Paul Gepts

List of Publications by Year
in descending order

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220 papers	18,745 citations	10956 71 h-index	15218 126 g-index
232 all docs	232 docs citations	232 times ranked	10252 citing authors

#	Article	IF	Citations
1	Release of tepary bean TARSâ€Tep 23 germplasm with broad abiotic stress tolerance and rust and common bacterial blight resistance. Journal of Plant Registrations, 2022, 16, 109-119.	0.4	6
2	Loss of pod strings in common bean is associated with gene duplication, retrotransposon insertion and overexpression of <scp>PvIND</scp>. New Phytologist, 2022, 235, 2454-2465.	3.5	6
3	Toward the introgression of PvPdh1 for increased resistance to pod shattering in common bean. Theoretical and Applied Genetics, 2021, 134, 313-325.	1.8	16
4	Phaseolus vulgaris MIR1511 genotypic variations differentially regulate plant tolerance to aluminum toxicity. Plant Journal, 2021, 105, 1521-1533.	2.8	9
5	Registration of â€˜UC Southwest Goldâ€™ heirloomâ€like gold and white mottled bean. Journal of Plant Registrations, 2021, 15, 48-52.	0.4	3
6	Registration of â€˜UC Tiger's Eyeâ€™ heirloomâ€like dry bean. Journal of Plant Registrations, 2021, 15, 16-20.	0.4	2
7	Registration of â€˜UC Southwest Redâ€™ heirloomâ€like red and white mottled bean. Journal of Plant Registrations, 2021, 15, 21-27.	0.4	3
8	Registration of â€˜UC Rio Zapeâ€™ heirloomâ€like dry bean. Journal of Plant Registrations, 2021, 15, 37-42.	0.4	3
9	Registration of â€˜UC Sunriseâ€™ heirloomâ€like orange and white mottled bean. Journal of Plant Registrations, 2021, 15, 43-47.	0.4	3
10	Pod shattering in grain legumes: emerging genetic and environment-related patterns. Plant Cell, 2021, 33, 179-199.	3.1	40
11	Population structure, genetic diversity and genomic selection signatures among a Brazilian common bean germplasm. Scientific Reports, 2021, 11, 2964.	1.6	46
12	Cowpea [Vigna unguiculata (L.) Walp.] maternal lineages, chloroplast captures, and wild cowpea evolution. Genetic Resources and Crop Evolution, 2021, 68, 2799-2812.	0.8	7
13	Genome-wide association study for grain mineral content in a Brazilian common bean diversity panel. Theoretical and Applied Genetics, 2021, 134, 2795-2811.	1.8	15
14	Genetic diversity among Brazilian carioca common bean cultivars for nitrogen use efficiency. Crop Science, 2021, 61, 2534-2547.	0.8	1
15	Characterization of Colletotrichum lindemuthianum Races in Zambia and Evaluation of the CIAT Phaseolus Core Collection for Resistance to Anthracnose. Plant Disease, 2021, , PDIS02210363RE.	0.7	1
16	Genome-Wide Association Study and Genomic Prediction for Soybean Cyst Nematode Resistance in USDA Common Bean (Phaseolus vulgaris) Core Collection. Frontiers in Plant Science, 2021, 12, 624156.	1.7	20
17	Genetic, anatomical, and environmental patterns related to pod shattering resistance in domesticated cowpea [Vigna unguiculata(L.) Walp]. Journal of Experimental Botany, 2021, 72, 6219-6229.	2.4	12
18	Genome-Environment Association Analysis for Bio-Climatic Variables in Common Bean (Phaseolus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	5

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19	Genetic variability and nitrogen response indices in common bean (Phaseolus vulgaris) cultivars under contrasting nitrogen environments. Plant Breeding, 2021, 140, 907.	1.0	3
20	Comprehensive genomic resources related to domestication and crop improvement traits in Lima bean. Nature Communications, 2021, 12, 702.	5.8	39
21	Population structure and genetic diversity in common bean accessions from Northeast Brazil. World Journal of Advanced Research and Reviews, 2021, 12, 287-297.	0.1	0
22	Genome-Wide Association Study Identifies Genomic Regions for Important Morpho-Agronomic Traits in Mesoamerican Common Bean. Frontiers in Plant Science, 2021, 12, 748829.	1.7	6
