

# Vikas K Singh

## List of Publications by Year in descending order

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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	A draft genome sequence of the pulse crop chickpea ( <i>Cicer arietinum</i> ). <i>Plant Journal</i> , 2013, 74, 715-729.	5.7	382
2	MAGIC populations in crops: current status and future prospects. <i>Theoretical and Applied Genetics</i> , 2015, 128, 999-1017.	3.6	230
3	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
4	Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. <i>Frontiers in Plant Science</i> , 2016, 7, 455.	3.6	180
5	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
6	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
7	5Gs for crop genetic improvement. <i>Current Opinion in Plant Biology</i> , 2020, 56, 190-196.	7.1	134
8	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
9	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
10	Incorporation of blast resistance into PRR78, an elite Basmati rice restorer line, through marker assisted backcross breeding. <i>Field Crops Research</i> , 2012, 128, 8-16.	5.1	121
11	FastTrack Introgression of a QTL hotspot 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
12	Next-generation sequencing for identification of candidate genes for Fusarium wilt and sterility mosaic disease in pigeonpea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , 2016, 14, 1183-1194.	8.3	108
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	Can genomics deliver climate-change ready crops?. <i>Current Opinion in Plant Biology</i> , 2018, 45, 205-211.	7.1	105
15	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
16	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	3.5	90
17	Haplotype analysis of key genes governing grain yield and quality traits across 3K RG 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
18	Molecular breeding for the development of multiple disease resistance in Basmati rice. <i>AoB PLANTS</i> , 2012, 2012, pls029-pls029.	2.3	79

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19	Analytical and Decision Support Tools for Genomics-Assisted Breeding. Trends in Plant Science, 2016, 21, 354-363.	8.8	70
20	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> ). Plant Biotechnology Journal, 2017, 15, 906-914.	8.3	67
21	Evaluation and Validation of Housekeeping Genes as Reference for Gene Expression Studies in Pigeonpea ( <i>Cajanus cajan</i> ) Under Drought Stress Conditions. PLoS ONE, 2015, 10, e0122847.	2.5	67
22	Superior haplotypes for haplotype-based breeding for drought tolerance in pigeonpea ( <i>Cajanus</i> ) Tj ETQq0 0 0 ggBT/Overlock 10 Tff	8.3	61
23	Genomics-assisted breeding for boosting crop improvement in pigeonpea ( <i>Cajanus cajan</i> ). Frontiers in Plant Science, 2015, 6, 50.	3.6	57
24	Construction of genotyping-by-sequencing based high-density genetic maps and QTL mapping for fusarium wilt resistance in pigeonpea. Scientific Reports, 2017, 7, 1911.	3.3	55
25	Identification of genomic region(s) responsible for high iron and zinc content in rice. Scientific Reports, 2019, 9, 8136.	3.3	52
26	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> . Plant Breeding, 2013, 132, 486-495.	1.9	49
27	Selection and Validation of Housekeeping Genes as Reference for Gene Expression Studies in Pigeonpea ( <i>Cajanus cajan</i> ) under Heat and Salt Stress Conditions. Frontiers in Plant Science, 2015, 6, 1071.	3.6	48
28	Genotyping-by-sequencing of three mapping populations for identification of candidate genomic regions for resistance to sterility mosaic disease in pigeonpea. Scientific Reports, 2017, 7, 1813.	3.3	48
29	Marker Assisted Forward Breeding to Combine Multiple Biotic-Abiotic Stress Resistance/Tolerance in Rice. Rice, 2020, 13, 29.	4.0	48
30	WheatQTLdb: a QTL database for wheat. Molecular Genetics and Genomics, 2021, 296, 1051-1056.	2.1	47
31	Genotyping-by-sequencing based QTL mapping for rice grain yield under reproductive stage drought stress tolerance. Scientific Reports, 2019, 9, 14326.	3.3	46
32	Identification and Validation of Selected Universal Stress Protein Domain Containing Drought-Responsive Genes in Pigeonpea ( <i>Cajanus cajan</i> L.). Frontiers in Plant Science, 2015, 6, 1065.	3.6	39
33	Genome-wide analysis of epigenetic and transcriptional changes associated with heterosis in pigeonpea. Plant Biotechnology Journal, 2020, 18, 1697-1710.	8.3	38
34	Deciphering the genetic basis of root morphology, nutrient uptake, yield, and yield-related traits in rice under dry direct-seeded cultivation systems. Scientific Reports, 2019, 9, 9334.	3.3	37
35	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. Functional and Integrative Genomics, 2020, 20, 739-761.	3.5	37
36	Epistatic interactions of major effect drought QTLs with genetic background loci determine grain yield of rice under drought stress. Scientific Reports, 2019, 9, 2616.	3.3	36

