

James Kijas

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

7,417
citations

53751

45
h-index

60583

81
g-index

101
all docs

101
docs citations

101
times ranked

6524
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Analysis of the World's Sheep Breeds Reveals High Levels of Historic Mixture and Strong Recent Selection. <i>PLoS Biology</i> , 2012, 10, e1001258.	2.6	719
2	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	9.4	479
3	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	6.0	436
4	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	3.8	331
5	A Genome Wide Survey of SNP Variation Reveals the Genetic Structure of Sheep Breeds. <i>PLoS ONE</i> , 2009, 4, e4668.	1.1	269
6	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	5.8	220
7	Genome-wide association mapping identifies the genetic basis of discrete and quantitative variation in sexual weaponry in a wild sheep population. <i>Molecular Ecology</i> , 2011, 20, 2555-2566.	2.0	217
8	Molecular Basis for the Dominant White Phenotype in the Domestic Pig. <i>Genome Research</i> , 1998, 8, 826-833.	2.4	195
9	The sheep genome reference sequence: a work in progress. <i>Animal Genetics</i> , 2010, 41, 449-453.	0.6	173
10	Five Ovine Mitochondrial Lineages Identified From Sheep Breeds of the Near East. <i>Genetics</i> , 2007, 175, 1371-1379.	1.2	155
11	Naturally occurring rhodopsin mutation in the dog causes retinal dysfunction and degeneration mimicking human dominant retinitis pigmentosa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6328-6333.	3.3	150
12	Adaptations to Climate-Mediated Selective Pressures in Sheep. <i>Molecular Biology and Evolution</i> , 2014, 31, 3324-3343.	3.5	149
13	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits. <i>Nature Communications</i> , 2020, 11, 2815.	5.8	142
14	Genetic diversity and signatures of selection in various goat breeds revealed by genome-wide SNP markers. <i>BMC Genomics</i> , 2017, 18, 229.	1.2	141
15	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. <i>Nature Communications</i> , 2018, 9, 859.	5.8	126
16	Linkage disequilibrium over short physical distances measured in sheep using a high-density SNP chip. <i>Animal Genetics</i> , 2014, 45, 754-757.	0.6	113
17	The extent of linkage disequilibrium in beef cattle breeds using high-density SNP genotypes. <i>Genetics Selection Evolution</i> , 2014, 46, 22.	1.2	113
18	Haplogroup relationships between domestic and wild sheep resolved using a mitogenome panel. <i>Heredity</i> , 2011, 106, 700-706.	1.2	112

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19	Genome-wide analysis reveals adaptation to high altitudes in Tibetan sheep. <i>Scientific Reports</i> , 2016, 6, 26770.	1.6	110
20	Selection signature analysis reveals genes associated with tail type in Chinese indigenous sheep. <i>Animal Genetics</i> , 2017, 48, 55-66.	0.6	108
21	Reference genome of wild goat (<i>capra aegagrus</i>) and sequencing of goat breeds provide insight into genic basis of goat domestication. <i>BMC Genomics</i> , 2015, 16, 431.	1.2	103
22	Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. <i>BMC Genomics</i> , 2017, 18, 484.	1.2	99
23	Accuracy of genotype imputation in sheep breeds. <i>Animal Genetics</i> , 2012, 43, 72-80.	0.6	98
24	Merino and Merino-derived sheep breeds: a genome-wide intercontinental study. <i>Genetics Selection Evolution</i> , 2015, 47, 64.	1.2	97
25	Genomic signatures of adaptive introgression from European mouflon into domestic sheep. <i>Scientific Reports</i> , 2017, 7, 7623.	1.6	92
26	Mitochondrial Sequence Reveals High Levels of Gene Flow Between Breeds of Domestic Sheep from Asia and Europe. <i>Journal of Heredity</i> , 2005, 96, 494-501.	1.0	91
27	Characterization of linkage disequilibrium, consistency of gametic phase and admixture in Australian and Canadian goats. <i>BMC Genomics</i> , 2015, 16, 67.	2.7	91
28	Evidence for multiple alleles effecting muscling and fatness at the Ovine GDF8 locus. <i>BMC Genomics</i> , 2007, 8, 80.	2.7	88
29	SNPs for Parentage Testing and Traceability in Globally Diverse Breeds of Sheep. <i>PLoS ONE</i> , 2014, 9, e94851.	1.1	88
30	Characterization of Ovine Nectin-4, a Novel Peste des Petits Ruminants Virus Receptor. <i>Journal of Virology</i> , 2013, 87, 4756-4761.	1.5	82
31	A genome-wide set of SNPs detects population substructure and long range linkage disequilibrium in wild sheep. <i>Molecular Ecology Resources</i> , 2011, 11, 314-322.	2.2	80
32	Whole-genome resequencing uncovers molecular signatures of natural and sexual selection in wild bighorn sheep. <i>Molecular Ecology</i> , 2015, 24, 5616-5632.	2.0	73
33	Globally dispersed Y chromosomal haplotypes in wild and domestic sheep. <i>Animal Genetics</i> , 2006, 37, 444-453.	0.6	72
34	Population structure and history of the Welsh sheep breeds determined by whole genome genotyping. <i>BMC Genomics</i> , 2015, 16, 65.	2.7	69
35	Linkage disequilibrium mapping in domestic dog breeds narrows the progressive rodent cone degeneration interval and identifies ancestral disease-transmitting chromosome. <i>Genomics</i> , 2006, 88, 541-550.	1.3	67
36	Diversity and linkage disequilibrium in farmed Tasmanian Atlantic salmon. <i>Animal Genetics</i> , 2017, 48, 237-241.	0.6	66

