## Thomas Henry Noel Ellis

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/826294/publications.pdf

Version: 2024-02-01

113 papers 8,294 citations

41258 49 h-index 48187 88 g-index

114 all docs

114 docs citations

times ranked

114

5636 citing authors

#	Article	IF	CITATIONS
1	An Integrated Linkage Map of Three Recombinant Inbred Populations of Pea (Pisum sativum L.). Genes, 2022, 13, 196.	1.0	3
2	How did Mendel arrive at his discoveries?. Nature Genetics, 2022, 54, 926-933.	9.4	9
3	Diversity of Pod Shape in Pisum. Diversity, 2021, 13, 203.	0.7	7
4	Retrotransposons and the Evolution of Genome Size in Pisum. BioTech, 2020, 9, 24.	1.3	3
5	A reference genome for pea provides insight into legume genome evolution. Nature Genetics, 2019, 51, 1411-1422.	9.4	363
6	Mendel's pea crosses: varieties, traits and statistics. Hereditas, 2019, 156, 33.	0.5	7
7	Genome-Wide Association Mapping for Agronomic and Seed Quality Traits of Field Pea (Pisum sativum) Tj ETQq1	1 0 78431 1.7	4 rgBT /Ove
8	Recombinant inbred lines derived from cultivars of pea for understanding the genetic basis of variation in breeders' traits. Plant Genetic Resources: Characterisation and Utilisation, 2018, 16, 424-436.	0.4	4
9	How Mendel's Interest in Inheritance Grew out of Plant Improvement. Genetics, 2018, 210, 347-355.	1.2	16
10	Identification of <i>Stipules reduced,</i> a leaf morphology gene in pea ( <i>Pisum sativum</i> ). New Phytologist, 2018, 220, 288-299.	3.5	21
11	NMR Metabolomics Defining Genetic Variation in Pea Seed Metabolites. Frontiers in Plant Science, 2018, 9, 1022.	1.7	18
12	Genetic Variation Controlling Wrinkled Seed Phenotypes in Pisum: How Lucky Was Mendel?. International Journal of Molecular Sciences, 2017, 18, 1205.	1.8	22
13	The Full Breadth of Mendel's Genetics. Genetics, 2016, 204, 1327-1336.	1.2	21
14	Translational Genomics in Agriculture: Some Examples in Grain Legumes. Critical Reviews in Plant Sciences, 2015, 34, 169-194.	2.7	83
15	Pea. Handbook of Plant Breeding, 2015, , 37-83.	0.1	25
16	Developmental specialisations in the legume family. Current Opinion in Plant Biology, 2014, 17, 153-158.	3.5	23
17	Exploiting a fast neutron mutant genetic resource in Pisum sativum (pea) for functional genomics. Functional Plant Biology, 2013, 40, 1261.	1.1	42
18	<i>NODULE ROOT</i> and <i>COCHLEATA</i> Maintain Nodule Development and Are Legume Orthologs of <i>Arabidopsis BLADE-ON-PETIOLE</i> Genes. Plant Cell, 2012, 24, 4498-4510.	3.1	116

#	Article	IF	Citations
19	The <i>b</i> Gene of Pea Encodes a Defective Flavonoid 3′,5′-Hydroxylase, and Confers Pink Flower Color  Â. Plant Physiology, 2012, 159, 759-768.	2.3	45
20	Conserved genetic determinant of motor organ identity in <i>Medicago truncatula</i> and related legumes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11723-11728.	3.3	57
21	VEGETATIVE1 is essential for development of the compound inflorescence in pea. Nature Communications, 2012, 3, 797.	5.8	85
22	Recombination, and chromosomes, in a changing environment. New Phytologist, 2012, 195, 8-9.	3.5	1
23	The Application of LTR Retrotransposons as Molecular Markers in Plants. Methods in Molecular Biology, 2012, 859, 115-153.	0.4	58
24	Phylogeny, phylogeography and genetic diversity of the Pisum genus. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 4-18.	0.4	128
25	Mendel, 150 years on. Trends in Plant Science, 2011, 16, 590-596.	4.3	58
26	Analysis of plant diversity with retrotransposon-based molecular markers. Heredity, 2011, 106, 520-530.	1.2	213
27	Natural Variation in Host-Specific Nodulation of Pea Is Associated with a Haplotype of the SYM37 LysM-Type Receptor-Like Kinase. Molecular Plant-Microbe Interactions, 2011, 24, 1396-1403.	1.4	24
28	Legume genetic resources: management, diversity assessment, and utilization in crop improvement. Euphytica, 2011, 180, 27-47.	0.6	47
29	Germplasm resources in legumes. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 1-3.	0.4	5
30	Genetic background and agronomic value of leaf types in pea (Pisum sativum). Ratarstvo I Povrtarstvo, 2011, 48, 275-284.	0.6	26
31	The genetic diversity and evolution of field pea (Pisum) studied by high throughput retrotransposon based insertion polymorphism (RBIP) marker analysis. BMC Evolutionary Biology, 2010, 10, 44.	3.2	169
32	Identification of Mendel's White Flower Character. PLoS ONE, 2010, 5, e13230.	1.1	135
33	THREaD Mapper Studio: a novel, visual web server for the estimation of genetic linkage maps. Nucleic Acids Research, 2010, 38, W188-W193.	6.5	24
34	Do Transcription Factors Play Special Roles in Adaptive Variation?: Figure 1 Plant Physiology, 2010, 154, 506-511.	2.3	46
35	Model legumes contribute to faba bean breeding. Field Crops Research, 2010, 115, 253-269.	2.3	64
36	<i>Tendril-less</i> Regulates Tendril Formation in Pea Leaves Â. Plant Cell, 2009, 21, 420-428.	3.1	129

