

Ajjamada C Kushalappa

List of Publications by Year in descending order

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50
papers

2,591
citations

172457

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197818

49
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50
docs citations

50
times ranked

2462
citing authors

#	ARTICLE	IF	CITATIONS
1	The caffeoyl-CoA O-methyltransferase gene SNP replacement in Russet Burbank potato variety enhances late blight resistance through cell wall reinforcement. <i>Plant Cell Reports</i> , 2021, 40, 237-254.	5.6	31
2	Identification and functional characterisation of late blight resistance polymorphic genes in Russet Burbank potato cultivar. <i>Functional Plant Biology</i> , 2021, 48, 88.	2.1	6
3	TaNAC032 transcription factor regulates lignin-biosynthetic genes to combat Fusarium head blight in wheat. <i>Plant Science</i> , 2021, 304, 110820.	3.6	23
4	Role of laccase gene in wheat NILs differing at QTL-Fhb1 for resistance against Fusarium head blight. <i>Plant Science</i> , 2020, 298, 110574.	3.6	25
5	Genome-wide in silico identification of LysM-RLK genes in potato (<i>Solanum tuberosum</i> L.). <i>Molecular Biology Reports</i> , 2019, 46, 5005-5017.	2.3	12
6	HvWRKY23 regulates flavonoid glycoside and hydroxycinnamic acid amide biosynthetic genes in barley to combat Fusarium head blight. <i>Plant Molecular Biology</i> , 2019, 100, 591-605.	3.9	54
7	Liquid chromatography and high resolution mass spectrometry-based metabolomics to identify quantitative resistance-related metabolites and genes in wheat QTL-2DL against Fusarium head blight. <i>European Journal of Plant Pathology</i> , 2018, 151, 125.	1.7	3
8	Macronutrient contents of potato genotype collections in the <i>Solanum tuberosum</i> Group Phureja. <i>Journal of Food Composition and Analysis</i> , 2018, 66, 179-184.	3.9	14
9	StWRKY8 transcription factor regulates benzyloisoquinoline alkaloid pathway in potato conferring resistance to late blight. <i>Plant Science</i> , 2017, 256, 208-216.	3.6	52
10	TaWRKY70 transcription factor in wheat QTL-2DL regulates downstream metabolite biosynthetic genes to resist Fusarium graminearum infection spread within spike. <i>Scientific Reports</i> , 2017, 7, 42596.	3.3	57
11	Potato NAC43 and MYB8 Mediated Transcriptional Regulation of Secondary Cell Wall Biosynthesis to Contain <i>Phytophthora infestans</i> Infection. <i>Plant Molecular Biology Reporter</i> , 2017, 35, 519-533.	1.8	22
12	Metabolo-transcriptome profiling of barley reveals induction of chitin elicitor receptor kinase gene (HvCERK1) conferring resistance against Fusarium graminearum. <i>Plant Molecular Biology</i> , 2017, 93, 247-267.	3.9	55
13	Identification and characterization of a fusarium head blight resistance gene <i>TaACT</i> in wheat QTL-2DL. <i>Plant Biotechnology Journal</i> , 2017, 15, 447-457.	8.3	66
14	Hydroxycinnamic acids in cooked potato tubers from <i>Solanum tuberosum</i> group Phureja. <i>Food Science and Nutrition</i> , 2017, 5, 380-389.	3.4	17
15	Corrigendum to: Integrated transcriptomics and metabolomics reveal induction of hierarchies of resistance genes in potato against late blight. <i>Functional Plant Biology</i> , 2016, 43, 1205.	2.1	0
16	WAX INDUCER1 (HvWIN1) transcription factor regulates free fatty acid biosynthetic genes to reinforce cuticle to resist Fusarium head blight in barley spikelets. <i>Journal of Experimental Botany</i> , 2016, 67, 4127-4139.	4.8	60
17	Plant Innate Immune Response: Qualitative and Quantitative Resistance. <i>Critical Reviews in Plant Sciences</i> , 2016, 35, 38-55.	5.7	137
18	Gene discovery and genome editing to develop cisgenic crops with improved resistance against pathogen infection. <i>Canadian Journal of Plant Pathology</i> , 2016, 38, 279-295.	1.4	17

