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List of Publications by Year
in descending order

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92 papers	7,261 citations	57758 44 h-index	56724 83 g-index
94 all docs	94 docs citations	94 times ranked	7432 citing authors

#	Article	IF	Citations
1	Toward nitrogen-fixing plants. Science, 2018, 359, 869-870.	12.6	82
2	Improving Nitrogen Use Efficient in Crop Plants Using Biotechnology Approaches. , 2018, , 15-35.		6
3	The Arabidopsis paraquat resistant1 mutant accumulates leucine upon dark treatment. Botany, 2017, 95, 751-761.	1.0	3
4	Understanding Plant Nitrogen Metabolism through Metabolomics and Computational Approaches. Plants, 2016, 5, 39.	3.5	41
5	Identification of Nitrogen Use Efficiency Genes in Barley: Searching for QTLs Controlling Complex Physiological Traits. Frontiers in Plant Science, 2016, 7, 1587.	3.6	59
6	The impact on nitrogen-efficient phenotypes when aspartate aminotransferase is expressed tissue-specifically in Brassica napus. New Negatives in Plant Science, 2016, 3-4, 1-9.	0.9	5
7	â€œGenes, Meet Gasesâ€: The Role of Plant Nutrition and Genomics in Addressing Greenhouse Gas Emissions. , 2016, , 149-172.		8
8	Yield and Production Gaps in Rainfed Wheat, Barley, and Canola in Alberta. Frontiers in Plant Science, 2015, 6, 990.	3.6	42
9	The Genetics of Nitrogen Use Efficiency in Crop Plants. Annual Review of Genetics, 2015, 49, 269-289.	7.6	217
10	Alanine Aminotransferase Variants Conferring Diverse NUE Phenotypes in Arabidopsis thaliana. PLoS ONE, 2015, 10, e0121830.	2.5	28
11	The challenges of commercializing second-generation transgenic crop traits necessitate the development of international public sector research infrastructure. Journal of Experimental Botany, 2014, 65, 5673-5682.	4.8	18
12	Physiological analysis of nitrogen-efficient rice overexpressing alanine aminotransferase under different N regimes. Botany, 2013, 91, 866-883.	1.0	36
13	Manipulation of microRNA expression to improve nitrogen use efficiency. Plant Science, 2013, 210, 70-81.	3.6	83
14	Gibberellin 3-oxidase Gene Expression Patterns Influence Gibberellin Biosynthesis, Growth, and Development in Pea. Plant Physiology, 2013, 163, 929-945.	4.8	97
15	Analysis of the Enzymatic Properties of a Broad Family of Alanine Aminotransferases. PLoS ONE, 2013, 8, e55032.	2.5	26
16	The Rice R2R3-MYB Transcription Factor OsMYB55 Is Involved in the Tolerance to High Temperature and Modulates Amino Acid Metabolism. PLoS ONE, 2012, 7, e52030.	2.5	163
17	Engineering nitrogen use efficient crop plants: the current status. Plant Biotechnology Journal, 2012, 10, 1011-1025.	8.3	332
18	Future Prospects for Cereals That Fix Nitrogen. Science, 2011, 333, 416-417.	12.6	160

