

Theodore Kalbfleisch

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

8,325
citations

257450

24
h-index

74163

75
g-index

80
all docs

80
docs citations

80
times ranked

9973
citing authors

#	ARTICLE	IF	CITATIONS
1	Delineating the Effects of Passaging and Exposure in a Longitudinal Study of Arsenic-Induced Squamous Cell Carcinoma in a HaCaT Cell Line Model. <i>Toxicological Sciences</i> , 2022, 185, 184-196.	3.1	6
2	Genetics of Thoroughbred Racehorse Performance. <i>Annual Review of Animal Biosciences</i> , 2022, 10, 131-150.	7.4	8
3	Transcriptomic analysis of equine placenta reveals key regulators and pathways involved in ascending placentitis. <i>Biology of Reproduction</i> , 2021, 104, 638-656.	2.7	9
4	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021, 112, 184-191.	2.4	25
5	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021, 112, 174-183.	2.4	14
6	Paternally expressed retrotransposon Gag-like 1 gene, RTL1, is one of the crucial elements for placental angiogenesis in horses. <i>Biology of Reproduction</i> , 2021, 104, 1386-1399.	2.7	5
7	Long non-coding RNA ZFAS1 is a major regulator of epithelial-mesenchymal transition through miR-200/ZEB1/E-cadherin, vimentin signaling in colon adenocarcinoma. <i>Cell Death Discovery</i> , 2021, 7, 61.	4.7	23
8	Parental bias in expression and interaction of genes in the equine placenta. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	9
9	Dynamic alteration in miRNA and mRNA expression profiles at different stages of chronic arsenic exposure-induced carcinogenesis in a human cell culture model of skin cancer. <i>Archives of Toxicology</i> , 2021, 95, 2351-2365.	4.2	25
10	Successful ATAC-Seq From Snap-Frozen Equine Tissues. <i>Frontiers in Genetics</i> , 2021, 12, 641788.	2.3	8
11	Transcriptomic analysis of equine chorioallantois reveals immune networks and molecular mechanisms involved in nocardioform placentitis. <i>Veterinary Research</i> , 2021, 52, 103.	3.0	8
12	Evaluating Large Spontaneous Deletions in a Bovine Cell Line Selected for Bovine Viral Diarrhea Virus Resistance. <i>Viruses</i> , 2021, 13, 2147.	3.3	4
13	Decoding the Equine Genome: Lessons from ENCODE. <i>Genes</i> , 2021, 12, 1707.	2.4	5
14	Transcriptional and Histochemical Signatures of Bone Marrow Mononuclear Cell-Mediated Resolution of Synovitis. <i>Frontiers in Immunology</i> , 2021, 12, 734322.	4.8	6
15	MC1R and KIT Haplotypes Associate With Pigmentation Phenotypes of North American Yak (<i>Bos</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	2.4	8
16	Genetics, Genomics, and Emergent Precision Medicine 12 Years After the Equine Reference Genome Was Published. <i>Veterinary Clinics of North America Equine Practice</i> , 2020, 36, 173-181.	0.7	1
17	Comparison of Poly-A+ Selection and rRNA Depletion in Detection of lncRNA in Two Equine Tissues Using RNA-seq. <i>Non-coding RNA</i> , 2020, 6, 32.	2.6	6
18	Inflamed synovial fluid induces a homeostatic response in bone marrow mononuclear cells in vitro: Implications for joint therapy. <i>FASEB Journal</i> , 2020, 34, 4430-4444.	0.5	13

