

Laurent Gentzbittel

List of Publications by Year in descending order

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72
papers

3,650
citations

117625

34
h-index

138484

58
g-index

74
all docs

74
docs citations

74
times ranked

3854
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic mapping of loci involved in oil tocopherol composition control in Russian sunflower (<i>Helianthus annuus</i> L.) lines. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	2
2	Activity assessment of tomato endophytic bacteria bioactive compounds for the postharvest biocontrol of <i>Botrytis cinerea</i> . <i>Postharvest Biology and Technology</i> , 2021, 172, 111389.	6.0	52
3	Identification of Key Metabolic Pathways and Biomarkers Underlying Flowering Time of Guar (<i>Cyamopsis tetragonoloba</i> (L.) Taub.) via Integrated Transcriptome-Metabolome Analysis. <i>Genes</i> , 2021, 12, 952.	2.4	5
4	Development of SNP Set for the Marker-Assisted Selection of Guar (<i>Cyamopsis tetragonoloba</i> (L.)) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	3.5	2
5	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106
6	WhoGEM: an admixture-based prediction machine accurately predicts quantitative functional traits in plants. <i>Genome Biology</i> , 2019, 20, 106.	8.8	9
7	Proteomics analysis of <i>Medicago truncatula</i> response to infection by the phytopathogenic bacterium <i>Ralstonia solanacearum</i> points to jasmonate and salicylate defence pathways. <i>Cellular Microbiology</i> , 2018, 20, e12796.	2.1	20
8	Cadmium-induced changes in antioxidative systems and differentiation in roots of contrasted <i>Medicago truncatula</i> lines. <i>Protoplasma</i> , 2017, 254, 473-489.	2.1	35
9	<i>Medicago truncatula</i> Oleanolic-Derived Saponins Are Correlated with Caterpillar Deterrence. <i>Journal of Chemical Ecology</i> , 2017, 43, 712-724.	1.8	16
10	Genetic determinism of reproductive fitness traits under drought stress in the model legume <i>Medicago truncatula</i> . <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	2.1	4
11	<i>Medicago truncatula</i> : Genetic and Genomic Resources. <i>Current Protocols in Plant Biology</i> , 2017, 2, 318-349.	2.8	12
12	Quantitative Resistance to Verticillium Wilt in <i>Medicago truncatula</i> Involves Eradication of the Fungus from Roots and Is Associated with Transcriptional Responses Related to Innate Immunity. <i>Frontiers in Plant Science</i> , 2016, 7, 1431.	3.6	13
13	Naturally occurring diversity helps to reveal genes of adaptive importance in legumes. <i>Frontiers in Plant Science</i> , 2015, 6, 269.	3.6	37
14	Effect of cadmium pollution on mobilization of embryo reserves in seedlings of six contrasted <i>Medicago truncatula</i> lines. <i>Phytochemistry</i> , 2015, 111, 98-106.	2.9	19
15	Achievements and Challenges in Legume Breeding for Pest and Disease Resistance. <i>Critical Reviews in Plant Sciences</i> , 2015, 34, 195-236.	5.7	153
16	Genetic variability and identification of quantitative trait loci affecting plant growth and chlorophyll fluorescence parameters in the model legume <i>Medicago truncatula</i> under control and salt stress conditions. <i>Functional Plant Biology</i> , 2014, 41, 983.	2.1	8
17	Banning of methyl bromide for seed treatment: could <i>Ditylenchus dipsaci</i> again become a major threat to alfalfa production in Europe?. <i>Pest Management Science</i> , 2014, 70, 1017-1022.	3.4	14
18	The small RNA diversity from <i>Medicago truncatula</i> roots under biotic interactions evidences the environmental plasticity of the miRNAome. <i>Genome Biology</i> , 2014, 15, 457.	8.8	78