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37	Linkage disequilibrium compared between five populations of domestic sheep. BMC Genetics, 2008, 9, 61.	2.7	65
38	Genome-wide search for signatures of selection in three major Brazilian locally adapted sheep breeds. Livestock Science, 2017, 197, 36-45.	0.6	57
39	Consistent divergence times and allele sharing measured from cross-species application of SNP chips developed for three domestic species. Molecular Ecology Resources, 2012, 12, 1145-1150.	2.2	56
40	Haplotype-based analysis of selective sweeps in sheep. Genome, 2014, 57, 433-437.	0.9	56
41	Introgression and the fate of domesticated genes in a wild mammal population. Molecular Ecology, 2013, 22, 4210-4221.	2.0	53
42	Diversity of copy number variation in a worldwide population of sheep. Genomics, 2018, 110, 143-148.	1.3	53
43	Cloning, Mapping, and Retinal Expression of the Canine Ciliary Neurotrophic Factor Receptor \pm (CNTFR \pm). , 2003, 44, 3642.		52
44	Microphthalmia in Texel Sheep Is Associated with a Missense Mutation in the Paired-Like Homeodomain 3 (PITX3) Gene. PLoS ONE, 2010, 5, e8689.	1.1	52
45	Using Regulatory and Epistatic Networks to Extend the Findings of a Genome Scan: Identifying the Gene Drivers of Pigmentation in Merino Sheep. PLoS ONE, 2011, 6, e21158.	1.1	52
46	Genetic diversity and investigation of polledness in divergent goat populations using 52,088 SNPs. Animal Genetics, 2013, 44, 325-335.	0.6	51
47	Evolution of Sex Determination Loci in Atlantic Salmon. Scientific Reports, 2018, 8, 5664.	1.6	51
48	Nucleotide diversity on the ovine Y chromosome. Animal Genetics, 2004, 35, 379-385.	0.6	50
49	The Effect of Genetic Variation of the Retinoic Acid Receptor-Related Orphan Receptor C Gene on Fatness in Cattle. Genetics, 2007, 175, 843-853.	1.2	49
50	Application of Selection Mapping to Identify Genomic Regions Associated with Dairy Production in Sheep. PLoS ONE, 2014, 9, e94623.	1.1	45
51	Historical Introgression from Wild Relatives Enhanced Climatic Adaptation and Resistance to Pneumonia in Sheep. Molecular Biology and Evolution, 2021, 38, 838-855.	3.5	44
52	Comparison of horse Chromosome 3 with donkey and human chromosomes by cross-species painting and heterologous FISH mapping. Mammalian Genome, 1999, 10, 277-282.	1.0	36
53	Genomic analysis identified a potential novel molecular mechanism for high-altitude adaptation in sheep at the Himalayas. Scientific Reports, 2016, 6, 29963.	1.6	36
54	Genetic Diversity Present Within the Near-Complete mtDNA Genome of 17 Breeds of Indigenous Chinese Pigs. , 2003, 94, 381-385.		35

