

Khalid Meksem

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6926690/publications.pdf>

Version: 2024-02-01

99
papers

3,957
citations

126708

33
h-index

128067

60
g-index

104
all docs

104
docs citations

104
times ranked

3129
citing authors

#	ARTICLE	IF	CITATIONS
1	The R1 gene for potato resistance to late blight (<i>Phytophthora infestans</i>) belongs to the leucine zipper/NBS/LRR class of plant resistance genes. <i>Plant Journal</i> , 2002, 30, 361-371.	2.8	381
2	A soybean cyst nematode resistance gene points to a new mechanism of plant resistance to pathogens. <i>Nature</i> , 2012, 492, 256-260.	13.7	332
3	TILLING to detect induced mutations in soybean. <i>BMC Plant Biology</i> , 2008, 8, 9.	1.6	259
4	Molecular cloning of the potato <i>Gro1-4</i> gene conferring resistance to pathotype Ro1 of the root cyst nematode <i>Globodera rostochiensis</i> , based on a candidate gene approach. <i>Plant Journal</i> , 2004, 38, 285-297.	2.8	211
5	A high-resolution map of the vicinity of the R1 locus on chromosome V of potato based on RFLP and AFLP markers. <i>Molecular Genetics and Genomics</i> , 1995, 249, 74-81.	2.4	198
6	Quantitative trait loci in Two Soybean Recombinant Inbred Line Populations Segregating for Yield and Disease Resistance. <i>Crop Science</i> , 2002, 42, 271-277.	0.8	114
7	A BAC- and BIBAC-Based Physical Map of the Soybean Genome. <i>Genome Research</i> , 2004, 14, 319-326.	2.4	111
8	An updated "Essex"™ by "Forrest"™ linkage map and first composite interval map of QTL underlying six soybean traits. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1015-1026.	1.8	106
9	Common loci underlie field resistance to soybean sudden death syndrome in Forrest, Pyramid, Essex, and Douglas. <i>Theoretical and Applied Genetics</i> , 2002, 104, 294-300.	1.8	98
10	The Soybean Genome Database (SoyGD): a browser for display of duplicated, polyploid, regions and sequence tagged sites on the integrated physical and genetic maps of <i>Glycine max</i> . <i>Nucleic Acids Research</i> , 2006, 34, D758-D765.	6.5	96
11	The soybean <i>GmSNAP18</i> gene underlies two types of resistance to soybean cyst nematode. <i>Nature Communications</i> , 2017, 8, 14822.	5.8	91
12	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016, 2, 16167.	4.7	90
13	SNP identification and marker assay development for high-throughput selection of soybean cyst nematode resistance. <i>BMC Genomics</i> , 2015, 16, 314.	1.2	86
14	Genetic and Physical Localization of the Soybean <i>Rpg1-b</i> Disease Resistance Gene Reveals a Complex Locus Containing Several Tightly Linked Families of NBS-LRR Genes. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 817-826.	1.4	77
15	Genomic analysis of the <i>rhg1</i> locus: candidate genes that underlie soybean resistance to the cyst nematode. <i>Molecular Genetics and Genomics</i> , 2006, 276, 503-516.	1.0	73
16	Characterization of the Soluble NSF Attachment Protein gene family identifies two members involved in additive resistance to a plant pathogen. <i>Scientific Reports</i> , 2017, 7, 45226.	1.6	69
17	Definition of Soybean Genomic Regions That Control Seed Phytoestrogen Amounts. <i>Journal of Biomedicine and Biotechnology</i> , 2004, 2004, 52-60.	3.0	67
18	Whole-genome resequencing reveals the impact of the interaction of copy number variants of the <i>rhg1</i> and <i>Rhg4</i> genes on broad-based resistance to soybean cyst nematode. <i>Plant Biotechnology Journal</i> , 2019, 17, 1595-1611.	4.1	65

