Claire M Wade

List of Publications by Year
in descending order

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84 papers	17,360 citations	136950 32 h-index	56724 83 g-index
92 all docs	92 docs citations	92 times ranked	20883 citing authors

#	Article	IF	Citations
1	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
2	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	27.8	2,215
3	Efficient Control of Population Structure in Model Organism Association Mapping. Genetics, 2008, 178, 1709-1723.	2.9	1,752
4	Insights from the genome of the biotrophic fungal plant pathogen Ustilago maydis. Nature, 2006, 444, 97-101.	27.8	1,113
5	Genome Sequence, Comparative Analysis, and Population Genetics of the Domestic Horse. Science, 2009, 326, 865-867.	12.6	680
6	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	27.8	661
7	Efficient mapping of mendelian traits in dogs through genome-wide association. Nature Genetics, 2007, 39, 1321-1328.	21.4	474
8	The mosaic structure of variation in the laboratory mouse genome. Nature, 2002, 420, 574-578.	27.8	448
9	A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. Nature, 2007, 448, 1050-1053.	27.8	406
10	A cis-acting regulatory mutation causes premature hair graying and susceptibility to melanoma in the horse. Nature Genetics, 2008, 40, 1004-1009.	21.4	271
11	Genome-Wide Analysis Reveals Selection for Important Traits in Domestic Horse Breeds. PLoS Genetics, 2013, 9, e1003211.	3.5	240
12	Genome-wide association analysis reveals a SOD1 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.	7.1	219
13	Genetic Diversity in the Modern Horse Illustrated from Genome-Wide SNP Data. PLoS ONE, 2013, 8, e54997.	2.5	214
14	A High Density SNP Array for the Domestic Horse and Extant Perissodactyla: Utility for Association Mapping, Genetic Diversity, and Phylogeny Studies. PLoS Genetics, 2012, 8, e1002451.	3.5	208
15	Duplication of FGF3, FGF4, FGF19 and ORAOV1 causes hair ridge and predisposition to dermoid sinus in Ridgeback dogs. Nature Genetics, 2007, 39, 1318-1320.	21.4	176
16	Glycogen synthase (GYS1) mutation causes a novel skeletal muscle glycogenosis. Genomics, 2008, 91, 458-466.	2.9	156
17	Genetic variation in laboratory mice. Nature Genetics, 2005, 37, 1175-1180.	21.4	143
18	A comprehensive biomedical variant catalogue based on whole genome sequences of 582 dogs and eight wolves. Animal Genetics, 2019, 50, 695-704.	1.7	138

#	Article	IF	Citations
19	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. BMC Genomics, 2017, 18, 565.	2.8	116
20	A truncating mutation in ATP13A2 is responsible for adult-onset neuronal ceroid lipofuscinosis in Tibetan terriers. Neurobiology of Disease, 2011, 42, 468-474.	4.4	109
21	Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource. Genetics, 2010, 185, 1081-1095.	2.9	95
22	Genome-Wide Association Studies in Dogs and Humans Identify ADAMTS20 as a Risk Variant for Cleft Lip and Palate. PLoS Genetics, 2015, 11, e1005059.	3.5	82
23	Segmental Phylogenetic Relationships of Inbred Mouse Strains Revealed by Fine-Scale Analysis of Sequence Variation Across 4.6 Mb of Mouse Genome. Genome Research, 2004, 14, 1493-1500.	5.5	78
24	A deletion in nephronophthisis 4 (NPHP4) is associated with recessive cone-rod dystrophy in standard wire-haired dachshund. Genome Research, 2008, 18, 1415-1421.	5.5	75
25	Regulatory mutations in TBX3 disrupt asymmetric hair pigmentation that underlies Dun camouflage color in horses. Nature Genetics, 2016, 48, 152-158.	21.4	59
26	Variants in the host genome may inhibit tumour growth in devil facial tumours: evidence from genome-wide association. Scientific Reports, 2017, 7, 423.	3.3	56
27	Identification of Novel Genes That Mediate Innate Immunity Using Inbred Mice. Genetics, 2009, 183, 1535-1544.	2.9	55
28	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.	2.7	49
29	A LINE-1 Insertion in DLX6 Is Responsible for Cleft Palate and Mandibular Abnormalities in a Canine Model of Pierre Robin Sequence. PLoS Genetics, 2014, 10, e1004257.	3.5	49
30	A genealogical survey of Australian registered dog breeds. Veterinary Journal, 2011, 189, 203-210.	1.7	41
31	Copy number expansion of the STX17 duplication in melanoma tissue from Grey horses. BMC Genomics, 2012, 13, 365.	2.8	34
32	Accumulating Mutations in Series of Haplotypes at the KIT and MITF Loci Are Major Determinants of White Markings in Franches-Montagnes Horses. PLoS ONE, 2013, 8, e75071.	2.5	34
33	Inbreeding and genetic diversity in dogs: Results from DNA analysis. Veterinary Journal, 2011, 189, 183-188.	1.7	32
34	A dominant TRPV4 variant underlies osteochondrodysplasia in Scottish fold cats. Osteoarthritis and Cartilage, 2016, 24, 1441-1450.	1.3	32
35	Evaluation of the Serotonergic Genes htr1A, htr1B, htr2A, and slc6A4 in Aggressive Behavior of Golden Retriever Dogs. Behavior Genetics, 2008, 38, 55-66.	2.1	31
36	Environmental Factors Associated with Success Rates of Australian Stock Herding Dogs. PLoS ONE, 2014, 9, e104457.	2.5	30