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19	Introgression potential between safflower (Carthamus tinctorius) and wild relatives of the genus Carthamus. BMC Plant Biology, 2011, 11, 47.	3.6	25
20	Analysis of B-Genome Chromosome Introgression in Interspecific Hybrids of Brassica napus Ã— B. carinata. Genetics, 2011, 187, 659-673.	2.9	48
21	Fertilizing Nature: A Tragedy of Excess in the Commons. PLoS Biology, 2011, 9, e1001124.	5.6	361
22	A phylogenetic investigation of Carthamus combining sequence and microsatellite data. Plant Systematics and Evolution, 2010, 287, 85-97.	0.9	26
23	Selection Efficiency across Environments in Improvement of Barley Yield for Moderately Low Nitrogen Environments. Crop Science, 2010, 50, 451-457.	1.8	22
24	The APETALA-2-Like Transcription Factor OsAP2-39 Controls Key Interactions between Abscisic Acid and Gibberellin in Rice. PLoS Genetics, 2010, 6, e1001098.	3.5	161
25	Nitrogen use efficiencies of spring barley grown under varying nitrogen conditions in the field and growth chamber. Annals of Botany, 2010, 105, 1171-1182.	2.9	78
26	Development of molecular markers and linkage maps for the Carthamus species C.Âtinctorius and C.Âoxyacanthus. Genome, 2010, 53, 266-276.	2.0	35
27	A high-throughput Agrobacterium tumefaciens-mediated transformation system for molecular breeding and functional genomics of rice (Oryza sativa L.). Plant Biotechnology, 2010, 27, 47-58.	1.0	5
28	Genetic Variability in Nitrogen Use Efficiency of Spring Barley. Crop Science, 2009, 49, 1259-1269.	1.8	77
29	Directed evolution of acyl-CoA:diacylglycerol acyltransferase: Development and characterization of Brassica napus DGAT1 mutagenized libraries. Plant Physiology and Biochemistry, 2009, 47, 456-461.	5.8	53
30	Potential for seed-mediated gene flow in agroecosystems from transgenic safflower (Carthamus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	2.4	18
31	Transcriptome analysis of nitrogenâ€efficient rice overâ€expressing alanine aminotransferase. Plant Biotechnology Journal, 2009, 7, 562-576.	8.3	74
32	Pollen-mediated gene flow from transgenic safflower (Carthamus tinctoriusL.) intended for plant molecular farming to conventional safflower. Environmental Biosafety Research, 2009, 8, 19-32.	1.1	13
33	Genetic engineering of improved nitrogen use efficiency in rice by the tissueâ€specific expression of alanine aminotransferase. Plant Biotechnology Journal, 2008, 6, 722-732.	8.3	270
34	Functional analysis of lactate dehydrogenase during hypoxic stress in Arabidopsis. Functional Plant Biology, 2008, 35, 131.	2.1	53
35	Detecting and Quantifying the Adventitious Presence of Transgenic Seeds in Safflower, Carthamus tinctorius L.. Journal of Agricultural and Food Chemistry, 2008, 56, 5506-5513.	5.2	10
36	Glutamate deamination by glutamate dehydrogenase plays a central role in amino acid catabolism in plants. Plant Signaling and Behavior, 2008, 3, 842-843.	2.4	28

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37	NAD(H)-dependent glutamate dehydrogenase is essential for the survival ofArabidopsis thalianaduring dark-induced carbon starvation. Journal of Experimental Botany, 2008, 59, 667-680.	4.8	138
38	Contribution of the GABA shunt to hypoxia-induced alanine accumulation in roots of Arabidopsis thaliana. Plant and Cell Physiology, 2008, 49, 92-102.	3.1	177
39	Interactions between Na⁺channels and Na⁺-HCO₃^{â^'}cotransporters in the freshwater fish gill MR cell: a model for transepithelial Na⁺uptake. American Journal of Physiology - Cell Physiology, 2007, 292, C935-C944.	4.6	62
40	Genetic use restriction technologies (GURTs): strategies to impede transgene movement. Trends in Plant Science, 2007, 12, 177-183.	8.8	56
41	Detection of naphthenic acids in fish exposed to commercial naphthenic acids and oil sands process-affected water. Chemosphere, 2007, 68, 518-527.	8.2	38
42	Blood and gill responses to HCl infusions in the Pacific hagfish (Eptatretus stoutii). Canadian Journal of Zoology, 2007, 85, 855-862.	1.0	28
43	Engineering nitrogen use efficiency with alanine aminotransferase. Canadian Journal of Botany, 2007, 85, 252-262.	1.1	201
44	Proteome Profile of Cytosolic Component of Zebrafish Liver Generated by LCâ^'ESI MS/MS Combined with Trypsin Digestion and Microwave-Assisted Acid Hydrolysis. Journal of Proteome Research, 2007, 6, 263-272.	3.7	69
45	V-H+-ATPase translocation during blood alkalosis in dogfish gills: interaction with carbonic anhydrase and involvement in the postfeeding alkaline tide. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2007, 292, R2012-R2019.	1.8	50
46	Analysis of the Arabidopsis cell suspension phosphoproteome in response to short-term low temperature and abscisic acid treatment. Physiologia Plantarum, 2007, 129, 687-697.	5.2	16
47	Alanine aminotransferase catalyses the breakdown of alanine after hypoxia in Arabidopsis thaliana. Plant Journal, 2007, 49, 1108-1121.	5.7	221
48	Recovery from blood alkalosis in the Pacific hagfish (Eptatretus stoutii): Involvement of gill Vâ€“H+â€“ATPase and Na+/K+â€“ATPase. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2007, 148, 133-141.	1.8	31
49	Quantitative trait loci for early maturity and their potential in breeding for earliness in Brassica juncea. Euphytica, 2007, 154, 101-111.	1.2	13
50	Mapping genes for resistance to Leptosphaeria maculans in Brassica juncea. Genome, 2006, 49, 30-41.	2.0	56
51	Extracellular Proteomes of Arabidopsis Thaliana and Brassica Napus Roots: Analysis and Comparison by MudPIT and LC-MS/MS. Plant and Soil, 2006, 286, 357-376.	3.7	60
52	Identification of quantitative trait loci (QTL) for oil and protein contents and their relationships with other seed quality traits in Brassica juncea. Theoretical and Applied Genetics, 2006, 113, 1211-1220.	3.6	60
53	Issues of Ferality or Potential for Ferality in Oats, Olives, the Vigna Group, Ryegrass Species, Safflower, and Sugarcane. , 2005, , 231-255.		8
54	Molecular markers for yield components in Brassica juncea â€“ do these assist in breeding for high seed yield?. Euphytica, 2005, 144, 157-167.	1.2	16

