Dharminder Bhatia

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Strategies and prospects of haploid induction in rice (<scp><i>Oryza sativa</i></scp>). Plant Breeding, 2022, 141, 1-11.	1.9	5
2	Molecular mapping of CLCuD resistance introgressed from synthetic cotton polyploid in upland cotton. Journal of Genetics, 2022, 101, 1.	0.7	6
3	Genetic Variation for Anaerobic Germination and Emergence from Deeper Soil Depth in Oryza nivara Accessions. Rice Science, 2022, 29, 304-308.	3.9	1
4	Genotyping-by-Sequencing Based Investigation of Population Structure and Genome Wide Association Studies for Seven Agronomically Important Traits in a Set of 346 Oryza rufipogon Accessions. Rice, 2022, 15, .	4.0	8
5	Identification of potential donors and QTLs for resistance to false smut in a subset of rice diversity panel. European Journal of Plant Pathology, 2021, 159, 461-470.	1.7	11
6	Genome-wide association study and identification of candidate genes for seed oil content in Brassica napus. Euphytica, 2021, 217, 1.	1.2	5
7	Phenotypic evaluation of genetic variability and selection of yield contributing traits in chickpea recombinant inbred line population under high temperature stress. Physiology and Molecular Biology of Plants, 2021, 27, 747-767.	3.1	14
8	Eighty years of gene-for-gene relationship and its applications in identification and utilization of R genes. Journal of Genetics, 2021, 100, 1.	0.7	20
9	Identification of stable heat tolerance QTLs using inter-specific recombinant inbred line population derived from GPF 2 and ILWC 292. PLoS ONE, 2021, 16, e0254957.	2.5	16
10	Characterization of evolutionarily distinct rice <i>BAHDâ€Acyltransferases</i> provides insight into their plausible role in rice susceptibility to <i>Rhizoctonia solani</i> . Plant Genome, 2021, 14, e20140.	2.8	5
11	Genome-wide association study for candidate genes controlling seed yield and its components in rapeseed (Brassica napus subsp. napus). Physiology and Molecular Biology of Plants, 2021, 27, 1933-1951.	3.1	9
12	Molecular mapping of quantitative trait loci for ascochyta blight and botrytis grey mould resistance in an inter-specific cross in chickpea (<i>Cicer arietinum</i> L.) using genotyping by sequencing. Breeding Science, 2021, 71, 229-239.	1.9	16
13	Eighty years of gene-for-gene relationship and its applications in identification and utilization of genes. Journal of Genetics, 2021, 100, .	0.7	3
14	High resolution genetic mapping and identification of a candidate gene(s) for the purple sheath color and plant height in an interspecific F2 population derived from Oryza nivara Sharma & Shastry × Oryza sativa L. cross. Genetic Resources and Crop Evolution, 2020, 67, 97-105.	1.6	3
15	High-resolution genetic mapping of a novel bacterial blight resistance gene xa-45(t) identified from Oryza glaberrima and transferred to Oryza sativa. Theoretical and Applied Genetics, 2020, 133, 689-705.	3.6	61
16	Advanced Quantitative Genetics Technologies for Accelerating Plant Breeding. , 2020, , 121-138.		1
17	Insect resistance in Rice (Oryza sativa L.): overview on current breeding interventions. International Journal of Tropical Insect Science, 2019, 39, 259-272.	1.0	6
18	Genome wide association studies for yield and its component traits under terminal heat stress in Indian mustardÂ(Brassica juncea L.). Euphytica, 2019, 215, 1.	1.2	6

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19	Reinventing heterosis phenomenon through deployment of alien introgression lines in rice (<i>Oryza) Tj ETQq1 I</i>	1 0,784314 1.9	l rgBT /Overl
20	Influence of explant collection period, antibrowning strategy and growth regulators composition on in vitro propagation of Bhagwa pomegranate. Indian Journal of Horticulture, 2019, 76, 273.	0.1	2
21	High-resolution genetic mapping of a novel brown planthopper resistance locus, Bph34 in Oryza sativa L. X Oryza nivara (Sharma & Shastry) derived interspecific F2 population. Theoretical and Applied Genetics, 2018, 131, 1163-1171.	3.6	65
22	Genotyping by sequencing of rice interspecific backcross inbred lines identifies QTLs for grain weight and grain length. Euphytica, 2018, 214, 1.	1.2	29
23	A novel QTL qSPP2.2 controlling spikelet per panicle identified from Oryza longistaminata (A. Chev. et) Tj ETQq1	1 <u>9.7</u> 8431 2.1	4 rgBT /Over
24	Heterotic response of genomic regions derived from <i>Oryza rufipogon</i> and <i>O. nivara</i> in improving grain morphology and quality of indica rice (<i>Oryza sativa</i> L). Indian Journal of Genetics and Plant Breeding, 2018, 78, 155.	0.5	5
25	Introgression of Yield Component Traits in Rice (<i>Oryza sativa</i> ssp. <i>indica</i>) through Interspecific Hybridization. Crop Science, 2017, 57, 1557-1573.	1.8	21
26	Advances in Breeding for Resistance to Hoppers in Rice. , 2017, , 101-130.		5
27	Incomplete block designs for plant breeding experiments. Agricultural Research Journal, 2017, 54, 607.	0.2	10
28	Induction of useful variability for pericarp colour and bacterial blight resistance in rice (<i>Oryza) Tj ETQq0 0 0 rg</i>	;BT/Overlo 0.2	ck 10 Tf 50 3
29	Access and Benefit Sharing on the Use of Indigenous Traditional Knowledge. , 2015, , 163-181.		1
30	Yield-Enhancing Heterotic QTL Transferred from Wild Species to Cultivated Rice Oryza sativa L. PLoS ONE, 2014, 9, e96939.	2.5	37
31	The International Oryza Map Alignment Project: development of a genus-wide comparative genomics platform to help solve the 9 billion-people question. Current Opinion in Plant Biology, 2013, 16, 147-156.	7.1	126
32	New PCR-based sequence-tagged site marker for bacterial blight resistance gene Xa38 of rice. Molecular Breeding, 2012, 30, 607-611.	2.1	81
33	Markerâ€Assisted Development of Bacterial Blight Resistant, Dwarf, and High Yielding Versions of Two Traditional Basmati Rice Cultivars. Crop Science, 2011, 51, 759-770.	1.8	29
34	A novel bacterial blight resistance gene from <i>Oryza nivara</i> mapped to 38Âkb region on chromosome 4L and transferred to <i>Oryza sativa</i> L Genetical Research, 2008, 90, 397-407.	0.9	128
35	Genetics and Genomics of Bacterial Blight Resistance in Rice. , 0, , .		16