

# Vikas K Singh

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

4,044  
citations

126907

33  
h-index

128289

60  
g-index

72  
all docs

72  
docs citations

72  
times ranked

3514  
citing authors

#	ARTICLE	IF	CITATIONS
1	Marker-assisted forward breeding to develop a drought-, bacterial leaf blight-, and blast-resistant rice cultivar. <i>Plant Genome</i> , 2022, 15, e20170.	2.8	10
2	Development and validation of a novel core set of KASP markers for the traits improving grain yield and adaptability of rice under direct-seeded cultivation conditions. <i>Genomics</i> , 2022, 114, 110269.	2.9	9
3	Multiparent-Derived, Marker-Assisted Introgression Lines of the Elite Indian Rice Cultivar, "Krishna Hamsa"™ Show Resistance against Bacterial Blight and Blast and Tolerance to Drought. <i>Plants</i> , 2022, 11, 622.	3.5	5
4	Genomic Designing for Biotic Stress Resistant Rice. , 2021, , 1-58.		0
5	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	3.5	90
6	Genomics and breeding innovations for enhancing genetic gain for climate resilience and nutrition traits. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1829-1843.	3.6	32
7	Superior haplotypes towards development of low glycemic index rice with preferred grain and cooking quality. <i>Scientific Reports</i> , 2021, 11, 10082.	3.3	15
8	WheatQTLdb: a QTL database for wheat. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1051-1056.	2.1	47
9	Effective Crop Management and Modern Breeding Strategies to Ensure Higher Crop Productivity under Direct Seeded Rice Cultivation System: A Review. <i>Agronomy</i> , 2021, 11, 1264.	3.0	12
10	Characterization of heterosis and genomic prediction-based establishment of heterotic patterns for developing better hybrids in pigeonpea. <i>Plant Genome</i> , 2021, 14, e20125.	2.8	6
11	Marker-assisted forward and backcross breeding for improvement of elite Indian rice variety Naveen for multiple biotic and abiotic stress tolerance. <i>PLoS ONE</i> , 2021, 16, e0256721.	2.5	19
12	Genomics-assisted breeding for successful development of multiple-stress-tolerant, climate-smart rice for southern and southeastern Asia. <i>Plant Genome</i> , 2021, 14, e20074.	2.8	14
13	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106
14	Genome-wide analysis of epigenetic and transcriptional changes associated with heterosis in pigeonpea. <i>Plant Biotechnology Journal</i> , 2020, 18, 1697-1710.	8.3	38
15	Identification of heterotic groups in South-Asian-bred hybrid parents of pearl millet. <i>Theoretical and Applied Genetics</i> , 2020, 133, 873-888.	3.6	15
16	Seeking Crops with Balanced Parts for the Ideal Whole. <i>Trends in Plant Science</i> , 2020, 25, 1189-1193.	8.8	18
17	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. <i>Functional and Integrative Genomics</i> , 2020, 20, 739-761.	3.5	37
18	More and more of less and less: Is genomics-based breeding of dry direct-seeded rice (DDSR) varieties the need of hour?. <i>Plant Biotechnology Journal</i> , 2020, 18, 2173-2186.	8.3	20

