

# Senapathy Senthilvel

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

1,015  
citations

471509

17  
h-index

434195

31  
g-index

35  
all docs

35  
docs citations

35  
times ranked

1120  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic regions associated with resistance to Fusarium wilt in castor identified through linkage and association mapping approaches. <i>Genome</i> , 2022, 65, 123-136.	2.0	9
2	Waxy bloom on capsules is a major determinant of early infection by gray mold ( <i>Amphobotrys</i> ) in castor. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2022, 170, 337-348.	1.0	2
3	Genetic mapping reveals a major QTL associated with tolerance to the aphid, <i>Uroleucon compositae</i> (Theobald) in safflower ( <i>Carthamus tinctorius</i> ). <i>Plant Breeding</i> , 2021, 140, 320-330.	1.9	6
4	Marker-assisted selection for fast-track breeding of high oleic lines in safflower ( <i>Carthamus tinctorius</i> ). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 98-104.	0.8	5
5	Development and characterization of tetraploid castor plants. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 98-104.	0.8	5
6	Wilt disease of castor: an overview. <i>Indian Phytopathology</i> , 2019, 72, 575-585.	1.2	7
7	Development and validation of an SNP genotyping array and construction of a high-density linkage map in castor. <i>Scientific Reports</i> , 2019, 9, 3003.	3.3	17
8	Genetic characterization of resistance to wilt disease caused by <i>Fusarium oxysporum</i> f. sp. <i>ricini</i> in castor ( <i>Ricinus communis</i> L.). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018, 16, 169-177.	0.8	10
9	Genetic variability and population structure in a collection of inbred lines derived from a core germplasm of castor. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 27-34.	1.7	17
10	Genetic diversity of safflower ( <i>Carthamus tinctorius</i> L.) germplasm as revealed by SSR markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 1-11.	0.8	25
11	Establishing a high throughput screening method for large scale phenotyping of castor genotypes for resistance to Fusarium wilt disease. <i>Phytoparasitica</i> , 2016, 44, 539-548.	1.2	17
12	QTL mapping of pearl millet rust resistance using an integrated DArT- and SSR-based linkage map. <i>Euphytica</i> , 2016, 209, 461-476.	1.2	24
13	Genetic Markers, Trait Mapping and Marker-Assisted Selection in Plant Breeding. , 2015, , 65-88.		7
14	Quantitative trait loci associated with constitutive traits control water use in pearl millet [ <i>Pennisetum glaucum</i> (L.) R. Br.]. <i>Plant Biology</i> , 2015, 17, 1073-1084.	3.8	22
15	Development of a Set of Chromosome Segment Substitution Lines in Pearl Millet [ <i>Pennisetum glaucum</i> (L.) R. Br.]. <i>Crop Science</i> , 2014, 54, 2175-2182.	1.8	12
16	Population structure and linkage disequilibrium of ICRISAT foxtail millet ( <i>Setaria italica</i> (L.) P. Beauv.) core collection. <i>Euphytica</i> , 2014, 196, 423-435.	1.2	16
17	Pearl millet [ <i>Pennisetum glaucum</i> (L.) R. Br.] consensus linkage map constructed using four RIL mapping populations and newly developed EST-SSRs. <i>BMC Genomics</i> , 2013, 14, 159.	2.8	94
18	Evaluation of genetic diversity in Magnaporthe grisea populations adapted to finger millet using simple sequence repeats (SSRs) markers. <i>Physiological and Molecular Plant Pathology</i> , 2013, 84, 10-18.	2.5	36

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19	Assessment of genetic diversity in the sorghum reference set using EST-SSR markers. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2051-2064.	3.6	73
20	Construction of Genetic Linkage Map and QTL Analysis of Sink-Size Traits in Pearl Millet ( <i>Pennisetum glaucum</i> ). <i>ISRN Genetics</i> , 2013, 2013, 1-14.	0.2	12
21	Assessing genetic diversity, allelic richness and genetic relationship among races in ICRISAT foxtail millet core collection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2012, 10, 214-223.	0.8	22
22	Water saving traits co-map with a major terminal drought tolerance quantitative trait locus in pearl millet [ <i>Pennisetum glaucum</i> (L.) R. Br.]. <i>Molecular Breeding</i> , 2012, 30, 1337-1353.	2.1	57
23	Development of new sources of tetraploid <i>Arachis</i> to broaden the genetic base of cultivated groundnut ( <i>Arachis hypogaea</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2011, 58, 889-907.	1.6	64
24	Identification and Characterization of Toxigenic <i>Fusaria</i> Associated with Sorghum Grain Mold Complex in India. <i>Mycopathologia</i> , 2011, 171, 223-230.	3.1	30
25	Development of a molecular linkage map of pearl millet integrating DArT and SSR markers. <i>Theoretical and Applied Genetics</i> , 2011, 123, 239-250.	3.6	75
26	SSR allelic diversity in relation to morphological traits and resistance to grain mould in sorghum. <i>Crop and Pasture Science</i> , 2010, 61, 230.	1.5	8
27	In silico mapping of important genes and markers available in the public domain for efficient sorghum breeding. <i>Molecular Breeding</i> , 2010, 26, 409-418.	2.1	32
28	Exploiting rice-sorghum synteny for targeted development of EST-SSRs to enrich the sorghum genetic linkage map. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1193-1204.	3.6	73
29	QTL and QTL-Environment Effects on Agronomic and Nitrogen Acquisition Traits in Rice. <i>Journal of Integrative Plant Biology</i> , 2008, 50, 1108-1117.	8.5	54
30	Development and mapping of Simple Sequence Repeat markers for pearl millet from data mining of Expressed Sequence Tags. <i>BMC Plant Biology</i> , 2008, 8, 119.	3.6	114
31	Laboratory Information Management Software for genotyping workflows: applications in high throughput crop genotyping. <i>BMC Bioinformatics</i> , 2006, 7, 383.	2.6	25
32	Genetics, fertility behaviour and molecular marker analysis of a new TGMS line, TS6, in rice. <i>Plant Breeding</i> , 2004, 123, 235-240.	1.9	6