

Matthew W Blair

List of Publications by Year in descending order

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85
papers

6,747
citations

76322

40
h-index

66906

78
g-index

87
all docs

87
docs citations

87
times ranked

4748
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.	21.4	1,159
2	Common bean breeding for resistance against biotic and abiotic stresses: From classical to MAS breeding. <i>Euphytica</i> , 2006, 147, 105-131.	1.2	448
3	Landrace Germplasm for Improving Yield and Abiotic Stress Adaptation. <i>Trends in Plant Science</i> , 2016, 21, 31-42.	8.8	293
4	Legume Crops Phylogeny and Genetic Diversity for Science and Breeding. <i>Critical Reviews in Plant Sciences</i> , 2015, 34, 43-104.	5.7	248
5	SNP marker diversity in common bean (<i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 123, 827-845.	3.6	182
6	Genetic diversity, inter-gene pool introgression and nutritional quality of common beans (<i>Phaseolus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.6	177
7	Extensive ribosomal DNA amplification during Andean common bean (<i>Phaseolus vulgaris</i> L.) evolution. <i>Theoretical and Applied Genetics</i> , 2006, 112, 924-933.	3.6	168
8	Genetic diversity, seed size associations and population structure of a core collection of common beans (<i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2009, 119, 955-972.	3.6	158
9	Gene-Based Single Nucleotide Polymorphism Markers for Genetic and Association Mapping in Common Bean. <i>BMC Genetics</i> , 2012, 13, 48.	2.7	143
10	Diversification and Population Structure in Common Beans (<i>Phaseolus vulgaris</i> L.). <i>PLoS ONE</i> , 2012, 7, e49488.	2.5	139
11	A high-throughput SNP marker system for parental polymorphism screening, and diversity analysis in common bean (<i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 535-548.	3.6	139
12	Drought Tolerance in Wild Plant Populations: The Case of Common Beans (<i>Phaseolus vulgaris</i> L.). <i>PLoS ONE</i> , 2013, 8, e62898.	2.5	137
13	Genetic diversity and population structure of common bean (<i>Phaseolus vulgaris</i> L.) landraces from the East African highlands. <i>Theoretical and Applied Genetics</i> , 2009, 120, 1-12.	3.6	134
14	Quantitative Trait Loci Associated with Drought Tolerance in Common Bean. <i>Crop Science</i> , 2014, 54, 923-938.	1.8	129
15	Genotyping by Sequencing and Genome-Environment Associations in Wild Common Bean Predict Widespread Divergent Adaptation to Drought. <i>Frontiers in Plant Science</i> , 2018, 9, 128.	3.6	129
16	Mineral Biofortification Strategies for Food Staples: The Example of Common Bean. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 8287-8294.	5.2	126
17	QTL Analysis of Seed Iron, Zinc, and Phosphorus Levels in an Andean Bean Population. <i>Crop Science</i> , 2009, 49, 1742-1750.	1.8	125
18	Identification of an ERECTA gene and its drought adaptation associations with wild and cultivated common bean. <i>Plant Science</i> , 2016, 242, 250-259.	3.6	122