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55	Identification, Mapping, and Economic Evaluation of QTLs Encoding Root Maggot Resistance inBrassica. Crop Science, 2005, 45, cropsci2005.0371.	1.8	14
56	Complexities of Chromosome Landing in a Highly Duplicated Genome: Toward Map-Based Cloning of a Gene Controlling Blackleg Resistance in Brassica napus. Genetics, 2005, 171, 1977-1988.	2.9	80
57	Molecular markers for seed colour in Brassica juncea. Genome, 2005, 48, 755-760.	2.0	20
58	Large-scale Identification of Tubulin-binding Proteins Provides Insight on Subcellular Trafficking, Metabolic Channeling, and Signaling in Plant Cells. Molecular and Cellular Proteomics, 2004, 3, 970-983.	3.8	110
59	Theoretical hybridization potential of transgenic safflower (Carthamus tinctorius L.) with weedy relatives in the New World. Canadian Journal of Plant Science, 2004, 84, 923-934.	0.9	48
60	Can less yield more? Is reducing nutrient input into the environment compatible with maintaining crop production?. Trends in Plant Science, 2004, 9, 597-605.	8.8	767
61	RFLP linkage analysis and mapping genes controlling the fatty acid profile of Brassica juncea using reciprocal DH populations. Theoretical and Applied Genetics, 2003, 107, 283-290.	3.6	42
62	Enhanced Low Oxygen Survival in Arabidopsis through Increased Metabolic Flux in the Fermentative Pathway. Plant Physiology, 2003, 132, 1292-1302.	4.8	243
63	Molecular mapping of seed aliphatic glucosinolates in Brassica juncea. Genome, 2003, 46, 753-760.	2.0	46
64	Vacuolar H+-ATPase, but not mitochondrial F1F0-ATPase, is required for NaCl tolerance inSaccharomyces cerevisiae. FEMS Microbiology Letters, 2002, 208, 227-232.	1.8	27
65	Vacuolar H+-ATPase, but not mitochondrial F1F0-ATPase, is required for NaCl tolerance in Saccharomyces cerevisiae. FEMS Microbiology Letters, 2002, 208, 227-232.	1.8	1
66	Transgenic Brassica napus plants overexpressing aluminium-induced mitochondrial manganese superoxide dismutase cDNA are resistant to aluminium. Plant, Cell and Environment, 2001, 24, 1278-1269.	5.7	173
67	Vacuolar H+-ATPase, but not mitochondrial F1F0-ATPase, is required for aluminum resistance in Saccharomyces cerevisiae. FEMS Microbiology Letters, 2001, 205, 231-236.	1.8	23
68	Molecular Basis of the Anaerobic Response in Plants. IUBMB Life, 2001, 51, 79-82.	3.4	15
69	Induction of Vacuolar ATPase and Mitochondrial ATP Synthase by Aluminum in an Aluminum-Resistant Cultivar of Wheat. Plant Physiology, 2001, 125, 2068-2077.	4.8	110
70	Identification and evaluation of flea beetle (Phyllotreta cruciferae) resistance within Brassicaceae. Canadian Journal of Plant Science, 2000, 80, 881-887.	0.9	23
71	Molecular strategies for improving waterlogging tolerance in plants. Journal of Experimental Botany, 2000, 51, 89-97.	4.8	277
72	Identification and evaluation of root maggot (Delia spp.) (Diptera: Anthomyiidae) resistance within Brassicaceae. Crop Protection, 2000, 19, 247-253.	2.1	34

