

# Thomas Henry Noel Ellis

## List of Publications by Year in descending order

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113  
papers

8,294  
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41258

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114  
docs citations

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times ranked

5636  
citing authors

#	ARTICLE	IF	CITATIONS
1	The wrinkled-seed character of pea described by Mendel is caused by a transposon-like insertion in a gene encoding starch-branching enzyme. <i>Cell</i> , 1990, 60, 115-122.	13.5	442
2	Estimating genome conservation between crop and model legume species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15289-15294.	3.3	416
3	UNIFOLIATA regulates leaf and flower morphogenesis in pea. <i>Current Biology</i> , 1997, 7, 581-587.	1.8	375
4	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	9.4	363
5	Conservation of Arabidopsis Flowering Genes in Model Legumes. <i>Plant Physiology</i> , 2005, 137, 1420-1434.	2.3	270
6	The potyvirus recessive resistance gene, <i>sbm1</i> , identifies a novel role for translation initiation factor eIF4E in cell-to-cell trafficking. <i>Plant Journal</i> , 2004, 40, 376-385.	2.8	248
7	DETERMINATE and LATE FLOWERING Are Two TERMINAL FLOWER1/CENTRORADIALIS Homologs That Control Two Distinct Phases of Flowering Initiation and Development in Pea. <i>Plant Cell</i> , 2003, 15, 2742-2754.	3.1	221
8	Chloroplast DNA deletions associated with wheat plants regenerated from pollen: possible basis for maternal inheritance of chloroplasts. <i>Cell</i> , 1984, 39, 359-368.	13.5	214
9	Analysis of plant diversity with retrotransposon-based molecular markers. <i>Heredity</i> , 2011, 106, 520-530.	1.2	213
10	Retrotransposon-based insertion polymorphisms (RBIP) for high throughput marker analysis. <i>Plant Journal</i> , 1998, 16, 643-650.	2.8	205
11	AFLP analysis of the diversity and phylogeny of <i>Lens</i> and its comparison with RAPD analysis. <i>Theoretical and Applied Genetics</i> , 1996, 93-93, 751-758.	1.8	191
12	The genetic diversity and evolution of field pea ( <i>Pisum</i> ) studied by high throughput retrotransposon based insertion polymorphism (RBIP) marker analysis. <i>BMC Evolutionary Biology</i> , 2010, 10, 44.	3.2	169
13	The <i>Sym35</i> Gene Required for Root Nodule Development in Pea Is an Ortholog of <i>Nin</i> from <i>Lotus japonicus</i> . <i>Plant Physiology</i> , 2003, 131, 1009-1017.	2.3	168
14	Deleted forms of plastid DNA in albino plants from cereal anther culture. <i>Current Genetics</i> , 1985, 9, 671-678.	0.8	165
15	Comparative mapping between <i>Medicago sativa</i> and <i>Pisum sativum</i> . <i>Molecular Genetics and Genomics</i> , 2004, 272, 235-246.	1.0	150
16	Polymorphism of insertion sites of Ty1-copia class retrotransposons and its use for linkage and diversity analysis in pea. <i>Molecular Genetics and Genomics</i> , 1998, 260, 9-19.	2.4	147
17	Legume genomes: more than peas in a pod. <i>Current Opinion in Plant Biology</i> , 2003, 6, 199-204.	3.5	142
18	Pea Compound Leaf Architecture Is Regulated by Interactions among the Genes UNIFOLIATA, COCHLEATA, AFILA, and TENDRIL-LESS. <i>Plant Cell</i> , 2000, 12, 1279-1294.	3.1	138

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19	Identification of Mendel's White Flower Character. PLoS ONE, 2010, 5, e13230.	1.1	135
20	<i>Tendrill-less</i> Regulates Tendril Formation in Pea Leaves. Plant Cell, 2009, 21, 420-428.	3.1	129
21	Phylogeny, phylogeography and genetic diversity of the Pisum genus. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 4-18.	0.4	128
22	<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
23	Genetic mapping in pea. 1. RAPD-based genetic linkage map of Pisum sativum. Theoretical and Applied Genetics, 1998, 97, 905-915.	1.8	115
24	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
25	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
26	The organization and genetics of rDNA length variants in peas. Chromosoma, 1984, 91, 74-81.	1.0	96
27	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
28	NMR profiling of transgenic peas. Plant Biotechnology Journal, 2004, 2, 27-35.	4.1	90
29	5S rRNA genes in Pisum: Sequence, long range and chromosomal organization. Molecular Genetics and Genomics, 1988, 214, 333-342.	2.4	88
30	The Mutant <i>crispa</i> Reveals Multiple Roles for PHANTASTICA in Pea Compound Leaf Development. Plant Cell, 2005, 17, 1046-1060.	3.1	86
31	The Application of LTR Retrotransposons as Molecular Markers in Plants. , 2004, 260, 145-174.		85
32	VEGETATIVE1 is essential for development of the compound inflorescence in pea. Nature Communications, 2012, 3, 797.	5.8	85
33	An integrated and comparative view of pea genetic and cytogenetic maps. New Phytologist, 2002, 153, 17-25.	3.5	83
34	Translational Genomics in Agriculture: Some Examples in Grain Legumes. Critical Reviews in Plant Sciences, 2015, 34, 169-194.	2.7	83
35	Genome-Wide Association Mapping for Agronomic and Seed Quality Traits of Field Pea (Pisum sativum) Tj ETQq1 1,0784314,rgBT /Ope	1.7	83
36	Rapid isolation of plant Ty1-copia group retrotransposon LTR sequences for molecular marker studies. Plant Journal, 1999, 19, 711-717.	2.8	82