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19	Development of introgression lines in high yielding, semi-dwarf genetic backgrounds to enable improvement of modern rice varieties for tolerance to multiple abiotic stresses free from undesirable linkage drag. <i>Scientific Reports</i> , 2020, 10, 13073.	3.3	16
20	Superior haplotypes for haplotype-based breeding for drought tolerance in pigeonpea ( <i>Cajanus cajan</i> ) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	8.3	61
21	Seed protein content and its relationships with agronomic traits in pigeonpea is controlled by both main and epistatic effects QTLs. <i>Scientific Reports</i> , 2020, 10, 214.	3.3	17
22	5Gs for crop genetic improvement. <i>Current Opinion in Plant Biology</i> , 2020, 56, 190-196.	7.1	134
23	Marker Assisted Forward Breeding to Combine Multiple Biotic-Abiotic Stress Resistance/Tolerance in Rice. <i>Rice</i> , 2020, 13, 29.	4.0	48
24	Unraveling candidate genomic regions responsible for delayed leaf senescence in rice. <i>PLoS ONE</i> , 2020, 15, e0240591.	2.5	4
25	Deciphering the genetic basis of root morphology, nutrient uptake, yield, and yield-related traits in rice under dry direct-seeded cultivation systems. <i>Scientific Reports</i> , 2019, 9, 9334.	3.3	37
26	Genotyping-by-sequencing based QTL mapping for rice grain yield under reproductive stage drought stress tolerance. <i>Scientific Reports</i> , 2019, 9, 14326.	3.3	46
27	Haplotype analysis of key genes governing grain yield and quality traits across 3K <scp>RG</scp> panel reveals scope for the development of tailor-made rice with enhanced genetic gains. <i>Plant Biotechnology Journal</i> , 2019, 17, 1612-1622.	8.3	87
28	Identification of genomic region(s) responsible for high iron and zinc content in rice. <i>Scientific Reports</i> , 2019, 9, 8136.	3.3	52
29	Genome-wide association study reveals significant genomic regions for improving yield, adaptability of rice under dry direct seeded cultivation condition. <i>BMC Genomics</i> , 2019, 20, 471.	2.8	26
30	Epistatic interactions of major effect drought QTLs with genetic background loci determine grain yield of rice under drought stress. <i>Scientific Reports</i> , 2019, 9, 2616.	3.3	36
31	Development of sequence-based markers for seed protein content in pigeonpea. <i>Molecular Genetics and Genomics</i> , 2019, 294, 57-68.	2.1	27
32	Toward the sequence-based breeding in legumes in the post-genome sequencing era. <i>Theoretical and Applied Genetics</i> , 2019, 132, 797-816.	3.6	147
33	Can genomics deliver climate-change ready crops?. <i>Current Opinion in Plant Biology</i> , 2018, 45, 205-211.	7.1	105
34	Current Status and Future Prospects of Next-Generation Data Management and Analytical Decision Support Tools for Enhancing Genetic Gains in Crops. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, 164, 277-292.	1.1	4
35	Development and Application of High-Density Axiom <i>Cajanus</i> SNP Array with 56K SNPs to Understand the Genome Architecture of Released Cultivars and Founder Genotypes. <i>Plant Genome</i> , 2018, 11, 180005.	2.8	35
36	Genetic variation and relationships of total seed protein content with some agronomic traits in pigeonpea ( <i>Cajanus cajan</i> (L.) Millsp.). <i>Australian Journal of Crop Science</i> , 2018, 12, 1859-1865.	0.3	19

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37	Marker-Assisted Improvement of the Elite Maintainer Line of Rice, IR 58025B for Wide Compatibility (S5n) Gene. <i>Frontiers in Plant Science</i> , 2018, 9, 1051.	3.6	10
38	Construction of genotyping-by-sequencing based high-density genetic maps and QTL mapping for fusarium wilt resistance in pigeonpea. <i>Scientific Reports</i> , 2017, 7, 1911.	3.3	55
39	Genotyping-by-sequencing of three mapping populations for identification of candidate genomic regions for resistance to sterility mosaic disease in pigeonpea. <i>Scientific Reports</i> , 2017, 7, 1813.	3.3	48
40	Indel-seq: a fast-forward genetics approach for identification of trait-associated putative candidate genomic regions and its application in pigeonpea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , 2017, 15, 906-914.	8.3	67
41	QTL-seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut ( <i>Arachis hypogaea</i> ). <i>Plant Biotechnology Journal</i> , 2017, 15, 927-941.	8.3	198
42	Sequencing Pigeonpea Genome. <i>Compendium of Plant Genomes</i> , 2017, , 93-97.	0.5	2
43	Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. <i>Frontiers in Plant Science</i> , 2016, 7, 455.	3.6	180
44	QTL-seq for rapid identification of candidate genes for 100-seed weight and root/total plant dry weight ratio under rainfed conditions in chickpea. <i>Plant Biotechnology Journal</i> , 2016, 14, 2110-2119.	8.3	177
45	Next-generation sequencing for identification of candidate genes for <i>Fusarium</i> wilt and sterility mosaic disease in pigeonpea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , 2016, 14, 1183-1194.	8.3	108
46	From Mendel's discovery on pea to today's plant genetics and breeding. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2267-2280.	3.6	26
47	Analytical and Decision Support Tools for Genomics-Assisted Breeding. <i>Trends in Plant Science</i> , 2016, 21, 354-363.	8.8	70
48	Improvement of Basmati rice varieties for resistance to blast and bacterial blight diseases using marker assisted backcross breeding. <i>Plant Science</i> , 2016, 242, 330-341.	3.6	99
49	Association of nad7a Gene with Cytoplasmic Male Sterility in Pigeonpea. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.11.0084.	2.8	28
50	Selection and Validation of Housekeeping Genes as Reference for Gene Expression Studies in Pigeonpea ( <i>Cajanus cajan</i> ) under Heat and Salt Stress Conditions. <i>Frontiers in Plant Science</i> , 2015, 6, 1071.	3.6	48
51	Genomics-assisted breeding for boosting crop improvement in pigeonpea ( <i>Cajanus cajan</i> ). <i>Frontiers in Plant Science</i> , 2015, 6, 50.	3.6	57
52	Introgression of multiple disease resistance into a maintainer of Basmati rice CMS line by marker assisted backcross breeding. <i>Euphytica</i> , 2015, 203, 97-107.	1.2	22
53	Identification of a non-redundant set of 202 in silico SSR markers and applicability of a select set in chickpea ( <i>Cicer arietinum</i> L.). <i>Euphytica</i> , 2015, 205, 381-394.	1.2	18
54	MAGIC populations in crops: current status and future prospects. <i>Theoretical and Applied Genetics</i> , 2015, 128, 999-1017.	3.6	230

