

# Erik H A Rikkerink

## List of Publications by Year in descending order

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64  
papers

4,582  
citations

147801

31  
h-index

118850

62  
g-index

71  
all docs

71  
docs citations

71  
times ranked

4170  
citing authors

#	ARTICLE	IF	CITATIONS
1	Actigard <sup>®</sup> induces a defence response to limit <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> in <i>Actinidia chinensis</i> var. <i>chinensis</i> Hort16A <sup>™</sup> tissue culture plants.. <i>Scientia Horticulturae</i> , 2022, 295, 110806.	3.6	7
2	Real-Time PCR and Droplet Digital PCR Are Accurate and Reliable Methods To Quantify <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> Biovar 3 in Kiwifruit Infected Plantlets. <i>Plant Disease</i> , 2021, 105, 1748-1757.	1.4	10
3	<i>Rpa1</i> mediates an immune response to <i>avrRpm1</i> and confers resistance against <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>Plant Journal</i> , 2020, 102, 688-702.	5.7	22
4	Computational Disorder Analysis in Ethylene Response Factors Uncovers Binding Motifs Critical to Their Diverse Functions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 74.	4.1	7
5	Construction of a kiwifruit yeast two-hybrid cDNA library to identify host targets of the <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> effector <i>AvrPto5</i> . <i>BMC Research Notes</i> , 2019, 12, 63.	1.4	3
6	Highly specific assays to detect isolates of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> biovar 3 and <i>Pseudomonas syringae</i> pv. <i>actinidifoliorum</i> directly from plant material. <i>Plant Pathology</i> , 2018, 67, 1220-1230.	2.4	12
7	Re-programming of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> gene expression during early stages of infection of kiwifruit. <i>BMC Genomics</i> , 2018, 19, 822.	2.8	42
8	A Single Effector Protein, <i>AvrRpt2</i> <sub>EA</sub> , from <i>Erwinia amylovora</i> Can Cause Fire Blight Disease Symptoms and Induces a Salicylic Acid-Dependent Defense Response. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 1179-1191.	2.6	19
9	Pathogens and Disease Play Havoc on the Host Epiproteome—The “First Line of Response” Role for Proteomic Changes Influenced by Disorder. <i>International Journal of Molecular Sciences</i> , 2018, 19, 772.	4.1	10
10	A bacterial acetyltransferase triggers immunity in <i>Arabidopsis thaliana</i> independent of hypersensitive response. <i>Scientific Reports</i> , 2017, 7, 3557.	3.3	69
11	A novel hairpin library-based approach to identify NBS-LRR genes required for effector-triggered hypersensitive response in <i>Nicotiana benthamiana</i> . <i>Plant Methods</i> , 2017, 13, 32.	4.3	25
12	Origin and Evolution of the Kiwifruit Canker Pandemic. <i>Genome Biology and Evolution</i> , 2017, 9, 932-944.	2.5	106
13	Transposon insertion libraries for the characterization of mutants from the kiwifruit pathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>PLoS ONE</i> , 2017, 12, e0172790.	2.5	26
14	Microarray analysis of kiwifruit ( <i>Actinidia chinensis</i> ) bark following challenge by the sucking insect <i>Hemiberlesia lataniae</i> (Hemiptera: Diaspididae). <i>Genomics Data</i> , 2016, 7, 281-283.	1.3	1
15	A <i>microRNA</i> allele that emerged prior to apple domestication may underlie fruit size evolution. <i>Plant Journal</i> , 2015, 84, 417-427.	5.7	95
16	Complete DNA Sequence of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> , the Causal Agent of Kiwifruit Canker Disease. <i>Genome Announcements</i> , 2015, 3, .	0.8	36
17	Characterisation, evolutionary trends and mapping of putative resistance and defence genes in <i>Actinidia</i> (kiwifruit). <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	7
18	Transcriptome Analysis of Kiwifruit ( <i>Actinidia chinensis</i> ) Bark in Response to Armoured Scale Insect ( <i>Hemiberlesia lataniae</i> ) Feeding. <i>PLoS ONE</i> , 2015, 10, e0141664.	2.5	18