#	ARTICLE	IF	CITATIONS
19	Characterization of the FAD2 Gene Family in Soybean Reveals the Limitations of Gel-Based TILLING in Genes with High Copy Number. <i>Frontiers in Plant Science</i> , 2017, 8, 324.	1.7	64
20	A SNP-Based Genetic Linkage Map of Soybean Using the SoyS - NP6K Illumina Infinium BeadChip Genotyping Array. <i>Journal of Plant Genome Sciences</i> , 2013, 1, 80-89.	0.2	62
21	Construction and characterization of a soybean bacterial artificial chromosome library and use of multiple complementary libraries for genome physical mapping. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1041-1050.	1.8	57
22	Construction of a HindIII Bacterial Artificial Chromosome library and its use in identification of clones associated with disease resistance in chickpea. <i>Theoretical and Applied Genetics</i> , 2004, 108, 663-669.	1.8	53
23	Identification of Quantitative Trait Loci (QTL) Underlying Protein, Oil, and Five Major Fatty Acids™ Contents in Soybean. <i>American Journal of Plant Sciences</i> , 2014, 05, 158-167.	0.3	51
24	An Integrated Map of <i>Arabidopsis thaliana</i> for Functional Analysis of Its Genome Sequence. <i>Genetics</i> , 2001, 159, 1231-1242.	1.2	48
25	Fine mapping and DNA fiber FISH analysis locates the tobamovirus resistance gene L 3 of <i>Capsicum chinense</i> in a 400-kb region of R-like genes cluster embedded in highly repetitive sequences. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1107-18.	1.8	44
26	Systematic Mutagenesis of Serine Hydroxymethyltransferase Reveals an Essential Role in Nematode Resistance. <i>Plant Physiology</i> , 2017, 175, 1370-1380.	2.3	43
27	A SNARE-Like Protein and Biotin Are Implicated in Soybean Cyst Nematode Virulence. <i>PLoS ONE</i> , 2015, 10, e0145601.	1.1	41
28	Soybean cyst nematode resistance in soybean is independent of the Rhg4 locus LRR-RLK gene. <i>Functional and Integrative Genomics</i> , 2011, 11, 539-549.	1.4	40
29	Tissue-specific gene expression in soybean (<i>Glycine max</i>) detected by cDNA microarray analysis. <i>Journal of Plant Physiology</i> , 2002, 159, 1361-1374.	1.6	39
30	Comparative sequence analysis of <i>Solanum</i> and <i>Arabidopsis</i> in a hot spot for pathogen resistance on potato chromosome V reveals a patchwork of conserved and rapidly evolving genome segments. <i>BMC Genomics</i> , 2007, 8, 112.	1.2	38
31	Title is missing!. <i>Molecular Breeding</i> , 2001, 7, 63-71.	1.0	35
32	Stearoyl-Acyl Carrier Protein Desaturase Mutations Uncover an Impact of Stearic Acid in Leaf and Nodule Structure. <i>Plant Physiology</i> , 2017, 174, 1531-1543.	2.3	35
33	Construction and characterization of two bacterial artificial chromosome libraries of pea (<i>Pisum</i>) Tj ETQq1 1 0.784314 rgBT/Overlacc	0.9	34
34	Loci underlying resistance to manganese toxicity mapped in a soybean recombinant inbred line population of 'Essex' x 'Forrest'. <i>Plant and Soil</i> , 2004, 260, 197-204.	1.8	33
35	A pathogenesis-related protein GmPR08β VI promotes a molecular interaction between the GmSHMT08 and GmSNAP18 in resistance to <i>Heterodera glycines</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 1810-1829.	4.1	29
36	The PI 438489B™ by Hamilton™ SNP-Based Genetic Linkage Map of Soybean [<i>Glycine max</i> (L.) Merr.] Identified Quantitative Trait Loci that Underlie Seedling SDS Resistance. <i>Journal of Plant Genome Sciences</i> , 2012, 1, 18-30.	0.2	28