23	Population Genomics of Phaseolus spp.: A Domestication Hotspot. Population Genomics, 2021, , 1.	0.2	4
24	Pod indehiscence is a domestication and aridity resilience trait in common bean. New Phytologist, 2020, 225, 558-570.	3.5	57
25	Is the USDA core collection of common bean representative of genetic diversity of the species, as assessed by SNP diversity?. Crop Science, 2020, 60, 1398-1414.	0.8	24
26	QTL analysis of seed size and yield-related traits in an inter-genepool population of common bean (Phaseolus vulgaris L.). Scientia Horticulturae, 2020, 274, 109678.	1.7	7
27	Identification of raceâ€specific quantitative trait loci for resistance to Colletotrichum lindemuthianum in an Andean population of common bean. Crop Science, 2020, 60, 2843-2856.	0.8	13
28	Determining the Genetic Control of Common Bean Early-Growth Rate Using Unmanned Aerial Vehicles. Remote Sensing, 2020, 12, 1748.	1.8	12
29	Identification of QTL for perenniality and floral scent in cowpea (Vigna unguiculataÂ[L.] Walp.). PLoS ONE, 2020, 15, e0229167.	1.1	13
30	Exploration of the Yield Potential of Mesoamerican Wild Common Beans From Contrasting Eco-Geographic Regions by Nested Recombinant Inbred Populations. Frontiers in Plant Science, 2020, 11, 346.	1.7	14
31	Beans: Origins and Development. , 2020, , 1362-1366.		0
32	Responses to selection for yield traits and key diseases among common bean genetic pyramids across locations. Journal of Crop Improvement, 2019, 33, 834-854.	0.9	0
33	Marker-Assisted Pyramiding Resistance Genes Against Angular Leaf Spot and Common Bacterial Blight Disease into Preferred Common Bean Cultivar "REDWOLAITA". Advances in Crop Science and Technology, 2019, 07, .	0.4	2
34	Evolution of SSR diversity from wild types to U.S. advanced cultivars in the Andean and Mesoamerican domestications of common bean (Phaseolus vulgaris). PLoS ONE, 2019, 14, e0211342.	1.1	39
35	DREBGenes from Common Bean (Phaseolus vulgarisL.) Show Broad to Specific Abiotic Stress Responses and Distinct Levels of Nucleotide Diversity. International Journal of Genomics, 2019, 2019, 1-28.	0.8	17
36	Effect of drought stress on the genetic architecture of photosynthate allocation and remobilization in pods of common bean (Phaseolus vulgaris L.), a key species for food security. BMC Plant Biology, 2019, 19, 171.	1.6	55

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37	Crop Biodiversity: An Unfinished Magnum Opus of Nature. Annual Review of Plant Biology, 2019, 70, 727-751.	8.6	74
38	Genetic diversity and re-classification of coffee (Coffea canephora Pierre ex A. Froehner) from South Western Nigeria through genotyping-by-sequencing-single nucleotide polymorphism analysis. Genetic Resources and Crop Evolution, 2019, 66, 685-696.	0.8	18
39	Recombination fraction and genetic linkage among key disease resistance genes (Co-42/Phg-2 and) Tj ETQq1 1 0.784314 rgBT /Overl	0.3	0
40	Root and shoot variation in relation to potential intermittent drought adaptation of Mesoamerican wild common bean (Phaseolus vulgaris L.). Annals of Botany, 2019, 124, 917-932.	1.4	49
41	Spatial and Temporal Scales of Range Expansion in Wild Phaseolus vulgaris. Molecular Biology and Evolution, 2018, 35, 119-131.	3.5	76
42	Genetic variation, Heritability estimates and GXE effects on yield traits of Mesoamerican common bean (Phaseolus vulgaris L) germplasm in Uganda. Plant Genetic Resources: Characterisation and Utilisation, 2018, 16, 237-248.	0.4	9
43	Alternative markers linked to the Phg-2 angular leaf spot resistance locus in common bean using the Phaseolus genes marker database. African Journal of Biotechnology, 2018, 17, 818-828.	0.3	14
44	Pathotypes Characterization and Virulence Diversity of Pseudocercospora griseola the Causal Agent of Angular Leaf Spot Disease Collected from Major Common Bean (Phaseolus vulgaris L.) Growing Areas of Ethiopia. Journal of Plant Pathology & Microbiology, 2018, 09, .	0.3	7
