

Jennifer R Meadows

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

2,652
citations

361296

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345118

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all docs

42
docs citations

42
times ranked

4325
citing authors

#	ARTICLE	IF	CITATIONS
1	Contribution of Rare Genetic Variation to Disease Susceptibility in a Large Scandinavian Myositis Cohort. <i>Arthritis and Rheumatology</i> , 2022, 74, 342-352.	2.9	7
2	Identification and functional characterization of a novel susceptibility locus for small vessel vasculitis with MPO-ANCA. <i>Rheumatology</i> , 2022, 61, 3461-3470.	0.9	8
3	Interpretable machine learning identifies paediatric Systemic Lupus Erythematosus subtypes based on gene expression data. <i>Scientific Reports</i> , 2022, 12, 7433.	1.6	7
4	A novel canine reference genome resolves genomic architecture and uncovers transcript complexity. <i>Communications Biology</i> , 2021, 4, 185.	2.0	59
5	Association of Protective HLA-A With HLA-B*27 Positive Ankylosing Spondylitis. <i>Frontiers in Genetics</i> , 2021, 12, 659042.	1.1	2
6	The ABCC4 gene is associated with pyometra in golden retriever dogs. <i>Scientific Reports</i> , 2021, 11, 16647.	1.6	5
7	OUP accepted manuscript. <i>Rheumatology</i> , 2021, 60, 837-848.	0.9	15
8	SweHLA: the high confidence HLA typing bio-resource drawn from 1000 Swedish genomes. <i>European Journal of Human Genetics</i> , 2020, 28, 627-635.	1.4	11
9	Targeted sequencing reveals the somatic mutation landscape in a Swedish breast cancer cohort. <i>Scientific Reports</i> , 2020, 10, 19304.	1.6	10
10	Common genetic variation in the autoimmune regulator (AIRE) locus is associated with autoimmune Addison's disease in Sweden. <i>Scientific Reports</i> , 2018, 8, 8395.	1.6	22
11	A potential regulatory region near the EDN3 gene may control both harness racing performance and coat color variation in horses. <i>Physiological Reports</i> , 2018, 6, e13700.	0.7	13
12	SETD2 Is Recurrently Mutated in Whole-Exome Sequenced Canine Osteosarcoma. <i>Cancer Research</i> , 2018, 78, 3421-3431.	0.4	76
13	Dissecting evolution and disease using comparative vertebrate genomics. <i>Nature Reviews Genetics</i> , 2017, 18, 624-636.	7.7	46
14	Absolute quantification reveals the stable transmission of a high copy number variant linked to autoinflammatory disease. <i>BMC Genomics</i> , 2016, 17, 299.	1.2	6
15	cgmisc: enhanced genome-wide association analyses and visualization. <i>Bioinformatics</i> , 2015, 31, 3830-3831.	1.8	14
16	A Simple Repeat Polymorphism in the MITF-M Promoter Is a Key Regulator of White Spotting in Dogs. <i>PLoS ONE</i> , 2014, 9, e104363.	1.1	50
17	A universal genomic coordinate translator for comparative genomics. <i>BMC Bioinformatics</i> , 2014, 15, 227.	1.2	7
18	An Improved Canine Genome and a Comprehensive Catalogue of Coding Genes and Non-Coding Transcripts. <i>PLoS ONE</i> , 2014, 9, e91172.	1.1	206

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19	Sheep: Domestication. , 2014, , 6597-6600.		1
20	Unsupervised genome-wide recognition of local relationship patterns. BMC Genomics, 2013, 14, 347.	1.2	59
21	Thorough Investigation of a Canine Autoinflammatory Disease (AID) Confirms One Main Risk Locus and Suggests a Modifier Locus for Amyloidosis. PLoS ONE, 2013, 8, e75242.	1.1	12
22	The same ELA class II risk factors confer equine insect bite hypersensitivity in two distinct populations. Immunogenetics, 2012, 64, 201-208.	1.2	40
23	A Novel Unstable Duplication Upstream of HAS2 Predisposes to a Breed-Defining Skin Phenotype and a Periodic Fever Syndrome in Chinese Shar-Pei Dogs. PLoS Genetics, 2011, 7, e1001332.	1.5	118
24	Whole-genome resequencing reveals loci under selection during chicken domestication. Nature, 2010, 464, 587-591.	13.7	985
25	Copy Number Variation in Intron 1 of SOX5 Causes the Pea-comb Phenotype in Chickens. PLoS Genetics, 2009, 5, e1000512.	1.5	219
26	Re-sequencing regions of the ovine Y chromosome in domestic and wild sheep reveals novel paternal haplotypes. Animal Genetics, 2009, 40, 119-123.	0.6	33
27	Bovine Muc1 is a highly polymorphic gene encoding an extensively glycosylated mucin that binds bacteria. Journal of Dairy Science, 2009, 92, 5276-5291.	1.4	58
28	Linkage disequilibrium compared between five populations of domestic sheep. BMC Genetics, 2008, 9, 61.	2.7	65
29	Five Ovine Mitochondrial Lineages Identified From Sheep Breeds of the Near East. Genetics, 2007, 175, 1371-1379.	1.2	155
30	Development of two microsatellite multiplex systems for black tiger shrimp <i>Penaeus monodon</i> and its application in genetic diversity study for two populations. Aquaculture, 2007, 266, 279-288.	1.7	45
31	Mitochondrial haplotypes reveal a strong genetic structure for three Indian sheep breeds. Animal Genetics, 2007, 38, 460-466.	0.6	22
32	Technical Note: Whole-Genome Amplification of DNA Extracted from Cattle Semen Samples. Journal of Dairy Science, 2006, 89, 2217-2221.	1.4	10
33	Application of DNA parentage analyses for determining relative growth rates of <i>Penaeus japonicus</i> families reared in commercial ponds. Aquaculture, 2006, 254, 171-181.	1.7	26
34	Globally dispersed Y chromosomal haplotypes in wild and domestic sheep. Animal Genetics, 2006, 37, 444-453.	0.6	72
35	Population genetic structure of the brown tiger prawn, <i>Penaeus esculentus</i> , in tropical northern Australia. Marine Biology, 2006, 148, 599-607.	0.7	13
36	Mitochondrial Sequence Reveals High Levels of Gene Flow Between Breeds of Domestic Sheep from Asia and Europe. Journal of Heredity, 2005, 96, 494-501.	1.0	91

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37	Parentage determination of Kuruma shrimp <i>Penaeus</i> (<i>Marsupenaeus</i>) <i>japonicus</i> using microsatellite markers (Bate). <i>Aquaculture</i> , 2004, 235, 237-247.	1.7	60