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19	TRANSPOSITION, INSERTION, DELETION AND RECOMBINATION DRIVE VARIABILITY IN THE TYPE 3 SECRETOME OF PSEUDOMONAS SYRINGAE PV. ACTINIDIAE, THE TRANSITION FROM GLOBAL EFFECTOR COMPARISONS TO KIWI FRUIT RESISTANCE BREEDING STRATEGIES. <i>Acta Horticulturae</i> , 2015, , 65-74.	0.2	3
20	The intrinsically disordered structural platform of the plant defence hub protein <scp>RPM</scp> interacting protein 4 provides insights into its mode of action in the host-pathogen interface and evolution of the nitrate-induced domain protein family. <i>FEBS Journal</i> , 2014, 281, 3955-3979.	4.7	50
21	Genomic Analysis of the Kiwifruit Pathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> Provides Insight into the Origins of an Emergent Plant Disease. <i>PLoS Pathogens</i> , 2013, 9, e1003503.	4.7	247
22	Using fundamental knowledge of induced resistance to develop control strategies for bacterial canker of kiwifruit caused by <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 24.	3.6	36
23	Multifarious Roles of Intrinsic Disorder in Proteins Illustrate Its Broad Impact on Plant Biology. <i>Plant Cell</i> , 2013, 25, 38-55.	6.6	138
24	GRAS proteins: the versatile roles of intrinsically disordered proteins in plant signalling. <i>Biochemical Journal</i> , 2012, 442, 1-12.	3.7	136
25	Revision of the Nomenclature of the Differential Host-Pathogen Interactions of <i>Venturia inaequalis</i> and <i>Malus</i> . <i>Annual Review of Phytopathology</i> , 2011, 49, 391-413.	7.8	176
26	A functionally required unfoldome from the plant kingdom: intrinsically disordered N-terminal domains of GRAS proteins are involved in molecular recognition during plant development. <i>Plant Molecular Biology</i> , 2011, 77, 205-223.	3.9	135
27	DEVELOPMENT OF A SET OF APPLE SSRS MARKERS SPANNING THE APPLE GENOME, GENOTYPING OF HIDRAS PLANT MATERIAL AND VALIDATION OF GENOTYPIC DATA. <i>Acta Horticulturae</i> , 2009, , 603-608.	0.2	3
28	Development and test of 21 multiplex PCRs composed of SSRs spanning most of the apple genome. <i>Tree Genetics and Genomes</i> , 2009, 5, 211-223.	1.6	52
29	BAC-end sequence-based SNPs and Bin mapping for rapid integration of physical and genetic maps in apple. <i>Genomics</i> , 2009, 93, 282-288.	2.9	31
30	"FAST-BREEDING" IN APPLE: A STRATEGY TO ACCELERATE INTROGRESSION OF NEW TRAITS INTO ELITE GERMPLASM. <i>Acta Horticulturae</i> , 2009, , 163-168.	0.2	20
31	A PROPOSAL FOR THE NOMENCLATURE OF <i>VENTURIA INAEQUALIS</i> RACES. <i>Acta Horticulturae</i> , 2009, , 739-746.	0.2	29
32	BREEDING FOR RED FLESH COLOUR IN APPLE: PROGRESS AND CHALLENGES. <i>Acta Horticulturae</i> , 2009, , 337-342.	0.2	47
33	Genome mapping of three major resistance genes to woolly apple aphid ( <i>Eriosoma lanigerum</i> Hausm.). <i>Tree Genetics and Genomes</i> , 2008, 4, 223-236.	1.6	84
34	Analysis of expressed sequence tags from Actinidia: applications of a cross species EST database for gene discovery in the areas of flavor, health, color and ripening. <i>BMC Genomics</i> , 2008, 9, 351.	2.8	178
35	Development of a set of SNP markers present in expressed genes of the apple. <i>Genomics</i> , 2008, 92, 353-358.	2.9	140
36	Two novel <i>Venturia inaequalis</i> genes induced upon morphogenetic differentiation during infection and in vitro growth on cellophane. <i>Fungal Genetics and Biology</i> , 2008, 45, 1329-1339.	2.1	35

