Tim Langdon

List of Publications by Year
in descending order

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Version: 2024-02-01

49 papers	3,256 citations	185998 28 h-index	233125 45 g-index
49 all docs	49 docs citations	49 times ranked	2681 citing authors

#	Article	IF	Citations
1	The regulatory gene areA mediating nitrogen metabolite repression in Aspergillus nidulans. Mutations affecting specificity of gene activation alter a loop residue of a putative zinc finger.. EMBO Journal, 1990, 9, 1355-1364.	3.5	386
2	Functional Rice Centromeres Are Marked by a Satellite Repeat and a Centromere-Specific Retrotransposon. Plant Cell, 2002, 14, 1691-1704.	3.1	375
3	The regulatory gene areA mediating nitrogen metabolite repression in Aspergillus nidulans. Mutations affecting specificity of gene activation alter a loop residue of a putative zinc finger. EMBO Journal, 1990, 9, 1355-64.	3.5	198
4	From The Cover: Chromatin immunoprecipitation cloning reveals rapid evolutionary patterns of centromeric DNA in Oryza species. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 11793-11798.	3.3	175
5	Evolution and taxonomic split of the model grass Brachypodium distachyon. Annals of Botany, 2012, 109, 385-405.	1.4	166
6	Subtle hydrophobic interactions between the seventh residue of the zinc finger loop and the first base of an HGATAR sequence determine promoter-specific recognition by the Aspergillus nidulans GATA factor AreA. EMBO Journal, 1997, 16, 3974-3986.	3.5	145
7	New DArT markers for oat provide enhanced map coverage and global germplasm characterization. BMC Genomics, 2009, 10, 39.	1.2	135
8	Nitrogen metabolite signalling involves the C-terminus and the GATA domain of the Aspergillus transcription factor AREA and the 3â€² untranslated region of its mRNA.. EMBO Journal, 1996, 15, 2791-2801.	3.5	125
9	Ribosomal DNA is an effective marker of Brassica chromosomes. Theoretical and Applied Genetics, 2001, 103, 486-490.	1.8	125
10	Retrotransposon Evolution in Diverse Plant Genomes. Genetics, 2000, 156, 313-325.	1.2	107
11	De Novo Evolution of Satellite DNA on the Rye B Chromosome. Genetics, 2000, 154, 869-884.	1.2	94
12	Mutational analysis reveals dispensability of the N-terminal region of the Aspergillus transcription factor mediating nitrogen metabolite repression. Molecular Microbiology, 1995, 17, 877-888.	1.2	91
13	A Consensus Map in Cultivated Hexaploid Oat Reveals Conserved Grass Synteny with Substantial Subgenome Rearrangement. Plant Genome, 2016, 9, plantgenome2015.10.0102.	1.6	85
14	Expression of a fungal ferulic acid esterase increases cell wall digestibility of tall fescue (Festuca) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	4.1	76
15	Crops that feed the world 9. Oats- a cereal crop for human and livestock feed with industrial applications. Food Security, 2013, 5, 13-33.	2.4	71
16	Nitrogen metabolite signalling involves the C-terminus and the GATA domain of the Aspergillus transcription factor AREA and the 3' untranslated region of its mRNA. EMBO Journal, 1996, 15, 2791-801.	3.5	67
17	Genomic insights from the first chromosome-scale assemblies of oat (Avena spp.) diploid species. BMC Biology, 2019, 17, 92.	1.7	58
18	High-density marker profiling confirms ancestral genomes of Avena species and identifies D-genome chromosomes of hexaploid oat. Theoretical and Applied Genetics, 2016, 129, 2133-2149.	1.8	56

