

Wouter Coppieters

List of Publications by Year in descending order

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54
papers

5,658
citations

126907

33
h-index

161849

54
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57
all docs

57
docs citations

57
times ranked

5788
citing authors

#	ARTICLE	IF	CITATIONS
1	The virulome of <i>Streptomyces scabiei</i> in response to cello-oligosaccharide elicitors. <i>Microbial Genomics</i> , 2022, 8, .	2.0	8
2	Benchmarking phasing software with a whole-genome sequenced cattle pedigree. <i>BMC Genomics</i> , 2022, 23, 130.	2.8	3
3	ABO genotype alters the gut microbiota by regulating GalNAc levels in pigs. <i>Nature</i> , 2022, 606, 358-367.	27.8	67
4	A High-Quality Genome Assembly of Striped Catfish (<i>Pangasianodon hypophthalmus</i>) Based on Highly Accurate Long-Read HiFi Sequencing Data. <i>Genes</i> , 2022, 13, 923.	2.4	3
5	A 12 kb multi-allelic copy number variation encompassing a GC gene enhancer is associated with mastitis resistance in dairy cattle. <i>PLoS Genetics</i> , 2021, 17, e1009331.	3.5	25
6	Analyses of Avascular Mutants Reveal Unique Transcriptomic Signature of Non-conventional Endothelial Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 589717.	3.7	6
7	SNP-based quantitative deconvolution of biological mixtures: application to the detection of cows with subclinical mastitis by whole-genome sequencing of tank milk. <i>Genome Research</i> , 2020, 30, 1201-1207.	5.5	1
8	Detection and identification of transgenic events by next generation sequencing combined with enrichment technologies. <i>Scientific Reports</i> , 2019, 9, 15595.	3.3	25
9	Analysis of Genes Associated With Monogenic Primary Immunodeficiency Identifies Rare Variants in XIAP in Patients With Crohn's Disease. <i>Gastroenterology</i> , 2018, 154, 2165-2177.	1.3	26
10	Isolation, Characterization, and Antibacterial Activity of Hard-to-Culture Actinobacteria from Cave Moonmilk Deposits. <i>Antibiotics</i> , 2018, 7, 28.	3.7	68
11	Complete Genome Sequence of <i>Streptomyces lunaelactis</i> MM109 T, Isolated from Cave Moonmilk Deposits. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
12	A novel SMAD3 mutation caused multiple aneurysms in a patient without osteoarthritis symptoms. <i>European Journal of Medical Genetics</i> , 2017, 60, 228-231.	1.3	10
13	Coding and noncoding variants in <i>HFM1</i> , <i>MLH3</i> , <i>MSH4</i> , <i>MSH5</i> , <i>RNF212</i> , and <i>RNF212B</i> affect recombination rate in cattle. <i>Genome Research</i> , 2016, 26, 1323-1332.	5.5	77
14	NGS-based reverse genetic screen for common embryonic lethal mutations compromising fertility in livestock. <i>Genome Research</i> , 2016, 26, 1333-1341.	5.5	71
15	Reverse genetic screen for loss-of-function mutations uncovers a frameshifting deletion in the <i>melanophilin</i> gene accountable for a distinctive coat color in Belgian Blue cattle. <i>Animal Genetics</i> , 2016, 47, 110-113.	1.7	21
16	A stop-gain in the <i>laminin, alpha 3</i> gene causes recessive junctional epidermolysis bullosa in Belgian Blue cattle. <i>Animal Genetics</i> , 2015, 46, 566-570.	1.7	11
17	On the use of the transmission disequilibrium test to detect pseudo-autosomal variants affecting traits with sex-limited expression. <i>Animal Genetics</i> , 2015, 46, 395-402.	1.7	4
18	Genome-wide next-generation DNA and RNA sequencing reveals a mutation that perturbs splicing of the phosphatidylinositol glycan anchor biosynthesis class H gene (<i>PIGH</i>) and causes arthrogyposis in Belgian Blue cattle. <i>BMC Genomics</i> , 2015, 16, 316.	2.8	13

