Karl Pauls

List of Publications by Year
in descending order

115 papers	3,446 citations	136950 32 h-index	161849 54 g-index
116 all docs	116 docs citations	116 times ranked	3927 citing authors

#	Article	IF	Citations
1	Cycling of extracellular DNA in the soil environment. Soil Biology and Biochemistry, 2007, 39, 2977-2991.	8.8	382
2	Seed and agronomic QTL in low linolenic acid, lipoxygenase-free soybean (Glycine max (L.) Merrill) germplasm. Genome, 2006, 49, 1510-1527.	2.0	194
3	Dehydrodimers of Ferulic Acid in Maize Grain Pericarp and Aleurone: Resistance Factors to Fusarium graminearum. Phytopathology, 2003, 93, 712-719.	2.2	140
4	In vitro starch digestibility, expected glycemic index and some physicochemical properties of starch and flour from common bean (Phaseolus vulgaris L.) varieties grown in Canada. Food Research International, 2008, 41, 869-875.	6.2	140
5	Reduced symptoms of Verticillium wilt in transgenic tomato expressing a bacterial ACC deaminase. Molecular Plant Pathology, 2001, 2, 135-145.	4.2	102
6	Genetic Mapping of Agronomic Traits in Common Bean. Crop Science, 2002, 42, 544-556.	1.8	100
7	Diets enriched with cranberry beans alter the microbiota and mitigate colitis severity and associated inflammation. Journal of Nutritional Biochemistry, 2016, 28, 129-139.	4.2	90
8	Cooked navy and black bean diets improve biomarkers of colon health and reduce inflammation during colitis. British Journal of Nutrition, 2014, 111, 1549-1563.	2.3	79
9	Molecular mapping of QTLs for resistance toGibberellaear rot, in corn, caused byFusarium graminearum. Genome, 2005, 48, 521-533.	2.0	76
10	Genetic Mapping of Agronomic Traits in Common Bean. Crop Science, 2002, 42, 544.	1.8	69
11	Antioxidant and anti-inflammatory polyphenols and peptides of common bean (Phaseolus vulga L.) milk and yogurt in Caco-2 and HT-29 cell models. Journal of Functional Foods, 2019, 53, 125-135.	3.4	65
12	Environmental effects on fatty acid levels in soybean seed oil. JAOCS, Journal of the American Oil Chemists' Society, 2006, 83, 759-763.	1.9	63
13	Aerobic and anaerobic de-epoxydation of mycotoxin deoxynivalenol by bacteria originating from agricultural soil. World Journal of Microbiology and Biotechnology, 2012, 28, 7-13.	3.6	60
14	Navy and black bean supplementation primes the colonic mucosal microenvironment to improve gut health. Journal of Nutritional Biochemistry, 2017, 49, 89-100.	4.2	59
15	OAC Rex common bean. Canadian Journal of Plant Science, 2006, 86, 733-736.	0.9	53
16	Separating the effect of crop from herbicide on soil microbial communities in glyphosate-resistant corn. Pedobiologia, 2009, 52, 253-262.	1.2	53
17	Effects of genetically modified, herbicideâ€tolerant crops and their management on soil food web properties and crop litter decomposition. Journal of Applied Ecology, 2009, 46, 388-396.	4.0	53
18	White and dark kidney beans reduce colonic mucosal damage and inflammation in response to dextran sodium sulfate. Journal of Nutritional Biochemistry, 2015, 26, 752-760.	4.2	52

