i>Nicotiana benthamiana</i> Infected by Tomato Blistering Mosaic Virus. Protein Journal, 2018, 37, 290-299.	1.6	9
21	Brassica oleracea resistance-related proteins identified at an early stage of black rot disease. Physiological and Molecular Plant Pathology, 2018, 104, 9-14.	2.5	20
22	Differential accumulation of <i>Xanthomonas campestris</i> pv. <i>campestris</i> proteins during the interaction with the host plant: Contributions of an in vivo system. Proteomics, 2017, 17, 1700086.	2.2	20
23	Validation of an in vitro system for studies of pathogenicity mechanisms in <i>Xanthomonas campestris</i> . FEMS Microbiology Letters, 2017, 364, .	1.8	3
24	Plant responses to tomato chlorotic mottle virus: Proteomic view of the resistance mechanisms to a bipartite begomovirus in tomato. Journal of Proteomics, 2017, 151, 284-292.	2.4	16
25	A year (2014-2015) of plants in <i>Proteomics</i> journal. Progress in wet and dry methodologies, moving from protein catalogs, and the view of classic plant biochemists. Proteomics, 2016, 16, 866-876.	2.2	9
26	Identification of proteins in susceptible and resistant Brassica oleracea responsive to <i>Xanthomonas campestris</i> pv. <i>campestris</i> infection. Journal of Proteomics, 2016, 143, 278-285.	2.4	27
27	MALDI-TOF MS profiling approach: how much can we get from it?. Frontiers in Plant Science, 2015, 6, 184.	3.6	23
28	Cowpea-Meloidogyne incognita interaction: Root proteomic analysis during early stages of nematode infection. Proteomics, 2015, 15, 1746-1759.	2.2	15
29	Comparing Acidovorax citrulli strains from melon and watermelon: Phenotypic characteristics, pathogenicity and genetic diversity. Tropical Plant Pathology, 2014, 39, 154-162.	1.5	10
30	Proteomic identification of differentially expressed proteins during the acquisition of somatic embryogenesis in oil palm (<i>Elaeis guineensis</i> Jacq.). Journal of Proteomics, 2014, 104, 112-127.	2.4	59
31	Proteomic Analysis of Upland Rice (<i>Oryza sativa</i> L.) Exposed to Intermittent Water Deficit. Protein Journal, 2014, 33, 221-230.	1.6	15
32	Proteomic pattern alterations of the cyanobacterium <i>Synechocystis</i> sp. PCC 6803 in response to cadmium, nickel and cobalt. Journal of Proteomics, 2014, 102, 98-112.	2.4	21
33	Biochemical Aspects of the Soybean Response to Herbivory Injury by the Brown Stink Bug <i>Euschistus heros</i> (Hemiptera: Pentatomidae). PLoS ONE, 2014, 9, e109735.	2.5	14
34	Effects of acute exercise over heart proteome from monogenic obese (<i>ob/ob</i>) mice. Journal of Cellular Physiology, 2013, 228, 824-834.	4.1	13
35	Identification of host proteins modulated by the virulence factor AC2 of Tomato chlorotic mottle virus in <i>Nicotiana benthamiana</i> . Proteomics, 2013, 13, 1947-1960.	2.2	25
36	Proteomic Analysis of Developing Somatic Embryos of <i>Coffea arabica</i> . Plant Molecular Biology Reporter, 2012, 30, 1393-1399.	1.8	27

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37	Comparative proteomics between natural <i>Microcystis</i> isolates with a focus on microcystin synthesis. <i>Proteome Science</i> , 2012, 10, 38.	1.7	17
38	Identification of defence-related genes expressed in coffee and citrus during infection by <i>Xylella fastidiosa</i> . <i>European Journal of Plant Pathology</i> , 2011, 130, 529-540.	1.7	5
39	A new chitinase-like xylanase inhibitor protein (XIP) from coffee (<i>Coffea arabica</i>) affects Soybean Asian rust (<i>Phakopsora pachyrhizi</i>) spore germination. <i>BMC Biotechnology</i> , 2011, 11, 14.	3.3	27
40	Comparative proteomic and metalloproteomic analyses of human plasma from patients with laryngeal cancer. <i>Cancer Immunology, Immunotherapy</i> , 2010, 59, 173-181.	4.2	9
41	METHODOLOGICAL EVALUATION OF 2-DE TO STUDY ROOT PROTEOMICS DURING NEMATODE INFECTION IN COTTON AND COFFEE PLANTS. <i>Preparative Biochemistry and Biotechnology</i> , 2010, 40, 152-163.	1.9	12
42	Variabilidade genética entre isolados de <i>Colletotrichum gossypii</i> do algodoeiro. <i>Summa Phytopathologica</i> , 2010, 36, 40-44.	0.1	1
43	Análise da diversidade genética de isolados de <i>Xanthomonas axonopodis</i> pv. <i>malvacearum</i> do algodoeiro. <i>Summa Phytopathologica</i> , 2009, 35, 105-109.	0.1	2