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37	Heritability and Phenotypic Variation of Canine Hip Dysplasia Radiographic Traits in a Cohort of Australian German Shepherd Dogs. PLoS ONE, 2012, 7, e39620.	2.5	29
38	Inheritance, Mode of Inheritance, and Candidate Genes for Primary Hyperparathyroidism in Keeshonden. Journal of Veterinary Internal Medicine, 2007, 21, 199-203.	1.6	27
39	Holding back the genes: limitations of research into canine behavioural genetics. Canine Genetics and Epidemiology, 2014, 1, 7.	2.8	27
40	Canine Disorder Mirrors Human Disease: Exonic Deletion in HES7 Causes Autosomal Recessive Spondylocostal Dysostosis in Miniature Schnauzer Dogs. PLoS ONE, 2015, 10, e0117055.	2.5	27
41	Progressive retinal atrophy in <scp>S</scp>hetland sheepdog is associated with a mutation in the <scp>CNGA</scp>1 gene. Animal Genetics, 2015, 46, 515-521.	1.7	22
42	A web resource on DNA tests for canine and feline hereditary diseases. Veterinary Journal, 2013, 197, 182-187.	1.7	21
43	Strong selection for behavioural resilience in Australian stock working dogs identified by selective sweep analysis. Canine Genetics and Epidemiology, 2015, 2, 6.	2.8	18
44	Using an owner-based questionnaire to phenotype dogs with separation-related distress: Do owners know what their dogs do when they are absent?. Journal of Veterinary Behavior: Clinical Applications and Research, 2018, 23, 58-65.	1.2	18
45	Estimated Breeding Values for Canine Hip Dysplasia Radiographic Traits in a Cohort of Australian German Shepherd Dogs. PLoS ONE, 2013, 8, e77470.	2.5	17
46	Manual muster: A critical analysis of the use of common terms in Australian working dog manuals. Journal of Veterinary Behavior: Clinical Applications and Research, 2014, 9, 370-374.	1.2	15
47	Canine coat pigmentation genetics: a review. Animal Genetics, 2022, 53, 3-34.	1.7	15
48	Risk factors of separation-related behaviours in Australian retrievers. Applied Animal Behaviour Science, 2018, 209, 71-77.	1.9	13
49	The Burmese cat as a genetic model of type 2 diabetes in humans. Animal Genetics, 2019, 50, 319-325.	1.7	13
50	Association analysis of candidate SNPs in TRPM1 with leopard complex spotting (LPâ€Š) and congenital stationary night blindness (CSNB) in horses. Animal Genetics, 2010, 41, 207-207.	1.7	12
51	Mapping the genetic basis of diabetes mellitus in the Australian Burmese cat (Felis catus). Scientific Reports, 2020, 10, 19194.	3.3	12
52	Genomic Characterization of External Morphology Traits in Kelpies Does Not Support Common Ancestry with the Australian Dingo. Genes, 2019, 10, 337.	2.4	11
53	A Coding Variant in the Gene Bardet-Biedl Syndrome 4 (BBS4) Is Associated with a Novel Form of Canine Progressive Retinal Atrophy. G3: Genes, Genomes, Genetics, 2017, 7, 2327-2335.	1.8	11
54	Symmetry of hip dysplasia traits in the German Shepherd Dog in Australia. Journal of Animal Breeding and Genetics, 2011, 128, 230-243.	2.0	10

