

Phillip E Mcclean

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

4,822
citations

126708

33
h-index

102304

66
g-index

84
all docs

84
docs citations

84
times ranked

4207
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Local to continental scale variation in fitness and heritability in common bean. <i>Crop Science</i> , 2022, 62, 767-779. | 0.8 | 7 |
| 2 | New genomic regions associated with white mold resistance in dry bean using a MAGIC population. <i>Plant Genome</i> , 2022, 15, e20190. | 1.6 | 3 |
| 3 | The Common Bean V Gene Encodes Flavonoid 3-Hydroxylase: A Major Mutational Target for Flavonoid Diversity in Angiosperms. <i>Frontiers in Plant Science</i> , 2022, 13, 869582. | 1.7 | 7 |
| 4 | Genetic diversity of Guatemalan climbing bean collections. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 639-656. | 0.8 | 10 |
| 5 | The genetics and physiology of seed dormancy, a crucial trait in common bean domestication. <i>BMC Plant Biology</i> , 2021, 21, 58. | 1.6 | 24 |
| 6 | Using Breeding Populations With a Dual Purpose: Cultivar Development and Gene Mapping—A Case Study Using Resistance to Common Bacterial Blight in Dry Bean (<i>Phaseolus vulgaris</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 621097. | 1.7 | 7 |
| 7 | Orthology and synteny analysis of receptor-like kinases and receptor-like proteins in legumes. <i>BMC Genomics</i> , 2021, 22, 113. | 1.2 | 4 |
| 8 | NAC Candidate Gene Marker for bgm-1 and Interaction With QTL for Resistance to Bean Golden Yellow Mosaic Virus in Common Bean. <i>Frontiers in Plant Science</i> , 2021, 12, 628443. | 1.7 | 12 |
| 9 | The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638. | 5.8 | 43 |
| 10 | Genome-Wide Association Mapping of bc-1 and bc-u Reveals Candidate Genes and New Adjustments to the Host-Pathogen Interaction for Resistance to Bean Common Mosaic Necrosis Virus in Common Bean. <i>Frontiers in Plant Science</i> , 2021, 12, 699569. | 1.7 | 10 |
| 11 | Faster cooking times and improved iron bioavailability are associated with the down regulation of procyandin synthesis in slow-darkening pinto beans (<i>Phaseolus vulgaris</i> L.). <i>Journal of Functional Foods</i> , 2021, 82, 104444. | 1.6 | 12 |
| 12 | Coding Mutations in Vacuolar Protein-Sorting 4 AAA+ ATPase Endosomal Sorting Complexes Required for Transport Protein Homologs Underlie bc-2 and New bc-4 Gene Conferring Resistance to Bean Common Mosaic Virus in Common Bean. <i>Frontiers in Plant Science</i> , 2021, 12, 769247. | 1.7 | 12 |
| 13 | Toward validation of QTLs associated with pod and seed size in common bean using two nested recombinant inbred line populations. <i>Molecular Breeding</i> , 2020, 40, 1. | 1.0 | 8 |
| 14 | Computational identification of receptor-like kinases and receptor-like proteins in legumes. <i>BMC Genomics</i> , 2020, 21, 459. | 1.2 | 16 |
| 15 | Sources of Resistance to <i>Fusarium solani</i> and Associated Genomic Regions in Common Bean Diversity Panels. <i>Frontiers in Genetics</i> , 2020, 11, 475. | 1.1 | 19 |
| 16 | Genetic Associations in Four Decades of Multienvironment Trials Reveal Agronomic Trait Evolution in Common Bean. <i>Genetics</i> , 2020, 215, 267-284. | 1.2 | 26 |
| 17 | Genetic Factors Associated With Nodulation and Nitrogen Derived From Atmosphere in a Middle American Common Bean Panel. <i>Frontiers in Plant Science</i> , 2020, 11, 576078. | 1.7 | 11 |
| 18 | Improving the Health Benefits of Snap Bean: Genome-Wide Association Studies of Total Phenolic Content. <i>Nutrients</i> , 2019, 11, 2509. | 1.7 | 27 |