#	ARTICLE	IF	CITATIONS
37	Identification of introduced and stably inherited DNA methylation variants in soybean associated with soybean cyst nematode parasitism. <i>New Phytologist</i> , 2020, 227, 168-184.	3.5	27
38	Genetic Analysis of Root and Shoot Traits in the "Essex" By "Forrest" Recombinant Inbred Line (RIL) Population of Soybean [<i>Glycine max</i> (L.) Merr.]. <i>Journal of Plant Genome Sciences</i> , 2012, 1, 1-9.	0.2	27
39	A Bacterial Artificial Chromosome Library of <i>Lotus japonicus</i> Constructed in an <i>Agrobacterium tumefaciens</i> -Transformable Vector. <i>Molecular Plant-Microbe Interactions</i> , 2001, 14, 422-425.	1.4	26
40	Neodiversification of homeologous <i>CLAVATA1</i> -like receptor kinase genes in soybean leads to distinct developmental outcomes. <i>Scientific Reports</i> , 2017, 7, 8878.	1.6	25
41	DNA Markers Associated with Loci Underlying Seed Phytoestrogen Content in Soybeans. <i>Journal of Medicinal Food</i> , 1999, 2, 185-187.	0.8	24
42	Quantitative Trait Loci for Seed Isoflavone Contents in "MD96-5722" by "Spencer" Recombinant Inbred Lines of Soybean. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 1464-1468.	2.4	24
43	Genome reorganization of the <i>GmSHMT</i> gene family in soybean showed a lack of functional redundancy in resistance to soybean cyst nematode. <i>Scientific Reports</i> , 2019, 9, 1506.	1.6	24
44	Soybean TILLING-by-Sequencing+ reveals the role of novel <i>GmSACPD</i> members in unsaturated fatty acid biosynthesis while maintaining healthy nodules. <i>Journal of Experimental Botany</i> , 2020, 71, 6969-6987.	2.4	22
45	Evaluation of Soybean Germplasm for Resistance to Multiple Nematode Species: <i>Heterodera glycines</i> , <i>Meloidogyne incognita</i> , and <i>Rotylenchulus reniformis</i> . <i>Crop Science</i> , 2018, 58, 2511-2522.	0.8	21
46	In silico comparison of transcript abundances during <i>Arabidopsis thaliana</i> and <i>Glycine max</i> resistance to <i>Fusarium virguliforme</i> . <i>BMC Genomics</i> , 2008, 9, S6.	1.2	20
47	Genome-wide identification and analysis of soybean acyl-ACP thioesterase gene family reveals the role of <i>GmFAT</i> to improve fatty acid composition in soybean seed. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3611-3623.	1.8	20
48	A SNP-Based Genetic Linkage Map of Soybean Using the SoySNP6K Illumina Infinium BeadChip Genotyping Array. <i>Journal of Plant Genome Sciences</i> , 2017, 1, 80-89.	0.2	20
49	Quantitative Trait Loci Associated with Foliar Trigonelline Accumulation in <i>Glycine Max</i> L. <i>Journal of Biomedicine and Biotechnology</i> , 2002, 2, 151-157.	3.0	19
50	TILLING-by-Sequencing+ Reveals the Role of Novel Fatty Acid Desaturases (<i>GmFAD2-2s</i>) in Increasing Soybean Seed Oleic Acid Content. <i>Cells</i> , 2021, 10, 1245.	1.8	19
51	Assessment of Phenotypic Variations and Correlation among Seed Composition Traits in Mutagenized Soybean Populations. <i>Genes</i> , 2019, 10, 975.	1.0	18
52	Mutations at the Serine Hydroxymethyltransferase Impact Its Interaction with a Soluble NSF Attachment Protein and a Pathogenesis-Related Protein in Soybean. <i>Vaccines</i> , 2020, 8, 349.	2.1	18
53	Quantitative trait loci underlying resistance to sudden death syndrome (SDS) in MD96-5722 by "Spencer" recombinant inbred line population of soybean. <i>3 Biotech</i> , 2015, 5, 203-210.	1.1	16
54	A SNP genetic linkage map based on the "Hamilton" by "Spencer" recombinant inbred line population identified QTL for seed isoflavone contents in soybean. <i>Plant Breeding</i> , 2015, 134, 580-588.	1.0	14