45	Simple and rapid detached leaf technique for screening common beans (Phaseolus vulgarise L.) in vitro against angular leaf spot (Pseudocercospora griseola) disease. African Journal of Biotechnology, 2018, 17, 1076-1081.	0.3	6
46	Integrating phenotypic evaluations with a molecular diversity assessment of an Ethiopian collection of common bean landraces. African Crop Science Journal, 2018, 26, 315.	0.1	2
47	Resequencing of Common Bean Identifies Regions of Interâ€“Gene Pool Introgression and Provides Comprehensive Resources for Molecular Breeding. Plant Genome, 2018, 11, 170068.	1.6	65
48	Highly structured genetic diversity of Bixa orellana var. urucurana, the wild ancestor of annatto, in Brazilian Amazonia. PLoS ONE, 2018, 13, e0198593.	1.1	14
49	Genetic Patterns of Common-Bean Seed Acquisition and Early-Stage Adoption Among Farmer Groups in Western Uganda. Frontiers in Plant Science, 2018, 9, 586.	1.7	10
50	Rep-PCR Genomic Fingerprinting Revealed Genetic Diversity and Population Structure among Ethiopian Isolates of Pseudocercospora griseola Pathogen of the Common Bean (Phaseolus vulgaris L.). Journal of Plant Pathology & Microbiology, 2018, 9, .	0.3	2
51	Unraveling agronomic and genetic aspects of runner bean (Phaseolus coccineus L.). Field Crops Research, 2017, 206, 86-94.	2.3	19
52	Low stomatal sensitivity to vapor pressure deficit in irrigated common, lima and tepary beans. Field Crops Research, 2017, 206, 128-137.	2.3	18
53	Genomic history of the origin and domestication of common bean unveils its closest sister species. Genome Biology, 2017, 18, 60.	3.8	142
54	Evolution of plant materials for ecological restoration: insights from the applied and basic literature. Journal of Applied Ecology, 2017, 54, 102-115.	1.9	72

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55	Nodulation ability in different genotypes of Phaseolus lunatus by rhizobia from California agricultural soils. Symbiosis, 2017, 73, 7-14.	1.2	11
56	A new species of Phaseolus (Leguminosae, Papilionoideae) sister to Phaseolus vulgaris, the common bean. Phytotaxa, 2017, 313, 259.	0.1	10
57	Agronomic qualities of genetic pyramids of common bean developed for multiple-disease-resistance. African Crop Science Journal, 2017, 25, 457.	0.1	7
58	Genetic diversity and population structure of common bean (Phaseolus vulgaris L) germplasm of Ethiopia as revealed by microsatellite markers. African Journal of Biotechnology, 2016, 15, 2824-2847.	0.3	20
59	Landscape genetics, adaptive diversity and population structure in Phaseolus vulgaris. New Phytologist, 2016, 209, 1781-1794.	3.5	86
60	Global agricultural intensification during climate change: a role for genomics. Plant Biotechnology Journal, 2016, 14, 1095-1098.	4.1	221
61	Genome-wide identification of SNPs and copy number variation in common bean (Phaseolus vulgaris L.) using genotyping-by-sequencing (GBS). Molecular Breeding, 2016, 36, 1.	1.0	87
62	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. Frontiers in Plant Science, 2015, 6, 563.	1.7	243
63	Origin and evolution of vertebrates. Nature, 2015, 520, 449-449.	13.7	1
64	Genome-wide identification and characterization of aquaporin gene family in common bean (Phaseolus) Tj ETQq0 0 0 rgBT /Overlock 10	1.0	80
65	Gene Pyramiding Improved Resistance to Angular Leaf Spot in Common Bean. American Journal of Experimental Agriculture, 2015, 9, 1-12.	0.2	12
66	Distribution and Variability of Pseudocercospora griseola in Uganda. Journal of Agricultural Science, 2014, 6, .	0.1	19
67	Domestication of Plants. , 2014, , 474-486.		21
68	Multiple lines of evidence for the origin of domesticated chili pepper, Capsicum annuum , in Mexico. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6165-6170.	3.3	203
