

Gail M Timmerman-Vaughan

List of Publications by Year in descending order

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34
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1,574
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257450

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1320
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| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Genomic Selection for Ascochyta Blight Resistance in Pea. <i>Frontiers in Plant Science</i> , 2018, 9, 1878. | 3.6 | 18 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | Overexpression of STARCH BRANCHING ENZYME II increases short-chain branching of amylopectin and alters the physicochemical properties of starch from potato tuber. <i>BMC Biotechnology</i> , 2015, 15, 28. | 3.3 | 43 |
| 6 | 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 |
| 7 | <i>Didymella pinodes</i> and its management in field pea: Challenges and opportunities. <i>Field Crops Research</i> , 2013, 148, 61-77. | 5.1 | 51 |
| 8 | A mass spectrometric method for quantifying C3 and C6 phosphorylation of starch. <i>Analytical Biochemistry</i> , 2012, 431, 115-119. | 2.4 | 9 |
| 9 | 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. <i>Genes and Genomics</i> , 2012, 34, 305-320. | 1.4 | 69 |
| 10 | Mendel, 150 years on. <i>Trends in Plant Science</i> , 2011, 16, 590-596. | 8.8 | 58 |
| 11 | 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 |
| 12 | 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 |
| 13 | Identification of Mendel's White Flower Character. <i>PLoS ONE</i> , 2010, 5, e13230. | 2.5 | 135 |
| 14 | Quantitative real-time PCR assays to detect DNA degradation in soybean-based food products. <i>Journal of the Science of Food and Agriculture</i> , 2009, 89, 1137-1144. | 3.5 | 23 |
| 15 | Marker development and characterisation of <i>Hordeum bulbosum</i> introgression lines: a resource for barley improvement. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1429-1437. | 3.6 | 46 |
| 16 | Analysis of the Accumulation of Pea enation mosaic virus 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 |
| 17 | Construction and characterization of two bacterial artificial chromosome libraries of pea (<i>Pisum</i>) Tj ETQq1 1 0.784314 rgBT /Overl | 2.0 | 34 |
| 18 | Use of Quantitative Real-Time PCR To Estimate Maize Endogenous DNA Degradation after Cooking and Extrusion or in Food Products. <i>Journal of Agricultural and Food Chemistry</i> , 2007, 55, 2231-2239. | 5.2 | 63 |

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|----|--|-----|-----------|
| 19 | Linkage Mapping of QTL for Seed Yield, Yield Components, and Developmental Traits in Pea. <i>Crop Science</i> , 2005, 45, 1336-1344. | 1.8 | 54 |
| 20 | Validation of quantitative trait loci for Ascochyta blight resistance in pea (<i>Pisum sativum</i> L.), using populations from two crosses. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1620-1631. | 3.6 | 82 |
| 21 | QTL Mapping of Partial Resistance to Field Epidemics of Ascochyta Blight of Pea. <i>Crop Science</i> , 2002, 42, 2100-2111. | 1.8 | 90 |
| 22 | 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 |
| 23 | 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 |
| 24 | Characterization and linkage mapping of R-gene analogous DNA sequences in pea (<i>Pisum sativum</i> L.). <i>Theoretical and Applied Genetics</i> , 2000, 101, 241-247. | 3.6 | 58 |
| 25 | Kanamycin is effective for selecting transformed peas. <i>Plant Science</i> , 1998, 139, 159-164. | 3.6 | 41 |
| 26 | A linkage map of the pea (<i>Pisum sativum</i> L.) genome containing cloned sequences of known function and expressed sequence tags (ESTs). <i>Theoretical and Applied Genetics</i> , 1997, 95, 1289-1299. | 3.6 | 82 |
| 27 | 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 |
| 28 | The transfer of a powdery mildew resistance gene from <i>Hordeum bulbosum</i> L to barley (<i>H. vulgare</i> L.) chromosome 2 (2l). <i>Theoretical and Applied Genetics</i> , 1995, 91, 1288-1292. | 3.6 | 106 |
| 29 | Linkage analysis of er-1, a recessive <i>Pisum sativum</i> gene for resistance to powdery mildew fungus (<i>Erysiphe pisi</i> D.C.). <i>Theoretical and Applied Genetics</i> , 1994, 88, 1050-1055. | 3.6 | 96 |
| 30 | 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 |
| 31 | Linkage mapping of sbm-1, a gene conferring resistance to pea seed-borne mosaic virus, using molecular markers in <i>Pisum sativum</i> . <i>Theoretical and Applied Genetics</i> , 1993, 85, 609-615. | 3.6 | 66 |
| 32 | 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 |
| 33 | Developmental cell cohesion in <i>Stigmatella aurantiaca</i> . <i>Archives of Microbiology</i> , 1982, 131, 334-337. | 2.2 | 11 |
| 34 | Morphogenetic movements and multicellular development in the fruiting myxobacterium, <i>Stigmatella aurantiaca</i> . <i>Developmental Biology</i> , 1978, 66, 270-274. | 2.0 | 67 |