

# Paula M Moolhuijzen

## List of Publications by Year in descending order

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48  
papers

1,922  
citations

236925

25  
h-index

254184

43  
g-index

52  
all docs

52  
docs citations

52  
times ranked

2726  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep Sequencing of Plant and Animal DNA Contained within Traditional Chinese Medicines Reveals Legality Issues and Health Safety Concerns. <i>PLoS Genetics</i> , 2012, 8, e1002657.	3.5	245
2	The first gene-based map of <i>Lupinus angustifolius</i> L.-location of domestication genes and conserved synteny with <i>Medicago truncatula</i> . <i>Theoretical and Applied Genetics</i> , 2006, 113, 225-238.	3.6	116
3	Genome Sequence of the Pathogenic Intestinal Spirochete <i>Brachyspira hyodysenteriae</i> Reveals Adaptations to Its Lifestyle in the Porcine Large Intestine. <i>PLoS ONE</i> , 2009, 4, e4641.	2.5	107
4	Identification of a mutation in the para-sodium channel gene of the cattle tick <i>Rhipicephalus (Boophilus) microplus</i> associated with resistance to synthetic pyrethroid acaricides. <i>International Journal for Parasitology</i> , 2009, 39, 775-779.	3.1	99
5	The Genetics of Symbiotic Nitrogen Fixation: Comparative Genomics of 14 Rhizobia Strains by Resolution of Protein Clusters. <i>Genes</i> , 2012, 3, 138-166.	2.4	94
6	Complete Genome Sequence of <i>Sporisorium scitamineum</i> and Biotrophic Interaction Transcriptome with Sugarcane. <i>PLoS ONE</i> , 2015, 10, e0129318.	2.5	93
7	Immunological Profiles of <i>Bos taurus</i> and <i>Bos indicus</i> Cattle Infested with the Cattle Tick, <i>Rhipicephalus (Boophilus) microplus</i> . <i>Vaccine Journal</i> , 2009, 16, 1074-1086.	3.1	86
8	De novo assembly of <i>Euphorbia fischeriana</i> root transcriptome identifies prostratin pathway related genes. <i>BMC Genomics</i> , 2011, 12, 600.	2.8	75
9	Aligning a New Reference Genetic Map of <i>Lupinus angustifolius</i> with the Genome Sequence of the Model Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2010, 17, 73-83.	3.4	73
10	Comparative genomics of the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> reveals chromosomal variations and genome plasticity. <i>BMC Genomics</i> , 2018, 19, 279.	2.8	56
11	CattleTickBase: An integrated Internet-based bioinformatics resource for <i>Rhipicephalus (Boophilus) microplus</i> . <i>International Journal for Parasitology</i> , 2012, 42, 161-169.	3.1	55
12	The Complete Genome Sequence of the Pathogenic Intestinal Spirochete <i>Brachyspira pilosicoli</i> and Comparison with Other <i>Brachyspira</i> Genomes. <i>PLoS ONE</i> , 2010, 5, e11455.	2.5	54
13	Genomic analysis of <i>Campylobacter fetus</i> subspecies: identification of candidate virulence determinants and diagnostic assay targets. <i>BMC Microbiology</i> , 2009, 9, 86.	3.3	51
14	Comparative microarray analysis of <i>Rhipicephalus (Boophilus) microplus</i> expression profiles of larvae pre-attachment and feeding adult female stages on <i>Bos indicus</i> and <i>Bos taurus</i> cattle. <i>BMC Genomics</i> , 2010, 11, 437.	2.8	48
15	Gene-enriched draft genome of the cattle tick <i>Rhipicephalus microplus</i> : assembly by the hybrid Pacific Biosciences/Illumina approach enabled analysis of the highly repetitive genome. <i>International Journal for Parasitology</i> , 2017, 47, 569-583.	3.1	48
16	Bread matters: a national initiative to profile the genetic diversity of Australian wheat. <i>Plant Biotechnology Journal</i> , 2012, 10, 703-708.	8.3	45
17	Genome Sequences of Six Wheat-Infecting <i>Fusarium</i> Species Isolates. <i>Genome Announcements</i> , 2013, 1, .	0.8	38
18	The genome structure of the 1-FEH genes in wheat ( <i>Triticum aestivum</i> L.): new markers to track stem carbohydrates and grain filling QTLs in breeding. <i>Molecular Breeding</i> , 2008, 22, 339-351.	2.1	36