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|----|---|-----|-----------|
| 19 | Genotypes and Genomic Regions Associated With <i>Rhizoctonia solani</i> Resistance in Common Bean. <i>Frontiers in Plant Science</i> , 2019, 10, 956. | 1.7 | 48 |
| 20 | Mapping and characterization of two stem rust resistance genes derived from cultivated emmer wheat accession PI 193883. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3177-3189. | 1.8 | 33 |
| 21 | Shovelomics for phenotyping root architectural traits of rapeseed/canola (<i>Brassica napus</i> L.) and genome-wide association mapping. <i>Molecular Genetics and Genomics</i> , 2019, 294, 985-1000. | 1.0 | 27 |
| 22 | Genome wide association study discovers genomic regions involved in resistance to soybean cyst nematode (<i>Heterodera glycines</i>) in common bean. <i>PLoS ONE</i> , 2019, 14, e0212140. | 1.1 | 14 |
| 23 | Single and Multi-trait GWAS Identify Genetic Factors Associated with Production Traits in Common Bean Under Abiotic Stress Environments. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1881-1892. | 0.8 | 76 |
| 24 | Investigation of a Stand-Alone Online Learning Module for Cellular Respiration Instruction. <i>Journal of Microbiology and Biology Education</i> , 2018, 19, . | 0.5 | 7 |
| 25 | Genetic Analysis of Flooding Tolerance in an Andean Diversity Panel of Dry Bean (<i>Phaseolus vulgaris</i>) Tj ETQq1 1 0.784314 rgBT /Over 1.7 67 | 1.7 | 67 |
| 26 | Genetic Architecture of Dietary Fiber and Oligosaccharide Content in a Middle American Panel of Edible Dry Bean. <i>Plant Genome</i> , 2018, 11, 170074. | 1.6 | 13 |
| 27 | White seed color in common bean (<i>Phaseolus vulgaris</i>) results from convergent evolution in the <i>P</i> (<i>pigment</i>) gene. <i>New Phytologist</i> , 2018, 219, 1112-1123. | 3.5 | 77 |
| 28 | Efficacy of a Meiosis Learning Module Developed for the Virtual Cell Animation Collection. <i>CBE Life Sciences Education</i> , 2017, 16, ar9. | 1.1 | 14 |
| 29 | Variation in external representations as part of the classroom lecture: An investigation of virtual cell animations in introductory photosynthesis instruction*. <i>Biochemistry and Molecular Biology Education</i> , 2017, 45, 226-234. | 0.5 | 5 |
| 30 | Common Bean Genomes: Mining New Knowledge of a Major Societal Crop. <i>Compendium of Plant Genomes</i> , 2017, , 129-145. | 0.3 | 4 |
| 31 | Genetic Architecture of Flooding Tolerance in the Dry Bean Middle-American Diversity Panel. <i>Frontiers in Plant Science</i> , 2017, 8, 1183. | 1.7 | 54 |
| 32 | Marker-Assisted Molecular Profiling, Deletion Mutant Analysis, and RNA-Seq Reveal a Disease Resistance Cluster Associated with <i>Uromyces appendiculatus</i> Infection in Common Bean <i>Phaseolus vulgaris</i> L.. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1109. | 1.8 | 3 |
| 33 | Phenotypic Diversity for Seed Mineral Concentration in North American Dry Bean Germplasm of Middle American Ancestry. <i>Crop Science</i> , 2017, 57, 3129-3144. | 0.8 | 29 |
| 34 | Targeted Analysis of Dry Bean Growth Habit: Interrelationship among Architectural, Phenological, and Yield Components. <i>Crop Science</i> , 2016, 56, 3005-3015. | 0.8 | 34 |
| 35 | Sequence-Based Introgression Mapping Identifies Candidate White Mold Tolerance Genes in Common Bean. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0092. | 1.6 | 10 |
| 36 | Genome-Wide Association Study Identifies Candidate Loci Underlying Agronomic Traits in a Middle American Diversity Panel of Common Bean. <i>Plant Genome</i> , 2016, 9, plantgenome2016.02.0012. | 1.6 | 136 |

