Harsh Raman

List of Publications by Year
in descending order

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Version: 2024-02-01

92	4,964	101543	98798
papers	citations	36 h-index	67 g-index

99	99	99	4467
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Speed breeding is a powerful tool to accelerate crop research and breeding. Nature Plants, 2018, 4, 23-29.	9.3	770
2	A high-density consensus map of barley linking DArT markers to SSR, RFLP and STS loci and agricultural traits. BMC Genomics, 2006, 7, 206.	2.8	305
3	A Second Mechanism for Aluminum Resistance in Wheat Relies on the Constitutive Efflux of Citrate from Roots Â Â. Plant Physiology, 2009, 149, 340-351.	4.8	248
4	Genome-Wide Delineation of Natural Variation for Pod Shatter Resistance in Brassica napus. PLoS ONE, 2014, 9, e101673.	2.5	182
5	Analysis of the Lr34/Yr18 Rust Resistance Region in Wheat Germplasm. Crop Science, 2008, 48, 1841-1852.	1.8	155
6	QTL mapping of multiple foliar disease and root-lesion nematode resistances in wheat. Molecular Breeding, 2010, 26, 107-124.	2.1	154
7	Molecular characterization and mapping ofALMT1, the aluminium-tolerance gene of bread wheat (Triticum aestivumL.). Genome, 2005, 48, 781-791.	2.0	149
8	High-resolution mapping of the Alp locus and identification of a candidate gene HvMATE controlling aluminium tolerance in barley (Hordeum vulgare L.). Theoretical and Applied Genetics, 2007, 115, 265-276.	3.6	123
9	Molecular mapping of qualitative and quantitative loci for resistance to Leptosphaeria maculans causing blackleg disease in canola (Brassica napus L.). Theoretical and Applied Genetics, 2012, 125, 405-418.	3.6	108
10	Genetic and physical mapping of flowering time loci in canola (Brassica napus L.). Theoretical and Applied Genetics, 2013, 126, 119-132.	3.6	105
11	A Tourist-like MITE insertion in the upstream region of the BnFLC.A10 gene is associated with vernalization requirement in rapeseed (Brassica napus L.). BMC Plant Biology, 2012, 12, 238.	3.6	94
12	Aluminium tolerance in barley (Hordeum vulgare L.): Physiological mechanisms, genetics and screening methods. Journal of Zhejiang University: Science B, 2006, 7, 769-787.	2.8	92
13	Identification of AFLP and microsatellite markers linked with an aluminium tolerance gene in barley (Hordeum vulgare L.). Theoretical and Applied Genetics, 2002, 105, 458-464.	3.6	82
14	Genomeâ€wide association analyses reveal complex genetic architecture underlying natural variation for flowering time in canola. Plant, Cell and Environment, 2016, 39, 1228-1239.	5.7	82
15	Multi-environment QTL studies suggest a role for cysteine-rich protein kinase genes in quantitative resistance to blackleg disease in Brassica napus. BMC Plant Biology, 2016, 16, 183.	3.6	81
16	Comparative Analysis of FLC Homologues in Brassicaceae Provides Insight into Their Role in the Evolution of Oilseed Rape. PLoS ONE, 2012, 7, e45751.	2.5	79
17	The multiple origins of aluminium resistance in hexaploid wheat include Aegilops tauschii and more recent cis mutations to TaALMT1. Plant Journal, 2010, 64, 446-455.	5.7	75
18	Genome-wide Association Study Identifies New Loci for Resistance to Leptosphaeria maculans in Canola. Frontiers in Plant Science, 2016, 7, 1513.	3.6	73