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55	Sequence diversity and rates of molecular evolution between sheep and cattle genes. <i>Animal Genetics</i> , 2006, 37, 171-174.	0.6	35
56	Analysis of copy number variants in the cattle genome. <i>Gene</i> , 2011, 482, 73-77.	1.0	34
57	Canine Models of Ocular Disease: Outcross Breedings Define a Dominant Disorder Present in the English Mastiff and Bull Mastiff Dog Breeds. , 2003, 94, 27-30.		33
58	Re-sequencing regions of the ovine Y chromosome in domestic and wild sheep reveals novel paternal haplotypes. <i>Animal Genetics</i> , 2009, 40, 119-123.	0.6	33
59	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. <i>Molecular Ecology Resources</i> , 2019, 19, 1497-1515.	2.2	31
60	Genetic Testing for TMEM154 Mutations Associated with Lentivirus Susceptibility in Sheep. <i>PLoS ONE</i> , 2013, 8, e55490.	1.1	28
61	Copy number variants in the sheep genome detected using multiple approaches. <i>BMC Genomics</i> , 2016, 17, 441.	1.2	27
62	Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. <i>GigaScience</i> , 2018, 7, 1-17.	3.3	27
63	Genomewide association for a dominant pigmentation gene in sheep. <i>Journal of Animal Breeding and Genetics</i> , 2013, 130, 468-475.	0.8	26
64	Genomewide association reveals the locus responsible for four-horned ruminant. <i>Animal Genetics</i> , 2016, 47, 258-262.	0.6	25
65	Polygenic and sex specific architecture for two maturation traits in farmed Atlantic salmon. <i>BMC Genomics</i> , 2019, 20, 139.	1.2	25
66	Cloning of the canine ABCA4 gene and evaluation in canine cone-rod dystrophies and progressive retinal atrophies. <i>Molecular Vision</i> , 2004, 10, 223-32.	1.1	25
67	Mitochondrial haplotypes reveal a strong genetic structure for three Indian sheep breeds. <i>Animal Genetics</i> , 2007, 38, 460-466.	0.6	22
68	Estimating the genetic merit of sires by using pooled DNA from progeny of undetermined pedigree. <i>Genetics Selection Evolution</i> , 2017, 49, 28.	1.2	19
69	A Frameshift Mutation within LAMC2 Is Responsible for Herlitz Type Junctional Epidermolysis Bullosa (HJEB) in Black Headed Mutton Sheep. <i>PLoS ONE</i> , 2011, 6, e18943.	1.1	19
70	Genetic architecture of gene expression in ovine skeletal muscle. <i>BMC Genomics</i> , 2011, 12, 607.	1.2	18
71	Selection signatures in tropical cattle are enriched for promoter and coding regions and reveal missense mutations in the damage response gene HELB. <i>Genetics Selection Evolution</i> , 2020, 52, 27.	1.2	17
72	Radiation hybrid map, physical map, and low-pass genomic sequence of the canine prcd region on CFA9 and comparative mapping with the syntenic region on human chromosome 17. Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under Accession Nos. AY178785, AY178786, AY178787, AY178788, AY178789, AY178790, AY178791, and AY178792.. <i>Genomics</i> , 2003, 81, 138-148.	1.3	16

