Bilal Ahmad Padder

List of Publications by Year
in descending order

41	585	759233 12	677142 22
papers	citations	h-index	g-index

44	44	44	460
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Optimizing the Agrobacterium tumefaciens-mediated transformation conditions in Colletotrichum lindemuthianum: a step forward to unravel the functions of pathogenicity arsenals. Letters in Applied Microbiology, 2022, 75, 293-307.	2.2	4
2	Phaseolus vulgaris-Colletotrichum lindemuthianum Pathosystem in the Post-Genomic Era: An Update. Current Microbiology, 2022, 79, 36.	2.2	14
3	First report of powdery mildew caused by Phyllactinia pyri-serotinae Sawada on pear (Pyrus communis) Tj ETQq1 1 0.784314 rgBT /Over	1.4	1
4	Insights on atypical adult plant resistance phenomenon in Andean bean cultivar Baspa (KRC-8) to Colletotrichum lindemuthianum, the bean anthracnose pathogen. Euphytica, 2022, 218, .	1.2	3
5	Multiplex PCR based detection method for Venturia species infecting pome and stone fruits. Indian Phytopathology, 2022, 75, 941-950.	1.2	1
6	Delineating binding potential, stability of Sulforaphaneâ€Nâ€acetylâ€cysteine in the active site of histone deacetylase 2 and testing its cytotoxicity against distinct cancer lines through stringent molecular dynamics, DFT and cellâ€based assays. Chemical Biology and Drug Design, 2021, 98, 363-376.	3.2	5
7	Heterothallism among spatiotemporally diverse Colletotrichum lindemuthianum isolates and its implication in common bean anthracnose resistance breeding in the Northwestern Himalayan region. Indian Phytopathology, 2021, 74, 939-947.	1.2	2
8	North-Western Himalayan Common Beans: Population Structure and Mapping of Quantitative Anthracnose Resistance Through Genome Wide Association Study. Frontiers in Plant Science, 2020, 11, 571618.	3.6	27
9	Population structure of Venturia inaequalis, a hemibiotrophic fungus, under different host resistance specificities in the Kashmir valley. Archives of Microbiology, 2020, 202, 2245-2253.	2.2	3
10	Thyrostroma carpophilum insertional mutagenesis: A step towards understanding its pathogenicity mechanism. Journal of Microbiological Methods, 2020, 171, 105885.	1.6	7
11	Population Genetics of Narcissus Species Reveals High Diversity and Multiple Introductions into Kashmir. Agricultural Research, 2020, 9, 536-542.	1.7	1
12	Morphometric and genetic characterization of medicinally important accessions of Physalis ixocarpa Brot.. Bangladesh Journal of Botany, 2020, 48, 105-111.	0.4	2
13	Temporal expression of candidate genes at the Co-1 locus and their interaction with other defense related genes in common bean. Physiological and Molecular Plant Pathology, 2019, 108, 101424.	2.5	24
14	Investigating the virulence and genetic diversity of Colletotrichum lindemuthianum populations distributed in the North Western Himalayan hill states. Journal of Plant Pathology, 2019, 101, 677-688.	1.2	20
15	Compendium of Colletotrichum graminicola responsive infection-induced transcriptomic shifts in the maize. Plant Gene, 2019, 17, 100166.	2.3	3
16	Venturia crataegi causing scab on CrataegusÂsongarica: Morpho-molecular characterization and a new record from India. Applied Biological Research, 2019, 21, 274.	0.2	2
17	Phylogenetic Relationship of Venturia carpophila, the Causal Agent of Almond Scab from Kashmir Valley as Inferred by ITS nr DNA. International Journal of Current Microbiology and Applied Sciences, 2019, 8, 2913-2919.	0.1	3
18	Marker Based Screening of F1 (Firdous x Gala) Mapping Population for Major Scab Resistance Gene Rvi6 in Apple (Malus Ã— Domestica). International Journal of Current Microbiology and Applied Sciences, 2019, 8, 2641-2646.	0.1	4