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19	A missense mutation accelerating the gating of the lysosomal Cl ⁻ /H ⁺ -exchanger CLC-7/Ostm1 causes osteopetrosis with gingival hamartomas in cattle. <i>DMM Disease Models and Mechanisms</i> , 2014, 7, 119-28.	2.4	36
20	Refined Candidate Region for F4ab/ac Enterotoxigenic <i>Escherichia coli</i> Susceptibility Situated Proximal to MUC13 in Pigs. <i>PLoS ONE</i> , 2014, 9, e105013.	2.5	28
21	Selection in action: dissecting the molecular underpinnings of the increasing muscle mass of Belgian Blue Cattle. <i>BMC Genomics</i> , 2014, 15, 796.	2.8	47
22	Exome sequencing reveals a novel Moroccan founder mutation in <i>SLC19A3</i> as a new cause of early-childhood fatal Leigh syndrome. <i>Brain</i> , 2013, 136, 882-890.	7.6	81
23	A Triad of Highly Divergent Polymeric Immunoglobulin Receptor (PIGR) Haplotypes with Major Effect on IgA Concentration in Bovine Milk. <i>PLoS ONE</i> , 2013, 8, e57219.	2.5	9
24	A Splice Site Variant in the Bovine RNF11 Gene Compromises Growth and Regulation of the Inflammatory Response. <i>PLoS Genetics</i> , 2012, 8, e1002581.	3.5	40
25	Genetic Variants in REC8, RNF212, and PRDM9 Influence Male Recombination in Cattle. <i>PLoS Genetics</i> , 2012, 8, e1002854.	3.5	128
26	Serial translocation by means of circular intermediates underlies colour sidedness in cattle. <i>Nature</i> , 2012, 482, 81-84.	27.8	137
27	A Deletion in the Bovine FANCI Gene Compromises Fertility by Causing Fetal Death and Brachyspina. <i>PLoS ONE</i> , 2012, 7, e43085.	2.5	82
28	Fast Homozygosity Mapping and Identification of a Zebrafish ENU-Induced Mutation by Whole-Genome Sequencing. <i>PLoS ONE</i> , 2012, 7, e34671.	2.5	41
29	Resequencing of positional candidates identifies low frequency IL23R coding variants protecting against inflammatory bowel disease. <i>Nature Genetics</i> , 2011, 43, 43-47.	21.4	175
30	Variants modulating the expression of a chromosome domain encompassing PLAG1 influence bovine stature. <i>Nature Genetics</i> , 2011, 43, 405-413.	21.4	300
31	Patrocles: a database of polymorphic miRNA-mediated gene regulation in vertebrates. <i>Nucleic Acids Research</i> , 2010, 38, D640-D651.	14.5	126
32	Balancing Selection of a Frame-Shift Mutation in the MRC2 Gene Accounts for the Outbreak of the Crooked Tail Syndrome in Belgian Blue Cattle. <i>PLoS Genetics</i> , 2009, 5, e1000666.	3.5	74
33	Mapping QTL influencing gastrointestinal nematode burden in Dutch Holstein-Friesian dairy cattle. <i>BMC Genomics</i> , 2009, 10, 96.	2.8	39
34	A high density linkage map of the bovine genome. <i>BMC Genetics</i> , 2009, 10, 18.	2.7	106
35	A nonsense mutation in cGMP-dependent type II protein kinase (<i>PRKG2</i>) causes dwarfism in American Angus cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19250-19255.	7.1	48
36	An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. <i>BMC Genetics</i> , 2008, 9, 37.	2.7	95

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37	Highly effective SNP-based association mapping and management of recessive defects in livestock. <i>Nature Genetics</i> , 2008, 40, 449-454.	21.4	263
38	Characterization of the bovine pseudoautosomal boundary: Documenting the evolutionary history of mammalian sex chromosomes. <i>Genome Research</i> , 2008, 18, 1884-1895.	5.5	60
39	Polymorphic miRNA-mediated gene regulation: contribution to phenotypic variation and disease. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 166-176.	3.3	131
40	Whole genome linkage disequilibrium maps in cattle. <i>BMC Genetics</i> , 2007, 8, 74.	2.7	201
41	Genetical metabolomics of flavonoid biosynthesis in <i>Populus</i> : a case study. <i>Plant Journal</i> , 2006, 47, 224-237.	5.7	140
42	Genetic identification of distinct loci controlling mammary tumor multiplicity, latency, and aggressiveness in the rat. <i>Mammalian Genome</i> , 2006, 17, 310-321.	2.2	28
43	Linkage Disequilibrium on the Bovine X Chromosome: Characterization and Use in Quantitative Trait Locus Mapping. <i>Genetics</i> , 2006, 173, 1777-1786.	2.9	24
44	Genetic and functional confirmation of the causality of the DGAT1 K232A quantitative trait nucleotide in affecting milk yield and composition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2398-2403.	7.1	370
45	Molecular Dissection of a Quantitative Trait Locus: A Phenylalanine-to-Tyrosine Substitution in the Transmembrane Domain of the Bovine Growth Hormone Receptor Is Associated With a Major Effect on Milk Yield and Composition. <i>Genetics</i> , 2003, 163, 253-266.	2.9	390
46	Positional Candidate Cloning of a QTL in Dairy Cattle: Identification of a Missense Mutation in the Bovine <i>DGAT1</i> Gene with Major Effect on Milk Yield and Composition. <i>Genome Research</i> , 2002, 12, 222-231.	5.5	803
47	Simultaneous Mining of Linkage and Linkage Disequilibrium to Fine Map Quantitative Trait Loci in Outbred Half-Sib Pedigrees: Revisiting the Location of a Quantitative Trait Locus With Major Effect on Milk Production on Bovine Chromosome 14. <i>Genetics</i> , 2002, 161, 275-287.	2.9	101
48	Extensive Genome-wide Linkage Disequilibrium in Cattle. <i>Genome Research</i> , 2000, 10, 220-227.	5.5	304
49	An imprinted QTL with major effect on muscle mass and fat deposition maps to the IGF2 locus in pigs. <i>Nature Genetics</i> , 1999, 21, 155-156.	21.4	376
50	The great-grand-daughter design: a simple strategy to increase the power of a grand-daughter design for QTL mapping. <i>Genetical Research</i> , 1999, 74, 189-199.	0.9	8
51	From phenotype to genotype : towards positional cloning of QTL in livestock?. <i>The Journal of Animal Genetics</i> , 1999, 27, 33-43.	0.1	3
52	A QTL with major effect on milk yield and composition maps to bovine Chromosome 14. <i>Mammalian Genome</i> , 1998, 9, 540-544.	2.2	110
53	A Rank-Based Nonparametric Method for Mapping Quantitative Trait Loci in Outbred Half-Sib Pedigrees: Application to Milk Production in a Granddaughter Design. <i>Genetics</i> , 1998, 149, 1547-1555.	2.9	43
54	Quantitative Trait Loci Analysis for Five Milk Production Traits on Chromosome <i>Six</i> in the Dutch Holstein-Friesian Population. <i>Genetics</i> , 1996, 144, 1799-1807.	2.9	198