## Allen G Good

## List of Publications by Year in descending order

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92 papers 7,261 citations

57758 44 h-index 83 g-index

94 all docs 94 docs citations

94 times ranked 7432 citing authors

#	Article	IF	CITATIONS
1	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
2	Fertilizing Nature: A Tragedy of Excess in the Commons. PLoS Biology, 2011, 9, e1001124.	5.6	361
3	Engineering nitrogen use efficient crop plants: the current status. Plant Biotechnology Journal, 2012, 10, 1011-1025.	8.3	332
4	Molecular strategies for improving waterlogging tolerance in plants. Journal of Experimental Botany, 2000, 51, 89-97.	4.8	277
5	Genetic engineering of improved nitrogen use efficiency in rice by the tissueâ€specific expression of <i>alanine aminotransferase</i> . Plant Biotechnology Journal, 2008, 6, 722-732.	8.3	270
6	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
7	Enhanced Low Oxygen Survival in Arabidopsis through Increased Metabolic Flux in the Fermentative Pathway. Plant Physiology, 2003, 132, 1292-1302.	4.8	243
8	Pollen flow between herbicide-resistantBrassica napusis the cause of multiple-resistantB. napusvolunteers1. Weed Science, 2000, 48, 688-694.	1.5	239
9	Alanine aminotransferase catalyses the breakdown of alanine after hypoxia in Arabidopsis thaliana. Plant Journal, 2007, 49, 1108-1121.	5.7	221
10	The Genetics of Nitrogen Use Efficiency in Crop Plants. Annual Review of Genetics, 2015, 49, 269-289.	7.6	217
11	Engineering nitrogen use efficiency with alanine aminotransferase. Canadian Journal of Botany, 2007, 85, 252-262.	1.1	201
12	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
13	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 <b>.</b> 7	173
14	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
15	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
16	Future Prospects for Cereals That Fix Nitrogen. Science, 2011, 333, 416-417.	12.6	160
17	NAD(H)-dependent glutamate dehydrogenase is essential for the survival of <i>Arabidopsis thaliana</i> during dark-induced carbon starvation. Journal of Experimental Botany, 2008, 59, 667-680.	4.8	138
18	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

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19	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
20	Anaerobic Induction of Alanine Aminotransferase in Barley Root Tissue. Plant Physiology, 1989, 90, 1305-1309.	4.8	109
21	Gibberellin 3-oxidase Gene Expression Patterns Influence Gibberellin Biosynthesis, Growth, and Development in Pea. Plant Physiology, 2013, 163, 929-945.	4.8	97
22	Manipulation of microRNA expression to improve nitrogen use efficiency. Plant Science, 2013, 210, 70-81.	3.6	83
23	Toward nitrogen-fixing plants. Science, 2018, 359, 869-870.	12.6	82
24	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
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	Genetic Variability in Nitrogen Use Efficiency of Spring Barley. Crop Science, 2009, 49, 1259-1269.	1.8	77
27	Transcriptome analysis of nitrogenâ€efficient rice overâ€expressing alanine aminotransferase. Plant Biotechnology Journal, 2009, 7, 562-576.	8.3	74
28	Molecular cloning and expression of a turgor-responsive gene in Brassica napus. Plant Molecular Biology, 1995, 27, 541-551.	3.9	69
29	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
30	Hypoxically inducible barley alanine aminotransferase: cDNA cloning and expression analysis. Plant Molecular Biology, 1994, 24, 417-427.	3.9	68
31	Molecular mapping of resistance to Leptosphaeria maculans in Australian cultivars of Brassica napus. Genome, 1997, 40, 294-301.	2.0	68
32	Purification and Characterization of an Anaerobically Induced Alanine Aminotransferase from Barley Roots. Plant Physiology, 1992, 99, 1520-1525.	4.8	63
33	Interactions between Na <sup>+</sup> channels and Na <sup>+</sup> -HCO <sub>3</sub> <sup>â^³</sup> cotransporters in the freshwater fish gill MR cell: a model for transepithelial Na <sup>+</sup> uptake. American Journal of Physiology - Cell Physiology, 2007. 292. C935-C944.	4.6	62
34	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
35	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
36	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

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37	Mapping genes for resistance to Leptosphaeria maculans in Brassica juncea. Genome, 2006, 49, 30-41.	2.0	56
38	Genetic use restriction technologies (GURTs): strategies to impede transgene movement. Trends in Plant Science, 2007, 12, 177-183.	8.8	56
39	Functional analysis of lactate dehydrogenase during hypoxic stress in Arabidopsis. Functional Plant Biology, 2008, 35, 131.	2.1	53
40	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
41	Induction of Alcohol Dehydrogenase and Lactate Dehydrogenase in Hypoxically Induced Barley. Plant Physiology, 1989, 90, 860-866.	4.8	51
42	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
43	Theoretical hybridization potential of transgenic safflower ( <i>Carthamus tinctorius</i> L.) with weedy relatives in the New World. Canadian Journal of Plant Science, 2004, 84, 923-934.	0.9	48
44	Analysis of B-Genome Chromosome Introgression in Interspecific Hybrids of <i>Brassica napus</i> Å- <i>B. carinata</i> . Genetics, 2011, 187, 659-673.	2.9	48
45	Molecular mapping of seed aliphatic glucosinolates in Brassica juncea. Genome, 2003, 46, 753-760.	2.0	46
46	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
47	Yield and Production Gaps in Rainfed Wheat, Barley, and Canola in Alberta. Frontiers in Plant Science, 2015, 6, 990.	3.6	42
48	Understanding Plant Nitrogen Metabolism through Metabolomics and Computational Approaches. Plants, 2016, 5, 39.	3.5	41
49	A 23-kDa, root exudate polypeptide co-segregates with aluminum resistance in Triticum aestivum. Physiologia Plantarum, 1999, 106, 53-61.	5.2	38
50	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
51	Physiological analysis of nitrogen-efficient rice overexpressing alanine aminotransferase under different N regimes. Botany, 2013, 91, 866-883.	1.0	36
52	Development of molecular markers and linkage maps for the Carthamus species C.Âtinctorius and C.Âoxyacanthus. Genome, 2010, 53, 266-276.	2.0	35
53	Identification and evaluation of root maggot (Delia spp.) (Diptera: Anthomyiidae) resistance within Brassicaceae. Crop Protection, 2000, 19, 247-253.	2.1	34
54	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