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73	Pollen flow between herbicide-resistantBrassica napusis the cause of multiple-resistantB. napusvolunteers1. Weed Science, 2000, 48, 688-694.	1.5	239
74	Arabidopsis thaliana: A source of candidate disease-resistance genes for Brassica napus. Genome, 2000, 43, 452-460.	2.0	17
75	A 23-kDa, root exudate polypeptide co-segregates with aluminum resistance in Triticum aestivum. Physiologia Plantarum, 1999, 106, 53-61.	5.2	38
76	Evolution of a functionally related lactate dehydrogenase and pyruvate decarboxylase pseudogene complex in maize. Genome, 1999, 42, 1167-1175.	2.0	0
77	Genetic mapping of plant disease resistance gene homologues using a minimal Brassica napus L. population. Genome, 1999, 42, 735-743.	2.0	7
78	Cloning and expression of a hypoxic and nitrogen inducible maize alanine aminotransferase gene. Physiologia Plantarum, 1998, 103, 503-512.	5.2	24
79	Molecular mapping of resistance to Leptosphaeria maculans in Australian cultivars of Brassica napus. Genome, 1997, 40, 294-301.	2.0	68
80	Al-Induced, 51-Kilodalton, Membrane-Bound Proteins Are Associated with Resistance to Al in a Segregating Population of Wheat. Plant Physiology, 1997, 114, 363-372.	4.8	33
81	Molecular cloning of a Brassica napus cysteine protease gene inducible by drought and low temperature stress. Physiologia Plantarum, 1997, 101, 389-397.	5.2	2
82	Molecular cloning and expression of a turgor-responsive gene in Brassica napus. Plant Molecular Biology, 1995, 27, 541-551.	3.9	69
83	Hypoxically inducible barley alanine aminotransferase: cDNA cloning and expression analysis. Plant Molecular Biology, 1994, 24, 417-427.	3.9	68
84	The effects of drought stress on free amino acid accumulation and protein synthesis in Brassica napus. Physiologia Plantarum, 1994, 90, 9-14.	5.2	244
85	Hypoxic metabolism in wild rice (Zizania palustris): enzyme induction and metabolite production. Physiologia Plantarum, 1993, 89, 165-171.	5.2	18
86	Effects of drought stress on the water relations in Brassica species. Canadian Journal of Plant Science, 1993, 73, 525-529.	0.9	21
87	Hypoxic metabolism in wild rice (Zizania palustris): enzyme induction and metabolite production. Physiologia Plantarum, 1993, 89, 165-171.	5.2	3
88	Purification and Characterization of an Anaerobically Induced Alanine Aminotransferase from Barley Roots. Plant Physiology, 1992, 99, 1520-1525.	4.8	63
89	Identification and characterization of a hypoxically induced maize lactate dehydrogenase gene. Plant Molecular Biology, 1992, 19, 693-697.	3.9	21
90	Induction of Alcohol Dehydrogenase and Lactate Dehydrogenase in Hypoxically Induced Barley. Plant Physiology, 1989, 90, 860-866.	4.8	51

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91	Anaerobic Induction of Alanine Aminotransferase in Barley Root Tissue. Plant Physiology, 1989, 90, 1305-1309.	4.8	109
92	Induced swarming in the predatory copepod Heterocope septentrionalis 1. Limnology and Oceanography, 1980, 25, 747-750.	3.1	17