69	Current perspectives and the future of domestication studies. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6139-6146.	3.3	594
70	The contribution of genetic and genomic approaches to plant domestication studies. Current Opinion in Plant Biology, 2014, 18, 51-59.	3.5	93
71	A reference genome for common bean and genome-wide analysis of dual domestications. Nature Genetics, 2014, 46, 707-713.	9.4	1,159
72	Beans: Origins and Development. , 2014, , 822-827.		8

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73	Co-segregation analysis and mapping of the anthracnose Co-10 and angular leaf spot Phg-ON disease-resistance genes in the common bean cultivar Ouro Negro. Theoretical and Applied Genetics, 2013, 126, 2245-2255.	1.8	64
74	Farmersâ€™ Varietal Identification in a Reference Sample of Local Phaseolus Species in the Sierra JuÃ¡rez, Oaxaca, Mexico. Economic Botany, 2013, 67, 283-298.	0.8	16
75	Spatially structured genetic diversity of the Amerindian yam (Dioscorea trifida L.) assessed by SSR and ISSR markers in Southern Brazil. Genetic Resources and Crop Evolution, 2013, 60, 2405-2420.	0.8	23
76	A new collection of wild populations of Capsicum in Mexico and the southern United States. Genetic Resources and Crop Evolution, 2013, 60, 225-232.	0.8	22
77	Feeding the future. Nature, 2013, 499, 23-24.	13.7	464
78	Identification and Characterization of a Homologue to the Arabidopsis INDEHISCENT Gene in Common Bean. Journal of Heredity, 2013, 104, 273-286.	1.0	39
79	Genetic Composition and Spatial Distribution of Farmerâ€managed Phaseolus Bean Plantings: An Example from a Village in Oaxaca, Mexico. Crop Science, 2012, 52, 1721-1735.	0.8	31
80	Multiple origins of the determinate growth habit in domesticated common bean (Phaseolus vulgaris). Annals of Botany, 2012, 110, 1573-1580.	1.4	100
81	Ecological Approaches to Crop Domestication. , 2012, , 377-406.		44
82	Genetic structure and mating system of wild cowpea populations in West Africa. BMC Plant Biology, 2012, 12, 113.	1.6	30
83	Introduction: The Domestication of Plants and Animals: Ten Unanswered Questions. , 2012, , 1-8.		4
84	Genetic Characterization of Cassava (Manihot esculenta Crantz) and Yam (Dioscorea trifida) Tj ETQq0 0 0 rgBT /Overlock 10 T		5
85	The common bean growth habit gene PvTFL1y is a functional homolog of Arabidopsis TFL1. Theoretical and Applied Genetics, 2012, 124, 1539-1547.	1.8	134
86	Biodiversity in Agriculture. , 2012, , .		57
87	Pathogenic and molecular characterization of Pythium species inducing root rot symptoms of common bean in Rwanda. African Journal of Microbiology Research, 2011, 5, 1169-1181.	0.4	20
88	Influence of cryptic population structure on observed mating patterns in the wild progenitor of maize (Zea mays ssp. parviglumis). Molecular Ecology, 2011, 20, 46-55.	2.0	16
89	Linkage mapping of the Phg-1 and Co-1 4 genes for resistance to angular leaf spot and anthracnose in the common bean cultivar AND 277. Theoretical and Applied Genetics, 2011, 122, 893-903.	1.8	99
90	Nucleotide diversity of a genomic sequence similar to SHATTERPROOF (PvSHP1) in domesticated and wild common bean (Phaseolus vulgaris L.). Theoretical and Applied Genetics, 2011, 123, 1341-1357.	1.8	44

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91	Leveraging Genomic Resources of Model Species for the Assessment of Diversity and Phylogeny in Wild and Domesticated Lentil. Journal of Heredity, 2011, 102, 315-329.	1.0	63
92	Integrating Phenotypic Evaluations with a Molecular Diversity Assessment of a Brazilian Collection of Common Bean Landraces. Crop Science, 2011, 51, 2668-2680.	0.8	12
93	Genetic Characterization and Molecular Mapping Pseâ€2 Gene for Resistance to Halo Blight in Common Bean. Crop Science, 2011, 51, 2439-2448.	0.8	22
