

# Gail M Timmerman-Vaughan

## List of Publications by Year in descending order

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34  
papers

1,574  
citations

257450

24  
h-index

361022

35  
g-index

36  
all docs

36  
docs citations

36  
times ranked

1320  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of Mendel's White Flower Character. PLoS ONE, 2010, 5, e13230.	2.5	135
2	The transfer of a powdery mildew resistance gene from <i>Hordeum bulbosum</i> L to barley ( <i>H. vulgare</i> L.) chromosome 2 (2L). Theoretical and Applied Genetics, 1995, 91, 1288-1292.	3.6	106
3	Linkage analysis of <i>er-1</i> , a recessive <i>Pisum sativum</i> gene for resistance to powdery mildew fungus ( <i>Erysiphe pisi</i> D.C.). Theoretical and Applied Genetics, 1994, 88, 1050-1055.	3.6	96
4	QTL Mapping of Partial Resistance to Field Epidemics of <i>Ascochyta</i> Blight of Pea. Crop Science, 2002, 42, 2100-2111.	1.8	90
5	A linkage map of the pea ( <i>Pisum sativum</i> L.) genome containing cloned sequences of known function and expressed sequence tags (ESTs). Theoretical and Applied Genetics, 1997, 95, 1289-1299.	3.6	82
6	Validation of quantitative trait loci for <i>Ascochyta</i> blight resistance in pea ( <i>Pisum sativum</i> L.), using populations from two crosses. Theoretical and Applied Genetics, 2004, 109, 1620-1631.	3.6	82
7	Genetic diversity, population structure and genome-wide marker-trait association analysis emphasizing seed nutrients of the USDA pea ( <i>Pisum sativum</i> L.) core collection. Genes and Genomics, 2012, 34, 305-320.	1.4	69
8	Morphogenetic movements and multicellular development in the fruiting myxobacterium, <i>Stigmatella aurantiaca</i> . Developmental Biology, 1978, 66, 270-274.	2.0	67
9	Linkage mapping of <i>sbm-1</i> , a gene conferring resistance to pea seed-borne mosaic virus, using molecular markers in <i>Pisum sativum</i> . Theoretical and Applied Genetics, 1993, 85, 609-615.	3.6	66
10	Use of Quantitative Real-Time PCR To Estimate Maize Endogenous DNA Degradation after Cooking and Extrusion or in Food Products. Journal of Agricultural and Food Chemistry, 2007, 55, 2231-2239.	5.2	63
11	Characterization and linkage mapping of R-gene analogous DNA sequences in pea ( <i>Pisum sativum</i> L.). Theoretical and Applied Genetics, 2000, 101, 241-247.	3.6	58
12	Mendel, 150 years on. Trends in Plant Science, 2011, 16, 590-596.	8.8	58
13	Linkage Mapping of QTL for Seed Yield, Yield Components, and Developmental Traits in Pea. Crop Science, 2005, 45, 1336-1344.	1.8	54
14	<i>Didymella pinodes</i> and its management in field pea: Challenges and opportunities. Field Crops Research, 2013, 148, 61-77.	5.1	51
15	Marker development and characterisation of <i>Hordeum bulbosum</i> introgression lines: a resource for barley improvement. Theoretical and Applied Genetics, 2009, 118, 1429-1437.	3.6	46
16	Overexpression of STARCH BRANCHING ENZYME II increases short-chain branching of amylopectin and alters the physicochemical properties of starch from potato tuber. BMC Biotechnology, 2015, 15, 28.	3.3	43
17	Kanamycin is effective for selecting transformed peas. Plant Science, 1998, 139, 159-164.	3.6	41
18	Construction and characterization of two bacterial artificial chromosome libraries of pea ( <i>Pisum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.0	34

#	ARTICLE	IF	CITATIONS
19	Partial Resistance of Transgenic Peas to Alfalfa Mosaic Virus under Greenhouse and Field Conditions. <i>Crop Science</i> , 2001, 41, 846-853.	1.8	32
20	Biochemical and Genetic Linkage Analysis of Green Seed Color in Field Pea. <i>Journal of the American Society for Horticultural Science</i> , 1997, 122, 218-225.	1.0	32
21	Starch phosphorylation in potato tubers is influenced by allelic variation in the genes encoding glucan water dikinase, starch branching enzymes I and II, and starch synthase III. <i>Frontiers in Plant Science</i> , 2015, 6, 143.	3.6	30
22	Ascochyta blight disease of pea ( <i>Pisum sativum</i> L.): defence-related candidate genes associated with QTL regions and identification of epistatic QTL. <i>Theoretical and Applied Genetics</i> , 2016, 129, 879-896.	3.6	27
23	Sequence tagged site markers linked to the sbm1 gene for resistance to pea seedborne mosaic virus in pea. <i>Plant Breeding</i> , 2002, 121, 512-516.	1.9	26
24	Nucleotide sequence of the coat protein gene of a necrotic strain of potato virus Y from New Zealand. <i>Archives of Virology</i> , 1989, 107, 111-122.	2.1	24
25	Quantitative real-time PCR assays to detect DNA degradation in soy-based food products. <i>Journal of the Science of Food and Agriculture</i> , 2009, 89, 1137-1144.	3.5	23
26	Haploid and doubled haploid plants from developing male and female gametes of <i>Gentiana triflora</i> . <i>Plant Cell Reports</i> , 2011, 30, 1055-1065.	5.6	22
27	Genomic Selection for Ascochyta Blight Resistance in Pea. <i>Frontiers in Plant Science</i> , 2018, 9, 1878.	3.6	18
28	Association mapping of starch chain length distribution and amylose content in pea ( <i>Pisum sativum</i> L.) using carbohydrate metabolism candidate genes. <i>BMC Plant Biology</i> , 2017, 17, 132.	3.6	17
29	Characterisation of progeny from backcrosses of triploid hybrids between <i>Hordeum vulgare</i> L. (2x) and <i>H. bulbosum</i> L. (4x) to <i>H. vulgare</i> . <i>Theoretical and Applied Genetics</i> , 1994, 88-88, 460-464.	3.6	16
30	Developmental cell cohesion in <i>Stigmatella aurantiaca</i> . <i>Archives of Microbiology</i> , 1982, 131, 334-337.	2.2	11
31	Analysis of the Accumulation of <i>Pea enation mosaic virus</i> Genomes in Seed Tissues and Lack of Evidence for Seed Transmission in Pea ( <i>Pisum sativum</i> ). <i>Phytopathology</i> , 2009, 99, 1281-1288.	2.2	11
32	Quantitative, small-scale, fluorophore-assisted carbohydrate electrophoresis implemented on a capillary electrophoresis-based DNA sequence analyzer. <i>Analytical Biochemistry</i> , 2011, 413, 104-113.	2.4	10
33	Phylogenetic analysis of New Zealand tomato spotted wilt virus isolates suggests likely incursion history scenarios and mechanisms for population evolution. <i>Archives of Virology</i> , 2014, 159, 993-1003.	2.1	10
34	A mass spectrometric method for quantifying C3 and C6 phosphorylation of starch. <i>Analytical Biochemistry</i> , 2012, 431, 115-119.	2.4	9