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19	Morpho-cultural, pathological and molecular variability in Thyrostroma carpophilum causing shot hole of stone fruits in India. European Journal of Plant Pathology, 2018, 151, 613-627.	1.7	14
20	Marker-assisted introgression of three dominant blast resistance genes into an aromatic rice cultivar Mushk Budji. Scientific Reports, 2018, 8, 4091.	3.3	32
21	In vitro evaluation of bioagents and fungitoxicants against Fusarium oxysporum and Fusarium solani causing corm rot of saffron (Crocus sativus) in Kashmir, India. Acta Horticulturae, 2018, , 125-132.	0.2	5
22	Microsatellite mining in the genus Colletotrichum. Gene Reports, 2018, 13, 84-93.	0.8	13
23	Management of corm rot of saffron (Crocus sativusL.) in Kashmir, India. Acta Horticulturae, 2018, , 111-114.	0.2	4
24	Population Structure of Colletotrichum truncatum in Himachal Pradesh and Identification of Broad-Spectrum Resistant Sources in Capsicum. Agricultural Research, 2017, 6, 296-303.	1.7	5
25	Diversity evaluation of fruit quality of apple (MalusÂÃ—Âdomestica Borkh.) germplasm through cluster and principal component analysis. Indian Journal of Plant Physiology, 2017, 22, 221-226.	0.8	8
26	Molecular marker-based validation of blast resistance gene Pi54 and identification of potential donors in temperate high altitude rice (Oryza sativa L.). Indian Journal of Genetics and Plant Breeding, 2017, 77, 266.	0.5	3
27	Genome-Wide Association Study of Anthracnose Resistance in Andean Beans (Phaseolus vulgaris). PLoS ONE, 2016, 11, e0156391.	2.5	138
28	Transcriptome Profiling of the Phaseolus vulgaris - Colletotrichum lindemuthianum Pathosystem. PLoS ONE, 2016, 11, e0165823.	2.5	51
29	Distribution of BCMV strains in Kashmir valley and identification of resistant sources ofPhaseolus vulgaris. Indian Journal of Genetics and Plant Breeding, 2016, 76, 107.	0.5	3
30	Distribution of Apple Scab Race Flora and Identification of Resistant Sources against Venturia inaequalis in Kashmir. Plant Pathology Journal, 2015, 14, 196-201.	0.2	6
31	Pathogenic and coat protein characterization confirming the occurrence of Bean common mosaic virus on common bean (Phaseolus vulgaris) in Kashmir, India. Phytoparasitica, 2014, 42, 317-322.	1.2	11
32	Plant Disease Resistance Genes: From Perception to Signal Transduction. , 2014, , 345-354.		3
33	Virulence and Molecular Diversity of <scp>V</scp>enturia inaequalis in Commercial Apple Growing Regions in <scp>K</scp>ashmir. Journal of Phytopathology, 2013, 161, 271-279.	1.0	15
34	Variability in Fusarium species Causing Wilt Disease in Crops: A Transcriptomic Approach to Characterize Dialogue Between Host and Pathogen. , 2013, , 269-293.		2
35	Identification and Genetic Diversity Analysis of Ascochyta Species Associated with Blight Complex of Pea in a Northwestern Hill State of India. Agricultural Research, 2012, 1, 325-337.	1.7	8
36	In vitro and in vivoantagonism of biocontrol agents againstColletotrichum lindemuthianumcausing bean anthracnose. Archives of Phytopathology and Plant Protection, 2011, 44, 961-969.	1.3	17

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37	Genetic Differentiation among Populations of Venturia inaequalis in Kashmir: A North-Western State of India. Asian Journal of Plant Pathology, 2011, 5, 75-83.	0.3	8
38	Evaluation of Bioagents and Biopesticides against Colletotrichum lindemuthianum and its Integrated Management in Common Bean. Notulae Scientia Biologicae, 2010, 2, 72-76.	0.4	13
39	Virulence and RAPD dataâ€"A tool to study the evolutionary trends ofColletotrichum lindemuthianumvirulences in the North Western Himalayan region of India. Archives of Phytopathology and Plant Protection, 2009, 42, 610-617.	1.3	13
40	Genetic diversity and gene flow estimates among five populations of Colletotrichum lindemuthianum across Himachal Pradesh. Physiological and Molecular Plant Pathology, 2007, 70, 8-12.	2.5	29
41	Pathological and molecular diversity inColletotrichum lindemuthianum(bean anthracnose) across Himachal Pradesh, a north-western Himalayan state of India. Australasian Plant Pathology, 2007, 36, 191.	1.0	37