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55	Identification and Validation of Selected Universal Stress Protein Domain Containing Drought-Responsive Genes in Pigeonpea ( <i>Cajanus cajan</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 1065.	3.6	39
56	Evaluation and Validation of Housekeeping Genes as Reference for Gene Expression Studies in Pigeonpea ( <i>Cajanus cajan</i> ) Under Drought Stress Conditions. <i>PLoS ONE</i> , 2015, 10, e0122847.	2.5	67
57	Validation of rapid DNA extraction protocol and their effectiveness in marker assisted selection in crop plants. <i>Indian Journal of Genetics and Plant Breeding</i> , 2015, 75, 110.	0.5	3
58	Marker-Assisted Backcrossing to Introgress Resistance to Fusarium Wilt Race 1 and Ascochyta Blight in C 214, an Elite Cultivar of Chickpea. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0035.	2.8	132
59	Marker-assisted simultaneous but stepwise backcross breeding for pyramiding blast resistance genes <i>Piz5</i> and <i>Pi54</i> into an elite Basmati rice restorer line <i>PRR78</i> <sup>TM</sup> . <i>Plant Breeding</i> , 2013, 132, 486-495.	1.9	49
60	A draft genome sequence of the pulse crop chickpea ( <i>Cicer arietinum</i> L.). <i>Plant Journal</i> , 2013, 74, 715-729.	5.7	382
61	Genetic analysis and molecular mapping of a new fertility restorer gene Rf8 for <i>Triticum timopheevi</i> cytoplasm in wheat ( <i>Triticum aestivum</i> L.) using SSR markers. <i>Genetica</i> , 2013, 141, 431-441.	1.1	21
62	Fast-track Introgression of <i>QTL Hotspot</i> for Root Traits and Other Drought Tolerance Traits in JG 11, an Elite and Leading Variety of Chickpea. <i>Plant Genome</i> , 2013, 6, plantgenome2013.07.0022.	2.8	118
63	Molecular breeding for the development of multiple disease resistance in Basmati rice. <i>AoB PLANTS</i> , 2012, 2012, pls029-pls029.	2.3	79
64	Population Structure and Genetic Diversity in Popular Rice Varieties of India as Evidenced from SSR Analysis. <i>Biochemical Genetics</i> , 2012, 50, 770-783.	1.7	24
65	Incorporation of blast resistance into <i>PRR78</i> , an elite Basmati rice restorer line, through marker assisted backcross breeding. <i>Field Crops Research</i> , 2012, 128, 8-16.	5.1	121
66	Determination of genetic relationships among elite thermosensitive genic male sterile lines (TGMS) of rice ( <i>Oryza sativa</i> L.) employing morphological and simple sequence repeat (SSR) markers. <i>Journal of Genetics</i> , 2011, 90, 11-19.	0.7	9
67	Prediction of hybrid performance based on the genetic distance of parental lines in two-line rice ( <i>Oryza sativa</i> L.) hybrids. <i>Journal of Crop Science and Biotechnology</i> , 2011, 14, 1-10.	1.5	15
68	Identification of Genotype Specific Alleles and Molecular Diversity Assessment of Popular Rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.5	23
69	Marker-assisted improvement of bacterial blight resistance in parental lines of Pusa RH10, a superfine grain aromatic rice hybrid. <i>Molecular Breeding</i> , 2010, 26, 293-305.	2.1	122