94	Microsatellite diversity and genetic structure among common bean (Phaseolus vulgaris L.) landraces in Brazil, a secondary center of diversity. Theoretical and Applied Genetics, 2010, 121, 801-813.	1.8	131
95	Different Seed Selection and Conservation Practices for Fresh Market and Dried Chile Farmers in Aguascalientes, Mexico. Economic Botany, 2010, 64, 318-328.	0.8	11
96	Cytogenetic map of common bean (Phaseolus vulgaris L.). Chromosome Research, 2010, 18, 487-502.	1.0	108
97	Extension of the core map of common bean with EST-SSR, RGA, AFLP, and putative functional markers. Molecular Breeding, 2010, 25, 25-45.	1.0	72
98	Cytogenetic mapping of common bean chromosomes reveals a less compartmentalized small-genome plant species. Chromosome Research, 2009, 17, 405-417.	1.0	60
99	Structure of genetic diversity in the two major gene pools of common bean (Phaseolus vulgaris L.,) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	280
100	Transgenes in Mexican maize: molecular evidence and methodological considerations for GMO detection in landrace populations. Molecular Ecology, 2009, 18, 750-761.	2.0	113
101	Resolution of the Mexican transgene detection controversy: error sources and scientific practice in commercial and ecological contexts. Molecular Ecology, 2009, 18, 4145-4150.	2.0	14
102	The Putative Mesoamerican Domestication Center of Phaseolus vulgaris Is Located in the Lermaâ€“Santiago Basin of Mexico. Crop Science, 2009, 49, 554-563.	0.8	108
103	Dispersal of Transgenes through Maize Seed Systems in Mexico. PLoS ONE, 2009, 4, e5734.	1.1	62
104	BAC end sequences corresponding to the B4 resistance gene cluster in common bean: a resource for markers and synteny analyses. Molecular Genetics and Genomics, 2008, 280, 521-33.	1.0	53
105	Mapping Homologous Sequences for Determinacy and Photoperiod Sensitivity in Common Bean (Phaseolus vulgaris). Journal of Heredity, 2008, 99, 283-291.	1.0	98
106	Phaseolus vulgaris: A Diploid Model for Soybean. , 2008, , 55-76.		28
107	Long-distance pollen flow assessment through evaluation of pollinator foraging range suggests transgene escape distances. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13456-13461.	3.3	174
108	Harvesting Data from Genetically Engineered Crops. Science, 2008, 320, 452-453.	6.0	20

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109	Tropical Environments, Biodiversity, and the Origin of Crops. , 2008, , 1-20.		12
110	Genomics of Phaseolus Beans, a Major Source of Dietary Protein and Micronutrients in the Tropics. , 2008, , 113-143.		114
111	Tagging the Signatures of Domestication in Common Bean (Phaseolus vulgaris) by Means of Pooled DNA Samples. Annals of Botany, 2007, 100, 1039-1051.	1.4	84
112	Prebreeding in Common Bean and Use of Genetic Diversity from Wild Germplasm. Crop Science, 2007, 47, S-44.	0.8	115
113	Gene Flow and Genetic Structure in the Wildâ€“Weedyâ€“Domesticated Complex of Phaseolus lunatus L. in its Mesoamerican Center of Domestication and Diversity. Crop Science, 2007, 47, 58-66.	0.8	38
114	Describing Maize (Zea mays L.) Landrace Persistence in the BajÃo of Mexico: A Survey of 1940s and 1950s Collection Locations. Economic Botany, 2007, 61, 60-72.	0.8	20
115	Genetic mapping of a new set of microsatellite markers in a reference common bean (Phaseolus) Tj ETQq1 1 0.784314 rgBT /Overlock	0.3	63
116	Structure and Genetic Diversity of Wild Populations of Lima Bean (Phaseolus lunatus L.) from the Yucatan Peninsula, Mexico. Crop Science, 2006, 46, 1071-1080.	0.8	31
117	The Future of Plant Breeding. Crop Science, 2006, 46, 1630-1634.	0.8	76
118	Plant Genetic Resources Conservation and Utilization: The Accomplishments and Future of a Societal Insurance Policy. Crop Science, 2006, 46, 2278-2292.	0.8	301
119	Development of PCR-based chloroplast DNA markers that characterize domesticated cowpea (Vigna) Tj ETQq1 1 0.784314 rgBT /Ove Systematics and Evolution, 2006, 262, 75-87.	0.3	19