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37	PROLIFERATING INFLORESCENCE MERISTEM, a MADS-Box Gene That Regulates Floral Meristem Identity in Pea. <i>Plant Physiology</i> , 2002, 129, 1150-1159.	2.3	75
38	Gene-Based Sequence Diversity Analysis of Field Pea ( <i>Pisum</i> ). <i>Genetics</i> , 2007, 177, 2263-2275.	1.2	74
39	Restriction fragment length polymorphism markers in relation to quantitative characters. <i>Theoretical and Applied Genetics</i> , 1986, 72, 1-2.	1.8	70
40	Identification of markers tightly linked to sbm recessive genes for resistance to Pea seed-borne mosaic virus. <i>Theoretical and Applied Genetics</i> , 2004, 109, 488-494.	1.8	70
41	A genetic linkage map of water yam ( <i>Dioscorea alata</i> L.) based on AFLP markers and QTL analysis for anthracnose resistance. <i>Theoretical and Applied Genetics</i> , 2002, 105, 726-735.	1.8	69
42	The relationship between genetic and cytogenetic maps of pea. II. Physical maps of linkage mapping populations. <i>Genome</i> , 1997, 40, 755-769.	0.9	66
43	Model legumes contribute to faba bean breeding. <i>Field Crops Research</i> , 2010, 115, 253-269.	2.3	64
44	Insertional Polymorphism and Antiquity of PDR1 Retrotransposon Insertions in <i>Pisum</i> Species. <i>Genetics</i> , 2005, 171, 741-752.	1.2	60
45	A microarray-based high throughput molecular marker genotyping method: the tagged microarray marker (TAM) approach. <i>Nucleic Acids Research</i> , 2003, 31, 115e-115.	6.5	58
46	Mendel, 150 years on. <i>Trends in Plant Science</i> , 2011, 16, 590-596.	4.3	58
47	The Application of LTR Retrotransposons as Molecular Markers in Plants. <i>Methods in Molecular Biology</i> , 2012, 859, 115-153.	0.4	58
48	Conserved genetic determinant of motor organ identity in <i>Medicago truncatula</i> and related legumes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11723-11728.	3.3	57
49	A genetic linkage map of Guinea yam ( <i>Dioscorea rotundata</i> Poir.) based on AFLP markers. <i>Theoretical and Applied Genetics</i> , 2002, 105, 716-725.	1.8	55
50	The sequence of a gene encoding convicilin from pea ( <i>Pisum sativum</i> L.) shows that convicilin differs from vicilin by an insertion near the N-terminus. <i>Biochemical Journal</i> , 1988, 251, 717-726.	1.7	53
51	The genetic control of patterning in pea leaves. <i>Trends in Plant Science</i> , 1998, 3, 439-444.	4.3	51
52	Pea lines carrying sym1 or sym2 can be nodulated by <i>Rhizobium</i> strains containing nodX; sym1 and sym2 are allelic. <i>Plant Science</i> , 1995, 108, 41-49.	1.7	49
53	Organization and mapping of legumin genes in <i>Pisum</i> . <i>Molecular Genetics and Genomics</i> , 1986, 202, 280-285.	2.4	48
54	Stability and inheritance of methylation states at PstI sites in <i>Pisum</i> . <i>Molecular Genetics and Genomics</i> , 2001, 265, 497-507.	1.0	47