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19	Analysis of TaALMT1 traces the transmission of aluminum resistance in cultivated common wheat (Triticum aestivum L.). Theoretical and Applied Genetics, 2008, 116, 343-354.	3.6	71
20	Genome-wide association analyses of common wheat (Triticum aestivum L.) germplasm identifies multiple loci for aluminium resistanceThis article is one of a selection of papers from the conference â€œExploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farmingâ€•. Genome, 2010, 53, 957-966.	2.0	70
21	Conventional and molecular genetic analysis of factors contributing to variation in the timing of heading among spring barley (Hordeum vulgare L.) genotypes grown over a mild winter growing season. Australian Journal of Agricultural Research, 2003, 54, 1277.	1.5	68
22	GWAS hints at pleiotropic roles for FLOWERING LOCUS T in flowering time and yield-related traits in canola. BMC Genomics, 2019, 20, 636.	2.8	65
23	A consensus map of rapeseed (Brassica napus L.) based on diversity array technology markers: applications in genetic dissection of qualitative and quantitative traits. BMC Genomics, 2013, 14, 277.	2.8	62
24	<scp>SNP</scp> markersâ€based map construction and genomeâ€wide linkage analysis in Brassica napus. Plant Biotechnology Journal, 2014, 12, 851-860.	8.3	59
25	Genetic and in silico comparative mapping of the polyphenol oxidase gene in bread wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Over	3.5	56
26	Molecular mapping and validation of Rlm1 gene for resistance to Leptosphaeria maculans in canola (Brassica napus L.). Crop and Pasture Science, 2012, 63, 1007.	1.5	55
27	Repetitive Indel Markers within the ALMT1 Gene Conditioning Aluminium Tolerance in Wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /O	2.1	55
28	Genetic mapping of the barley Rrs14 scald resistance gene with RFLP, isozyme and seed storage protein markers. Plant Breeding, 2000, 119, 193-196.	1.9	52
29	Mapping of genomic regions associated with net form of netblotch resistance in barley. Australian Journal of Agricultural Research, 2003, 54, 1359.	1.5	50
30	Stable Quantitative Resistance Loci to Blackleg Disease in Canola (Brassica napus L.) Over Continents. Frontiers in Plant Science, 2018, 9, 1622.	3.6	48
31	Diversity Array Technology Markers: Genetic Diversity Analyses and Linkage Map Construction in Rapeseed (Brassica napus L.). DNA Research, 2012, 19, 51-65.	3.4	47
32	A DArT platform for quantitative bulked segregant analysis. BMC Genomics, 2007, 8, 196.	2.8	45
33	Identification and characterization of candidate Rlm4 blackleg resistance genes in Brassica napus using nextâ€generation sequencing. Plant Biotechnology Journal, 2012, 10, 709-715.	8.3	44
34	Modelling of gene loss propensity in the pangenomes of three Brassica species suggests different mechanisms between polyploids and diploids. Plant Biotechnology Journal, 2021, 19, 2488-2500.	8.3	44
35	A high-throughput SNP array in the amphidiploid species Brassica napus shows diversity in resistance genes. Functional and Integrative Genomics, 2014, 14, 643-655.	3.5	43
36	Localisation of quantitative trait loci for quality attributes in a doubled haploid population of wheat (Triticum aestivumL.). Genome, 2009, 52, 701-715.	2.0	42

