

# 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	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
2	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
3	<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
4	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
5	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
6	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
7	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
8	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106
9	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
10	A composite map of expressed sequences and phenotypic traits of the sunflower ( <i>Helianthus annuus</i> ) Tj ETQq0 0 0,rgBT /Overlock 10 Tf	3.8	101
11	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
12	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
13	Title is missing!. <i>Molecular Breeding</i> , 1998, 4, 215-226.	2.1	93
14	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
15	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
16	RFLP and RAPD mapping of the sunflower PI1 locus for resistance to <i>Plasmopara halstedii</i> race 1. <i>Theoretical and Applied Genetics</i> , 1995, 91, 733-737.	3.6	75
17	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
18	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

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19	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
20	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
21	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
22	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
23	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
24	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
25	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
26	Colocation of downy mildew ( <i>Plasmopara halstedii</i> ) resistance genes in sunflower ( <i>Helianthus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462	1.2	51
27	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
28	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
29	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
30	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
31	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
32	<i>MtQRRS1</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
33	Naturally occurring diversity helps to reveal genes of adaptive importance in legumes. <i>Frontiers in Plant Science</i> , 2015, 6, 269.	3.6	37
34	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
35	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
36	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

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37	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
38	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
39	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
40	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
41	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
42	Properties and nucleotide sequence of a mitochondrial plasmid from sunflower. <i>Current Genetics</i> , 1989, 15, 283-289.	1.7	23
43	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
44	QTL mapping of partial resistance to <i>Phoma</i> basal stem and root necrosis in sunflower ( <i>Helianthus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	20
45	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
46	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
47	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
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	Comparative analysis of early embryonic sunflower cDNA libraries. <i>Plant Molecular Biology</i> , 2005, 57, 255-270.	3.9	18
50	<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
51	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
52	HACRE1, a recently inserted copia-like retrotransposon of sunflower ( <i>Helianthus annuus</i> L.). <i>Genome</i> , 2009, 52, 904-911.	2.0	15
53	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
54	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

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55	Banning of methyl bromide for seed treatment: could <i>Ditylenchus dipsaci</i> again become a major threat to alfalfa production in Europe?. Pest Management Science, 2014, 70, 1017-1022.	3.4	14
56	Quantitative trait loci associated with resistance to a potato isolate of <i>Verticillium albo-atrum</i> in <i>Medicago truncatula</i> . Plant Pathology, 2014, 63, 308-315.	2.4	13
57	Quantitative Resistance to Verticillium Wilt in Medicago truncatula Involves Eradication of the Fungus from Roots and Is Associated with Transcriptional Responses Related to Innate Immunity. Frontiers in Plant Science, 2016, 7, 1431.	3.6	13
58	Genetic control of in vitro-organogenesis in recombinant inbred lines of sunflower (Helianthus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	1.9	12
59	<i>Medicago truncatula</i> : Genetic and Genomic Resources. Current Protocols in Plant Biology, 2017, 2, 318-349.	2.8	12
60	Combining-ability analysis of somatic embryogenesis from epidermal layers in the sunflower (Helianthus annuus L.). Theoretical and Applied Genetics, 2000, 100, 621-624.	3.6	9
61	WhoGEM: an admixture-based prediction machine accurately predicts quantitative functional traits in plants. Genome Biology, 2019, 20, 106.	8.8	9
62	Genetic variability and identification of quantitative trait loci affecting plant growth and chlorophyll fluorescence parameters in the model legume Medicago truncatula under control and salt stress conditions. Functional Plant Biology, 2014, 41, 983.	2.1	8
63	A BASIC Program to Construct Evolutionary Trees from Restriction Endonuclease Data. Journal of Heredity, 1989, 80, 254-254.	2.4	7
64	Somatic embryogenesis from thin epidermal layers in sunflower and chromosomal regions controlling the response. Plant Science, 2007, 173, 247-252.	3.6	7
65	Detection of partial resistance quantitative trait loci against Didymella pinodes in Medicago truncatula. Molecular Breeding, 2014, 33, 589-599.	2.1	7
66	Differential expression of defence-related genes between compatible and partially compatible sunflower-Phoma macdonaldii interactions. Crop Protection, 2008, 27, 740-746.	2.1	6
67	Identification of Key Metabolic Pathways and Biomarkers Underlying Flowering Time of Guar (Cyamopsis tetragonoloba (L.) Taub.) via Integrated Transcriptome-Metabolome Analysis. Genes, 2021, 12, 952.	2.4	5
68	Mass cloning of differential and nondifferential transcript-derived fragments from cDNA-AFLP experiments in sunflower. Plant Molecular Biology Reporter, 2004, 22, 165-171.	1.8	4
69	Genetic determinism of reproductive fitness traits under drought stress in the model legume Medicago truncatula. Acta Physiologiae Plantarum, 2017, 39, 1.	2.1	4
70	Somatic embryogenesis by liquid culture of epidermal layers in sunflower: from genetic control to cell development. Plant Cell, Tissue and Organ Culture, 2005, 81, 331-337.	2.3	3
71	Development of SNP Set for the Marker-Assisted Selection of Guar (Cyamopsis tetragonoloba (L.)) Tj ETQq1 1 0.784314 rgBT /Overlock 2	3.5	2
72	Genetic mapping of loci involved in oil tocopherol composition control in Russian sunflower ( <i>Helianthus annuus</i> L.) lines. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	2