

# James Kijas

## List of Publications by Year in descending order

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Version: 2024-02-01

97  
papers

7,417  
citations

53794

45  
h-index

60623

81  
g-index

101  
all docs

101  
docs citations

101  
times ranked

6524  
citing authors

#	ARTICLE	IF	CITATIONS
1	Leveraging transcriptome and epigenome landscapes to infer regulatory networks during the onset of sexual maturation. <i>BMC Genomics</i> , 2022, 23, .	2.8	3
2	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.	3.9	5
3	Historical Introgression from Wild Relatives Enhanced Climatic Adaptation and Resistance to Pneumonia in Sheep. <i>Molecular Biology and Evolution</i> , 2021, 38, 838-855.	8.9	44
4	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.	8.9	15
5	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.	3.0	16
6	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.	4.0	9
7	Ovine congenital progressive muscular dystrophy (OCPMD) is a model of <i>TNNT1</i> congenital myopathy. <i>Acta Neuropathologica Communications</i> , 2020, 8, 142.	5.2	4
8	Selection signatures in tropical cattle are enriched for promoter and coding regions and reveal missense mutations in the damage response gene <i>HELB</i> . <i>Genetics Selection Evolution</i> , 2020, 52, 27.	3.0	17
9	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits. <i>Nature Communications</i> , 2020, 11, 2815.	12.8	142
10	Changed Patterns of Genomic Variation Following Recent Domestication: Selection Sweeps in Farmed Atlantic Salmon. <i>Frontiers in Genetics</i> , 2020, 11, 264.	2.3	15
11	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. <i>Molecular Ecology Resources</i> , 2019, 19, 1497-1515.	4.8	31
12	Assessment of genetic diversity and population structure in cultured Australian Pacific oysters. <i>Animal Genetics</i> , 2019, 50, 686-694.	1.7	9
13	Polygenic and sex specific architecture for two maturation traits in farmed Atlantic salmon. <i>BMC Genomics</i> , 2019, 20, 139.	2.8	25
14	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	12.8	220
15	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. <i>Nature Communications</i> , 2018, 9, 859.	12.8	126
16	Evolution of Sex Determination Loci in Atlantic Salmon. <i>Scientific Reports</i> , 2018, 8, 5664.	3.3	51
17	Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. <i>GigaScience</i> , 2018, 7, 1-17.	6.4	27
18	Diversity of copy number variation in a worldwide population of sheep. <i>Genomics</i> , 2018, 110, 143-148.	2.9	53

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19	Multi-Tissue Transcriptome Profiling of North American Derived Atlantic Salmon. <i>Frontiers in Genetics</i> , 2018, 9, 369.	2.3	11
20	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.	2.3	14
21	Genome-wide search for signatures of selection in three major Brazilian locally adapted sheep breeds. <i>Livestock Science</i> , 2017, 197, 36-45.	1.6	57
22	Genetic diversity and signatures of selection in various goat breeds revealed by genome-wide SNP markers. <i>BMC Genomics</i> , 2017, 18, 229.	2.8	141
23	Genomic signatures of adaptive introgression from European mouflon into domestic sheep. <i>Scientific Reports</i> , 2017, 7, 7623.	3.3	92
24	Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. <i>BMC Genomics</i> , 2017, 18, 484.	2.8	99
25	Estimating the genetic merit of sires by using pooled DNA from progeny of undetermined pedigree. <i>Genetics Selection Evolution</i> , 2017, 49, 28.	3.0	19
26	Diversity and linkage disequilibrium in farmed Tasmanian Atlantic salmon. <i>Animal Genetics</i> , 2017, 48, 237-241.	1.7	66
27	Selection signature analysis reveals genes associated with tail type in Chinese indigenous sheep. <i>Animal Genetics</i> , 2017, 48, 55-66.	1.7	108
28	The "heritability" of domestication and its functional partitioning in the pig. <i>Heredity</i> , 2017, 118, 160-168.	2.6	7
29	Mapping the sheep genome. <i>Burleigh Dodds Series in Agricultural Science</i> , 2017, , 115-132.	0.2	0
30	Copy number variants in the sheep genome detected using multiple approaches. <i>BMC Genomics</i> , 2016, 17, 441.	2.8	27
31	Genomic analysis identified a potential novel molecular mechanism for high-altitude adaptation in sheep at the Himalayas. <i>Scientific Reports</i> , 2016, 6, 29963.	3.3	36
32	Genome-wide association reveals the locus responsible for four-horned ruminant. <i>Animal Genetics</i> , 2016, 47, 258-262.	1.7	25
33	Genome-wide analysis reveals adaptation to high altitudes in Tibetan sheep. <i>Scientific Reports</i> , 2016, 6, 26770.	3.3	110
34	Merino and Merino-derived sheep breeds: a genome-wide intercontinental study. <i>Genetics Selection Evolution</i> , 2015, 47, 64.	3.0	97
35	Compression distance can discriminate animals by genetic profile, build relationship matrices and estimate breeding values. <i>Genetics Selection Evolution</i> , 2015, 47, 78.	3.0	7
36	Whole-genome resequencing uncovers molecular signatures of natural and sexual selection in wild bighorn sheep. <i>Molecular Ecology</i> , 2015, 24, 5616-5632.	3.9	73

