

Claire M Wade

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

17,360
citations

136740

32
h-index

56606

83
g-index

92
all docs

92
docs citations

92
times ranked

20883
citing authors

#	ARTICLE	IF	CITATIONS
1	Canine coat pigmentation genetics: a review. <i>Animal Genetics</i> , 2022, 53, 3-34.	0.6	15
2	Forensic DNA phenotyping: <i>Canis familiaris</i> breed classification and skeletal phenotype prediction using functionally significant skeletal SNPs and indels. <i>Animal Genetics</i> , 2022, 53, 247-263.	0.6	5
3	Valued personality traits in livestock herding Kelpies—Development and application of a livestock herding dog assessment form. <i>PLoS ONE</i> , 2022, 17, e0267266.	1.1	0
4	Roan, ticked and clear coat patterns in the canine are associated with three haplotypes near <i>usherin</i> on CFA38. <i>Animal Genetics</i> , 2021, 52, 198-207.	0.6	4
5	Inbreeding levels in an open-registry pedigreed dog breed: The Australian working kelpie. <i>Veterinary Journal</i> , 2021, 269, 105609.	0.6	3
6	Genetics of canine myxomatous mitral valve disease. <i>Animal Genetics</i> , 2021, 52, 409-421.	0.6	9
7	Sequence variants of the canine melanocyte inducing transcription factor (<i>MITF</i>) locus reveal a common <i>MITF</i> processed pseudogene. <i>Animal Genetics</i> , 2021, 52, 777-778.	0.6	2
8	Exploiting genomic synteny in Felidae: cross-species genome alignments and SNV discovery can aid conservation management. <i>BMC Genomics</i> , 2021, 22, 601.	1.2	3
9	A large deletion on CFA28 omitting <i>ACSL5</i> gene is associated with intestinal lipid malabsorption in the Australian Kelpie dog breed. <i>Scientific Reports</i> , 2020, 10, 18223.	1.6	4
10	Mapping the genetic basis of diabetes mellitus in the Australian Burmese cat (<i>Felis catus</i>). <i>Scientific Reports</i> , 2020, 10, 19194.	1.6	12
11	Characterization of a Homozygous Deletion of Steroid Hormone Biosynthesis Genes in Horse Chromosome 29 as a Risk Factor for Disorders of Sex Development and Reproduction. <i>Genes</i> , 2020, 11, 251.	1.0	9
12	Sequential Analysis of Livestock Herding Dog and Sheep Interactions. <i>Animals</i> , 2020, 10, 352.	1.0	3
13	The Perceived Value of Behavioural Traits in Australian Livestock Herding Dogs Varies with the Operational Context. <i>Animals</i> , 2019, 9, 448.	1.0	2
14	A comprehensive biomedical variant catalogue based on whole genome sequences of 582 dogs and eight wolves. <i>Animal Genetics</i> , 2019, 50, 695-704.	0.6	138
15	The Burmese cat as a genetic model of type 2 diabetes in humans. <i>Animal Genetics</i> , 2019, 50, 319-325.	0.6	13
16	Genomic Characterization of External Morphology Traits in Kelpies Does Not Support Common Ancestry with the Australian Dingo. <i>Genes</i> , 2019, 10, 337.	1.0	11
17	Association between coat colour and the behaviour of Australian Labrador retrievers. <i>Canine Genetics and Epidemiology</i> , 2019, 6, 10.	2.9	5
18	Behavioral Genetics of Dog Breeds. , 2019, , 312-322.		2

