

# 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	New insights into the genomic structure of the oats ( <i>Avena</i> L., Poaceae): intragenomic polymorphism of ITS1 sequences of rare endemic species <i>Avena bruhnsiana</i> Gruner and its relationship to other species with C-genomes. <i>Euphytica</i> , 2022, 218, 1.	0.6	7
2	Population genomics of Mediterranean oat ( <i>A. sativa</i> ) reveals high genetic diversity and three loci for heading date. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2063-2077.	1.8	10
3	Subtelomeric assembly of a multi-gene pathway for antimicrobial defense compounds in cereals. <i>Nature Communications</i> , 2021, 12, 2563.	5.8	51
4	Genotype and Environment Affect the Grain Quality and Yield of Winter Oats ( <i>Avena sativa</i> L.). <i>Foods</i> , 2021, 10, 2356.	1.9	12
5	Genomic Approaches for Climate Resilience Breeding in Oats. , 2020, , 133-169.		9
6	Genomic insights from the first chromosome-scale assemblies of oat ( <i>Avena</i> spp.) diploid species. <i>BMC Biology</i> , 2019, 17, 92.	1.7	58
7	Detached Leaf Assays for Resistance to Crown Rust Reveal Diversity Within Populations of <i>Avena sterilis</i> . <i>Plant Disease</i> , 2019, 103, 832-840.	0.7	12
8	Towards takeâ€all control: a Câ€21Î² oxidase required for acylation of triterpene defence compounds in oat. <i>New Phytologist</i> , 2019, 221, 1544-1555.	3.5	25
9	A noncanonical vacuolar sugar transferase required for biosynthesis of antimicrobial defense compounds in oat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 27105-27114.	3.3	27
10	Analysis of Two New Arabinosyltransferases Belonging to the Carbohydrate-Active Enzyme (CAZY) Glycosyl Transferase Family1 Provides Insights into Disease Resistance and Sugar Donor Specificity. <i>Plant Cell</i> , 2018, 30, 3038-3057.	3.1	43
11	Multi-Environmental Trials Reveal Genetic Plasticity of Oat Agronomic Traits Associated With Climate Variable Changes. <i>Frontiers in Plant Science</i> , 2018, 9, 1358.	1.7	12
12	Expression of a fungal ferulic acid esterase in suspension cultures of tall fescue ( <i>Festuca</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 Td ( Tissue and Organ Culture, 2017, 129, 181-193.	1.2	5
13	High-density marker profiling confirms ancestral genomes of <i>Avena</i> species and identifies D-genome chromosomes of hexaploid oat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2133-2149.	1.8	56
14	A Consensus Map in Cultivated Hexaploid Oat Reveals Conserved Grass Synteny with Substantial Subgenome Rearrangement. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0102.	1.6	85
15	Genome-wide association study for crown rust ( <i>Puccinia coronata</i> f. sp. <i>avenae</i> ) and powdery mildew ( <i>Blumeria graminis</i> f. sp. <i>avenae</i> ) resistance in an oat ( <i>Avena sativa</i> ) collection of commercial varieties and landraces. <i>Frontiers in Plant Science</i> , 2015, 6, 103.	1.7	43
16	Functional co-expression of a fungal ferulic acid esterase and a Î²-1,4 endoxylanase in <i>Festuca arundinacea</i> (tall fescue) modifies post-harvest cell wall deconstruction. <i>Planta</i> , 2015, 242, 97-111.	1.6	18
17	Genetic Identification of Kazakhstan OAT Varieties. <i>Biosciences, Biotechnology Research Asia</i> , 2015, 12, 2227-2233.	0.2	1
18	Genetic Diversity and Population Structure Among Oat Cultivars and Landraces. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 1305-1314.	1.0	55