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19	Oxidative injury and antioxidant genes regulation in cadmium-exposed radicles of six contrasted <i>Medicago truncatula</i> genotypes. <i>Environmental Science and Pollution Research</i> , 2014, 21, 8070-8083.	5.3	27
20	Quantitative trait loci associated with resistance to a potato isolate of <i>Verticillium albo-atrum</i> in <i>Medicago truncatula</i> . <i>Plant Pathology</i> , 2014, 63, 308-315.	2.4	13
21	Detection of partial resistance quantitative trait loci against <i>Didymella pinodes</i> in <i>Medicago truncatula</i> . <i>Molecular Breeding</i> , 2014, 33, 589-599.	2.1	7
22	An improved genome release (version Mt4.0) for the model legume <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2014, 15, 312.	2.8	381
23	Natural diversity in the model legume <i>Medicago truncatula</i> allows identifying distinct genetic mechanisms conferring partial resistance to <i>Verticillium</i> wilt. <i>Journal of Experimental Botany</i> , 2013, 64, 317-332.	4.8	63
24	<i>QRRS1</i> , an <i>R</i> -locus required for <i>Medicago truncatula</i> quantitative resistance to <i>Ralstonia solanacearum</i> . <i>New Phytologist</i> , 2013, 199, 758-772.	7.3	37
25	Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume <i>Medicago truncatula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E864-70.	7.1	220
26	HACRE1, a recently inserted copia-like retrotransposon of sunflower (<i>Helianthus annuus</i> L.). <i>Genome</i> , 2009, 52, 904-911.	2.0	15
27	Dissection of Bacterial Wilt on <i>Medicago truncatula</i> Revealed Two Type III Secretion System Effectors Acting on Root Infection Process and Disease Development. <i>Plant Physiology</i> , 2009, 150, 1713-1722.	4.8	65
28	Real-time PCR monitoring of signal transduction related genes involved in water stress tolerance mechanism of sunflower. <i>Plant Physiology and Biochemistry</i> , 2009, 47, 139-145.	5.8	20
29	The <i>RAP1</i> Gene Confers Effective, Race-Specific Resistance to the Pea Aphid in <i>Medicago truncatula</i> Independent of the Hypersensitive Reaction. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1645-1655.	2.6	50
30	Differential expression of defence-related genes between compatible and partially compatible sunflower- <i>Phoma macdonaldii</i> interactions. <i>Crop Protection</i> , 2008, 27, 740-746.	2.1	6
31	A Comprehensive Analysis of the Combined Effects of High Light and High Temperature Stresses on Gene Expression in Sunflower. <i>Annals of Botany</i> , 2008, 102, 127-140.	2.9	42
32	Characterization of the Interaction Between the Bacterial Wilt Pathogen <i>Ralstonia solanacearum</i> and the Model Legume Plant <i>Medicago truncatula</i> . <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 159-167.	2.6	106
33	Genetic analysis of plant water status and osmotic adjustment in recombinant inbred lines of sunflower under two water treatments. <i>Plant Science</i> , 2007, 172, 773-787.	3.6	125
34	QTL mapping of partial resistance to <i>Phoma</i> basal stem and root necrosis in sunflower (<i>Helianthus</i>). <i>Plant Pathology</i> , 2007, 56, 855-861.	3.6	20
35	Somatic embryogenesis from thin epidermal layers in sunflower and chromosomal regions controlling the response. <i>Plant Science</i> , 2007, 173, 247-252.	3.6	7
36	Quantitative trait loci associated with isolate specific and isolate nonspecific partial resistance to <i>Phoma macdonaldii</i> in sunflower. <i>Plant Pathology</i> , 2007, 56, 855-861.	2.4	27

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37	Transcriptional profiles of primary metabolism and signal transduction-related genes in response to water stress in field-grown sunflower genotypes using a thematic cDNA microarray. <i>Planta</i> , 2007, 226, 601-617.	3.2	37
38	A cDNA microarray approach to decipher sunflower (<i>Helianthus annuus</i>) responses to the necrotrophic fungus <i>Phoma macdonaldii</i> . <i>New Phytologist</i> , 2006, 170, 523-536.	7.3	38
39	Primary metabolic pathways and signal transduction in sunflower (<i>Helianthus annuus</i> L.): comparison of transcriptional profiling in leaves and immature embryos using cDNA microarrays. <i>Planta</i> , 2006, 223, 948-964.	3.2	15
40	Genetic variability for physiological traits under drought conditions and differential expression of water stress-associated genes in sunflower (<i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 2006, 114, 193-207.	3.6	104
41	<i>Ralstonia solanacearum</i> requires F-box-like domain-containing type III effectors to promote disease on several host plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14620-14625.	7.1	202
42	Transcriptional profiling of sunflower plants growing under low temperatures reveals an extensive down-regulation of gene expression associated with chilling sensitivity. <i>Journal of Experimental Botany</i> , 2006, 57, 3109-3122.	4.8	39
43	Somatic embryogenesis by liquid culture of epidermal layers in sunflower: from genetic control to cell development. <i>Plant Cell, Tissue and Organ Culture</i> , 2005, 81, 331-337.	2.3	3
44	Comparative analysis of early embryonic sunflower cDNA libraries. <i>Plant Molecular Biology</i> , 2005, 57, 255-270.	3.9	18
45	Identification of QTLs for germination and seedling development in sunflower (<i>Helianthus annuus</i> L.). <i>Plant Science</i> , 2005, 169, 221-227.	3.6	24
46	The Iccare web server: an attempt to merge sequence and mapping information for plant and animal species. <i>Nucleic Acids Research</i> , 2004, 32, W429-W434.	14.5	35
47	Differential regulation of ACC synthase genes in cold-dependent and -independent ripening in pear fruit. <i>Plant, Cell and Environment</i> , 2004, 27, 1197-1210.	5.7	67
48	Sequence evaluation of four specific cDNA libraries for developmental genomics of sunflower. <i>Molecular Genetics and Genomics</i> , 2004, 271, 367-375.	2.1	18
49	Mass cloning of differential and nondifferential transcript-derived fragments from cDNA-AFLP experiments in sunflower. <i>Plant Molecular Biology Reporter</i> , 2004, 22, 165-171.	1.8	4
50	Genotypic variation and identification of QTLs for agronomic traits, using AFLP and SSR markers in RILs of sunflower (<i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 2004, 109, 1353-1360.	3.6	58
51	Combined mapping of DALP and AFLP markers in cultivated sunflower using F9 recombinant inbred lines. <i>Theoretical and Applied Genetics</i> , 2003, 106, 1068-1074.	3.6	20
52	Mapping and analysis of quantitative trait loci for grain oil content and agronomic traits using AFLP and SSR in sunflower (<i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 2002, 106, 149-156.	3.6	52
53	A QTL analysis of sunflower partial resistance to downy mildew (<i>Plasmopara halstedii</i>) and black stem (<i>Phoma macdonaldii</i>) by the use of recombinant inbred lines (RILs). <i>Theoretical and Applied Genetics</i> , 2002, 104, 490-496.	3.6	54
54	A bacterial artificial chromosome (BAC) library for sunflower, and identification of clones containing genes for putative transmembrane receptors. <i>Molecular Genetics and Genomics</i> , 2002, 266, 979-987.	2.1	25