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55	Legume genetic resources: management, diversity assessment, and utilization in crop improvement. <i>Euphytica</i> , 2011, 180, 27-47.	0.6	47
56	Two genes encoding "minor" legumin polypeptides in pea ( <i>Pisum sativum</i> L.). Characterization and complete sequence of the <i>LegJ</i> gene. <i>Biochemical Journal</i> , 1988, 250, 15-24.	1.7	46
57	Do Transcription Factors Play Special Roles in Adaptive Variation?: Figure 1.. <i>Plant Physiology</i> , 2010, 154, 506-511.	2.3	46
58	The organisation and expression of the genes encoding the mitochondrial glycine decarboxylase complex and serine hydroxymethyltransferase in pea ( <i>Pisum sativum</i> ). <i>Molecular Genetics and Genomics</i> , 1993, 236-236, 402-408.	2.4	45
59	The <i>b</i> Gene of Pea Encodes a Defective Flavonoid 3,5-Hydroxylase, and Confers Pink Flower Color. <i>Plant Physiology</i> , 2012, 159, 759-768.	2.3	45
60	Mapping of the nodulation loci <i>sym9</i> and <i>sym10</i> of pea ( <i>Pisum sativum</i> L.). <i>Theoretical and Applied Genetics</i> , 2002, 104, 1312-1316.	1.8	43
61	The relationship between genetic and cytogenetic maps of pea. I. Standard and translocation karyotypes. <i>Genome</i> , 1997, 40, 744-754.	0.9	42
62	Exploiting a fast neutron mutant genetic resource in <i>Pisum sativum</i> (pea) for functional genomics. <i>Functional Plant Biology</i> , 2013, 40, 1261.	1.1	42
63	Genetic mapping and functional analysis of a nodulation-defective mutant ( <i>sym19</i> ) of pea ( <i>Pisum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	2.4	40
64	GERMINATE. A Generic Database for Integrating Genotypic and Phenotypic Information for Plant Genetic Resource Collections. <i>Plant Physiology</i> , 2005, 139, 619-631.	2.3	35
65	Genetic and genomic analysis of legume flowers and seeds. <i>Current Opinion in Plant Biology</i> , 2006, 9, 133-141.	3.5	35
66	Vicilin genes of <i>Pisum</i> . <i>Molecular Genetics and Genomics</i> , 1986, 205, 164.	2.4	33
67	Methylated and undermethylated rDNA repeats are interspersed at random in two higher plant species. <i>Plant Molecular Biology</i> , 1990, 14, 73-80.	2.0	32
68	Association of dominant loci for resistance to <i>Pseudomonas syringae</i> pv. <i>pti</i> with linkage groups II, VI and VII of <i>Pisum sativum</i> . <i>Theoretical and Applied Genetics</i> , 2001, 103, 129-135.	1.8	28
69	Ramped field inversion gel electrophoresis: a cautionary note. <i>Nucleic Acids Research</i> , 1987, 15, 5489-5489.	6.5	27
70	Genetic background and agronomic value of leaf types in pea ( <i>Pisum sativum</i> ). <i>Ratarstvo I Povrtarstvo</i> , 2011, 48, 275-284.	0.6	26
71	Pea. <i>Handbook of Plant Breeding</i> , 2015, , 37-83.	0.1	25
72	An RFLP marker for <i>rb</i> in pea. <i>Theoretical and Applied Genetics</i> , 1988, 75, 362-365.	1.8	24

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73	Genetic Control of Leaf Morphology: A Partial View. <i>Annals of Botany</i> , 2001, 88, 1129-1139.	1.4	24
74	THREaD Mapper Studio: a novel, visual web server for the estimation of genetic linkage maps. <i>Nucleic Acids Research</i> , 2010, 38, W188-W193.	6.5	24
75	Natural Variation in Host-Specific Nodulation of Pea Is Associated with a Haplotype of the SYM37 LysM-Type Receptor-Like Kinase. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1396-1403.	1.4	24
76	Three classes of proteinase inhibitor gene have distinct but overlapping patterns of expression in <i>Pisum sativum</i> plants. <i>Plant Molecular Biology</i> , 2002, 48, 319-329.	2.0	23
77	Developmental specialisations in the legume family. <i>Current Opinion in Plant Biology</i> , 2014, 17, 153-158.	3.5	23
78	Genetic Variation Controlling Wrinkled Seed Phenotypes in <i>Pisum</i> : How Lucky Was Mendel?. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1205.	1.8	22
79	Heterogeneity of the internal structure of PDR1, a family of Ty1/copia-like retrotransposons in pea. <i>Molecular Genetics and Genomics</i> , 1999, 262, 703-713.	2.4	21
80	The Full Breadth of Mendel's Genetics. <i>Genetics</i> , 2016, 204, 1327-1336.	1.2	21
81	Identification of <i>Stipules reduced</i> , a leaf morphology gene in pea ( <i>Pisum sativum</i> ). <i>New Phytologist</i> , 2018, 220, 288-299.	3.5	21
82	Identification of translocations in pea by in situ hybridization with chromosome-specific DNA probes. <i>Genome</i> , 1990, 33, 745-749.	0.9	20
83	The pea early nodulin gene PsENOD7 maps in the region of linkage group I containing sym2 and leghaemoglobin. <i>Plant Molecular Biology</i> , 1996, 31, 149-156.	2.0	20
84	High-throughput retrotransposon-based fluorescent markers: improved information content and allele discrimination. <i>Plant Methods</i> , 2009, 5, 10.	1.9	20
85	Neighbour mapping as a method for ordering genetic markers. <i>Genetical Research</i> , 1997, 69, 35-43.	0.3	19
86	Nodule-Expressed Cyp15a Cysteine Protease Genes Map to Syntenic Genome Regions in <i>Pisum</i> and <i>Medicago</i> spp.. <i>Molecular Plant-Microbe Interactions</i> , 2000, 13, 715-723.	1.4	19
87	Isolation by PCR of a cDNA clone from pea petals with similarity to petunia and wheat zinc finger proteins. <i>Plant Molecular Biology</i> , 1996, 30, 1051-1058.	2.0	18
88	Genetic diversity within <i>Lablab purpureus</i> and the application of gene-specific markers from a range of legume species. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2007, 5, 154-171.	0.4	18
89	NMR Metabolomics Defining Genetic Variation in Pea Seed Metabolites. <i>Frontiers in Plant Science</i> , 2018, 9, 1022.	1.7	18
90	How Mendel's Interest in Inheritance Grew out of Plant Improvement. <i>Genetics</i> , 2018, 210, 347-355.	1.2	16