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19	QTL for seed iron and zinc concentration and content in a Mesoamerican common bean (<i>Phaseolus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 119	3.6	119
20	Nucleotide diversity patterns at the drought-related DREB2 encoding genes in wild and cultivated common bean (<i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2012, 125, 1069-1085.	3.6	114
21	Genomics of <i>Phaseolus</i> Beans, a Major Source of Dietary Protein and Micronutrients in the Tropics. , 2008, , 113-143.		114
22	Uneven recombination rate and linkage disequilibrium across a reference SNP map for common bean (<i>Phaseolus vulgaris</i> L.). <i>PLoS ONE</i> , 2018, 13, e0189597.	2.5	108
23	Genetic diversity of Chinese common bean (<i>Phaseolus vulgaris</i> L.) landraces assessed with simple sequence repeat markers. <i>Theoretical and Applied Genetics</i> , 2008, 117, 629-640.	3.6	103
24	QTL analyses for seed iron and zinc concentrations in an intra-genepool population of Andean common beans (<i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 122, 511-521.	3.6	102
25	Molecular ecology and selection in the drought-related <i>Asr</i> gene polymorphisms in wild and cultivated common bean (<i>Phaseolus vulgaris</i> L.). <i>BMC Genetics</i> , 2012, 13, 58.	2.7	100
26	Resequencing of 683 common bean genotypes identifies yield component trait associations across a north-south cline. <i>Nature Genetics</i> , 2020, 52, 118-125.	21.4	81
27	A legume biofortification quandary: variability and genetic control of seed coat micronutrient accumulation in common beans. <i>Frontiers in Plant Science</i> , 2013, 4, 275.	3.6	80
28	Gene-based SSR markers for common bean (<i>Phaseolus vulgaris</i> L.) derived from root and leaf tissue ESTs: an integration of the BMC series. <i>BMC Plant Biology</i> , 2011, 11, 50.	3.6	79
29	Use of the advanced backcross-QTL method to transfer seed mineral accumulation nutrition traits from wild to Andean cultivated common beans. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1015-1031.	3.6	77
30	A review of breeding objectives, genomic resources, and marker-assisted methods in common bean (<i>Phaseolus vulgaris</i> L.). <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	72
31	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.	1.9	70
32	Quantitative trait loci for rooting pattern traits of common beans grown under drought stress versus non-stress conditions. <i>Molecular Breeding</i> , 2012, 30, 681-695.	2.1	65
33	Meta-QTL analysis of seed iron and zinc concentration and content in common bean (<i>Phaseolus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 119	3.6	65
34	Development and diversity of Andean-derived, gene-based microsatellites for common bean (<i>Phaseolus</i>) Tj ETQq0 0,0 rgBT /Overlock 119	3.6	62
35	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.	2.5	61
36	Integration of physical and genetic maps of common bean through BAC-derived microsatellite markers. <i>BMC Genomics</i> , 2010, 11, 436.	2.8	59