#	ARTICLE	IF	CITATIONS
55	Characterization of a plant-transformation-ready large-insert BIBAC library of <i>Arabidopsis</i> and bombardment transformation of a large-insert BIBAC of the library into tobacco. <i>Genome</i> , 2011, 54, 437-447.	0.9	13
56	A bacterial artificial chromosome based physical map of the <i>Ustilago maydis</i> genome. <i>Genome</i> , 2005, 48, 207-216.	0.9	12
57	TILLING: A Reverse Genetics and a Functional Genomics Tool in Soybean. , 0, , 251-265.		12
58	Dissecting nematode resistance regions in soybean revealed pleiotropic effect of soybean cyst and reniform nematode resistance genes. <i>Plant Genome</i> , 2021, 14, e20083.	1.6	12
59	TILLING-by-Sequencing+ to Decipher Oil Biosynthesis Pathway in Soybeans: A New and Effective Platform for High-Throughput Gene Functional Analysis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4219.	1.8	12
60	Quantitative Trait Loci Underlying Seed Sugars Content in 'MD96-5722' by 'Spencer' Recombinant Inbred Line Population of Soybean. <i>Food and Nutrition Sciences (Print)</i> , 2015, 06, 964-973.	0.2	12
61	Genetic Analysis of Root and Shoot Traits in the 'Essex' By 'Forrest' Recombinant Inbred Line (RIL) Population of Soybean [<i>Glycine max</i> (L.) Merr.]. <i>Journal of Plant Genome Sciences</i> , 2017, 1, 1-9.	0.2	12
62	Mapping of QTL Associated with Seed Amino Acids Content in 'MD96-5722' by 'Spencer' RIL Population of Soybean Using SNP Markers. <i>Food and Nutrition Sciences (Print)</i> , 2015, 06, 974-984.	0.2	11
63	Quantitative Trait Loci Associated with Moisture, Protein, and Oil Content in Soybean [<i>Glycine max</i> (L.) Merr.]. <i>Journal of Agricultural Science</i> , 2012, 4, .	0.1	10
64	Additional Quantitative Trait Loci and Candidate Genes for Seed Isoflavone Content in Soybean. <i>Journal of Agricultural Science</i> , 2013, 5, .	0.1	10
65	The Soybean High Density 'Forrest' by 'Williams 82' SNP-Based Genetic Linkage Map Identifies QTL and Candidate Genes for Seed Isoflavone Content. <i>Plants</i> , 2021, 10, 2029.	1.6	10
66	Detection of QTL underlying seed quality components in soybean [<i>Glycine max</i> (L.) Merr.]. <i>Canadian Journal of Plant Science</i> , 2018, 98, 881-888.	0.3	9
67	EMS-Induced Mutagenesis of <i>Clostridium carboxidivorans</i> for Increased Atmospheric CO ₂ Reduction Efficiency and Solvent Production. <i>Microorganisms</i> , 2020, 8, 1239.	1.6	8
68	Evaluating Physical Maps by Clone Location Comparisons. <i>Journal of Genome Science and Technology</i> , 2003, 2, 98-105.	0.7	8
69	Effect of Row Spacing on Seed Isoflavone Contents in Soybean [<i>Glycine max</i> (L.) Merr.]. <i>American Journal of Plant Sciences</i> , 2014, 05, 4003-4010.	0.3	8
70	The 'PI 438489B' by 'Hamilton' SNP-Based Genetic Linkage Map of Soybean [<i>Glycine max</i> (L.) Merr.] Identified Quantitative Trait Loci that Underlie Seedling SDS Resistance. <i>Journal of Plant Genome Sciences</i> , 2017, 1, 18-30.	0.2	8
71	Quantitative Trait Loci (QTL) that Underlie SCN Resistance in Soybean [<i>Glycine max</i> (L.) Merr.] PI438489B by 'Hamilton' Re - combinant Inbred Line (RIL) Population. <i>Atlas Journal of Plant Biology</i> , 2014, 1, 29-38.	0.1	7
72	Genome Wide MeDIP-Seq Profiling of Wild and Cultivated Olives Trees Suggests DNA Methylation Fingerprint on the Sensory Quality of Olive Oil. <i>Plants</i> , 2021, 10, 1405.	1.6	6