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19	Natural variation of sucrose, glucose and fructose contents in Colombian genotypes of <i>Solanum tuberosum</i> Group Phureja at harvest. <i>Journal of the Science of Food and Agriculture</i> , 2016, 96, 4288-4294.	3.5	27
20	Integrated transcriptomics and metabolomics reveal induction of hierarchies of resistance genes in potato against late blight. <i>Functional Plant Biology</i> , 2016, 43, 766.	2.1	24
21	Hydroxycinnamic acid functional ingredients and their biosynthetic genes in tubers of <i>Solanum tuberosum</i> Group Phureja. <i>Cogent Food and Agriculture</i> , 2016, 2, .	1.4	6
22	Tuber metabolic profiling of resistant and susceptible potato varieties challenged with <i>Phytophthora infestans</i> . <i>European Journal of Plant Pathology</i> , 2016, 145, 277-287.	1.7	19
23	Functional molecular markers for crop improvement. <i>Critical Reviews in Biotechnology</i> , 2016, 36, 917-930.	9.0	63
24	Integrated Metabolo-Transcriptomics Reveals Fusarium Head Blight Candidate Resistance Genes in Wheat QTL-Fhb2. <i>PLoS ONE</i> , 2016, 11, e0155851.	2.5	100
25	Transcription factor <i>StWRKY1</i> regulates phenylpropanoid metabolites conferring late blight resistance in potato. <i>Journal of Experimental Botany</i> , 2015, 66, 7377-7389.	4.8	107
26	Metabolomics deciphers quantitative resistance mechanisms in diploid potato clones against late blight. <i>Functional Plant Biology</i> , 2015, 42, 284.	2.1	53
27	Nutritional contents of advanced breeding clones of <i>Solanum tuberosum</i> group Phureja. <i>LWT - Food Science and Technology</i> , 2015, 62, 76-82.	5.2	32
28	Real-time quantitative PCR based method for the quantification of fungal biomass to discriminate quantitative resistance in barley and wheat genotypes to fusarium head blight. <i>Journal of Cereal Science</i> , 2015, 64, 16-22.	3.7	26
29	Development and validation of a liquid chromatographic method to quantify sucrose, glucose, and fructose in tubers of <i>Solanum tuberosum</i> Group Phureja. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2015, 975, 18-23.	2.3	41
30	Quantitative resistance in potato leaves to late blight associated with induced hydroxycinnamic acid amides. <i>Functional and Integrative Genomics</i> , 2014, 14, 285-298.	3.5	76
31	Identification of fusarium head blight resistance related metabolites specific to doubled-haploid lines in barley. <i>European Journal of Plant Pathology</i> , 2014, 138, 67-78.	1.7	30
32	Identification of Late Blight Resistance-Related Metabolites and Genes in Potato through Nontargeted Metabolomics. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 584-595.	1.8	65
33	Metabolomics deciphers the host resistance mechanisms in wheat cultivar Sumai-3, against trichothecene producing and non-producing isolates of <i>Fusarium graminearum</i> . <i>Plant Physiology and Biochemistry</i> , 2014, 83, 40-50.	5.8	98
34	Metabolo-proteomics to discover plant biotic stress resistance genes. <i>Trends in Plant Science</i> , 2013, 18, 522-531.	8.8	105
35	Differential metabolic response of barley genotypes, varying in resistance, to trichothecene-producing and non-producing (<i>tri5⁺</i>) isolates of <i>Fusarium graminearum</i> . <i>Plant Pathology</i> , 2012, 61, 509-521.	2.4	42
36	Integrated Metabolo-Proteomic Approach to Decipher the Mechanisms by Which Wheat QTL (Fhb1) Contributes to Resistance against <i>Fusarium graminearum</i> . <i>PLoS ONE</i> , 2012, 7, e40695.	2.5	244

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37	Metabolomics technology to phenotype resistance in barley against <i>Gibberella zeae</i> . <i>European Journal of Plant Pathology</i> , 2011, 130, 29-43.	1.7	68
38	Mass Spectrometry Based Metabolomics to Identify Potential Biomarkers for Resistance in Barley against <i>Fusarium Head Blight</i> (<i>Fusarium graminearum</i>). <i>Journal of Chemical Ecology</i> , 2011, 37, 846-856.	1.8	63
39	Identification of metabolites related to mechanisms of resistance in barley against <i>Fusarium graminearum</i> , based on mass spectrometry. <i>Plant Molecular Biology</i> , 2011, 77, 355-370.	3.9	96
40	Mass spectrometry-based metabolomics application to identify quantitative resistance-related metabolites in barley against <i>Fusarium</i> head blight. <i>Molecular Plant Pathology</i> , 2010, 11, 769-782.	4.2	153
41	Detection and discrimination of two fungal diseases of mango (cv. Keitt) fruits based on volatile metabolite profiles using GC/MS. <i>Postharvest Biology and Technology</i> , 2007, 45, 117-125.	6.0	46
42	Metabolic fingerprinting to discriminate diseases of stored carrots. <i>Annals of Applied Biology</i> , 2006, 148, 17-26.	2.5	39
43	Volatile metabolite profiling to detect and discriminate stem-end rot and anthracnose diseases of mango fruits. <i>Plant Pathology</i> , 2006, 55, 792-802.	2.4	26
44	Volatile metabolic profiling for discrimination of potato tubers inoculated with dry and soft rot pathogens. <i>American Journal of Potato Research</i> , 2005, 82, 1-8.	0.9	45
45	Discrimination of three fungal diseases of potato tubers based on volatile metabolic profiles developed using GC/MS. <i>Potato Research</i> , 2005, 48, 85-96.	2.7	23
46	Metabolic profiling and factor analysis to discriminate quantitative resistance in wheat cultivars against <i>Fusarium</i> head blight. <i>Physiological and Molecular Plant Pathology</i> , 2005, 66, 119-133.	2.5	101
47	Volatile metabolite profiling to discriminate diseases of McIntosh apple inoculated with fungal pathogens. <i>Journal of the Science of Food and Agriculture</i> , 2004, 84, 1333-1340.	3.5	62
48	Models to predict potato tuber infection by <i>Pythium ultimum</i> from duration of wetness and temperature, and leak-lesion expansion from storage duration and temperature. <i>Postharvest Biology and Technology</i> , 2003, 27, 313-322.	6.0	8
49	PHYSICAL, PHYSIOLOGICAL AND CHEMICAL CHANGES IN POTATO AS INFLUENCED BY <i>ERWINIA CAROTOVORA</i> INFECTION. <i>Journal of Food Processing and Preservation</i> , 2002, 26, 339-359.	2.0	11
50	Calculation of Apparent Infection Rate in Plant Diseases: Development of a Method to Correct for Host Growth. <i>Phytopathology</i> , 1982, 72, 1373.	2.2	41