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55	QTL analysis of photosynthesis and water status traits in sunflower (<i>Helianthus annuus</i> L.) under greenhouse conditions. <i>Journal of Experimental Botany</i> , 2001, 52, 1857-1864.	4.8	99
56	Combining-ability analysis of somatic embryogenesis from epidermal layers in the sunflower (<i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 2000, 100, 621-624.	3.6	9
57	AFLP mapping of QTLs for in vitro organogenesis traits using recombinant inbred lines in sunflower (<i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 2000, 101, 1299-1306.	3.6	59
58	Genotypic variation and chromosomal location of QTLs for somatic embryogenesis revealed by epidermal layers culture of recombinant inbred lines in the sunflower (<i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 2000, 101, 1307-1312.	3.6	31
59	Genetic control of in vitro-organogenesis in recombinant inbred lines of sunflower (<i>Helianthus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 1.9 12		
60	Influence of genotype and gelling agents on in vitro regeneration by organogenesis in sunflower. <i>Plant Cell, Tissue and Organ Culture</i> , 1999, 59, 65-69.	2.3	14
61	A composite map of expressed sequences and phenotypic traits of the sunflower (<i>Helianthus annuus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 3.6 FO1		
62	Title is missing!. <i>Molecular Breeding</i> , 1998, 4, 215-226.	2.1	93
63	Cloning of molecular markers for disease resistance in sunflower, <i>Helianthus annuus</i> L.. <i>Theoretical and Applied Genetics</i> , 1998, 96, 519-525.	3.6	95
64	The genetics of resistance to five races of downy mildew (<i>Plasmopara halstedii</i>) in sunflower (<i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 1997, 95, 584-589.	3.6	84
65	Colocation of downy mildew (<i>Plasmopara halstedii</i>) resistance genes in sunflower (<i>Helianthus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 1.2 51		
66	RFLP and RAPD mapping of the sunflower Pl1 locus for resistance to <i>Plasmopara halstedii</i> race 1. <i>Theoretical and Applied Genetics</i> , 1995, 91, 733-737.	3.6	75
67	Development of a consensus linkage RFLP map of cultivated sunflower (<i>Helianthus annuus</i> L.). <i>Theoretical and Applied Genetics</i> , 1995, 90, 1079-1086.	3.6	157
68	Assessment of inter- and intra-inbred line variability in sunflower (<i>Helianthus annuus</i>) by RFLPs. <i>Genome</i> , 1995, 38, 1040-1048.	2.0	29
69	RFLP studies of genetic relationships among inbred lines of the cultivated sunflower, <i>Helianthus annuus</i> L.: evidence for distinct restorer and maintainer germplasm pools. <i>Theoretical and Applied Genetics</i> , 1994, 89, 419-425.	3.6	68
70	Improvement of a BASIC Program to Construct Evolutionary Trees from Restriction Endonuclease Data with the Use of PASCAL. <i>Journal of Heredity</i> , 1990, 81, 491-492.	2.4	14
71	Properties and nucleotide sequence of a mitochondrial plasmid from sunflower. <i>Current Genetics</i> , 1989, 15, 283-289.	1.7	23
72	A BASIC Program to Construct Evolutionary Trees from Restriction Endonuclease Data. <i>Journal of Heredity</i> , 1989, 80, 254-254.	2.4	7