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37	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	8.8	331
38	Characterization of linkage disequilibrium, consistency of gametic phase and admixture in Australian and Canadian goats. <i>BMC Genetics</i> , 2015, 16, 67.	2.7	91
39	Beta-globin gene evolution in the ruminants: evidence for an ancient origin of sheep haplotype <i>Animal Genetics</i> , 2015, 46, 506-514.	1.7	5
40	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.	2.8	103
41	Population structure and history of the Welsh sheep breeds determined by whole genome genotyping. <i>BMC Genetics</i> , 2015, 16, 65.	2.7	69
42	SNP discovery in nonmodel organisms: strand bias and base substitution errors reduce conversion rates. <i>Molecular Ecology Resources</i> , 2015, 15, 723-736.	4.8	9
43	Haplotype-based analysis of selective sweeps in sheep. <i>Genome</i> , 2014, 57, 433-437.	2.0	56
44	Linkage disequilibrium over short physical distances measured in sheep using a high-density SNP chip. <i>Animal Genetics</i> , 2014, 45, 754-757.	1.7	113
45	Adaptations to Climate-Mediated Selective Pressures in Sheep. <i>Molecular Biology and Evolution</i> , 2014, 31, 3324-3343.	8.9	149
46	The extent of linkage disequilibrium in beef cattle breeds using high-density SNP genotypes. <i>Genetics Selection Evolution</i> , 2014, 46, 22.	3.0	113
47	Information compression exploits patterns of genome composition to discriminate populations and highlight regions of evolutionary interest. <i>BMC Bioinformatics</i> , 2014, 15, 66.	2.6	15
48	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	12.6	436
49	Application of Selection Mapping to Identify Genomic Regions Associated with Dairy Production in Sheep. <i>PLoS ONE</i> , 2014, 9, e94623.	2.5	45
50	SNPs for Parentage Testing and Traceability in Globally Diverse Breeds of Sheep. <i>PLoS ONE</i> , 2014, 9, e94851.	2.5	88
51	Brachygnathia, cardiomegaly and renal hypoplasia syndrome (BCRHS) in Merino sheep maps to a 1.1 megabase region on ovine chromosome OAR2. <i>Animal Genetics</i> , 2013, 44, 231-233.	1.7	12
52	Understanding parasitic infection in sheep to design more efficient animal selection strategies. <i>Veterinary Journal</i> , 2013, 197, 143-152.	1.7	9
53	Characterization of Ovine Nectin-4, a Novel Peste des Petits Ruminants Virus Receptor. <i>Journal of Virology</i> , 2013, 87, 4756-4761.	3.4	82
54	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat ( <i>Capra</i> )	17.8	479

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55	Genetic diversity and investigation of polledness in divergent goat populations using 52,088 <sc>SNPs</sc>. <i>Animal Genetics</i> , 2013, 44, 325-335.	1.7	51
56	Introgression and the fate of domesticated genes in a wild mammal population. <i>Molecular Ecology</i> , 2013, 22, 4210-4221.	3.9	53
57	Detecting Regions of Homozygosity to Map the Cause of Recessively Inherited Disease. <i>Methods in Molecular Biology</i> , 2013, 1019, 331-345.	0.9	14
58	Genomewide association for a dominant pigmentation gene in sheep. <i>Journal of Animal Breeding and Genetics</i> , 2013, 130, 468-475.	2.0	26
59	Genetic Testing for TMEM154 Mutations Associated with Lentivirus Susceptibility in Sheep. <i>PLoS ONE</i> , 2013, 8, e55490.	2.5	28
60	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.	5.6	719
61	Consistent divergence times and allele sharing measured from cross-species application of <sc>SNP</sc> chips developed for three domestic species. <i>Molecular Ecology Resources</i> , 2012, 12, 1145-1150.	4.8	56
62	Tracking the Emergence of a New Breed Using 49,034 SNP in Sheep. <i>PLoS ONE</i> , 2012, 7, e41508.	2.5	9
63	Accuracy of genotype imputation in sheep breeds. <i>Animal Genetics</i> , 2012, 43, 72-80.	1.7	98
64	Analysis of copy number variants in the cattle genome. <i>Gene</i> , 2011, 482, 73-77.	2.2	34
65	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.	4.8	80
66	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.	3.9	217
67	Haplogroup relationships between domestic and wild sheep resolved using a mitogenome panel. <i>Heredity</i> , 2011, 106, 700-706.	2.6	112
68	Genetic architecture of gene expression in ovine skeletal muscle. <i>BMC Genomics</i> , 2011, 12, 607.	2.8	18
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.	2.5	19
70	Using Regulatory and Epistatic Networks to Extend the Findings of a Genome Scan: Identifying the Gene Drivers of Pigmentation in Merino Sheep. <i>PLoS ONE</i> , 2011, 6, e21158.	2.5	52
71	Evaluation of 16 loci to examine the cross-species utility of single nucleotide polymorphism arrays. <i>Animal Genetics</i> , 2010, 41, 199-202.	1.7	12
72	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.	1.7	10