#	Article	IF	Citations
37	High-throughput retrotransposon-based fluorescent markers: improved information content and allele discrimination. Plant Methods, 2009, 5, 10.	1.9	20
38	Genetic Diversity and Core Collection of Alien <l>Pisum sativum</l> L. Germplasm. Acta Agronomica Sinica(China), 2009, 34, 1518-1528.	0.1	1
39	Genetic diversity within Lablab purpureus and the application of gene-specific markers from a range of legume species. Plant Genetic Resources: Characterisation and Utilisation, 2007, 5, 154-171.	0.4	18
40	Gene-Based Sequence Diversity Analysis of Field Pea (Pisum). Genetics, 2007, 177, 2263-2275.	1.2	74
41	Genetic and genomic analysis of legume flowers and seeds. Current Opinion in Plant Biology, 2006, 9, 133-141.	3.5	35
42	A crispa null mutant facilitates identification of a crispa-like pseudogene in pea. Functional Plant Biology, 2006, 33, 757.	1.1	3
43	Conservation of Arabidopsis Flowering Genes in Model Legumes. Plant Physiology, 2005, 137, 1420-1434.	2.3	270
44	The Mutant crispa Reveals Multiple Roles for PHANTASTICA in Pea Compound Leaf Development. Plant Cell, 2005, 17, 1046-1060.	3.1	86
45	GERMINATE. A Generic Database for Integrating Genotypic and Phenotypic Information for Plant Genetic Resource Collections. Plant Physiology, 2005, 139, 619-631.	2.3	35
46	Insertional Polymorphism and Antiquity of PDR1 Retrotransposon Insertions in Pisum Species. Genetics, 2005, 171, 741-752.	1.2	60
47	The Application of LTR Retrotransposons as Molecular Markers in Plants. , 2004, 260, 145-174.		85
48	Estimating genome conservation between crop and model legume species. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15289-15294.	3.3	416
49	The potyvirus recessive resistance gene, sbm1 , identifies a novel role for translation initiation factor eIF4E in cellâ€toâ€cell trafficking. Plant Journal, 2004, 40, 376-385.	2.8	248
50	Using bioinformatics to analyse germplasm collections. Euphytica, 2004, 137, 39-54.	0.6	8
51	Comparative mapping between Medicago sativa and Pisum sativum. Molecular Genetics and Genomics, 2004, 272, 235-246.	1.0	150
52	Identification of markers tightly linked to sbm recessive genes for resistance to Pea seed-borne mosaic virus. Theoretical and Applied Genetics, 2004, 109, 488-494.	1.8	70
53	NMR profiling of transgenic peas. Plant Biotechnology Journal, 2004, 2, 27-35.	4.1	90
54	Legume genomes: more than peas in a pod. Current Opinion in Plant Biology, 2003, 6, 199-204.	3.5	142