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19	Suppressive subtractive hybridization analysis of <i>Rhipicephalus (Boophilus) microplus</i> larval and adult transcript expression during attachment and feeding. <i>Veterinary Parasitology</i> , 2010, 167, 304-320.	1.8	36
20	Analysis of Multiple <i>Brachyspira hyodysenteriae</i> Genomes Confirms That the Species Is Relatively Conserved but Has Potentially Important Strain Variation. <i>PLoS ONE</i> , 2015, 10, e0131050.	2.5	36
21	Evolutionary conserved microRNAs are ubiquitously expressed compared to tick-specific miRNAs in the cattle tick <i>Rhipicephalus (Boophilus) microplus</i> . <i>BMC Genomics</i> , 2011, 12, 328.	2.8	33
22	Transcriptome and toxin family analysis of the paralysis tick, <i>Ixodes holocyclus</i> . <i>International Journal for Parasitology</i> , 2018, 48, 71-82.	3.1	33
23	Differential recognition by tick-resistant cattle of the recombinantly expressed <i>Rhipicephalus microplus</i> serine protease inhibitor-3 (RMS-3). <i>Ticks and Tick-borne Diseases</i> , 2012, 3, 159-169.	2.7	32
24	Reassociation kinetics-based approach for partial genome sequencing of the cattle tick, <i>Rhipicephalus (Boophilus) microplus</i> . <i>BMC Genomics</i> , 2010, 11, 374.	2.8	31
25	The transcript repeat element: the human Alu sequence as a component of gene networks influencing cancer. <i>Functional and Integrative Genomics</i> , 2010, 10, 307-319.	3.5	28
26	An automated and combinative method for the predictive ranking of candidate effector proteins of fungal plant pathogens. <i>Scientific Reports</i> , 2021, 11, 19731.	3.3	27
27	<i>Rhipicephalus microplus</i> lipocalins (LRMs): Genomic identification and analysis of the bovine immune response using in silico predicted B and T cell epitopes. <i>International Journal for Parasitology</i> , 2013, 43, 739-752.	3.1	24
28	Genomic Regions Associated with Virulence in <i>Pyrenophora teres</i> f. <i>teres</i> Identified by Genome-Wide Association Analysis and Biparental Mapping. <i>Phytopathology</i> , 2020, 110, 881-891.	2.2	21
29	Genome-level identification of cell wall invertase genes in wheat for the study of drought tolerance. <i>Functional Plant Biology</i> , 2012, 39, 569.	2.1	18
30	Next-generation sequencing: a challenge to meet the increasing demand for training workshops in Australia. <i>Briefings in Bioinformatics</i> , 2013, 14, 563-574.	6.5	17
31	Shoot transcriptome of the giant reed, <i>Arundo donax</i> . <i>Data in Brief</i> , 2015, 3, 1-6.	1.0	17
32	Genomic distribution of a novel <i>Pyrenophora tritici-repentis</i> ToxA insertion element. <i>PLoS ONE</i> , 2018, 13, e0206586.	2.5	16
33	PacBio genome sequencing reveals new insights into the genomic organisation of the multi-copy ToxB gene of the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> . <i>BMC Genomics</i> , 2020, 21, 645.	2.8	15
34	Hierarchical clustering of MS/MS spectra from the firefly metabolome identifies new lucibufagin compounds. <i>Scientific Reports</i> , 2020, 10, 6043.	3.3	13
35	Expansion and Conservation of Biosynthetic Gene Clusters in Pathogenic <i>Pyrenophora</i> spp.. <i>Toxins</i> , 2020, 12, 242.	3.4	13
36	A new PacBio genome sequence of an Australian <i>Pyrenophora tritici-repentis</i> race 1 isolate. <i>BMC Research Notes</i> , 2019, 12, 642.	1.4	12

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37	The identification and deletion of the polyketide synthaseâ€nonribosomal peptide synthase gene responsible for the production of the phytotoxic triticone A/B in the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> . <i>Environmental Microbiology</i> , 2019, 21, 4875-4886.	3.8	12
38	Acetylcholinesterase 1 in populations of organophosphate-resistant North American strains of the cattle tick, <i>Rhipicephalus microplus</i> (Acari: Ixodidae). <i>Parasitology Research</i> , 2015, 114, 3027-3040.	1.6	11
39	A conserved hypothetical gene is required but not sufficient for <i>Ptr ToxC</i> production in <i>Pyrenophora tritici-repentis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, , .	2.6	11
40	A genome-wide genetic linkage map and reference quality genome sequence for a new race in the wheat pathogen <i>Pyrenophora tritici-repentis</i> . <i>Fungal Genetics and Biology</i> , 2021, 152, 103571.	2.1	8
41	Exploration of wheat and pathogen transcriptomes during tan spot infection. <i>BMC Research Notes</i> , 2018, 11, 907.	1.4	7
42	Remote homology clustering identifies lowly conserved families of effector proteins in plant-pathogenic fungi. <i>Microbial Genomics</i> , 2021, 7, .	2.0	7
43	Immunomic Investigation of Holocyclotoxins to Produce the First Protective Anti-Venom Vaccine Against the Australian Paralysis Tick, <i>Ixodes holocyclus</i> . <i>Frontiers in Immunology</i> , 2021, 12, 744795.	4.8	6
44	Physiological Changes in Barley mlo-11 Powdery Mildew Resistance Conditioned by Tandem Repeat Copy Number. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8769.	4.1	5
45	Potentiators of Disease During Barley Infection by <i>Pyrenophora teres</i> f. <i>teres</i> in a Susceptible Interaction. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 779-792.	2.6	5
46	The first genome assembly of fungal pathogen <i>Pyrenophora tritici-repentis</i> race 1 isolate using Oxford Nanopore MinION sequencing. <i>BMC Research Notes</i> , 2021, 14, 334.	1.4	3
47	Draft Genome Sequences of <i>Campylobacter fetus</i> subsp. <i>venerealis</i> bv. <i>venerealis</i> Strain B6 and bv. <i>intermedius</i> Strain 642-21. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
48	Proteomics of the wheat tan spot pathogen <i>Pyrenophora tritici-repentis</i> . <i>BMC Research Notes</i> , 2018, 11, 846.	1.4	1