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37	Does the Genomic Landscape of Species Divergence in Phaseolus Beans Coerce Parallel Signatures of Adaptation and Domestication?. <i>Frontiers in Plant Science</i> , 2018, 9, 1816.	3.6	56
38	Single strand conformation polymorphism based SNP and Indel markers for genetic mapping and synteny analysis of common bean (<i>Phaseolus vulgaris</i> L.). <i>BMC Genomics</i> , 2009, 10, 629.	2.8	55
39	QTL Analysis of Root Architecture Traits and Low Phosphorus Tolerance in an Andean Bean Population. <i>Crop Science</i> , 2009, 49, 59-68.	1.8	51
40	Variation and inheritance of iron reductase activity in the roots of common bean (<i>Phaseolus vulgaris</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	3.6	51
41	Differentially Expressed Genes in Resistant and Susceptible Common Bean (<i>Phaseolus vulgaris</i> L.) Genotypes in Response to <i>Fusarium oxysporum</i> f. sp. <i>phaseoli</i> . <i>PLoS ONE</i> , 2015, 10, e0127698.	2.5	51
42	Diversity in Grain Amaranths and Relatives Distinguished by Genotyping by Sequencing (GBS). <i>Frontiers in Plant Science</i> , 2017, 8, 1960.	3.6	44
43	Genetic mapping of the bean golden yellow mosaic geminivirus resistance gene <i>bgm-1</i> and linkage with potyvirus resistance in common bean (<i>Phaseolus vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2006, 114, 261-271.	3.6	42
44	CEL I Nuclease Digestion for SNP Discovery and Marker Development in Common Bean (<i>Phaseolus</i>) Tj ETQq0 0 0 ggBT /Overlock 10 T	1.8	40
45	Morphological Assessment of Cultivated and Wild Amaranth Species Diversity. <i>Agronomy</i> , 2018, 8, 272.	3.0	38
46	Allelic Diversity at Abiotic Stress Responsive Genes in Relationship to Ecological Drought Indices for Cultivated Tepary Bean, <i>Phaseolus acutifolius</i> A. Gray, and Its Wild Relatives. <i>Genes</i> , 2021, 12, 556.	2.4	38
47	Development of microsatellite markers for common bean (<i>Phaseolus vulgaris</i> L.) based on screening of non-enriched, small-insert genomic libraries. <i>Genome</i> , 2009, 52, 772-782.	2.0	37
48	Genetic mapping of microsatellite markers around the arcelin bruchid resistance locus in common bean. <i>Theoretical and Applied Genetics</i> , 2010, 121, 393-402.	3.6	37
49	Inheritance of seed phytate and phosphorus levels in common bean (<i>Phaseolus vulgaris</i> L.) and association with newly-mapped candidate genes. <i>Molecular Breeding</i> , 2012, 30, 1265-1277.	2.1	36
50	Hybrid weakness controlled by the dosage-dependent lethal (DL) gene system in common bean (<i>Phaseolus vulgaris</i>) is caused by a shoot-derived inhibitory signal leading to salicylic acid-associated root death. <i>New Phytologist</i> , 2007, 176, 537-549.	7.3	34
51	Construction and EST sequencing of full-length, drought stress cDNA libraries for common beans (<i>Phaseolus vulgaris</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 171.	3.6	28
52	Extensive diversity and inter-genepool introgression in a world-wide collection of indeterminate snap bean accessions. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1381-1391.	3.6	26
53	Linkage disequilibrium at the APA insecticidal seed protein locus of common bean (<i>Phaseolus vulgaris</i>) Tj ETQq1 1 0,784314 ggBT /Overl	3.6	26
54	Molecular Characterization of Mung Bean Germplasm from the USDA Core Collection Using Newly Developed KASP-based SNP Markers. <i>Crop Science</i> , 2018, 58, 1659-1670.	1.8	25

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55	Role of Legumes for and as Horticultural Crops in Sustainable Agriculture. Sustainable Development and Biodiversity, 2016, , 185-211.	1.7	22
56	Hairy root transgene expression analysis of a secretory peroxidase (PvPOX1) from common bean infected by Fusarium wilt. Plant Science, 2017, 260, 1-7.	3.6	22
57	Linkage and mapping of quantitative trait loci associated with angular leaf spot and powdery mildew resistance in common beans. Genetics and Molecular Biology, 2017, 40, 109-122.	1.3	21
58	Genetic diversity of Colombian landraces of common bean as detected through the use of silver-stained and fluorescently labelled microsatellites. Plant Genetic Resources: Characterisation and Utilisation, 2011, 9, 86-96.	0.8	20
59	QTL and candidate genes associated with common bacterial blight resistance in the common bean cultivar Longyundou 5 from China. Crop Journal, 2016, 4, 344-352.	5.2	18
60	Identification and Mapping of Simple Sequence Repeat Markers from Common Bean (<i>Phaseolus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Geneticâ€Physical Map Integration. Plant Genome, 2010, 3, .	2.8	17
61	Salicylic Acid Enhances Resistance to <i>Fusarium oxysporum</i> f. sp. <i>phaseoli</i> in Common Beans (<i>Phaseolus</i>) Tj ETQq1 1,0,784314 rgBT /Ove	5.1	17
62	Genetic Relatedness of Mexican Common Bean Cultivars Revealed by Microsatellite Markers. Crop Science, 2011, 51, 2655-2667.	1.8	16
63	EST â€SSR markers from five sequenced cDNA libraries of common bean (<i>Phaseolus vulgaris</i> L.) comparing three bioinformatic algorithms. Molecular Ecology Resources, 2013, 13, 688-695.	4.8	16
64	Development of mapped simple sequence repeat markers from common bean (<i>Phaseolus vulgaris</i> L.) based on genome sequences of a Chinese landrace and diversity evaluation. Molecular Breeding, 2014, 33, 489-496.	2.1	16
65	Relationship of Cultivated Grain Amaranth Species and Wild Relative Accessions. Genes, 2021, 12, 1849.	2.4	14
66	Bases for the Establishment of Robusta Coffee (<i>Coffea canephora</i>) as a New Crop for Colombia. Agronomy, 2021, 11, 2550.	3.0	14
67	Development and mapping of SSR markers linked to resistance-gene homologue clusters in common bean. Crop Journal, 2014, 2, 183-194.	5.2	13
68	New geneâ€derived simple sequence repeat markers for common bean (<i>Phaseolus vulgaris</i> L.). Molecular Ecology Resources, 2012, 12, 661-668.	4.8	12
69	Cloning and characterization of a novel secretory root-expressed peroxidase gene from common bean (<i>Phaseolus vulgaris</i> L.) infected with <i>Fusarium oxysporum</i> f. sp. <i>Phaseoli</i> . Molecular Breeding, 2014, 34, 855-870.	2.1	12
70	Lessons from Common Bean on How Wild Relatives and Landraces Can Make Tropical Crops More Resistant to Climate Change. , 2018, , .		10
71	Isolation and Characterization of Nucleotide-Binding Site Resistance Gene Homologues in Common Bean (<i>Phaseolus vulgaris</i>). Phytopathology, 2013, 103, 156-168.	2.2	9
72	Naturally Available Genetic Adaptation in Common Bean and Its Response to Climate Change. , 2018, , .		9

