

# Lars G Kamphuis

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

2,533  
citations

236925

25  
h-index

206112

48  
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59  
all docs

59  
docs citations

59  
times ranked

3570  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of Sclerotinia stem rot resistance quantitative trait loci in a chickpea ( <i>Cicer arietinum</i> ) recombinant inbred line population. <i>Functional Plant Biology</i> , 2022, , .	2.1	1
2	The novel avirulence effector <i>AlAvr1</i> from <i>Ascochyta lentis</i> mediates host cultivar specificity of ascochyta blight in lentil. <i>Molecular Plant Pathology</i> , 2022, , .	4.2	5
3	Identification of Novel Sources of Resistance to <i>Ascochyta</i> Blight in a Collection of Wild <i>Cicer</i> Accessions. <i>Phytopathology</i> , 2021, 111, 369-379.	2.2	17
4	Modeling first order additive $\tilde{A}$ — additive epistasis improves accuracy of genomic prediction for sclerotinia stem rot resistance in canola. <i>Plant Genome</i> , 2021, 14, e20088.	2.8	8
5	Genomic resources for lupins are coming of age. , 2021, 3, e77.		5
6	Identification of sources of <i>Sclerotinia sclerotiorum</i> resistance in a collection of wild <i>Cicer</i> germplasm. <i>Plant Disease</i> , 2021, 105, 2314-2324.	1.4	4
7	Analysis of differentially expressed <i>Sclerotinia sclerotiorum</i> genes during the interaction with moderately resistant and highly susceptible chickpea lines. <i>BMC Genomics</i> , 2021, 22, 333.	2.8	10
8	A Trimethylguanosine Synthase1-like (TGS1) homologue is implicated in vernalisation and flowering time control. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3411-3426.	3.6	9
9	Identification of <i>Brassica napus</i> small RNAs responsive to infection by a necrotrophic pathogen. <i>BMC Plant Biology</i> , 2021, 21, 366.	3.6	9
10	A multiplex PCR marker distinguishes between a series of four <i>LanFTc1</i> alleles regulating flowering time in narrow-leafed lupin ( <i>Lupinus angustifolius</i> ). <i>Plant Breeding</i> , 2021, 140, 1090-1101.	1.9	0
11	A detailed in silico analysis of secondary metabolite biosynthesis clusters in the genome of the broad host range plant pathogenic fungus <i>Sclerotinia sclerotiorum</i> . <i>BMC Genomics</i> , 2020, 21, 7.	2.8	36
12	A functional genomics approach to dissect spotted alfalfa aphid resistance in <i>Medicago truncatula</i> . <i>Scientific Reports</i> , 2020, 10, 22159.	3.3	3
13	Ethylene Is Not Essential for R-Gene Mediated Resistance but Negatively Regulates Moderate Resistance to Some Aphids in <i>Medicago truncatula</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 4657.	4.1	3
14	Ecophysiology and Phenology: Genetic Resources for Genetic/Genomic Improvement of Narrow-Leafed Lupin. <i>Compendium of Plant Genomes</i> , 2020, , 19-30.	0.5	6
15	Overview of Genomic Resources Available for Lupins with a Focus on Narrow-Leafed Lupin ( <i>Lupinus</i> ) <i>TJ ETQq1 1 0.784314 rgBT /Overl</i>	0.5	1
16	Transcriptome Resources Paving the Way for Lupin Crop Improvement. <i>Compendium of Plant Genomes</i> , 2020, , 53-71.	0.5	3
17	Genomic Applications and Resources to Dissect Flowering Time Control in Narrow-Leafed Lupin. <i>Compendium of Plant Genomes</i> , 2020, , 109-137.	0.5	2
18	An RNAi supplemented diet as a reverse genetics tool to control bluegreen aphid, a major pest of legumes. <i>Scientific Reports</i> , 2020, 10, 1604.	3.3	13