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|----|---|-----|-----------|
| 37 | Transcriptome Analysis of Piperlongumine-Treated Human Pancreatic Cancer Cells Reveals Involvement of Oxidative Stress and Endoplasmic Reticulum Stress Pathways. <i>Journal of Medicinal Food</i> , 2016, 19, 578-585. | 0.8 | 21 |
| 38 | Optimization of genotyping by sequencing (GBS) data in common bean (<i>Phaseolus vulgaris</i> L.). <i>Molecular Breeding</i> , 2016, 36, 1. | 1.0 | 65 |
| 39 | High Level of Nonsynonymous Changes in Common Bean Suggests That Selection under Domestication Increased Functional Diversity at Target Traits. <i>Frontiers in Plant Science</i> , 2016, 7, 2005. | 1.7 | 19 |
| 40 | The Virtual Cell Animation Collection: Tools for Teaching Molecular and Cellular Biology. <i>PLoS Biology</i> , 2015, 13, e1002118. | 2.6 | 12 |
| 41 | New QTL alleles for quality-related traits in spring wheat revealed by RIL population derived from supernumerary—non-supernumerary spikelet genotypes. <i>Theoretical and Applied Genetics</i> , 2015, 128, 893-912. | 1.8 | 47 |
| 42 | SNP Assay Development for Linkage Map Construction, Anchoring Whole-Genome Sequence, and Other Genetic and Genomic Applications in Common Bean. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2285-2290. | 0.8 | 147 |
| 43 | Genome-Wide Association Mapping for Resistance to Leaf and Stripe Rust in Winter-Habit Hexaploid Wheat Landraces. <i>PLoS ONE</i> , 2015, 10, e0129580. | 1.1 | 120 |
| 44 | Developing market class specific InDel markers from next generation sequence data in <i>Phaseolus vulgaris</i> L.. <i>Frontiers in Plant Science</i> , 2014, 5, 185. | 1.7 | 79 |
| 45 | Quantitative trait loci mapping of seed colour, hairy leaf, seedling anthocyanin, leaf chlorosis and days to flowering in <i>F₂</i> population of <i>B_{rassica rapa}</i> L.. <i>Plant Breeding</i> , 2014, 133, 381-389. | 1.0 | 11 |
| 46 | Application of in silico bulked segregant analysis for rapid development of markers linked to Bean common mosaic virus resistance in common bean. <i>BMC Genomics</i> , 2014, 15, 903. | 1.2 | 58 |
| 47 | A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713. | 9.4 | 1,159 |
| 48 | Common Bean Genomics and Its Applications in Breeding Programs. , 2014, , 185-206. | | 4 |
| 49 | Genome-Wide Association Studies Identifies Seven Major Regions Responsible for Iron Deficiency Chlorosis in Soybean (<i>Glycine max</i>). <i>PLoS ONE</i> , 2014, 9, e107469. | 1.1 | 92 |
| 50 | A re-sequencing based assessment of genomic heterogeneity and fast neutron-induced deletions in a common bean cultivar. <i>Frontiers in Plant Science</i> , 2013, 4, 210. | 1.7 | 18 |
| 51 | In silico comparison of genomic regions containing genes coding for enzymes and transcription factors for the phenylpropanoid pathway in <i>Phaseolus vulgaris</i> L. and <i>Glycine max</i> L. <i>Merr. Frontiers in Plant Science</i> , 2013, 4, 317. | 1.7 | 30 |
| 52 | Genetic Analysis on Flowering Time and Root System in <i>Brassica napus</i> L. <i>Crop Science</i> , 2013, 53, 141-147. | 0.8 | 21 |
| 53 | Tan spot susceptibility governed by the <i>Tsn1</i> locus and race-nonspecific resistance quantitative trait loci in a population derived from the wheat lines Salamouni and Katepwa. <i>Molecular Breeding</i> , 2012, 30, 1669-1678. | 1.0 | 42 |
| 54 | Whole-Genome QTL Analysis of <i>Stagonospora nodorum</i> Blotch Resistance and Validation of the <i>Snn4</i> — <i>Snn4</i> Interaction in Hexaploid Wheat. <i>Phytopathology</i> , 2012, 102, 94-104. | 1.1 | 22 |