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37	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
38	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
39	Association of nad7a Gene with Cytoplasmic Male Sterility in Pigeonpea. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.11.0084.	2.8	28
40	Development of sequence-based markers for seed protein content in pigeonpea. <i>Molecular Genetics and Genomics</i> , 2019, 294, 57-68.	2.1	27
41	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
42	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
43	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
44	Identification of Genotype Specific Alleles and Molecular Diversity Assessment of Popular Rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	23
45	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
46	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
47	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
48	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
49	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
50	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
51	Seeking Crops with Balanced Parts for the Ideal Whole. <i>Trends in Plant Science</i> , 2020, 25, 1189-1193.	8.8	18
52	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
53	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
54	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

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55	Identification of heterotic groups in South-Asian-bred hybrid parents of pearl millet. Theoretical and Applied Genetics, 2020, 133, 873-888.	3.6	15
56	Superior haplotypes towards development of low glycemic index rice with preferred grain and cooking quality. Scientific Reports, 2021, 11, 10082.	3.3	15
57	Genomics-assisted breeding for successful development of multiple-stress-tolerant, climate-smart rice for southern and southeastern Asia. Plant Genome, 2021, 14, e20074.	2.8	14
58	Effective Crop Management and Modern Breeding Strategies to Ensure Higher Crop Productivity under Direct Seeded Rice Cultivation System: A Review. Agronomy, 2021, 11, 1264.	3.0	12
59	Marker-Assisted Improvement of the Elite Maintainer Line of Rice, IR 58025B for Wide Compatibility (S5n) Gene. Frontiers in Plant Science, 2018, 9, 1051.	3.6	10
60	Marker-assisted forward breeding to develop a drought-, bacterial leaf blight-, and blast-resistant rice cultivar. Plant Genome, 2022, 15, e20170.	2.8	10
61	Determination of genetic relationships among elite thermosensitive genic male sterile lines (TCMS) of rice ( <i>Oryza sativa</i> L.) employing morphological and simple sequence repeat (SSR) markers. Journal of Genetics, 2011, 90, 11-19.	0.7	9
62	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. Genomics, 2022, 114, 110269.	2.9	9
63	Characterization of heterosis and genomic prediction-based establishment of heterotic patterns for developing better hybrids in pigeonpea. Plant Genome, 2021, 14, e20125.	2.8	6
64	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. Plants, 2022, 11, 622.	3.5	5
65	Current Status and Future Prospects of Next-Generation Data Management and Analytical Decision Support Tools for Enhancing Genetic Gains in Crops. Advances in Biochemical Engineering/Biotechnology, 2018, 164, 277-292.	1.1	4
66	Unraveling candidate genomic regions responsible for delayed leaf senescence in rice. PLoS ONE, 2020, 15, e0240591.	2.5	4
67	Validation of rapid DNA extraction protocol and their effectiveness in marker assisted selection in crop plants. Indian Journal of Genetics and Plant Breeding, 2015, 75, 110.	0.5	3
68	Sequencing Pigeonpea Genome. Compendium of Plant Genomes, 2017, , 93-97.	0.5	2
69	Genomic Designing for Biotic Stress Resistant Rice. , 2021, , 1-58.		0