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19	PDC1, a corn defensin peptide expressed in Escherichia coli and Pichia pastoris inhibits growth of Fusarium graminearum. Peptides, 2009, 30, 1593-1599.	2.4	50
20	Mapping quantitative trait loci for a common bean (Phaseolus vulgaris L.) ideotype. Genome, 2003, 46, 411-422.	2.0	49
21	Effects of Nitrogen Application on Nitrogen Fixation in Common Bean Production. Frontiers in Plant Science, 2020, 11, 1172.	3.6	49
22	Mycorrhizal and Rhizobial Colonization of Genetically Modified and Conventional Soybeans. Applied and Environmental Microbiology, 2007, 73, 4365-4367.	3.1	46
23	Economics of genomic selection: the role of prediction accuracy and relative genotyping costs. Euphytica, 2016, 210, 259-276.	1.2	45
24	Molecular basis of the low linolenic acid trait in soybean EMS mutant line RG10. Plant Breeding, 2009, 128, 253-258.	1.9	44
25	Effect of glyphosate on the tripartite symbiosis formed by Glomus intraradices, Bradyrhizobium japonicum, and genetically modified soybean. Applied Soil Ecology, 2009, 41, 128-136.	4.3	44
26	Characterization of seed coat post harvest darkening in common bean (Phaseolus vulgaris L.). Theoretical and Applied Genetics, 2011, 123, 1467-1472.	3.6	43
27	Navy bean supplemented high-fat diet improves intestinal health, epithelial barrier integrity and critical aspects of the obese inflammatory phenotype. Journal of Nutritional Biochemistry, 2019, 70, 91-104.	4.2	41
28	Identification of RAPD markers linked to common bacterial blight resistance genes in Phaseolus vulgaris L.. Genome, 1997, 40, 544-551.	2.0	40
29	Anti-inflammatory effects of phenolic-rich cranberry bean (Phaseolus vulgaris L.) extracts and enhanced cellular antioxidant enzyme activities in Caco-2 cells. Journal of Functional Foods, 2017, 38, 675-685.	3.4	39
30	Agronomic Performance and Nitrogen Fixation of Heirloom and Conventional Dry Bean Varieties Under Low-Nitrogen Field Conditions. Frontiers in Plant Science, 2019, 10, 952.	3.6	39
31	Quantitation of Transgenic Plant DNA in Leachate Water:Â Real-Time Polymerase Chain Reaction Analysis. Journal of Agricultural and Food Chemistry, 2005, 53, 5858-5865.	5.2	35
32	Real-Time Polymerase Chain Reaction Quantification of the Transgenes for Roundup Ready Corn and Roundup Ready Soybean in Soil Samples. Journal of Agricultural and Food Chemistry, 2005, 53, 1337-1342.	5.2	34
33	Response to selection for improved nitrogen fixation in common bean (Phaseolus vulgaris L.). Euphytica, 2017, 213, 1.	1.2	33
34	Proanthocyanidin accumulation and transcriptional responses in the seed coat of cranberry beans (Phaseolus vulgaris L.) with different susceptibility to postharvest darkening. BMC Plant Biology, 2017, 17, 89.	3.6	32
35	Microbial detoxification of eleven food and feed contaminating trichothecene mycotoxins. BMC Biotechnology, 2017, 17, 30.	3.3	32
36	Application of Image Analysis in Studies of Quantitative Disease Resistance, Exemplified Using Common Bacterial Blightâ€“Common Bean Pathosystem. Phytopathology, 2012, 102, 434-442.	2.2	30