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19	Using an owner-based questionnaire to phenotype dogs with separation-related distress: Do owners know what their dogs do when they are absent?. <i>Journal of Veterinary Behavior: Clinical Applications and Research</i> , 2018, 23, 58-65.	0.5	18
20	Work-type influences perceived livestock herding success in Australian Working Kelpies. <i>Canine Genetics and Epidemiology</i> , 2018, 5, 5.	2.9	4
21	Risk factors of separation-related behaviours in Australian retrievers. <i>Applied Animal Behaviour Science</i> , 2018, 209, 71-77.	0.8	13
22	Umbilical tissue as a sampling technique for DNA testing in neonate dogs. <i>Animal Genetics</i> , 2018, 49, 499-500.	0.6	0
23	A rapid multiplex PCR assay for presumptive species identification of rhinoceros horns and its implementation in Vietnam. <i>PLoS ONE</i> , 2018, 13, e0198565.	1.1	5
24	Relationship between transitional lumbosacral vertebrae and eight lumbar vertebrae in a breeding colony of Labrador Retrievers and Labrador Crosses. <i>Australian Veterinary Journal</i> , 2017, 95, 33-36.	0.5	5
25	Variants in the host genome may inhibit tumour growth in devil facial tumours: evidence from genome-wide association. <i>Scientific Reports</i> , 2017, 7, 423.	1.6	56
26	Exclusion of known progressive retinal atrophy genes for blindness in the Hungarian Puli. <i>Animal Genetics</i> , 2017, 48, 500-501.	0.6	2
27	Exclusion of known gene loci for cerebellar atrophy in the Australian Working Kelpie. <i>Animal Genetics</i> , 2017, 48, 730-732.	0.6	3
28	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. <i>BMC Genomics</i> , 2017, 18, 565.	1.2	116
29	A Coding Variant in the Gene Bardet-Biedl Syndrome 4 (<i>BBS4</i>) Is Associated with a Novel Form of Canine Progressive Retinal Atrophy. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2327-2335.	0.8	11
30	Inheritance of chronic superficial keratitis in Australian Greyhounds. <i>Animal Genetics</i> , 2016, 47, 629-629.	0.6	4
31	Interval dogs: Results and evaluation of Global Positioning System units in measuring athletic performance in stock-herding dogs. <i>Journal of Veterinary Behavior: Clinical Applications and Research</i> , 2016, 14, 1-4.	0.5	5
32	A dominant TRPV4 variant underlies osteochondrodysplasia in Scottish fold cats. <i>Osteoarthritis and Cartilage</i> , 2016, 24, 1441-1450.	0.6	32
33	Digging for known genetic mutations underlying inherited bone and cartilage characteristics and disorders in the dog and cat. <i>Veterinary and Comparative Orthopaedics and Traumatology</i> , 2016, 29, 269-276.	0.2	5
34	Regulatory mutations in <i>TBX3</i> disrupt asymmetric hair pigmentation that underlies Dun camouflage color in horses. <i>Nature Genetics</i> , 2016, 48, 152-158.	9.4	59
35	Progressive retinal atrophy in <i>hetland</i> sheepdog is associated with a mutation in the <i>CNGA1</i> gene. <i>Animal Genetics</i> , 2015, 46, 515-521.	0.6	22
36	Canine Disorder Mirrors Human Disease: Exonic Deletion in <i>HES7</i> Causes Autosomal Recessive Spondylocostal Dysostosis in Miniature Schnauzer Dogs. <i>PLoS ONE</i> , 2015, 10, e0117055.	1.1	27

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37	Strong selection for behavioural resilience in Australian stock working dogs identified by selective sweep analysis. <i>Canine Genetics and Epidemiology</i> , 2015, 2, 6.	2.9	18
38	Simple, rapid and accurate genotyping-by-sequencing from aligned whole genomes with ArrayMaker. <i>Bioinformatics</i> , 2015, 31, 599-601.	1.8	1
39	Genome-Wide Association Studies in Dogs and Humans Identify ADAMTS20 as a Risk Variant for Cleft Lip and Palate. <i>PLoS Genetics</i> , 2015, 11, e1005059.	1.5	82
40	Environmental Factors Associated with Success Rates of Australian Stock Herding Dogs. <i>PLoS ONE</i> , 2014, 9, e104457.	1.1	30
41	A LINE-1 Insertion in DLX6 Is Responsible for Cleft Palate and Mandibular Abnormalities in a Canine Model of Pierre Robin Sequence. <i>PLoS Genetics</i> , 2014, 10, e1004257.	1.5	49
42	Manual muster: A critical analysis of the use of common terms in Australian working dog manuals. <i>Journal of Veterinary Behavior: Clinical Applications and Research</i> , 2014, 9, 370-374.	0.5	15
43	Holding back the genes: limitations of research into canine behavioural genetics. <i>Canine Genetics and Epidemiology</i> , 2014, 1, 7.	2.9	27
44	From the Phenotype to the Genotype via Bioinformatics. <i>Methods in Molecular Biology</i> , 2014, 1168, 1-16.	0.4	4
45	Analysis of the canine genome and canine health: Bridging a gap. <i>Veterinary Journal</i> , 2013, 196, 1-3.	0.6	1
46	Empirical assessment of competitive hybridization and noise in ultra high density canine tiling arrays. <i>BMC Bioinformatics</i> , 2013, 14, 231.	1.2	0
47	A web resource on DNA tests for canine and feline hereditary diseases. <i>Veterinary Journal</i> , 2013, 197, 182-187.	0.6	21
48	Genetic Diversity in the Modern Horse Illustrated from Genome-Wide SNP Data. <i>PLoS ONE</i> , 2013, 8, e54997.	1.1	214
49	Genome-Wide Analysis Reveals Selection for Important Traits in Domestic Horse Breeds. <i>PLoS Genetics</i> , 2013, 9, e1003211.	1.5	240
50	Accumulating Mutations in Series of Haplotypes at the KIT and MITF Loci Are Major Determinants of White Markings in Franches-Montagnes Horses. <i>PLoS ONE</i> , 2013, 8, e75071.	1.1	34
51	Genetic Correlations among Canine Hip Dysplasia Radiographic Traits in a Cohort of Australian German Shepherd Dogs, and Implications for the Design of a More Effective Genetic Control Program. <i>PLoS ONE</i> , 2013, 8, e78929.	1.1	7
52	Estimated Breeding Values for Canine Hip Dysplasia Radiographic Traits in a Cohort of Australian German Shepherd Dogs. <i>PLoS ONE</i> , 2013, 8, e77470.	1.1	17
53	A High Density SNP Array for the Domestic Horse and Extant Perissodactyla: Utility for Association Mapping, Genetic Diversity, and Phylogeny Studies. <i>PLoS Genetics</i> , 2012, 8, e1002451.	1.5	208
54	Copy number expansion of the STX17 duplication in melanoma tissue from Grey horses. <i>BMC Genomics</i> , 2012, 13, 365.	1.2	34