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19	Targeting expression of a fungal ferulic acid esterase to the apoplast, endoplasmic reticulum or golgi can disrupt feruloylation of the growing cell wall and increase the biodegradability of tall fescue (Festuca arundinacea). Plant Biotechnology Journal, 2010, 8, 316-331.	4.1	55
20	Genetic Diversity and Population Structure Among Oat Cultivars and Landraces. Plant Molecular Biology Reporter, 2013, 31, 1305-1314.	1.0	55
21	Subtelomeric assembly of a multi-gene pathway for antimicrobial defense compounds in cereals. Nature Communications, 2021, 12, 2563.	5.8	51
22	C-terminal truncation of the transcriptional activator encoded by areA in Aspergillus nidulans results in both loss-of-function and gain-of-function phenotypes. Molecular Microbiology, 1993, 7, 81-87.	1.2	46
23	Genome-wide association study for crown rust (Puccinia coronata f. sp. avenae) and powdery mildew (Blumeria graminis f. sp. avenae) resistance in an oat (Avena sativa) collection of commercial varieties and landraces. Frontiers in Plant Science, 2015, 6, 103.	1.7	43
24	Analysis of Two New Arabinosyltransferases Belonging to the Carbohydrate-Active Enzyme (CAZY) Glycosyl Transferase Family1 Provides Insights into Disease Resistance and Sugar Donor Specificity. Plant Cell, 2018, 30, 3038-3057.	3.1	43
25	Notch signaling targets the Wingless responsiveness of a Ubx visceral mesoderm enhancer in Drosophila. Current Biology, 2001, 11, 375-385.	1.8	41
26	Compact genomes and complex evolution in the genus Brachypodium. Chromosoma, 2011, 120, 199-212.	1.0	36
27	Manipulating the Phenolic Acid Content and Digestibility of Italian Ryegrass (Lolium multiflorum) by Vacuolar-Targeted Expression of a Fungal Ferulic Acid Esterase. , 2006, 129-132, 416-426.		33
28	A High-Copy-Number CACTA Family Transposon in Temperate Grasses and Cereals. Genetics, 2003, 163, 1097-1108.	1.2	32
29	Multi-substrate chromosome preparations for high throughput comparative FISH. BMC Biotechnology, 2006, 6, 20.	1.7	31
30	A noncanonical vacuolar sugar transferase required for biosynthesis of antimicrobial defense compounds in oat. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 27105-27114.	3.3	27
31	Towards takeâ€all control: a Câ€21Î² oxidase required for acylation of triterpene defence compounds in oat. New Phytologist, 2019, 221, 1544-1555.	3.5	25
32	Expression of a Trichoderma reesei Î²-1,4 endo-xylanase in tall fescue modifies cell wall structure and digestibility and elicits pathogen defence responses. Planta, 2012, 236, 1757-1774.	1.6	23
33	Notch receptor encodes two structurally separable functions inDrosophila: A genetic analysis. Developmental Dynamics, 2006, 235, 998-1013.	0.8	22
34	Mutational analysis of the C-terminal region of AREA, the transcription factor mediating nitrogen metabolite repression inAspergillus nidulans. Molecular Genetics and Genomics, 1996, 250, 106-114.	2.4	21
35	Functional co-expression of a fungal ferulic acid esterase and a Î²-1,4 endoxylanase in Festuca arundinacea (tall fescue) modifies post-harvest cell wall deconstruction. Planta, 2015, 242, 97-111.	1.6	18
36	Strategies for the study of meiosis in rye. Cytogenetic and Genome Research, 2005, 109, 221-227.	0.6	17

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37	The nature and destiny of translocated B-chromosome-specific satellite DNA of rye. Chromosome Research, 2002, 10, 83-86.	1.0	15
38	Fragments of the key flowering gene GIGANTEA are associated with helitron-type sequences in the Pooideae grass Lolium perenne. BMC Plant Biology, 2009, 9, 70.	1.6	13
39	Multi-Environmental Trials Reveal Genetic Plasticity of Oat Agronomic Traits Associated With Climate Variable Changes. Frontiers in Plant Science, 2018, 9, 1358.	1.7	12
40	Detached Leaf Assays for Resistance to Crown Rust Reveal Diversity Within Populations of Avena sterilis. Plant Disease, 2019, 103, 832-840.	0.7	12
41	Genotype and Environment Affect the Grain Quality and Yield of Winter Oats (Avena sativa L.). Foods, 2021, 10, 2356.	1.9	12
42	Population genomics of Mediterranean oat (A. sativa) reveals high genetic diversity and three loci for heading date. Theoretical and Applied Genetics, 2021, 134, 2063-2077.	1.8	10
43	Genomic Approaches for Climate Resilience Breeding in Oats. , 2020, , 133-169.		9
44	New insights into the genomic structure of the oats (Avena L., Poaceae): intragenomic polymorphism of ITS1 sequences of rare endemic species Avena bruhnsiana Gruner and its relationship to other species with C-genomes. Euphytica, 2022, 218, 1.	0.6	7
45	Expression of a fungal ferulic acid esterase in suspension cultures of tall fescue (Festuca) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 Tissue and Organ Culture, 2017, 129, 181-193.	1.2	5
46	The Plant Nucleus at War and Peace: Genome Organization in the Interphase Nucleus. , 2013, , 13-31.		3
47	Mutational analysis of the C-terminal region of AREA, the transcription factor mediating nitrogen metabolite repression in. Molecular Genetics and Genomics, 1996, 250, 106.	2.4	3
48	Genetic Identification of Kazakhstan OAT Varieties. Biosciences, Biotechnology Research Asia, 2015, 12, 2227-2233.	0.2	1
49	C-terminal truncation of the transcriptional activator encoded by area in Aspergillus nidulans results in both loss-of-function and gain-of-function phenotypes. Molecular Microbiology, 1993, 7, 1025-1025.	1.2	0