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37	In silico comparison of genomic regions containing genes coding for enzymes and transcription factors for the phenylpropanoid pathway in Phaseolus vulgaris L. and Glycine max L. Merr. Frontiers in Plant Science, 2013, 4, 317.	3.6	30
38	Candidate Gene Identification with SNP Marker-Based Fine Mapping of Anthracnose Resistance Gene Co-4 in Common Bean. PLoS ONE, 2015, 10, e0139450.	2.5	30
39	Genome-wide single nucleotide polymorphism and Insertion-Deletion discovery through next-generation sequencing of reduced representation libraries in common bean. Molecular Breeding, 2014, 33, 769-778.	2.1	29
40	Flow Cytometric Characterization of Embryogenic and Gametophytic Development in Brassica napus Microspore Cultures. Plant and Cell Physiology, 1998, 39, 226-234.	3.1	27
41	When microspores decide to become embryos â€" cellular and molecular changesThis review is one of a selection of papers published in the Special Issue on Plant Cell Biology.. Canadian Journal of Botany, 2006, 84, 668-678.	1.1	27
42	Identification of putative genes in bean (Phaseolus vulgaris) genomic (Bng) RFLP clones and their conversion to STSs. Genome, 2002, 45, 1013-1024.	2.0	26
43	Quantitative trait loci for leafhopper (Empoasca fabae and Empoasca kraemeri) resistance and seed weight in the common bean. Plant Breeding, 2004, 123, 474-479.	1.9	26
44	A guanylyl cyclase-like gene is associated with Gibberella ear rot resistance in maize (Zea mays L.). Theoretical and Applied Genetics, 2008, 116, 465-479.	3.6	25
45	Plant Growth Environment Effects on Rapeseed Microspore Development and Culture. Plant Physiology, 1992, 99, 468-472.	4.8	23
46	Flow cytometric analysis of cellulose tracks development of embryogenic Brassica cells in microspore cultures. New Phytologist, 2002, 154, 249-254.	7.3	23
47	Brassica napus Rop GTPases and their expression in microspore cultures. Planta, 2006, 225, 469-484.	3.2	23
48	Rexeter common bean. Canadian Journal of Plant Science, 2012, 92, 351-353.	0.9	23
49	Detection of transgenic cp4 epsps genes in the soil food web. Agronomy for Sustainable Development, 2009, 29, 497-501.	5.3	22
50	OAC Inferno common bean. Canadian Journal of Plant Science, 2012, 92, 589-592.	0.9	21
51	Developmental, tissue culture, and genotypic factors affecting plant regeneration from shoot apical meristems of germinated Zea mays L. Seedlings. In Vitro Cellular and Developmental Biology - Plant, 2002, 38, 285-292.	2.1	20
52	The performance of dry bean cultivars with and without common bacterial blight resistance in field studies across Canada. Canadian Journal of Plant Science, 2009, 89, 405-410.	0.9	20
53	Dynasty kidney bean. Canadian Journal of Plant Science, 2016, 96, 215-217.	0.9	19
54	Lighthouse Common Bean. Canadian Journal of Plant Science, 0, , .	0.9	19

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55	Mapping the non-darkening trait from â€˜Wit-rood boontjeâ€™ in bean (Phaseolus vulgaris). Theoretical and Applied Genetics, 2018, 131, 1331-1343.	3.6	19
56	Flow cytometric characterization and sorting of cultured Brassica napus microspores. Biochimica Et Biophysica Acta - Molecular Cell Research, 1991, 1091, 165-172.	4.1	18
57	Transformation of isolated barley (Hordeum vulgare L.) microspores: I. The influence of pretreatments and osmotic treatment on the time of DNA synthesis. Genome, 2009, 52, 166-174.	2.0	16
58	Molecular basis of seed lipoxygenase null traits in soybean line OX948. Theoretical and Applied Genetics, 2011, 122, 1247-1264.	3.6	16
59	Stability of the association of molecular markers with common bacterial blight resistance in common bean (Phascolus vulgaris L.). Plant Breeding, 1998, 117, 553-558.	1.9	15
60	Evaluation of beneficial and inhibitory effects of nitrate on nodulation and nitrogen fixation in common bean (Phaseolus vulgaris). , 2020, 2, e45.		15
61	Title is missing!. Euphytica, 2003, 130, 423-432.	1.2	14
62	Transformation of isolated barley (Hordeum vulgare L.) microspores: II. Timing of pretreatment and temperatures relative to results of bombardment. Genome, 2009, 52, 175-190.	2.0	14
63	Determination of traits associated with leafhopper (Empoasca fabae and Empoasca kraemeri) resistance and dissection of leafhopper damage symptoms in the common bean (Phaseolus vulgaris). Annals of Applied Biology, 2001, 139, 319-327.	2.5	13
64	Real-Time Polymerase Chain Reaction Monitoring of Recombinant DNA Entry into Soil from Decomposing Roundup Ready Leaf Biomass. Journal of Agricultural and Food Chemistry, 2008, 56, 6339-6347.	5.2	13
65	Development of candidate gene markers associated to common bacterial blight resistance in common bean. Theoretical and Applied Genetics, 2012, 125, 1525-1537.	3.6	13
66	Microsomal Omega-3 Fatty Acid Desaturase Genes in Low Linolenic Acid Soybean Line RG10 and Validation of Major Linolenic Acid QTL. Frontiers in Genetics, 2016, 7, 38.	2.3	13
67	Mist Common Bean. Canadian Journal of Plant Science, 0, , .	0.9	13
68	Postharvest seed coat darkening in pinto bean (Phaseolus vulgaris) is regulated by P^{sd}, an allele of the basic helixâ€loopâ€helix transcription factor P. Plants People Planet, 2020, 2, 663-677.	3.3	13
69	A R2R3-MYB gene-based marker for the non-darkening seed coat trait in pinto and cranberry beans (Phaseolus vulgaris L.) derived from â€˜Wit-rood boontjeâ€™. Theoretical and Applied Genetics, 2020, 133, 1977-1994.	3.6	13
70	Agrobacterium tumefaciens-mediated transformation of corn (Zea maysL.) multiple shoots. Biotechnology and Biotechnological Equipment, 2014, 28, 208-216.	1.3	12
71	Regulation of Expression of the prb-1b / ACC Deaminase Gene by UV-8 in Transgenic Tomatoes. Journal of Plant Biochemistry and Biotechnology, 2003, 12, 25-29.	1.7	11
72	Evaluation of Tomato Plants with Constitutive, Root-Specific, and Stress-Induced ACC Deaminase Gene Expression. Russian Journal of Plant Physiology, 2005, 52, 359-364.	1.1	11