120	Development of four phylogenetically-arrayed BAC libraries and sequence of the APA locus in Phaseolus vulgaris. Theoretical and Applied Genetics, 2006, 112, 987-998.	1.8	73
121	Detecting (trans)gene flow to landraces in centers of crop origin: lessons from the case of maize in Mexico. Environmental Biosafety Research, 2005, 4, 197-208.	1.1	44
122	Population Structure and Evolutionary Dynamics of Wild-Weedy-Domesticated Complexes of Common Bean in a Mesoamerican Region. Crop Science, 2005, 45, 1073-1083.	0.8	81
123	A genome-wide analysis of differentiation between wild and domesticated Phaseolus vulgaris from Mesoamerica. Theoretical and Applied Genetics, 2005, 111, 1147-1158.	1.8	102
124	Spatial Distribution of Genetic Diversity in Wild Populations of Phaseolus vulgarisL. from Guanajuato and MichoacÃ¡n, MÃ©xico. Genetic Resources and Crop Evolution, 2005, 52, 589-599.	0.8	36
125	A Method of Controlling Corn Rootworm Feeding Using a Bacillus thuringiensis Protein Expressed in Transgenic Maize. Crop Science, 2005, 45, 931-938.	0.8	233
126	Assessment of Inter Simple Sequence Repeat Markers to Differentiate Sympatric Wild and Domesticated Populations of Common Bean. Crop Science, 2005, 45, 606-615.	0.8	48

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127	GENETICALLY ENGINEERED ORGANISMS AND THE ENVIRONMENT: CURRENT STATUS AND RECOMMENDATIONS1. , 2005, 15, 377-404.		260
128	Trading the Genome. Investigating the Commodification of Bio-Information. Economic Botany, 2005, 59, 395-395.	0.8	0
129	The Genetic Anatomy of a Patented Yellow Bean. Crop Science, 2004, 44, 968-977.	0.8	51
130	Who Owns Biodiversity, and How Should the Owners Be Compensated?. Plant Physiology, 2004, 134, 1295-1307.	2.3	72
131	Genetic diversity in cowpea [Vigna unguiculata (L.) Walp.] as revealed by RAPD markers. Genetic Resources and Crop Evolution, 2004, 51, 539-550.	0.8	102
132	Genetics of resistance to the geminivirus, Bean dwarf mosaic virus, and the role of the hypersensitive response in common bean. Theoretical and Applied Genetics, 2004, 108, 786-793.	1.8	36
133	Genetic Diversity and Pathogenic Variation of Common Blight Bacteria (Xanthomonas campestris pv.) Tj ETQq1 1 0.784314 rgBT /Ove Common Bean. Phytopathology, 2004, 94, 593-603.	1.1	68
134	Asymmetric gene flow and introgression between domesticated and wild populations.. , 2004, , 125-138.		11
135	Quantitative Trait Locus Analyses of the Domestication Syndrome and Domestication Process. , 2004, , 1069-1073.		10
136	Gene Flow Between Crops and Their Wild Progenitors. , 2004, , 488-491.		9
137	Genomics and Genetic Diversity in Common Bean. , 2004, , .		13
138	The Genetic Anatomy of a Patented Yellow Bean. Crop Science, 2004, 44, 968.	0.8	17
139	Beans (Phaseolus spp.) â€“ model food legumes. Plant and Soil, 2003, 252, 55-128.	1.8	1,100
140	Asymmetry of gene flow and differential geographical structure of molecular diversity in wild and domesticated common bean (Phaseolus vulgaris L.) from Mesoamerica. Theoretical and Applied Genetics, 2003, 106, 239-250.	1.8	209
141	Development of a genome-wide anchored microsatellite map for common bean (Phaseolus vulgaris L.). Theoretical and Applied Genetics, 2003, 107, 1362-1374.	1.8	342
142	Tagging and mapping of genes and QTL and molecular marker-assisted selection for traits of economic importance in bean and cowpea. Field Crops Research, 2003, 82, 135-154.	2.3	250
143	Possible effects of (trans)gene flow from crops on the genetic diversity from landraces and wild relatives. Environmental Biosafety Research, 2003, 2, 89-103.	1.1	129
144	An improved genetic linkage map for cowpea (Vigna unguiculataL.) Combining AFLP, RFLP, RAPD, biochemical markers, and biological resistance traits. Genome, 2002, 45, 175-188.	0.9	119