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55	Empowering international canine inherited disorder management. Mammalian Genome, 2012, 23, 195-202.	2.2	10
56	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. Genes, 2020, 11, 251.	2.4	9
57	Genetics of canine myxomatous mitral valve disease. Animal Genetics, 2021, 52, 409-421.	1.7	9
58	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. PLoS ONE, 2013, 8, e78929.	2.5	7
59	Canine genetics: A very Special Issue. Veterinary Journal, 2011, 189, 123-125.	1.7	6
60	Interval dogs: Results and evaluation of Global Positioning System units in measuring athletic performance in stock-herding dogs. Journal of Veterinary Behavior: Clinical Applications and Research, 2016, 14, 1-4.	1.2	5
61	Digging for known genetic mutations underlying inherited bone and cartilage characteristics and disorders in the dog and cat. Veterinary and Comparative Orthopaedics and Traumatology, 2016, 29, 269-276.	0.5	5
62	Relationship between transitional lumbosacral vertebrae and eight lumbar vertebrae in a breeding colony of Labrador Retrievers and Labrador Crosses. Australian Veterinary Journal, 2017, 95, 33-36.	1.1	5
63	A rapid multiplex PCR assay for presumptive species identification of rhinoceros horns and its implementation in Vietnam. PLoS ONE, 2018, 13, e0198565.	2.5	5
64	Association between coat colour and the behaviour of Australian Labrador retrievers. Canine Genetics and Epidemiology, 2019, 6, 10.	2.8	5
65	Forensic DNA phenotyping: Canis familiaris breed classification and skeletal phenotype prediction using functionally significant skeletal SNPs and indels. Animal Genetics, 2022, 53, 247-263.	1.7	5
66	Inheritance of chronic superficial keratitis in Australian Greyhounds. Animal Genetics, 2016, 47, 629-629.	1.7	4
67	Work-type influences perceived livestock herding success in Australian Working Kelpies. Canine Genetics and Epidemiology, 2018, 5, 5.	2.8	4
68	A large deletion on CFA28 omitting ACSL5 gene is associated with intestinal lipid malabsorption in the Australian Kelpie dog breed. Scientific Reports, 2020, 10, 18223.	3.3	4
69	Roan, ticked and clear coat patterns in the canine are associated with three haplotypes near usherin on CFA38. Animal Genetics, 2021, 52, 198-207.	1.7	4
70	From the Phenotype to the Genotype via Bioinformatics. Methods in Molecular Biology, 2014, 1168, 1-16.	0.9	4
71	Exclusion of known gene loci for cerebellar abiotrophy in the Australian Working Kelpie. Animal Genetics, 2017, 48, 730-732.	1.7	3
72	Sequential Analysis of Livestock Herding Dog and Sheep Interactions. Animals, 2020, 10, 352.	2.3	3

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73	Inbreeding levels in an open-registry pedigreed dog breed: The Australian working kelpie. Veterinary Journal, 2021, 269, 105609.	1.7	3
74	Exploiting genomic synteny in Felidae: cross-species genome alignments and SNV discovery can aid conservation management. BMC Genomics, 2021, 22, 601.	2.8	3
75	Inheritance, Mode of Inheritance, and Candidate Genes for Primary Hyperparathyroidism in Keeshonden. Journal of Veterinary Internal Medicine, 2007, 21, 199.	1.6	3
76	Exclusion of known progressive retinal atrophy genes for blindness in the Hungarian Puli. Animal Genetics, 2017, 48, 500-501.	1.7	2
77	The Perceived Value of Behavioural Traits in Australian Livestock Herding Dogs Varies with the Operational Context. Animals, 2019, 9, 448.	2.3	2
78	Behavioral Genetics of Dog Breeds. , 2019, , 312-322.		2
79	Sequence variants of the canine melanocyte inducing transcription factor (MITF) locus reveal a common MITFâ€A processed pseudogene. Animal Genetics, 2021, 52, 777-778.	1.7	2
80	Analysis of the canine genome and canine health: Bridging a gap. Veterinary Journal, 2013, 196, 1-3.	1.7	1
81	Simple, rapid and accurate genotyping-by-sequencing from aligned whole genomes with ArrayMaker. Bioinformatics, 2015, 31, 599-601.	4.1	1
82	Empirical assessment of competitive hybridization and noise in ultra high density canine tiling arrays. BMC Bioinformatics, 2013, 14, 231.	2.6	0
83	Umbilical tissue as a sampling technique for DNA testing in neonate dogs. Animal Genetics, 2018, 49, 499-500.	1.7	0
84	Valued personality traits in livestock herding Kelpiesâ€"Development and application of a livestock herding dog assessment form. PLoS ONE, 2022, 17, e0267266.	2.5	0