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73	Increased expression of a cGMP-dependent protein kinase in rotation-adapted western corn rootworm (Diabrotica virgifera virgifera L.). Insect Biochemistry and Molecular Biology, 2008, 38, 697-704.	2.7	11
74	Interaction of common bacterial blight quantitative trait loci in a resistant interâ€cross population of common bean. Plant Breeding, 2013, 132, 658-666.	1.9	11
75	Inheritance of plant regeneration from maize (Zea mays L.) shoot meristem cultures derived from germinated seeds and the identification of associated RAPD and SSR markers. Theoretical and Applied Genetics, 2004, 108, 681-687.	3.6	10
76	Quantification and Persistence of Recombinant DNA of Roundup Ready Corn and Soybean in Rotation. Journal of Agricultural and Food Chemistry, 2007, 55, 10226-10231.	5.2	10
77	Navy Bean Supplementation in Established High-Fat Diet-Induced Obesity Attenuates the Severity of the Obese Inflammatory Phenotype. Nutrients, 2021, 13, 757.	4.1	10
78	The utility of doubled haploid populations for studying the genetic control of traits determinated by recessive alleles. Current Plant Science and Biotechnology in Agriculture, 1996, , 125-144.	0.0	9
79	Optimizing and quantifying fusion of liposomes to mammalian sperm using resonance energy transfer and flow cytometric methods. Cytometry, 2002, 49, 22-27.	1.8	8
80	Dual Role for Ethylene in Susceptibility of Tomato to Verticillium Wilt. Journal of Phytopathology, 2001, 149, 385-388.	1.0	8
81	Construction of a BAC library and a physical map of a major QTL for CBB resistance of common bean (Phaseolus vulgaris L.). Genetica, 2010, 138, 709-716.	1.1	8
82	Relationships and inheritance of linolenic acid and seed lipoxygenases in soybean crosses designed to combine these traits. Canadian Journal of Plant Science, 2005, 85, 593-602.	0.9	7
83	An empirical approach to target DNA quantification in environmental samples using real-time polymerase chain reactions. Soil Biology and Biochemistry, 2007, 39, 1956-1967.	8.8	7
84	Factors Affecting the Presence and Persistence of Plant DNA in the Soil Environment in Corn and Soybean Rotations. Weed Science, 2008, 56, 767-774.	1.5	7
85	Apex common bean. Canadian Journal of Plant Science, 2013, 93, 131-135.	0.9	7
86	Interaction of quantitative trait loci for resistance to common bacterial blight and pathogen isolates in Phaseolus vulgaris L.. Molecular Breeding, 2017, 37, 1.	2.1	7
87	Genome-Wide Association Study of Seed Folate Content in Common Bean. Frontiers in Plant Science, 2021, 12, 696423.	3.6	7
88	Identification, Gene Structure, and Expression of BnMicEmUP: A Gene Upregulated in Embryogenic Brassica napus Microspores. Frontiers in Plant Science, 2020, 11, 576008.	3.6	7
89	Draft Genome Sequence of Citrobacter freundii Strain A47, Resistant to the Mycotoxin Deoxynivalenol. Genome Announcements, 2017, 5, .	0.8	6
90	Flow cytometric characterization of microspore development in Brassica napus. Canadian Journal of Botany, 1992, 70, 802-809.	1.1	5