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19	Abiotic conditions governing the myceliogenic germination of <i>Sclerotinia sclerotiorum</i> allowing the basal infection of <i>Brassica napus</i> . <i>Australasian Plant Pathology</i> , 2019, 48, 85-91.	1.0	13
20	Additive and epistatic interactions between AKR and AIN loci conferring bluegreen aphid resistance and hypersensitivity in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 4887-4902.	4.8	8
21	A whole genome scan of SNP data suggests a lack of abundant hard selective sweeps in the genome of the broad host range plant pathogenic fungus <i>Sclerotinia sclerotiorum</i> . <i>PLoS ONE</i> , 2019, 14, e0214201.	2.5	23
22	The role of jasmonate signalling in quinolizidine alkaloid biosynthesis, wounding and aphid predation response in narrow-leafed lupin. <i>Functional Plant Biology</i> , 2019, 46, 443.	2.1	10
23	Identification and profiling of narrow-leafed lupin ( <i>Lupinus angustifolius</i> ) microRNAs during seed development. <i>BMC Genomics</i> , 2019, 20, 135.	2.8	22
24	The host generalist phytopathogenic fungus <i>Sclerotinia sclerotiorum</i> differentially expresses multiple metabolic enzymes on two different plant hosts. <i>Scientific Reports</i> , 2019, 9, 19966.	3.3	21
25	INDEL variation in the regulatory region of the major flowering time gene <i>LanFTc1</i> is associated with vernalization response and flowering time in narrow-leafed lupin ( <i>Lupinus angustifolius</i> ) <i>Tj ETQq1 1 05784314 rsgBT /Over</i>		
26	Characterization of the genetic factors affecting quinolizidine alkaloid biosynthesis and its response to abiotic stress in narrow-leafed lupin ( <i>Lupinus angustifolius</i> L.). <i>Plant, Cell and Environment</i> , 2018, 41, 2155-2168.	5.7	32
27	Partial stem resistance in <i>Brassica napus</i> to highly aggressive and genetically diverse <i>Sclerotinia sclerotiorum</i> isolates from Australia. <i>Canadian Journal of Plant Pathology</i> , 2018, 40, 551-561.	1.4	30
28	The Arabidopsis RNA Polymerase II Carboxyl Terminal Domain (CTD) Phosphatase-Like1 (CPL1) is a biotic stress susceptibility gene. <i>Scientific Reports</i> , 2018, 8, 13454.	3.3	18
29	Exploring the genetic and adaptive diversity of a pan-Mediterranean crop wild relative: narrow-leafed lupin. <i>Theoretical and Applied Genetics</i> , 2018, 131, 887-901.	3.6	50
30	A comprehensive draft genome sequence for lupin ( <i>Lupinus angustifolius</i> ), an emerging health food: insights into plant-microbe interactions and legume evolution. <i>Plant Biotechnology Journal</i> , 2017, 15, 318-330.	8.3	153
31	Quinolizidine Alkaloid Biosynthesis in Lupins and Prospects for Grain Quality Improvement. <i>Frontiers in Plant Science</i> , 2017, 8, 87.	3.6	89
32	Genetic Mapping of a Major Resistance Gene to Pea Aphid ( <i>Acyrtosipon pisum</i> ) in the Model Legume <i>Medicago truncatula</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 1224.	4.1	11
33	Narrow-Leafed Lupin ( <i>Lupinus angustifolius</i> ) Î²1- and Î²6-Conglutin Proteins Exhibit Antifungal Activity, Protecting Plants against Necrotrophic Pathogen Induced Damage from <i>Sclerotinia sclerotiorum</i> and <i>Phytophthora nicotianae</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1856.	3.6	17
34	Comparative genomics and prediction of conditionally dispensable sequences in legume-infecting <i>Fusarium oxysporum</i> formae speciales facilitates identification of candidate effectors. <i>BMC Genomics</i> , 2016, 17, 191.	2.8	109
35	A rapid method for profiling of volatile and semi-volatile phytohormones using methyl chloroformate derivatisation and GC-MS. <i>Metabolomics</i> , 2015, 11, 1922-1933.	3.0	26
36	Analysis of conglutin seed storage proteins across lupin species using transcriptomic, protein and comparative genomic approaches. <i>BMC Plant Biology</i> , 2015, 15, 106.	3.6	49