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55	Recovery from blood alkalosis in the Pacific hagfish (Eptatretus stoutii): Involvement of gill V–H+–ATPase and Na+/K+–ATPase. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2007, 148, 133-141.	1.8	31
56	Blood and gill responses to HCl infusions in the Pacific hagfish ( <i>Eptatretus stoutii</i> ). Canadian Journal of Zoology, 2007, 85, 855-862.	1.0	28
57	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
58	Alanine Aminotransferase Variants Conferring Diverse NUE Phenotypes in Arabidopsis thaliana. PLoS ONE, 2015, 10, e0121830.	2.5	28
59	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
60	A phylogenetic investigation of Carthamus combining sequence and microsatellite data. Plant Systematics and Evolution, 2010, 287, 85-97.	0.9	26
61	Analysis of the Enzymatic Properties of a Broad Family of Alanine Aminotransferases. PLoS ONE, 2013, 8, e55032.	2.5	26
62	Introgression potential between safflower (Carthamus tinctorius) and wild relatives of the genus Carthamus. BMC Plant Biology, 2011, 11, 47.	3.6	25
63	Cloning and expression of a hypoxic and nitrogen inducible maize alanine aminotransferase gene. Physiologia Plantarum, 1998, 103, 503-512.	5.2	24
64	Identification and evaluation of flea beetle ( <i>Phyllotreta cruciferae</i> ) resistance within Brassicaceae. Canadian Journal of Plant Science, 2000, 80, 881-887.	0.9	23
65	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
66	Selection Efficiency across Environments in Improvement of Barley Yield for Moderately Low Nitrogen Environments. Crop Science, 2010, 50, 451-457.	1.8	22
67	Identification and characterization of a hypoxically induced maize lactate dehydrogenase gene. Plant Molecular Biology, 1992, 19, 693-697.	3.9	21
68	Effects of drought stress on the water relations in <i>Brassica</i> species. Canadian Journal of Plant Science, 1993, 73, 525-529.	0.9	21
69	Molecular markers for seed colour in Brassica juncea. Genome, 2005, 48, 755-760.	2.0	20
70	Hypoxic metabolism in wild rice (Zizania palustris): enzyme induction and metabolite production. Physiologia Plantarum, 1993, 89, 165-171.	5.2	18
71	Potential for seed-mediated gene flow in agroecosystems from transgenic safflower (Carthamus) Tj ETQq1 1 0.7	84314 rgB 2.4	T <u> Q</u> verlock
72	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

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73	Induced swarming in the predatory copepod Heterocope septentrionalis 1. Limnology and Oceanography, 1980, 25, 747-750.	3.1	17
74	<i>Arabidopsis thaliana</i> : A source of candidate disease-resistance genes for <i>Brassica napus</i> Genome, 2000, 43, 452-460.	2.0	17
75	Molecular markers for yield components in Brassica juncea – do these assist in breeding for high seed yield?. Euphytica, 2005, 144, 157-167.	1.2	16
76	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
77	Molecular Basis of the Anaerobic Response in Plants. IUBMB Life, 2001, 51, 79-82.	3.4	15
78	Identification, Mapping, and Economic Evaluation of QTLs Encoding Root Maggot Resistance in <i>Brassica</i> . Crop Science, 2005, 45, cropsci2005.0371.	1.8	14
79	Quantitative trait loci for early maturity and their potential in breeding for earliness in Brassica juncea. Euphytica, 2007, 154, 101-111.	1.2	13
80	Pollen-mediated gene flow from transgenic safflower ( <i>Carthamustinctorius</i> L.) intended for plant molecular farming to conventional safflower. Environmental Biosafety Research, 2009, 8, 19-32.	1.1	13
81	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
82	Issues of Ferality or Potential for Ferality in Oats, Olives, the Vigna Group, Ryegrass Species, Safflower, and Sugarcane., 2005,, 231-255.		8
83	"Genes, Meet Gases― The Role of Plant Nutrition and Genomics in Addressing Greenhouse Gas Emissions. , 2016, , 149-172.		8
84	Genetic mapping of plant disease resistance gene homologues using a minimal <i>Brassica napus</i> L. population. Genome, 1999, 42, 735-743.	2.0	7
85	Improving Nitrogen Use Efficient in Crop Plants Using Biotechnology Approaches. , 2018, , 15-35.		6
86	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
87	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
88	The <i>Arabidopsis</i> paraquat resistant1 mutant accumulates leucine upon dark treatment. Botany, 2017, 95, 751-761.	1.0	3
89	Hypoxic metabolism in wild rice (Zizania palustris): enzyme induction and metabolite production. Physiologia Plantarum, 1993, 89, 165-171.	5.2	3
90	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

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91	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
92	Evolution of a functionally related lactate dehydrogenase and pyruvate decarboxylase pseudogene complex in maize. Genome, 1999, 42, 1167-1175.	2.0	0