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19	The Plant Nucleus at War and Peace: Genome Organization in the Interphase Nucleus. , 2013, , 13-31.		3
20	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
21	Evolution and taxonomic split of the model grass <i>Brachypodium distachyon</i> . Annals of Botany, 2012, 109, 385-405.	1.4	166
22	Expression of a <i>Trichoderma reesei</i> $\beta$ -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
23	Compact genomes and complex evolution in the genus <i>Brachypodium</i> . Chromosoma, 2011, 120, 199-212.	1.0	36
24	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 ( <i>Festuca arundinacea</i> ). Plant Biotechnology Journal, 2010, 8, 316-331.	4.1	55
25	New DArT markers for oat provide enhanced map coverage and global germplasm characterization. BMC Genomics, 2009, 10, 39.	1.2	135
26	Fragments of the key flowering gene <i>GIGANTEA</i> are associated with helitron-type sequences in the Poideae grass <i>Lolium perenne</i> . BMC Plant Biology, 2009, 9, 70.	1.6	13
27	Expression of a fungal ferulic acid esterase increases cell wall digestibility of tall fescue ( <i>Festuca</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	4.1	76
28	Multi-substrate chromosome preparations for high throughput comparative FISH. BMC Biotechnology, 2006, 6, 20.	1.7	31
29	Notch receptor encodes two structurally separable functions in <i>Drosophila</i> : A genetic analysis. Developmental Dynamics, 2006, 235, 998-1013.	0.8	22
30	Manipulating the Phenolic Acid Content and Digestibility of Italian Ryegrass ( <i>Lolium multiflorum</i> ) by Vacuolar-Targeted Expression of a Fungal Ferulic Acid Esterase. , 2006, 129-132, 416-426.		33
31	Strategies for the study of meiosis in rye. Cytogenetic and Genome Research, 2005, 109, 221-227.	0.6	17
32	From The Cover: Chromatin immunoprecipitation cloning reveals rapid evolutionary patterns of centromeric DNA in <i>Oryza</i> species. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 11793-11798.	3.3	175
33	A High-Copy-Number CACTA Family Transposon in Temperate Grasses and Cereals. Genetics, 2003, 163, 1097-1108.	1.2	32
34	Functional Rice Centromeres Are Marked by a Satellite Repeat and a Centromere-Specific Retrotransposon. Plant Cell, 2002, 14, 1691-1704.	3.1	375
35	The nature and destiny of translocated B-chromosome-specific satellite DNA of rye. Chromosome Research, 2002, 10, 83-86.	1.0	15
36	Ribosomal DNA is an effective marker of Brassica chromosomes. Theoretical and Applied Genetics, 2001, 103, 486-490.	1.8	125

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37	Notch signaling targets the Wingless responsiveness of a Ubx visceral mesoderm enhancer in <i>Drosophila</i> . <i>Current Biology</i> , 2001, 11, 375-385.	1.8	41
38	De Novo Evolution of Satellite DNA on the Rye B Chromosome. <i>Genetics</i> , 2000, 154, 869-884.	1.2	94
39	Retrotransposon Evolution in Diverse Plant Genomes. <i>Genetics</i> , 2000, 156, 313-325.	1.2	107
40	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 <i>Aspergillus nidulans</i> GATA factor AreA. <i>EMBO Journal</i> , 1997, 16, 3974-3986.	3.5	145
41	Nitrogen metabolite signalling involves the C-terminus and the GATA domain of the <i>Aspergillus</i> transcription factor AREA and the 3' untranslated region of its mRNA.. <i>EMBO Journal</i> , 1996, 15, 2791-2801.	3.5	125
42	Mutational analysis of the C-terminal region of AREA, the transcription factor mediating nitrogen metabolite repression in <i>Aspergillus nidulans</i> . <i>Molecular Genetics and Genomics</i> , 1996, 250, 106-114.	2.4	21
43	Mutational analysis of the C-terminal region of AREA, the transcription factor mediating nitrogen metabolite repression in. <i>Molecular Genetics and Genomics</i> , 1996, 250, 106.	2.4	3
44	Nitrogen metabolite signalling involves the C-terminus and the GATA domain of the <i>Aspergillus</i> transcription factor AREA and the 3' untranslated region of its mRNA. <i>EMBO Journal</i> , 1996, 15, 2791-801.	3.5	67
45	Mutational analysis reveals dispensability of the N-terminal region of the <i>Aspergillus</i> transcription factor mediating nitrogen metabolite repression. <i>Molecular Microbiology</i> , 1995, 17, 877-888.	1.2	91
46	C-terminal truncation of the transcriptional activator encoded by <i>areA</i> in <i>Aspergillus nidulans</i> results in both loss-of-function and gain-of-function phenotypes. <i>Molecular Microbiology</i> , 1993, 7, 81-87.	1.2	46
47	C-terminal truncation of the transcriptional activator encoded by <i>area</i> in <i>Aspergillus nidulans</i> results in both loss-of-function and gain-of-function phenotypes. <i>Molecular Microbiology</i> , 1993, 7, 1025-1025.	1.2	0
48	The regulatory gene <i>areA</i> mediating nitrogen metabolite repression in <i>Aspergillus nidulans</i> . Mutations affecting specificity of gene activation alter a loop residue of a putative zinc finger.. <i>EMBO Journal</i> , 1990, 9, 1355-1364.	3.5	386
49	The regulatory gene <i>areA</i> mediating nitrogen metabolite repression in <i>Aspergillus nidulans</i> . Mutations affecting specificity of gene activation alter a loop residue of a putative zinc finger. <i>EMBO Journal</i> , 1990, 9, 1355-64.	3.5	198