#	Article	IF	Citations
55	DETERMINATE and LATE FLOWERING Are Two TERMINAL FLOWER1/CENTRORADIALIS Homologs That Control Two Distinct Phases of Flowering Initiation and Development in Pea. Plant Cell, 2003, 15, 2742-2754.	3.1	221
56	The Sym35 Gene Required for Root Nodule Development in Pea Is an Ortholog of Nin from Lotus japonicus Â. Plant Physiology, 2003, 131, 1009-1017.	2.3	168
57	A microarray-based high throughput molecular marker genotyping method: the tagged microarray marker (TAM) approach. Nucleic Acids Research, 2003, 31, 115e-115.	6.5	58
58	Transposable Elements Reveal the Impact of Introgression, Rather than Transposition, in Pisum Diversity, Evolution, and Domestication. Molecular Biology and Evolution, 2003, 20, 2067-2075.	3.5	111
59	PROLIFERATING INFLORESCENCE MERISTEM, a MADS-Box Gene That Regulates Floral Meristem Identity in Pea. Plant Physiology, 2002, 129, 1150-1159.	2.3	75
60	Three classes of proteinase inhibitor gene have distinct but overlapping patterns of expression in Pisum sativum plants. Plant Molecular Biology, 2002, 48, 319-329.	2.0	23
61	Conservation and diversification of gene function in plant development. Current Opinion in Plant Biology, 2002, 5, 56-61.	3.5	10
62	Mapping of the nodulation loci sym9 and sym10 of pea (Pisum sativum L.). Theoretical and Applied Genetics, 2002, 104, 1312-1316.	1.8	43
63	A genetic linkage map of Guinea yam (Dioscorea rotundata Poir.) based on AFLP markers. Theoretical and Applied Genetics, 2002, 105, 716-725.	1.8	55
64	A genetic linkage map of water yam (Dioscorea alata L.) based on AFLP markers and QTL analysis for anthracnose resistance. Theoretical and Applied Genetics, 2002, 105, 726-735.	1.8	69
65	An integrated and comparative view of pea genetic and cytogenetic maps. New Phytologist, 2002, 153, 17-25.	3.5	83
66	Genetic Control of Leaf Morphology: A Partial View. Annals of Botany, 2001, 88, 1129-1139.	1.4	24
67	Association of dominant loci for resistance to Pseudomonas syringae pv. pisi with linkage groups II, VI and VII of Pisum sativum. Theoretical and Applied Genetics, 2001, 103, 129-135.	1.8	28
68	Stability and inheritance of methylation states at Pstl sites in Pisum. Molecular Genetics and Genomics, 2001, 265, 497-507.	1.0	47
69	Expression of a class 1 knotted1-like homeobox gene is down-regulated in pea compound leaf primordia. Plant Molecular Biology, 2001, 45, 387-398.	2.0	96
70	Nodule-Expressed Cyp15a Cysteine Protease Genes Map to Syntenic Genome Regions in Pisum and Medicago spp Molecular Plant-Microbe Interactions, 2000, 13, 715-723.	1.4	19
71	Pea Ty1-copia group retrotransposons: transpositional activity and use as markers to study genetic diversity in Pisum. Molecular Genetics and Genomics, 2000, 263, 898-907.	2.4	107
72	Pea Compound Leaf Architecture Is Regulated by Interactions among the Genes UNIFOLIATA, COCHLEATA, AFILA, and TENDRIL-LESS. Plant Cell, 2000, 12, 1279.	3.1	0

#	Article	IF	Citations
73	Pea Compound Leaf Architecture Is Regulated by Interactions among the Genes UNIFOLIATA, COCHLEATA, AFILA, and TENDRIL-LESS. Plant Cell, 2000, 12, 1279-1294.	3.1	138
74	Rapid isolation of plant Ty1-copia group retrotransposon LTR sequences for molecular marker studies. Plant Journal, 1999, 19, 711-717.	2.8	82
75	Genetic mapping and functional analysis of a nodulation-defective mutant (sym19) of pea (Pisum) Tj ETQq1 1 0	.784314 r 2.4	gBT <sub>4</sub> Overlo <mark>ck</mark>
76	Heterogeneity of the internal structure of PDR1, a family of Ty1/copia-like retrotransposons in pea. Molecular Genetics and Genomics, 1999, 262, 703-713.	2.4	21
77	Genetic mapping in pea. 1. RAPD-based genetic linkage map of Pisum sativum. Theoretical and Applied Genetics, 1998, 97, 905-915.	1.8	115
78	Polymorphism of insertion sites of Ty1-copia class retrotransposons and its use for linkage and diversity analysis in pea. Molecular Genetics and Genomics, 1998, 260, 9-19.	2.4	147
79	Retrotransposon-based insertion polymorphisms (RBIP) for high throughput marker analysis. Plant Journal, 1998, 16, 643-650.	2.8	205
80	The genetic control of patterning in pea leaves. Trends in Plant Science, 1998, 3, 439-444.	4.3	51
81	Neighbour mapping as a method for ordering genetic markers. Genetical Research, 1997, 69, 35-43.	0.3	19
82	The relationship between genetic and cytogenetic maps of pea. I. Standard and translocation karyotypes. Genome, 1997, 40, 744-754.	0.9	42
83	The relationship between genetic and cytogenetic maps of pea. II. Physical maps of linkage mapping populations. Genome, 1997, 40, 755-769.	0.9	66
84	UNIFOLIATA regulates leaf and flower morphogenesis in pea. Current Biology, 1997, 7, 581-587.	1.8	375
85	Repeated sequence markers in pea (Pisum sativum). New Phytologist, 1997, 137, 35-41.	3.5	3
86	The pea early nodulin gene PsENOD7 maps in the region of linkage group I containing sym2 and leghaemoglobin. Plant Molecular Biology, 1996, 31, 149-156.	2.0	20
87	Isolation by PCR of a cDNA clone from pea petals with similarity to petunia and wheat zinc finger proteins. Plant Molecular Biology, 1996, 30, 1051-1058.	2.0	18
88	AFLP analysis of the diversity and phylogeny of Lens and its comparison with RAPD analysis. Theoretical and Applied Genetics, 1996, 93-93, 751-758.	1.8	191
89	Pea lines carrying syml or sym2 can be nodulated by Rhizobium strains containing nodX; sym1 and sym2 are allelic. Plant Science, 1995, 108, 41-49.	1.7	49
90	Estimating map distances. Trends in Genetics, 1994, 10, 113-114.	2.9	2