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37	Quantitative genetic analysis of grain yield in an Australian Brassica napus doubled-haploid population. Crop and Pasture Science, 2016, 67, 298.	1.5	42
38	Leaf scald resistance genes in Hordeum vulgare and Hordeum vulgare ssp. spontaneum: parallels between cultivated and wild barley. Australian Journal of Agricultural Research, 2003, 54, 1335.	1.5	39
39	Mapping and QTL analysis of the barley population Sloop Ã— Halcyon. Australian Journal of Agricultural Research, 2003, 54, 1145.	1.5	37
40	Molecular diversity and genetic structure of modern and traditional landrace cultivars of wheat (Triticum aestivum L.). Crop and Pasture Science, 2010, 61, 222.	1.5	34
41	Genetic Dissection of Blackleg Resistance Loci in Rapeseed (Brassica napus L.). , 0, , .		34
42	A new variant of Puccinia striiformis causing stripe rust on barley and wild Hordeum species in Australia. Plant Pathology, 2000, 49, 803-803.	2.4	33
43	Co-linearity and divergence of the A subgenome of Brassica juncea compared with other Brassica species carrying different A subgenomes. BMC Genomics, 2016, 17, 18.	2.8	32
44	Development and allele diversity of microsatellite markers linked to the aluminium tolerance gene Alp in barley. Australian Journal of Agricultural Research, 2003, 54, 1315.	1.5	32
45	Functional gene markers for polyphenol oxidase locus in bread wheat (Triticum aestivum L.). Molecular Breeding, 2007, 19, 315-328.	2.1	31
46	Evaluating landraces of bread wheat Triticum aestivum L. for tolerance to aluminium under low pH conditions. Genetic Resources and Crop Evolution, 2007, 54, 759-766.	1.6	31
47	Molecular mapping and physical location of major gene conferring seedling resistance to Septoria tritici blotch in wheat. Molecular Breeding, 2009, 24, 153-164.	2.1	31
48	Genetic and physical mapping of loci for resistance to blackleg disease in canola (Brassica napus L.). Scientific Reports, 2020, 10, 4416.	3.3	30
49	Molecular Diversity Analysis and Genetic Mapping of Pod Shatter Resistance Loci in Brassica carinata L.. Frontiers in Plant Science, 2017, 8, 1765.	3.6	29
50	Constructing a dense genetic linkage map and mapping QTL for the traits of flower development in Brassica carinata. Theoretical and Applied Genetics, 2014, 127, 1593-1605.	3.6	28
51	Multigenic Control of Pod Shattering Resistance in Chinese Rapeseed Germplasm Revealed by Genome-Wide Association and Linkage Analyses. Frontiers in Plant Science, 2016, 7, 1058.	3.6	25
52	Analyses Using SSR and DArT Molecular Markers Reveal that Ethiopian Accessions of White Lupin (<i>Lupinus albus</i> L.) Represent a Unique Genepool. Open Journal of Genetics, 2014, 04, 87-98.	0.1	25
53	Assessment of molecular diversity in landraces of bread wheat (Triticum aestivum L.) held in an ex situ collection with Diversity Arrays Technology (DArTâ„¢). Australian Journal of Agricultural Research, 2007, 58, 1174.	1.5	24
54	Arbuscular mycorrhizal fungal diversity in perennial pastures; responses to long-term lime application. Plant and Soil, 2012, 351, 389-403.	3.7	24

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55	Investigation of the Genetic Diversity and Quantitative Trait Loci Accounting for Important Agronomic and Seed Quality Traits in Brassica carinata. Frontiers in Plant Science, 2017, 8, 615.	3.6	23
56	Mapping genes for resistance to Puccinia hordei in barley. Australian Journal of Agricultural Research, 2003, 54, 1323.	1.5	22
57	Construction of integrated linkage map of a recombinant inbred line population of white lupin (<i>Lupinus albus</i> L.). Breeding Science, 2013, 63, 292-300.	1.9	22
58	Identifying genetic diversity of avirulence genes in Leptosphaeria maculans using whole genome sequencing. Functional and Integrative Genomics, 2013, 13, 295-308.	3.5	21
59	Development of SSR Markers for Genetic Analysis of Silverleaf Nightshade (Solanum elaeagnifolium) and Related Species. Plant Molecular Biology Reporter, 2013, 31, 248-254.	1.8	20
60	Predicting polymorphic EST â€•SSR s in silico. Molecular Ecology Resources, 2013, 13, 538-545.	4.8	20
61	A Major Locus for Manganese Tolerance Maps on Chromosome A09 in a Doubled Haploid Population of Brassica napus L.. Frontiers in Plant Science, 2017, 8, 1952.	3.6	20
62	AFLP and SSR analysis of genetic diversity among landraces of bread wheat (Triticum aestivum L. em.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.5	19
63	Quantitative trait loci controlling kernel discoloration in barley (Hordeum vulgare L.). Australian Journal of Agricultural Research, 2003, 54, 1251.	1.5	19
64	A copia-like retrotransposon insertion in the upstream region of the SHATTERPROOF1 gene, BnSHP1.A9, is associated with quantitative variation in pod shattering resistance in oilseed rape. Journal of Experimental Botany, 2020, 71, 5402-5413.	4.8	18
65	De novo design of future rapeseed crops: Challenges and opportunities. Crop Journal, 2022, 10, 587-596.	5.2	18
66	Can genomics assist the phenological adaptation of canola to new and changing environments?. Crop and Pasture Science, 2016, 67, 284.	1.5	17
67	Validation of an Alt locus for aluminium tolerance scored with eriochrome cyanine R staining method in barley cultivar Honen (Hordeum vulgare L.). Australian Journal of Agricultural Research, 2006, 57, 113.	1.5	17
68	Evaluation of simple sequence repeat (SSR) markers from Solanum crop species for Solanum elaeagnifolium. Weed Research, 2012, 52, 217-223.	1.7	16
69	Microsatellite marker-based identification of mother plants for the reliable propagation of olive (Olea europaea L.) cultivars in Australia. Journal of Horticultural Science and Biotechnology, 2012, 87, 647-653.	1.9	14
70	Identification of QTLs associated with resistance to Phomopsis pod blight (<i>Diaporthe) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142	1.9	14
71	Genome-Wide Association Mapping Identifies Novel Loci for Quantitative Resistance to Blackleg Disease in Canola. Frontiers in Plant Science, 2020, 11, 1184.	3.6	14
72	The Rlm13 Gene, a New Player of Brassica napusâ€“Leptosphaeria maculans Interaction Maps on Chromosome C03 in Canola. Frontiers in Plant Science, 2021, 12, 654604.	3.6	14