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37	Screening a BAC Library With Nonradioactive Overlapping Oligonucleotide (Overgo) Probes. , 2007, 353, 79-92.		6
38	Linkage Disequilibrium. , 2007, , 11-39.		18
39	Prospects of Association Mapping in Perennial Horticultural Crops. , 2007, , 249-269.		21
40	CONSTRUCTION OF KIWIFRUIT BAC CONTIG MAPS BY OVERGO HYBRIDIZATION AND THEIR USE FOR MAPPING THE SEX LOCUS. Acta Horticulturae, 2007, , 185-190.	0.2	3
41	Analyses of Expressed Sequence Tags from Apple. Plant Physiology, 2006, 141, 147-166.	4.8	246
42	The Vh8 locus of a new gene-for-gene interaction between <i>Venturia inaequalis</i> and the wild apple <i>Malus sieversii</i> is closely linked to the Vh2 locus in <i>Malus pumila</i> R12740-7A. New Phytologist, 2005, 166, 1035-1049.	7.3	92
43	Estimation of allele frequencies in polyploids under certain patterns of inheritance. Heredity, 2005, 95, 327-334.	2.6	100
44	The Vh2 and Vh4 scab resistance genes in two differential hosts derived from Russian apple R12740-7A map to the same linkage group of apple. Molecular Breeding, 2005, 15, 103-116.	2.1	85
45	Analysis of a Secreted Aspartic Peptidase Disruption Mutant of <i>Glomerella cingulata</i> . European Journal of Plant Pathology, 2004, 110, 265-274.	1.7	18
46	AN UPDATE ON APPLE SCAB RESISTANCE BREEDING IN NEW ZEALAND. Acta Horticulturae, 2002, , 43-47.	0.2	15
47	Aligning male and female linkage maps of apple ( <i>Malus pumila</i> Mill.) using multi-allelic markers. Theoretical and Applied Genetics, 1998, 97, 60-73.	3.6	391
48	Effect of Disruption of a Cutinase Gene ( <i>cutA</i> ) on Virulence and Tissue Specificity of <i>Fusarium solani</i> f. sp. <i>cucurbitae</i> race 2 Toward <i>Cucurbita maxima</i> and <i>C. moschata</i> . Molecular Plant-Microbe Interactions, 1997, 10, 355-368.	2.6	44
49	Microsatellites in <i>Malus X domestica</i> (apple): abundance, polymorphism and cultivar identification. Theoretical and Applied Genetics, 1997, 94, 249-254.	3.6	288
50	A detailed linkage map around an apple scab resistance gene demonstrates that two disease resistance classes both carry the V f gene. Theoretical and Applied Genetics, 1996, 93, 485-493.	3.6	64
51	Gene inactivation in the plant pathogen <i>Glomerella cingulata</i> : three strategies for the disruption of the pectin lyase gene <i>pnlA</i> . Molecular Genetics and Genomics, 1995, 246, 196-205.	2.4	48
52	Integration of vectors by homologous recombination in the plant pathogen <i>Glomerella cingulata</i> . Current Genetics, 1994, 25, 202-208.	1.7	26
53	The use of species-specific DNA probes for the identification of <i>Mycosphaerella fijiensis</i> and <i>M. musicola</i> , the causal agents of Sigatoka disease of banana. Plant Pathology, 1994, 43, 701-707.	2.4	30
54	The pectin lyase-encoding gene ( <i>pnl</i> ) family from <i>Glomerella cingulata</i> : characterization of <i>pnlA</i> and its expression in yeast. Gene, 1994, 142, 141-146.	2.2	49

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55	The ARG4 gene of <i>Candida albicans</i> . <i>Gene</i> , 1994, 142, 213-218.	2.2	19
56	Cloning and molecular characterization of the glyceraldehyde-3-phosphate dehydrogenase-encoding gene and cDNA from the plant pathogenic fungus <i>Glomerella cingulata</i> . <i>Gene</i> , 1992, 122, 225-230.	2.2	285
57	Genetics of the white-opaque transition in <i>Candida albicans</i> : demonstration of switching recessivity and mapping of switching genes. <i>Journal of Bacteriology</i> , 1992, 174, 2951-2957.	2.2	17
58	High efficiency transformation of <i>Fusarium solani</i> f. sp. <i>cucurbitae</i> race 2 (mating population V). <i>Current Genetics</i> , 1992, 21, 463-469.	1.7	20
59	Differentiation of <i>Fusarium solani</i> f. sp. <i>cucurbitae</i> races 1 and 2 by random amplification of polymorphic DNA. <i>Current Genetics</i> , 1991, 20, 391-396.	1.7	221
60	Genomic structure of <i>Candida stellatoidea</i> : extra chromosomes and gene duplication. <i>Infection and Immunity</i> , 1990, 58, 949-954.	2.2	19
61	Methods for the genetics and molecular biology of <i>Candida albicans</i> . <i>Analytical Biochemistry</i> , 1988, 175, 361-372.	2.4	35
62	Opaque-white phenotype transition: a programmed morphological transition in <i>Candida albicans</i> . <i>Journal of Bacteriology</i> , 1988, 170, 895-899.	2.2	185
63	Heat shock induces chromosome loss in the yeast <i>Candida albicans</i> . <i>Molecular Genetics and Genomics</i> , 1985, 200, 162-8.	2.4	74
64	Genetic analysis of red, adenine-requiring mutants of <i>Candida albicans</i> . <i>Journal of Bacteriology</i> , 1983, 156, 1066-1077.	2.2	71