#	Article	IF	CITATIONS
91	The organisation and expression of the genes encoding the mitochondrial glycine decarboxylase complex and serine hydroxymethyltransferase in pea (Pisum sativum). Molecular Genetics and Genomics, 1993, 236-236, 402-408.	2.4	45
92	Pisum lipoxygenase genes. Theoretical and Applied Genetics, 1991, 81, 800-805.	1.8	14
93	A developmentally regulated early-embryogenesis protein in pea (Pisum sativum L.) is related to the heat-shock protein (HSP70) gene family. Planta, 1991, 184, 350-5.	1.6	11
94	Evidence for the presence of hairpin chloroplast DNA molecules in barley cultivars. Current Genetics, 1991, 20, 253-258.	0.8	8
95	Identification and Genetic Regulation of the Chalcone Synthase Multigene Family in Pea. Plant Cell, 1990, 2, 185.	3.1	3
96	Methylated and undermethylated rDNA repeats are interspersed at random in two higher plant species. Plant Molecular Biology, 1990, 14, 73-80.	2.0	32
97	Identification of translocations in pea by in situ hybridization with chromosome-specific DNA probes. Genome, 1990, 33, 745-749.	0.9	20
98	The wrinkled-seed character of pea described by Mendel is caused by a transposon-like insertion in a gene encoding starch-branching enzyme. Cell, 1990, 60, 115-122.	13.5	442
99	An RFLP marker for rb in pea. Theoretical and Applied Genetics, 1988, 75, 362-365.	1.8	24
100	Trisomy: a useful adjunct to RFLP mapping in pea. Chromosoma, 1988, 96, 91-94.	1.0	11
101	5S rRNA genes in Pisum: Sequence, long range and chromosomal organization. Molecular Genetics and Genomics, 1988, 214, 333-342.	2.4	88
102	The Structure, Expression and Arrangement of Legumin Genes in Peas. Biochemie Und Physiologie Der Pflanzen, 1988, 183, 173-180.	0.5	5
103	Two genes encoding â€~minor' legumin polypeptides in pea ( <i>Pisum sativum</i> L.). Characterization and complete sequence of the <i>LegJ</i> gene. Biochemical Journal, 1988, 250, 15-24.	1.7	46
104	The sequence of a gene encoding convicilin from pea (Pisum sativum L.) shows that convicilin differs from vicilin by an insertion near the N-terminus. Biochemical Journal, 1988, 251, 717-726.	1.7	53
105	Ramped field inversion gel electrophoresis: a cautionary note. Nucleic Acids Research, 1987, 15, 5489-5489.	6.5	27
106	Restriction fragment length polymorphism markers in relation to quantitative characters. Theoretical and Applied Genetics, 1986, 72, 1-2.	1.8	70
107	Organization and mapping of legumin genes in Pisum. Molecular Genetics and Genomics, 1986, 202, 280-285.	2.4	48
108	Vicilin genes of Pisum. Molecular Genetics and Genomics, 1986, 205, 164.	2.4	33

#	Article	IF	CITATIONS
109	Deleted forms of plastid DNA in albino plants from cereal anther culture. Current Genetics, 1985, 9, 671-678.	0.8	165
110	The organization and genetics of rDNA length variants in peas. Chromosoma, 1984, 91, 74-81.	1.0	96
111	Chloroplast DNA deletions associated with wheat plants regenerated from pollen: possible basis for maternal inheritance of chloroplasts. Cell, 1984, 39, 359-368.	13.5	214
112	Aleksandar Mikić, the legume (re)searcher. , 0, , .		0
113	Mendel's reaction to Darwin's provisional hypothesis of pangenesis and the experiment that could not wait. Heredity, 0, , .	1.2	4