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37	Characterization and mapping of LanrBo: a locus conferring anthracnose resistance in narrow-leaved lupin ( <i>Lupinus angustifolius</i> L.). <i>Theoretical and Applied Genetics</i> , 2015, 128, 2121-2130.	3.6	25
38	Transcriptome sequencing of different narrow-leaved lupin tissue types provides a comprehensive uni-gene assembly and extensive gene-based molecular markers. <i>Plant Biotechnology Journal</i> , 2015, 13, 14-25.	8.3	70
39	The Arabidopsis KH-Domain RNA-Binding Protein ESR1 Functions in Components of Jasmonate Signalling, Unlinking Growth Restraint and Resistance to Stress. <i>PLoS ONE</i> , 2015, 10, e0126978.	2.5	45
40	The essential role of genetic resources in narrow-leaved lupin improvement. <i>Crop and Pasture Science</i> , 2013, 64, 361.	1.5	44
41	Characterization and genetic dissection of resistance to spotted alfalfa aphid ( <i>Therioaphis trifolii</i> ) in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2013, 64, 5157-5172.	4.8	33
42	Plant-aphid interactions with a focus on legumes. <i>Functional Plant Biology</i> , 2013, 40, 1271.	2.1	40
43	Identification of distinct quantitative trait loci associated with defence against the closely related aphids <i>Acyrtosiphon pisum</i> and <i>A. kondoi</i> in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2012, 63, 3913-3922.	4.8	36
44	Identification and characterization of resistance to cowpea aphid ( <i>Aphis craccivora</i> Koch) in <i>Medicago truncatula</i> . <i>BMC Plant Biology</i> , 2012, 12, 101.	3.6	50
45	<i>Phoma medicaginis</i> stimulates the induction of the octadecanoid and phenylpropanoid pathways in <i>Medicago truncatula</i> . <i>Molecular Plant Pathology</i> , 2012, 13, 593-603.	4.2	25
46	Development of genomic resources for the narrow-leaved lupin ( <i>Lupinus angustifolius</i> ): construction of a bacterial artificial chromosome (BAC) library and BAC-end sequencing. <i>BMC Genomics</i> , 2011, 12, 521.	2.8	53
47	Identification of potential early regulators of aphid resistance in <i>Medicago truncatula</i> via transcription factor expression profiling. <i>New Phytologist</i> , 2010, 186, 980-994.	7.3	36
48	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	5.6	913
49	Two independent resistance genes in the <i>Medicago truncatula</i> cultivar Jester confer resistance to two different aphid species of the genus <i>Acyrtosiphon</i> . <i>Plant Signaling and Behavior</i> , 2009, 4, 328-331.	2.4	25
50	Two alternative recessive quantitative trait loci influence resistance to spring black stem and leaf spot in <i>Medicago truncatula</i> . <i>BMC Plant Biology</i> , 2008, 8, 30.	3.6	34
51	The <i>Medicago truncatula</i> reference accession A17 has an aberrant chromosomal configuration. <i>New Phytologist</i> , 2007, 174, 299-303.	7.3	42
52	A cDNA-AFLP based strategy to identify transcripts associated with avirulence in <i>Phytophthora infestans</i> . <i>Fungal Genetics and Biology</i> , 2006, 43, 111-123.	2.1	29
53	Identification of Sources of Resistance to <i>Phoma medicaginis</i> Isolates in <i>Medicago truncatula</i> SARDI Core Collection Accessions, and Multigene Differentiation of Isolates. <i>Phytopathology</i> , 2006, 96, 1330-1336.	2.2	34
54	Agroinfection-based high-throughput screening reveals specific recognition of INF elicitors in <i>Solanum</i> . <i>Molecular Plant Pathology</i> , 2006, 7, 499-510.	4.2	50

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55	SSR analysis of the <i>Medicago truncatula</i> SARDI core collection reveals substantial diversity and unusual genotype dispersal throughout the Mediterranean basin. <i>Theoretical and Applied Genetics</i> , 2006, 112, 977-983.	3.6	69
56	A pan-genome and chromosome-length reference genome of narrow-leaved lupin ( <i>Lupinus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Journal, 0, , .	5.7	9