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91	Yield and insect injury in leafhopper (Empoasca fabae Harris and Empoasca kraemeri Ross) Tj ETQq1 1 0.784314 rgBT /Ove 891-900.	0.9	5
92	Agronomic performance of soybean with seed lipoxygenase nulls and low linolenic acid content. Canadian Journal of Plant Science, 2006, 86, 379-387.	0.9	5
93	Enhancing In-crop Diversity in Common Bean by Planting Cultivar Mixtures and Its Effect on Productivity. Frontiers in Sustainable Food Systems, 2020, 4, .	3.9	5
94	Genetic Diversity, Nitrogen Fixation, and Water Use Efficiency in a Panel of Honduran Common Bean (Phaseolus vulgaris L.) Landraces and Modern Genotypes. Plants, 2020, 9, 1238.	3.5	5
95	Oviposition site selected by the western corn rootworm (Diabrotica virgifera virgifera Leconte) in southern Ontario strip plots. Canadian Journal of Plant Science, 2005, 85, 949-954.	0.9	4
96	Lightning common bean. Canadian Journal of Plant Science, 2009, 89, 303-305.	0.9	4
97	Genome Regions Associated with Functional Performance of Soybean Stem Fibers in Polypropylene Thermoplastic Composites. PLoS ONE, 2015, 10, e0130371.	2.5	4
98	Pectin acetylesterase 8 influences pectin acetylation in the seed coat, seed imbibition, and dormancy in common bean (<scp>Phaseolus vulgaris</scp> L.). , 2022, 4, e130.		4
99	Roundup ReadyÃ‚Â®soybean gene concentrations in field soil aggregate size classes. FEMS Microbiology Letters, 2009, 291, 175-179.	1.8	3
100	Draft Genome Sequence of Enterobacter cloacae 3D9 (Phylum Proteobacteria). Microbiology Resource Announcements, 2018, 7, .	0.6	3
101	Yield and antiyield genes in common bean (<scp>Phaseolus vulgaris</scp> L.). , 2021, 3, e91.		3
102	Investigations of the effects of the nonâ€darkening seed coat trait coded by the recessive jj alleles on agronomic, sensory, and cooking characteristics in pinto beans. Crop Science, 2021, 61, 1843-1863.	1.8	3
103	The Induction of the Isoflavone Biosynthesis Pathway Is Associated with Resistance to Common Bacterial Blight in Phaseolus vulgaris L.. Metabolites, 2021, 11, 433.	2.9	3
104	A Comparison of Screening Techniques for Resistance to Verticillium Wilt in Alfalfa (Medicago sativa) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.0	2
105	Predicting progeny performance in common bean (Phaseolus vulgaris L.) using molecular marker-based cluster analysis. Genome, 2003, 46, 259-267.	2.0	2
106	OAC Spark Common Bean. Canadian Journal of Plant Science, 2016, , .	0.9	2
107	Molecular characterization of dihydroneopterin aldolase and aminodeoxychorismate synthase in common beanâ€”genes coding for enzymes in the folate synthesis pathway. Genome, 2017, 60, 588-600.	2.0	2
108	OAC Derkeller common bean. Canadian Journal of Plant Science, 2010, 90, 715-717.	0.9	1

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109	Root and hypocotyl growth in transgenic tomatoes that express the bacterial enzyme ACC deaminase. Journal of Plant Biology, 2003, 46, 181-186.	2.1	0
110	OAC Lyrik common bean. Canadian Journal of Plant Science, 2009, 89, 307-308.	0.9	0
111	OAC Redstar common bean. Canadian Journal of Plant Science, 2009, 89, 309-311.	0.9	0
112	OAC Dublin common bean. Canadian Journal of Plant Science, 2010, 90, 511-514.	0.9	0
113	AAC Argosy navy dry bean. Canadian Journal of Plant Science, 0, , .	0.9	0
114	AAC Shock navy dry bean. Canadian Journal of Plant Science, 0, , .	0.9	0
115	Draft Genome Sequence of Enterobacter cloacae 3F11 (Phylum Proteobacteria). Microbiology Resource Announcements, 2018, 7, .	0.6	0