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55	Heritability and Phenotypic Variation of Canine Hip Dysplasia Radiographic Traits in a Cohort of Australian German Shepherd Dogs. PLoS ONE, 2012, 7, e39620.	1.1	29
56	Empowering international canine inherited disorder management. Mammalian Genome, 2012, 23, 195-202.	1.0	10
57	Symmetry of hip dysplasia traits in the German Shepherd Dog in Australia. Journal of Animal Breeding and Genetics, 2011, 128, 230-243.	0.8	10
58	Canine genetics: A very Special Issue. Veterinary Journal, 2011, 189, 123-125.	0.6	6
59	Inbreeding and genetic diversity in dogs: Results from DNA analysis. Veterinary Journal, 2011, 189, 183-188.	0.6	32
60	A genealogical survey of Australian registered dog breeds. Veterinary Journal, 2011, 189, 203-210.	0.6	41
61	A truncating mutation in ATP13A2 is responsible for adult-onset neuronal ceroid lipofuscinosis in Tibetan terriers. Neurobiology of Disease, 2011, 42, 468-474.	2.1	109
62	Association analysis of candidate SNPs in <i>TRPM1</i> with leopard complex spotting (<i>LP</i>) and congenital stationary night blindness (CSNB) in horses. Animal Genetics, 2010, 41, 207-207.	0.6	12
63	Fine-mapping and mutation analysis of TRPM1: a candidate gene for leopard complex (LP) spotting and congenital stationary night blindness in horses. Briefings in Functional Genomics, 2010, 9, 193-207.	1.3	49
64	Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource. Genetics, 2010, 185, 1081-1095.	1.2	95
65	Genome-wide association analysis reveals a <i>SOD1</i> mutation in canine degenerative myelopathy that resembles amyotrophic lateral sclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2794-2799.	3.3	219
66	Identification of Novel Genes That Mediate Innate Immunity Using Inbred Mice. Genetics, 2009, 183, 1535-1544.	1.2	55
67	Genome Sequence, Comparative Analysis, and Population Genetics of the Domestic Horse. Science, 2009, 326, 865-867.	6.0	680
68	Evaluation of the Serotonergic Genes <i>htr1A</i> , <i>htr1B</i> , <i>htr2A</i> , and <i>slc6A4</i> in Aggressive Behavior of Golden Retriever Dogs. Behavior Genetics, 2008, 38, 55-66.	1.4	31
69	A cis-acting regulatory mutation causes premature hair graying and susceptibility to melanoma in the horse. Nature Genetics, 2008, 40, 1004-1009.	9.4	271
70	Glycogen synthase (<i>GYS1</i>) mutation causes a novel skeletal muscle glycogenosis. Genomics, 2008, 91, 458-466.	1.3	156
71	Efficient Control of Population Structure in Model Organism Association Mapping. Genetics, 2008, 178, 1709-1723.	1.2	1,752
72	A deletion in nephronophthisis 4 (<i>NPHP4</i>) is associated with recessive cone-rod dystrophy in standard wire-haired dachshund. Genome Research, 2008, 18, 1415-1421.	2.4	75

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73	Inheritance, Mode of Inheritance, and Candidate Genes for Primary Hyperparathyroidism in Keeshonden. <i>Journal of Veterinary Internal Medicine</i> , 2007, 21, 199-203.	0.6	27
74	Efficient mapping of mendelian traits in dogs through genome-wide association. <i>Nature Genetics</i> , 2007, 39, 1321-1328.	9.4	474
75	Duplication of FGF3, FGF4, FGF19 and ORAOV1 causes hair ridge and predisposition to dermoid sinus in Ridgeback dogs. <i>Nature Genetics</i> , 2007, 39, 1318-1320.	9.4	176
76	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
77	A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. <i>Nature</i> , 2007, 448, 1050-1053.	13.7	406
78	Inheritance, mode of inheritance, and candidate genes for primary hyperparathyroidism in Keeshonden. <i>Journal of Veterinary Internal Medicine</i> , 2007, 21, 199-203.	0.6	3
79	Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 2006, 444, 97-101.	13.7	1,113
80	Genetic variation in laboratory mice. <i>Nature Genetics</i> , 2005, 37, 1175-1180.	9.4	143
81	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	13.7	2,215
82	Segmental Phylogenetic Relationships of Inbred Mouse Strains Revealed by Fine-Scale Analysis of Sequence Variation Across 4.6 Mb of Mouse Genome. <i>Genome Research</i> , 2004, 14, 1493-1500.	2.4	78
83	The mosaic structure of variation in the laboratory mouse genome. <i>Nature</i> , 2002, 420, 574-578.	13.7	448
84	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319