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73	Molecular breeding for Septoria tritici blotch resistance in wheat. Cereal Research Communications, 2012, 40, 451-466.	1.6	13
74	QTL mapping reveals genomic regions for yield based on an incremental tolerance index to drought stress and related agronomic traits in canola. Crop and Pasture Science, 2020, 71, 562.	1.5	13
75	Refining the biological factors affecting virulence of Botryosphaeriaceae on grapevines. Annals of Applied Biology, 2011, 159, 467-477.	2.5	12
76	Characterisation of genetic variation for aluminium resistance and polyphenol oxidase activity in genebank accessions of spelt wheat. Breeding Science, 2009, 59, 373-381.	1.9	11
77	Multienvironment QTL analysis delineates a major locus associated with homoeologous exchanges for waterâ€use efficiency and seed yield in canola. Plant, Cell and Environment, 2022, 45, 2019-2036.	5.7	11
78	Characterization of SNP and Structural Variations in the Mitochondrial Genomes of Tilletia indica and Its Closely Related Species Formed Basis for a Simple Diagnostic Assay. PLoS ONE, 2016, 11, e0166086.	2.5	10
79	Genetic Solutions to Improve Resilience of Canola to Climate Change. , 2019, , 75-131.		10
80	Morphological variation of <scp>S</scp>olanum elaeagnifolium in southâ€eastern <scp>A</scp>ustralia. Weed Research, 2013, 53, 344-354.	1.7	9
81	Time of emergence impacts the growth and reproduction of silverleaf nightshade (Solanum) Tj ETQq1 1 0.784314 rgBT /Overlock	1.4	7
82	Genetic and physiological bases for variation in water use efficiency in canola. Food and Energy Security, 2020, 9, e237.	4.3	7
83	Breeding Brassica napus for Shatter Resistance. , 0, , .		7
84	In VitroScreening of Apple Germplasm for Resistance Against Black Spot Caused byVenturia inaequalis. Journal of New Seeds, 2001, 2, 37-46.	0.3	4
85	Molecular Breeding of Cereals for Aluminum Resistance. , 2011, , 251-287.		4
86	Synthetic hexaploid wheat as a source of novel genetic loci for aluminium tolerance. Euphytica, 2020, 216, 1.	1.2	3
87	Genetic Diversity and Lineage Based on SSR Markers of Two Genomic Resources among <i>Trifolium</i> Collections Held within the Australian Pastures Genebank. Open Journal of Genetics, 2019, 09, 1-14.	0.1	3
88	Genetic variation and structure of <scp>S</scp>olanum elaeagnifolium in <scp>A</scp>ustralia analysed by amplified fragment length polymorphism markers. Weed Research, 2013, 53, 337-343.	1.7	2
89	Genetic Variation for Weed Competition and Allelopathy in Rapeseed (Brassica napus L.). , 0, , .		2
90	Localisation of Loci Involved in Resistance to <i>Diaporthe toxica</i> and <i>Pleiochaeta setosa</i> in White Lupin (<i>Lupinus albus</i> L.). Open Journal of Genetics, 2014, 04, 210-226.	0.1	2

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91	Editorial: Advances in Breeding for Quantitative Disease Resistance. Frontiers in Plant Science, 2022, 13, 890002.	3.6	1
92	Validation of Competitive Ability of Diverse Canola Accessions against Annual Ryegrass under Glasshouse and Field Conditions. Open Journal of Genetics, 2020, 10, 17-34.	0.1	0