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73	The sheep genome reference sequence: a work in progress. <i>Animal Genetics</i> , 2010, 41, 449-453.	1.7	173
74	Microphthalmia in Texel Sheep Is Associated with a Missense Mutation in the Paired-Like Homeodomain 3 (PITX3) Gene. <i>PLoS ONE</i> , 2010, 5, e8689.	2.5	52
75	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.	0.5	11
76	Molecular Cytogenetics and Gene Mapping in Sheep ( <i>Ovis aries</i> , 2n = 54). <i>Cytogenetic and Genome Research</i> , 2009, 126, 63-76.	1.1	15
77	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.	1.7	33
78	A Genome Wide Survey of SNP Variation Reveals the Genetic Structure of Sheep Breeds. <i>PLoS ONE</i> , 2009, 4, e4668.	2.5	269
79	Linkage disequilibrium compared between five populations of domestic sheep. <i>BMC Genetics</i> , 2008, 9, 61.	2.7	65
80	The Effect of Genetic Variation of the Retinoic Acid Receptor-Related Orphan Receptor C Gene on Fatness in Cattle. <i>Genetics</i> , 2007, 175, 843-853.	2.9	49
81	Five Ovine Mitochondrial Lineages Identified From Sheep Breeds of the Near East. <i>Genetics</i> , 2007, 175, 1371-1379.	2.9	155
82	Evidence for multiple alleles effecting muscling and fatness at the Ovine GDF8 locus. <i>BMC Genetics</i> , 2007, 8, 80.	2.7	88
83	Mitochondrial haplotypes reveal a strong genetic structure for three Indian sheep breeds. <i>Animal Genetics</i> , 2007, 38, 460-466.	1.7	22
84	Linkage disequilibrium mapping in domestic dog breeds narrows the progressive rod-cone degeneration interval and identifies ancestral disease-transmitting chromosome. <i>Genomics</i> , 2006, 88, 541-550.	2.9	67
85	Sequence diversity and rates of molecular evolution between sheep and cattle genes. <i>Animal Genetics</i> , 2006, 37, 171-174.	1.7	35
86	Globally dispersed Y chromosomal haplotypes in wild and domestic sheep. <i>Animal Genetics</i> , 2006, 37, 444-453.	1.7	72
87	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.	2.4	91
88	Nucleotide diversity on the ovine Y chromosome. <i>Animal Genetics</i> , 2004, 35, 379-385.	1.7	50
89	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
90	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.	2.9	16

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91	Genetic Diversity Present Within the Near-Complete mtDNA Genome of 17 Breeds of Indigenous Chinese Pigs. , 2003, 94, 381-385.		35
92	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
93	Cloning, Mapping, and Retinal Expression of the Canine Ciliary Neurotrophic Factor Receptor $\hat{\pm}$ (CNTFR $\hat{\pm}$ ). , 2003, 44, 3642.		52
94	Naturally occurring rhodopsin mutation in the dog causes retinal dysfunction and degeneration mimicking human dominant retinitis pigmentosa. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6328-6333.	7.1	150
95	Cloning and characterization of the canine photoreceptor specific cone-rod homeobox (CRX) gene and evaluation as a candidate for early onset photoreceptor diseases in the dog. Molecular Vision, 2002, 8, 79-84.	1.1	11
96	Comparison of horse Chromosome 3 with donkey and human chromosomes by cross-species painting and heterologous FISH mapping. Mammalian Genome, 1999, 10, 277-282.	2.2	36
97	Molecular Basis for the Dominant White Phenotype in the Domestic Pig. Genome Research, 1998, 8, 826-833.	5.5	195