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73	BAC-End Microsatellites from Intra and Inter-Genic Regions of the Common Bean Genome and Their Correlation with Cytogenetic Features. PLoS ONE, 2014, 9, e101873.	2.5	8
74	Introgression of the Afla Gene into Climbing Garden Pea (<i>Pisum sativum</i> L.). Agronomy, 2020, 10, 1537.	3.0	7
75	Sources of Resistance to Common Bacterial Blight and Charcoal Rot Disease for the Production of Mesoamerican Common Beans in the Southern United States. Plants, 2021, 10, 998.	3.5	7
76	Parallel Sequencing of Expressed Sequence Tags from Two Complementary DNA Libraries for High and Low Phosphorus Adaptation in Common Beans. Plant Genome, 2011, 4, .	2.8	6
77	Condensed Tannin Accumulation during Seed Coat Development in Five Common Bean Genotypes. Crop Science, 2015, 55, 2826-2832.	1.8	6
78	A methyl esterase 1 (PvMES1) promotes the salicylic acid pathway and enhances Fusarium wilt resistance in common beans. Theoretical and Applied Genetics, 2021, 134, 2379-2398.	3.6	6
79	Diversity of Common Bean Landraces, Breeding Lines, and Varieties from Cuba. Crop Science, 2016, 56, 322-330.	1.8	5
80	Editorial: Food Legume Diversity and Legume Research Policies. Crop Journal, 2016, 4, 339-343.	5.2	5
81	Genetic differentiation of grain, fodder and pod vegetable type cowpeas (<i>Vigna unguiculata</i> L.) identified through single nucleotide polymorphisms from genotyping-by-sequencing. Molecular Horticulture, 2022, 2, .	5.8	5
82	Novel Alleles for Black and Gray Seed Color Genes in Common Bean. Crop Science, 2017, 57, 1603-1610.	1.8	4
83	Genetic Diversity of Purple Passion Fruit, <i>Passiflora edulis</i> f. <i>edulis</i> , Based on Single-Nucleotide Polymorphism Markers Discovered through Genotyping by Sequencing. Diversity, 2021, 13, 144.	1.7	3
84	Genetic Diversity of Bolivian Accessions of <i>Phaseolus</i> Species Evaluated with Fluorescent Microsatellite Markers. Crop Science, 2012, 52, 2619-2627.	1.8	1
85	Agronomic evaluation of biofortified beans in Antioquia producers' farms. Revista Facultad Nacional De Agronomia Medellin, 2020, 73, 9143-9149.	0.5	1