44	Proteomic evaluation of coffee zygotic embryos in two different stages of seed development. <i>Plant Physiology and Biochemistry</i> , 2009, 47, 1046-1050.	5.8	13
45	Comparative proteome analysis of <i>Xanthomonas campestris</i> pv. <i>campestris</i> in the interaction with the susceptible and the resistant cultivars of <i>Brassica oleracea</i> . <i>FEMS Microbiology Letters</i> , 2009, 298, 260-266.	1.8	31
46	In vivo proteome analysis of <i>Xanthomonas campestris</i> pv. <i>campestris</i> in the interaction with the host plant <i>Brassica oleracea</i> . <i>FEMS Microbiology Letters</i> , 2008, 281, 167-174.	1.8	47
47	Plant-pathogen interactions: what is proteomics telling us?. <i>FEBS Journal</i> , 2008, 275, 3731-3746.	4.7	122
48	Identification of drought-responsive genes in roots of upland rice (<i>Oryza sativa</i> L). <i>BMC Genomics</i> , 2008, 9, 485.	2.8	104
49	Post-secretory events alter the peptide content of the skin secretion of <i>Hypsiboas raniceps</i> . <i>Biochemical and Biophysical Research Communications</i> , 2008, 377, 1057-1061.	2.1	33
50	Comparative Proteomic Analysis of Zygotic Embryo and Endosperm from <i>Coffea arabica</i> Seeds. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 10922-10926.	5.2	8
51	Proteomic analysis of <i>Metarhizium anisopliae</i> secretion in the presence of the insect pest <i>Callosobruchus maculatus</i> . <i>Microbiology (United Kingdom)</i> , 2008, 154, 3766-3774.	1.8	24
52	Rootomics: The Challenge of Discovering Plant Defense-Related Proteins in Roots. <i>Current Protein and Peptide Science</i> , 2008, 9, 108-116.	1.4	31
53	Diversity analysis of <i>Bemisia tabaci</i> biotypes: RAPD, PCR-RFLP and sequencing of the ITS1 rDNA region. <i>Genetics and Molecular Biology</i> , 2008, 31, 585-590.	1.3	11
54	Screening and secretomic analysis of entomopathogenic <i>Beauveria bassiana</i> isolates in response to cowpea weevil (<i>Callosobruchus maculatus</i>) exoskeleton. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2007, 145, 333-338.	2.6	22

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55	Genes associated with hypersensitive response (HR) in the citrus EST database (CitEST). <i>Genetics and Molecular Biology</i> , 2007, 30, 943-956.	1.3	16
56	Signaling pathways in a Citrus EST database. <i>Genetics and Molecular Biology</i> , 2007, 30, 734-751.	1.3	2
57	Differentiation of <i>Xanthomonas</i> species by PCR-RFLP of <i>rpfB</i> and <i>atpD</i> genes. <i>FEMS Microbiology Letters</i> , 2007, 271, 33-39.	1.8	15
58	Identification of differentially expressed genes of <i>Xanthomonas axonopodis</i> pv. <i>citri</i> by representational difference analysis of cDNA. <i>Genetics and Molecular Biology</i> , 2005, 28, 140-149.	1.3	7
59	A Simple Method for In Vivo Expression Studies of <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <i>Current Microbiology</i> , 2003, 47, 400-3.	2.2	25
60	Proteins induced by <i>Xanthomonas axonopodis</i> pv. <i>passiflorae</i> with leaf extract of the host plant (<i>Passiflorae edulis</i>). <i>Proteomics</i> , 2003, 3, 95-102.	2.2	44
61	ERIC and REP-PCR Banding Patterns and Sequence Analysis of the Internal Transcribed Spacer of rDNA of <i>Stemphylium solani</i> Isolates from Cotton. <i>Current Microbiology</i> , 2002, 44, 323-328.	2.2	26
62	ERIC- and REP-PCR amplify non-repetitive fragments from the genome of <i>Drechslera avenae</i> and <i>Stemphylium solani</i> . <i>FEMS Microbiology Letters</i> , 2002, 211, 51-55.	1.8	13
63	ERIC- and REP-PCR amplify non-repetitive fragments from the genome of <i>Drechslera avenae</i> and <i>Stemphylium solani</i> . <i>FEMS Microbiology Letters</i> , 2002, 211, 51-55.	1.8	0
64	Differentially expressed proteins in the interaction of <i>Xanthomonas axonopodis</i> pv. <i>citri</i> with leaf extract of the host plant. <i>Proteomics</i> , 2001, 1, 1111-1118.	2.2	55
65	Assessment of the genetic diversity of <i>Xylella fastidiosa</i> isolated from citrus in Brazil by PCR-RFLP of the 16S rDNA and 16S-23S intergenic spacer and rep-PCR fingerprinting. <i>Antonie Van Leeuwenhoek</i> , 2001, 79, 53-59.	1.7	23