

# 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	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
2	Artificial selection for determinate growth habit in soybean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8563-8568.	3.3	330
3	Mesoamerican origin of the common bean ( <i>Phaseolus vulgaris</i> L.) is revealed by sequence data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E788-96.	3.3	327
4	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
5	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
6	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
7	Association mapping of iron deficiency chlorosis loci in soybean ( <i>Glycine max</i> L. Merr.) advanced breeding lines. <i>Theoretical and Applied Genetics</i> , 2008, 116, 777-787.	1.8	111
8	Molecular and Cellular Biology Animations: Development and Impact on Student Learning. <i>CBE: Life Sciences Education</i> , 2005, 4, 169-179.	0.7	107
9	Genome-Wide Association Analysis Identifies Candidate Genes Associated with Iron Deficiency Chlorosis in Soybean. <i>Plant Genome</i> , 2011, 4, 154-164.	1.6	106
10	Synteny mapping between common bean and soybean reveals extensive blocks of shared loci. <i>BMC Genomics</i> , 2010, 11, 184.	1.2	100
11	Syntenic relationships among legumes revealed using a gene-based genetic linkage map of common bean ( <i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2010, 121, 1103-1116.	1.8	99
12	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
13	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
14	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
15	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
16	Investigation of the domestication of common bean ( <i>Phaseolus vulgaris</i> ) using multilocus sequence data. <i>Functional Plant Biology</i> , 2011, 38, 953.	1.1	75
17	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean ( <i>Phaseolus vulgaris</i> L.) Genome. <i>Tropical Plant Biology</i> , 2008, 1, 40-48.	1.0	70
18	MITOCHONDRIAL DNA SEQUENCE DIVERGENCE AMONG LYCOPERSICON AND RELATED SOLANUM SPECIES. <i>Genetics</i> , 1986, 112, 649-667.	1.2	69

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19	Crop improvement in the era of climate change: an integrated, multi-disciplinary approach for common bean ( <i>Phaseolus vulgaris</i> ). <i>Functional Plant Biology</i> , 2011, 38, 927.	1.1	67
20	Genetic Analysis of Flooding Tolerance in an Andean Diversity Panel of Dry Bean ( <i>Phaseolus vulgaris</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.7	67
21	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
22	Saturation of an Intra-Gene Pool Linkage Map: Towards a Unified Consensus Linkage Map for Fine Mapping and Synteny Analysis in Common Bean. <i>PLoS ONE</i> , 2011, 6, e28135.	1.1	61
23	Application of in silico bulked segregant analysis for rapid development of markers linked to Bean common mosaic virusresistance in common bean. <i>BMC Genomics</i> , 2014, 15, 903.	1.2	58
24	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
25	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
26	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
27	New QTL alleles for quality-related traits in spring wheat revealed by RIL population derived from supernumerary—Anon-supernumerary spikelet genotypes. <i>Theoretical and Applied Genetics</i> , 2015, 128, 893-912.	1.8	47
28	Coefficient of Parentage and Cluster Analysis of North American Dry Bean Cultivars. <i>Crop Science</i> , 1993, 33, 190-197.	0.8	46
29	The isolation of mitochondria and mitochondrial DNA. <i>Methods in Enzymology</i> , 1986, 118, 437-453.	0.4	45
30	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
31	Population structure and genetic differentiation among the USDA common bean ( <i>Phaseolus vulgaris</i> ) Tj ETQq1 1 0,784314 rgBT /Over 45	0.8	45
32	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	5.8	43
33	Sequence diversity analysis of dihydroflavonol 4-reductase intron 1 in common bean. <i>Genome</i> , 2004, 47, 266-280.	0.9	42
34	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
35	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
36	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

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37	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. Merr. <i>Frontiers in Plant Science</i> , 2013, 4, 317.	1.7	30
38	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
39	<i>Phaseolus vulgaris</i> : A Diploid Model for Soybean. , 2008, , 55-76.		28
40	Improving the Health Benefits of Snap Bean: Genome-Wide Association Studies of Total Phenolic Content. <i>Nutrients</i> , 2019, 11, 2509.	1.7	27
41	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
42	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
43	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
44	Whole-Genome QTL Analysis of <i>Stagonospora nodorum</i> Blotch Resistance and Validation of the <i>Snn4</i> Interaction in Hexaploid Wheat. <i>Phytopathology</i> , 2012, 102, 94-104.	1.1	22
45	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
46	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
47	Identification of candidate genes associated with CBB resistance in common bean HR45 ( <i>Phaseolus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tff	1.0	20
48	Genetic architecture of chalcone isomerase non-coding regions in common bean ( <i>Phaseolus vulgaris</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tff	0.9	19
49	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
50	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
51	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
52	A molecular marker tightly linked to <i>P</i> , a gene required for flower and seedcoat color in common bean ( <i>Phaseolus vulgaris</i> L.), contains the Ty3-gypsyretrotransposon <i>Tpv3g</i> . <i>Genome</i> , 2002, 45, 728-736.	0.9	16
53	Computational identification of receptor-like kinases and receptor-like proteins in legumes. <i>BMC Genomics</i> , 2020, 21, 459.	1.2	16
54	Classical and Molecular Genetic Studies of the Strong Greenish Yellow Seedcoat Color in 'Wagenaar' and 'Enola' Common Bean. <i>Journal of the American Society for Horticultural Science</i> , 2002, 127, 50-55.	0.5	16

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55	Organization and transcription of the gene encoding potato UDP-glucose pyrophosphorylase. <i>Gene</i> , 1997, 186, 293-297.	1.0	14
56	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
57	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
58	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
59	The Virtual Cell Animation Collection: Tools for Teaching Molecular and Cellular Biology. <i>PLoS Biology</i> , 2015, 13, e1002118.	2.6	12
60	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
61	Faster cooking times and improved iron bioavailability are associated with the down regulation of procyanidin synthesis in slow-darkening pinto beans ( <i>Phaseolus vulgaris</i> L.). <i>Journal of Functional Foods</i> , 2021, 82, 104444.	1.6	12
62	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
63	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
64	Quantitative trait loci mapping of seed colour, hairy leaf, seedling anthocyanin, leaf chlorosis and days to flowering in <i>F<sub>2</sub></i> population of <i>B<sub>rassica rapa</sub></i> L.. <i>Plant Breeding</i> , 2014, 133, 381-389.	1.0	11
65	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
66	A tandemly repeated sequence from the <i>Plasmopara halstedii</i> genome. <i>Gene</i> , 1993, 124, 127-130.	1.0	10
67	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
68	Genetic diversity of Guatemalan climbing bean collections. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 639-656.	0.8	10
69	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
70	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
71	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
72	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

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73	Local to continental scale variation in fitness and heritability in common bean. <i>Crop Science</i> , 2022, 62, 767-779.	0.8	7
74	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
75	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
76	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
77	Common Bean Genomes: Mining New Knowledge of a Major Societal Crop. <i>Compendium of Plant Genomes</i> , 2017, , 129-145.	0.3	4
78	Orthology and synteny analysis of receptor-like kinases and receptor-like proteins in legumes. <i>BMC Genomics</i> , 2021, 22, 113.	1.2	4
79	Common Bean Genomics and Its Applications in Breeding Programs. , 2014, , 185-206.		4
80	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
81	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
82	Bean rust resistance in the Guatemalan climbing bean germplasm collection. , 0, , .		2