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|----|---|-----|-----------|
| 55 | Mesoamerican origin of the common bean (<i>Phaseolus vulgaris</i> L.) is revealed by sequence data. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E788-96. | 3.3 | 327 |
| 56 | Population structure and genetic differentiation among the USDA common bean (<i>Phaseolus vulgaris</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf | 0.8 | 45 |
| 57 | Investigation of the domestication of common bean (<i>Phaseolus vulgaris</i>) using multilocus sequence data. Functional Plant Biology, 2011, 38, 953. | 1.1 | 75 |
| 58 | Genome-Wide Association Analysis Identifies Candidate Genes Associated with Iron Deficiency Chlorosis in Soybean. Plant Genome, 2011, 4, 154-164. | 1.6 | 106 |
| 59 | Crop improvement in the era of climate change: an integrated, multi-disciplinary approach for common bean (<i>Phaseolus vulgaris</i>). Functional Plant Biology, 2011, 38, 927. | 1.1 | 67 |
| 60 | Identification of candidate genes associated with CBB resistance in common bean HR45 (<i>Phaseolus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf | 1.0 | 20 |
| 61 | Saturation of an Intra-Gene Pool Linkage Map: Towards a Unified Consensus Linkage Map for Fine Mapping and Synteny Analysis in Common Bean. PLoS ONE, 2011, 6, e28135. | 1.1 | 61 |
| 62 | Syntenic relationships among legumes revealed using a gene-based genetic linkage map of common bean (<i>Phaseolus vulgaris</i> L.). Theoretical and Applied Genetics, 2010, 121, 1103-1116. | 1.8 | 99 |
| 63 | Synteny mapping between common bean and soybean reveals extensive blocks of shared loci. BMC Genomics, 2010, 11, 184. | 1.2 | 100 |
| 64 | Artificial selection for determinate growth habit in soybean. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8563-8568. | 3.3 | 330 |
| 65 | Association mapping of iron deficiency chlorosis loci in soybean (<i>Glycine max</i> L. Merr.) advanced breeding lines. Theoretical and Applied Genetics, 2008, 116, 777-787. | 1.8 | 111 |
| 66 | BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (<i>Phaseolus vulgaris</i> L.) Genome. Tropical Plant Biology, 2008, 1, 40-48. | 1.0 | 70 |
| 67 | <i>Phaseolus vulgaris</i> : A Diploid Model for Soybean., 2008, , 55-76. | | 28 |
| 68 | Genetic architecture of chalcone isomerase non-coding regions in common bean (<i>Phaseolus vulgaris</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf | 0.9 | 19 |
| 69 | Molecular and Cellular Biology Animations: Development and Impact on Student Learning. CBE: Life Sciences Education, 2005, 4, 169-179. | 0.7 | 107 |
| 70 | Sequence diversity analysis of dihydroflavonol 4-reductase intron 1 in common bean. Genome, 2004, 47, 266-280. | 0.9 | 42 |
| 71 | A molecular marker tightly linked toP, a gene required for flower and seedcoat color in common bean (<i>Phaseolus vulgaris</i> L.), contains the Ty3-gypsyretrotransposonTpv3g. Genome, 2002, 45, 728-736. | 0.9 | 16 |
| 72 | Classical and Molecular Genetic Studies of the Strong Greenish Yellow Seedcoat Color in 'Wagenaar' and 'Enola' Common Bean. Journal of the American Society for Horticultural Science, 2002, 127, 50-55. | 0.5 | 16 |

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|----|--|-----|-----------|
| 73 | Inheritance of Reverse Margo Seedcoat Pattern and Allelism between the Genes J for Seedcoat Color and L for Partly Colored Seedcoat Pattern in Common Bean. <i>Journal of the American Society for Horticultural Science</i> , 2002, 127, 56-61. | 0.5 | 12 |
| 74 | Organization and transcription of the gene encoding potato UDP-glucose pyrophosphorylase. <i>Gene</i> , 1997, 186, 293-297. | 1.0 | 14 |
| 75 | Effect of Expression of UDP-Glucose Pyrophosphorylase Ribozyme and Antisense RNAs on the Enzyme Activity and Carbohydrate Composition of Field-Grown Transgenic Potato Plants. <i>Journal of Plant Physiology</i> , 1996, 147, 644-652. | 1.6 | 57 |
| 76 | A tandemly repeated sequence from the <i>Plasmopara halstedii</i> genome. <i>Gene</i> , 1993, 124, 127-130. | 1.0 | 10 |
| 77 | Coefficient of Parentage and Cluster Analysis of North American Dry Bean Cultivars. <i>Crop Science</i> , 1993, 33, 190-197. | 0.8 | 46 |
| 78 | Estimating Phenylalanine Ammonia-lyase Activity in Common Beans Inoculated with <i>Sclerotinia sclerotiorum</i> . <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 1993, 28, 937-938. | 0.5 | 6 |
| 79 | Susceptibility of dry bean (<i>Phaseolus vulgaris</i> L.) to <i>Agrobacterium</i> infection: Transformation of cotyledonary and hypocotyl tissues. <i>Plant Cell, Tissue and Organ Culture</i> , 1991, 24, 131-138. | 1.2 | 45 |
| 80 | The isolation of mitochondria and mitochondrial DNA. <i>Methods in Enzymology</i> , 1986, 118, 437-453. | 0.4 | 45 |
| 81 | MITOCHONDRIAL DNA SEQUENCE DIVERGENCE AMONG LYCOPERSICON AND RELATED SOLANUM SPECIES. <i>Genetics</i> , 1986, 112, 649-667. | 1.2 | 69 |
| 82 | Bean rust resistance in the Guatemalan climbing bean germplasm collection. , 0, , . | | 2 |