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145	Molecular and Phenotypic Mapping of Genes Controlling Seed Coat Pattern and Color in Common Bean (Phaseolus vulgaris L.). , 2002, 93, 148-152.		121
146	A Comparison between Crop Domestication, Classical Plant Breeding, and Genetic Engineering. Crop Science, 2002, 42, 1780-1790.	0.8	171
147	Protein Structures of Common Bean (Phaseolus vulgaris) Î±-Amylase Inhibitors. Journal of Agricultural and Food Chemistry, 2002, 50, 6618-6627.	2.4	26
148	AFLP analysis of the phenetic organization and genetic diversity of Vigna unguiculata L. Walp. reveals extensive gene flow between wild and domesticated types. Theoretical and Applied Genetics, 2002, 104, 358-366.	1.8	155
149	Title is missing!. Euphytica, 2002, 125, 69-79.	0.6	65
150	(SMV) and the SMV Resistance Gene (). Crop Science, 2002, 42, 178.	0.8	10
151	QTL Conditioning Physiological Resistance and Avoidance to White Mold in Dry Bean. Crop Science, 2001, 41, 309-315.	0.8	129
152	Inheritance of Partial Resistance Against Colletotrichum lindemuthianum in Phaseolus vulgaris and Co-localization of Quantitative Trait Loci with Genes Involved in Specific Resistance. Molecular Plant-Microbe Interactions, 2000, 13, 287-296.	1.4	164
153	Integration of simple sequence repeat (SSR) markers into a molecular linkage map of common bean (Phaseolus vulgaris L.). , 2000, 91, 429-434.		219
154	A Phylogenetic and Genomic Analysis of Crop Germplasm: A Necessary Condition for its Rational Conservation and Use. Stadler Genetics Symposia Series, 2000, , 163-181.	0.0	8
155	Genetic Linkage Mapping and Location of Genomic Regions Associated with Nodulation and Bacterial Diseases in Phaseolus vulgaris L.. Current Plant Science and Biotechnology in Agriculture, 2000, , 317-318.	0.0	0
156	Isozyme Diversity in Bambara Groundnut. Crop Science, 1999, 39, 1228-1236.	0.8	42
157	Title is missing!. , 1999, 106, 45-56.		28
158	Identification of an Ancestral Resistance Gene Cluster Involved in the Coevolution Process Between Phaseolus vulgaris and Its Fungal Pathogen Colletotrichum lindemuthianum. Molecular Plant-Microbe Interactions, 1999, 12, 774-784.	1.4	176
159	Detection and Differentiation of Phaeoisariopsis griseola Isolates with the Polymerase Chain Reaction and Group-Specific Primers. Plant Disease, 1999, 83, 37-42.	0.7	20
160	Development of an Integrated Linkage Map. Developments in Plant Breeding, 1999, , 53-91.	0.2	27
161	QTL mapping for nodule number and common bacterial blight in Phaseolus vulgaris L.. Plant and Soil, 1998, 204, 135-145.	1.8	34
162	A family of LRR sequences in the vicinity of the Co-2 locus for anthracnose resistance in Phaseolus vulgaris and its potential use in marker-assisted selection. Theoretical and Applied Genetics, 1998, 96, 494-502.	1.8	103

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163	Towards an integrated linkage map of common bean. 4. Development of a core linkage map and alignment of RFLP maps. Theoretical and Applied Genetics, 1998, 97, 847-856.	1.8	275
164	Musculoskeletal Rehabilitation. Clinics in Geriatric Medicine, 1998, 14, 641-660.	1.0	6
165	Origin and Evolution of Common Bean: Past Events and Recent Trends. Hortscience: A Publication of the American Society for Hortcultural Science, 1998, 33, 1124-1130.	0.5	160
166	Molecular Tagging of the bcâ€3 Gene for Introgression into Andean Common Bean. Crop Science, 1997, 37, 248-254.	0.8	72
167	A genetic linkage map of cowpea (Vigna unguiculata) developed from a cross between two inbred, domesticated lines. Theoretical and Applied Genetics, 1997, 95, 1210-1217.	1.8	139
168	Pulsed-field gel electrophoresis analysis of the phaseolin locus region inPhaseolus vulgaris. Genome, 1996, 39, 722-729.	0.9	10
169	Genetic Control of the Domestication Syndrome in Common Bean. Crop Science, 1996, 36, 1037-1045.	0.8	400
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