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91	Pisum lipoyxygenase genes. <i>Theoretical and Applied Genetics</i> , 1991, 81, 800-805.	1.8	14
92	Trisomy: a useful adjunct to RFLP mapping in pea. <i>Chromosoma</i> , 1988, 96, 91-94.	1.0	11
93	A developmentally regulated early-embryogenesis protein in pea ( <i>Pisum sativum</i> L.) is related to the heat-shock protein (HSP70) gene family. <i>Planta</i> , 1991, 184, 350-5.	1.6	11
94	Conservation and diversification of gene function in plant development. <i>Current Opinion in Plant Biology</i> , 2002, 5, 56-61.	3.5	10
95	How did Mendel arrive at his discoveries?. <i>Nature Genetics</i> , 2022, 54, 926-933.	9.4	9
96	Evidence for the presence of hairpin chloroplast DNA molecules in barley cultivars. <i>Current Genetics</i> , 1991, 20, 253-258.	0.8	8
97	Using bioinformatics to analyse germplasm collections. <i>Euphytica</i> , 2004, 137, 39-54.	0.6	8
98	Mendel's pea crosses: varieties, traits and statistics. <i>Hereditas</i> , 2019, 156, 33.	0.5	7
99	Diversity of Pod Shape in <i>Pisum</i> . <i>Diversity</i> , 2021, 13, 203.	0.7	7
100	The Structure, Expression and Arrangement of Legumin Genes in Peas. <i>Biochemie Und Physiologie Der Pflanzen</i> , 1988, 183, 173-180.	0.5	5
101	Germplasm resources in legumes. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 1-3.	0.4	5
102	Recombinant inbred lines derived from cultivars of pea for understanding the genetic basis of variation in breeders' traits. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018, 16, 424-436.	0.4	4
103	Mendel's reaction to Darwin's provisional hypothesis of pangenesis and the experiment that could not wait. <i>Heredity</i> , 0, , .	1.2	4
104	Identification and Genetic Regulation of the Chalcone Synthase Multigene Family in Pea. <i>Plant Cell</i> , 1990, 2, 185.	3.1	3
105	Repeated sequence markers in pea ( <i>Pisum sativum</i> ). <i>New Phytologist</i> , 1997, 137, 35-41.	3.5	3
106	Retrotransposons and the Evolution of Genome Size in <i>Pisum</i> . <i>BioTech</i> , 2020, 9, 24.	1.3	3
107	A <i>crispa</i> null mutant facilitates identification of a <i>crispa</i> -like pseudogene in pea. <i>Functional Plant Biology</i> , 2006, 33, 757.	1.1	3
108	An Integrated Linkage Map of Three Recombinant Inbred Populations of Pea ( <i>Pisum sativum</i> L.). <i>Genes</i> , 2022, 13, 196.	1.0	3

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109	Estimating map distances. <i>Trends in Genetics</i> , 1994, 10, 113-114.	2.9	2
110	Recombination, and chromosomes, in a changing environment. <i>New Phytologist</i> , 2012, 195, 8-9.	3.5	1
111	Genetic Diversity and Core Collection of Alien <i>Pisum sativum</i> L. Germplasm. <i>Acta Agronomica Sinica</i> (China), 2009, 34, 1518-1528.	0.1	1
112	Pea Compound Leaf Architecture Is Regulated by Interactions among the Genes UNIFOLIATA, COCHLEATA, AFILA, and TENDRIL-LESS. <i>Plant Cell</i> , 2000, 12, 1279.	3.1	0
113	Aleksandar Mikić, the legume (re)searcher. , 0, , .		0