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73	VarGoats project: a dataset of 1159 whole-genome sequences to dissect <i>Capra hircus</i> global diversity. <i>Genetics Selection Evolution</i> , 2021, 53, 86.	1.2	16
74	Molecular Cytogenetics and Gene Mapping in Sheep (<i>Ovis aries</i> , 2n = 54). <i>Cytogenetic and Genome Research</i> , 2009, 126, 63-76.	0.6	15
75	Information compression exploits patterns of genome composition to discriminate populations and highlight regions of evolutionary interest. <i>BMC Bioinformatics</i> , 2014, 15, 66.	1.2	15
76	Changed Patterns of Genomic Variation Following Recent Domestication: Selection Sweeps in Farmed Atlantic Salmon. <i>Frontiers in Genetics</i> , 2020, 11, 264.	1.1	15
77	Analysis of Polycerate Mutants Reveals the Evolutionary Co-option of <i>HOXD1</i> for Horn Patterning in Bovidae. <i>Molecular Biology and Evolution</i> , 2021, 38, 2260-2272.	3.5	15
78	Detecting Regions of Homozygosity to Map the Cause of Recessively Inherited Disease. <i>Methods in Molecular Biology</i> , 2013, 1019, 331-345.	0.4	14
79	Genome Sequencing of Blacklip and Greenlip Abalone for Development and Validation of a SNP Based Genotyping Tool. <i>Frontiers in Genetics</i> , 2018, 9, 687.	1.1	14
80	Evaluation of 16 loci to examine the cross-species utility of single nucleotide polymorphism arrays. <i>Animal Genetics</i> , 2010, 41, 199-202.	0.6	12
81	Brachygnathia, cardiomegaly and renal hypoplasia syndrome (<i>BCRHS</i>) in <i>Merin</i> sheep maps to a 1.1 megabase region on ovine chromosome <i>OAR</i> 2. <i>Animal Genetics</i> , 2013, 44, 231-233.	0.6	12
82	Technical note: High fidelity of whole-genome amplified sheep (<i>Ovis aries</i>) deoxyribonucleic acid using a high-density single nucleotide polymorphism array-based genotyping platform1. <i>Journal of Animal Science</i> , 2010, 88, 3183-3186.	0.2	11
83	Multi-Tissue Transcriptome Profiling of North American Derived Atlantic Salmon. <i>Frontiers in Genetics</i> , 2018, 9, 369.	1.1	11
84	Cloning and characterization of the canine photoreceptor specific cone-rod homeobox (<i>CRX</i>) gene and evaluation as a candidate for early onset photoreceptor diseases in the dog. <i>Molecular Vision</i> , 2002, 8, 79-84.	1.1	11
85	East Friesian sheep carry a <i>Myostatin</i> allele known to cause muscle hypertrophy in other breeds. <i>Animal Genetics</i> , 2010, 41, 445-446.	0.6	10
86	Tracking the Emergence of a New Breed Using 49,034 SNP in Sheep. <i>PLoS ONE</i> , 2012, 7, e41508.	1.1	9
87	Understanding parasitic infection in sheep to design more efficient animal selection strategies. <i>Veterinary Journal</i> , 2013, 197, 143-152.	0.6	9
88	SNP discovery in nonmodel organisms: strand bias and base substitution errors reduce conversion rates. <i>Molecular Ecology Resources</i> , 2015, 15, 723-736.	2.2	9
89	Assessment of genetic diversity and population structure in cultured Australian Pacific oysters. <i>Animal Genetics</i> , 2019, 50, 686-694.	0.6	9
90	Genomic data suggest environmental drivers of fish population structure in the deep sea: A case study for the orange roughy (<i>Hoplostethus atlanticus</i>). <i>Journal of Applied Ecology</i> , 2020, 57, 296-306.	1.9	9

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91	Compression distance can discriminate animals by genetic profile, build relationship matrices and estimate breeding values. <i>Genetics Selection Evolution</i> , 2015, 47, 78.	1.2	7
92	The "heritability" of domestication and its functional partitioning in the pig. <i>Heredity</i> , 2017, 118, 160-168.	1.2	7
93	Beta-globin gene evolution in the ruminants: evidence for an ancient origin of sheep haplotype <i>B</i> . <i>Animal Genetics</i> , 2015, 46, 506-514.	0.6	5
94	Geographical contrasts of Y-chromosomal haplogroups from wild and domestic goats reveal ancient migrations and recent introgressions. <i>Molecular Ecology</i> , 2022, 31, 4364-4380.	2.0	5
95	Ovine congenital progressive muscular dystrophy (OCPMD) is a model of TNNT1 congenital myopathy. <i>Acta Neuropathologica Communications</i> , 2020, 8, 142.	2.4	4
96	Leveraging transcriptome and epigenome landscapes to infer regulatory networks during the onset of sexual maturation. <i>BMC Genomics</i> , 2022, 23, .	1.2	3
97	Mapping the sheep genome. <i>Burleigh Dodds Series in Agricultural Science</i> , 2017, , 115-132.	0.1	0