#	ARTICLE	IF	CITATIONS
73	Identification of QTL Underlying Seed Micronutrients Accumulation in "MD 96-5722"™ by "Spencer"™ Recombinant Inbred Lines of Soybean. Atlas Journal of Plant Biology, 2017, 1, 39-49.	0.1	6
74	Genetic Analysis of Yield Components in the PI 438489B by "Hamilton"™ Recombinant Inbred Line (RIL) Population of Soybean [Glycine max (L.) Merr.]. Journal of Agricultural Science, 2012, 4, .	0.1	5
75	Correlation between the Chemical and Genetic Relationships among <i>Thymus saturejoides</i> Genotypes Cultured under <i>in vitro</i> and <i>in vivo</i> Environments. Chemistry and Biodiversity, 2016, 13, 387-394.	1.0	5
76	Genetic Mapping of QTL Associated with Seed Macronutrients Accumulation in "MD 96-5722"™ by "Spencer"™ Recombinant Inbred Lines of Soybean. Atlas Journal of Biology, 2017, 3, 224-235.	0.1	5
77	Quantitative Trait Loci (QTL) that Underlie SCN Resistance in Soybean [Glycine max (L.) Merr.] PI438489B by "Hamilton"™ Recombinant Inbred Line (RIL) Population. Atlas Journal of Plant Biology, 2017, 1, 29-38.	0.1	5
78	Genetic Analysis of Relative Water Content (RWC) in Two Recombinant Inbred Line Populations of Soybean [Glycine max (L.) Merr.]. Journal of Plant Genome Sciences, 0, , 46-53.	0.2	5
79	Soybean Genomic Libraries, TILLING, and Genetic Resources. Compendium of Plant Genomes, 2017, , 131-149.	0.3	4
80	Positional Cloning of Plant Developmental Genes. , 2005, , 233-256.		3
81	Integration of Physical and Genetic Maps. , 2005, , 215-232.		3
82	Nonhypothesis Analysis of a Mutagenic Soybean (<sc><i>Glycine max</i></sc> [L.] Population for Protein and Fatty Acid Composition. JAOCS, Journal of the American Oil Chemists' Society, 2018, 95, 461-471.	0.8	3
83	Genetic Analysis of Relative Water Content (RWC) in Two Recombinant Inbred Line Populations of Soybean [Glycine max (L.) Merr.]. Journal of Plant Genome Sciences, 2017, 1, 46-53.	0.2	3
84	Evaluation of Several Agronomic Traits in "Essex"™ By "Forrest"™ Recombinant Inbred Line Population of Soybean [Glycine max (L.) Merr.]. Atlas Journal of Plant Biology, 2017, 1, 13-17.	0.1	3
85	Effect of Two Row Spaces on Several Agronomic Traits in Soybean [Glycine max (L.) Merr.]. Atlas Journal of Plant Biology, 2013, 1, 18-23.	0.1	3
86	QTL and Candidate Genes for Seed Tocopherol Content in "Forrest"™ by "Williams 82"™ Recombinant Inbred Line (RIL) Population of Soybean. Plants, 2022, 11, 1258.	1.0	3
87	Agarose Gel Electrophoresis and Polyacrylamide Gel Electrophoresis for Visualization of Simple Sequence Repeats. Methods in Molecular Biology, 2013, 1006, 167-177.	0.4	2
88	Influence of Drought Stress on Several Root Traits and their Correlation with Seed Protein and Oil Contents in Soybean. Atlas Journal of Biology, 0, , 267-273.	0.1	2
89	Effect of Two Row Spaces on Several Agronomic Traits in Soybean [Glycine max (L.) Merr.]. Atlas Journal of Plant Biology, 2017, 1, 18-23.	0.1	2
90	Transcript Abundance Responses of Resistance Pathways of Arabidopsis thaliana to Deoxynivalenol. Atlas Journal of Biology, 2013, 2, 154-161.	0.1	1

#	ARTICLE	IF	CITATIONS
91	Evaluation of Several Agronomic Traits in "Essex"™ By "Forrest"™ Recombinant Inbred Line Population of Soybean [Glycine max (L.) Merr.]. Atlas Journal of Plant Biology, 2011, 1, 13-17.	0.1	1
92	Characterization of Diversity of Bradyrhizobia on Cowpea in Iraq Reveals Unusual Strain Characteristics. Atlas Journal of Biology, 0, , 392-401.	0.1	0
93	Additional Polymorphisms Linked to Soybean Cyst Nematode Resistance At The Rhg4 Locus. Atlas Journal of Biology, 0, , 376-383.	0.1	0
94	Transcript Abundance Responses of Resistance Pathways of Arabidopsis thaliana to Deoxynivalenol. Atlas Journal of Biology, 2017, 2, 154-161.	0.1	0
95	Annotation of Cultivar Variations at the Multigeneic Rhg1/Rfs2 Locus:. Atlas Journal of Biology, 0, , 407-416.	0.1	0
96	Evaluation of Yield Performance of Soybean Mutant FM6-847 in North Carolina. Atlas Journal of Plant Biology, 0, , 96-105.	0.1	0
97	Genetic Mapping of QTL Associated with Seed Macronutrients Accumulation in "MD 96-5722"™ by "Spencer"™ Recombinant In - bred Lines of Soybean. Atlas Journal of Biology, 2015, 3, 224-235.	0.1	0
98	Influence of Drought Stress on Several Root Traits and their Correlation with Seed Protein and Oil Contents in Soybean. Atlas Journal of Biology, 0, , 267-273.	0.1	0
99	Identification of QTL Underlying Seed Micronutrients Accumulation in "MD 96-5722"™ by "Spencer"™ Recombinant Inbred Lines of Soybean. Atlas Journal of Plant Biology, 2015, 1, 39-49.	0.1	0