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19	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	6.4	46
20	Using triallelic SNPs for determining parentage in North American yak (<i>Bos grunniens</i>) and estimating cattle (<i>B. taurus</i>) introgression. <i>F1000Research</i> , 2020, 9, 1096.	1.6	1
21	Using triallelic SNPs for determining parentage in North American yak (<i>Bos grunniens</i>) and estimating cattle (<i>B. taurus</i>) introgression. <i>F1000Research</i> , 2020, 9, 1096.	1.6	1
22	Landscape of Overlapping Gene Expression in the Equine Placenta. <i>Genes</i> , 2019, 10, 503.	2.4	8
23	Equine arteritis virus long-term persistence is orchestrated by CD8+ T lymphocyte transcription factors, inhibitory receptors, and the CXCL16/CXCR6 axis. <i>PLoS Pathogens</i> , 2019, 15, e1007950.	4.7	20
24	Characterization of the placental transcriptome through mid to late gestation in the mare. <i>PLoS ONE</i> , 2019, 14, e0224497.	2.5	15
25	Coding RNA Sequencing of Equine Endometrium during Maternal Recognition of Pregnancy. <i>Genes</i> , 2019, 10, 749.	2.4	13
26	Non-Coding RNA Sequencing of Equine Endometrium During Maternal Recognition of Pregnancy. <i>Genes</i> , 2019, 10, 821.	2.4	8
27	Exclusion of adrenoceptor alpha 2 variants in a horse insensitive to medetomidine. <i>Animal Genetics</i> , 2018, 49, 141-141.	1.7	1
28	Downregulation of MicroRNA eca-mir-128 in Seminal Exosomes and Enhanced Expression of CXCL16 in the Stallion Reproductive Tract Are Associated with Long-Term Persistence of Equine Arteritis Virus. <i>Journal of Virology</i> , 2018, 92, .	3.4	14
29	Next generation sequencing analysis of soy glyceollins and 17- β estradiol: Effects on transcript abundance in the female mouse brain. <i>Molecular and Cellular Endocrinology</i> , 2018, 471, 15-21.	3.2	8
30	Improved reference genome for the domestic horse increases assembly contiguity and composition. <i>Communications Biology</i> , 2018, 1, 197.	4.4	148
31	Ruling out <i>BGN</i> variants as simple X-linked causative mutations for bilateral corneal stromal loss in Friesian horses. <i>Animal Genetics</i> , 2018, 49, 656-657.	1.7	6
32	Generation of an equine biobank to be used for Functional Annotation of Animal Genomes project. <i>Animal Genetics</i> , 2018, 49, 564-570.	1.7	33
33	A SNP resource for studying North American moose. <i>F1000Research</i> , 2018, 7, 40.	1.6	7
34	A bovine CD18 signal peptide variant with increased binding activity to <i>Mannheimia hemolytica</i> leukotoxin. <i>F1000Research</i> , 2018, 7, 1985.	1.6	4
35	Molecular cloning and functional expression of the K ⁺ channel KV 7.1 and the regulatory subunit KCNE1 from equine myocardium. <i>Research in Veterinary Science</i> , 2017, 113, 79-86.	1.9	7
36	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. <i>BMC Genomics</i> , 2017, 18, 565.	2.8	116

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37	Using sheep genomes from diverse U.S. breeds to identify missense variants in genes affecting fecundity. <i>F1000Research</i> , 2017, 6, 1303.	1.6	18
38	Using diverse U.S. beef cattle genomes to identify missense mutations in <i>EPAS1</i> , a gene associated with pulmonary hypertension. <i>F1000Research</i> , 2016, 5, 2003.	1.6	21
39	Genomic signatures of <i>Mannheimia haemolytica</i> that associate with the lungs of cattle with respiratory disease, an integrative conjugative element, and antibiotic resistance genes. <i>BMC Genomics</i> , 2016, 17, 982.	2.8	46
40	Observations on macrolide resistance and susceptibility testing performance in field isolates collected from clinical bovine respiratory disease cases. <i>Veterinary Microbiology</i> , 2016, 192, 186-193.	1.9	13
41	Equine Arteritis Virus Uses Equine CXCL16 as an Entry Receptor. <i>Journal of Virology</i> , 2016, 90, 3366-3384.	3.4	19
42	Using diverse U.S. beef cattle genomes to identify missense mutations in <i>EPAS1</i> , a gene associated with high-altitude pulmonary hypertension. <i>F1000Research</i> , 2016, 5, 2003.	1.6	27
43	Allelic Variation in CXCL16 Determines CD3+ T Lymphocyte Susceptibility to Equine Arteritis Virus Infection and Establishment of Long-Term Carrier State in the Stallion. <i>PLoS Genetics</i> , 2016, 12, e1006467.	3.5	18
44	Annotation of the Protein Coding Regions of the Equine Genome. <i>PLoS ONE</i> , 2015, 10, e0124375.	2.5	29
45	Comparison of the Equine Reference Sequence with Its Sanger Source Data and New Illumina Reads. <i>PLoS ONE</i> , 2015, 10, e0126852.	2.5	6
46	Interaction between smoking history and gene expression levels impacts survival of breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2015, 152, 545-556.	2.5	28
47	Health Status, Perceptions and Needs of Hispanics in Rural Shelbyville, Kentucky. <i>Journal of Immigrant and Minority Health</i> , 2015, 17, 148-155.	1.6	1
48	Characterization of an APC Promoter 1B deletion in a Patient Diagnosed with Familial Adenomatous Polyposis via Whole Genome Shotgun Sequencing. <i>F1000Research</i> , 2015, 4, 170.	1.6	5
49	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5661-9.	7.1	260
50	SNPs for Parentage Testing and Traceability in Globally Diverse Breeds of Sheep. <i>PLoS ONE</i> , 2014, 9, e94851.	2.5	88
51	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
52	Genetic Testing for <i>TMEM154</i> Mutations Associated with Lentivirus Susceptibility in Sheep. <i>PLoS ONE</i> , 2013, 8, e55490.	2.5	28
53	The Intersection of Genetics and Epigenetics: Reactivation of Mammalian LINE-1 Retrotransposons by Environmental Injury. <i>Epigenetics and Human Health</i> , 2013, , 127-160.	0.2	4
54	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. <i>F1000Research</i> , 2013, 2, 244.	1.6	13

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55	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. <i>F1000Research</i> , 2013, 2, 244.	1.6	9
56	Reduced Lentivirus Susceptibility in Sheep with TMEM154 Mutations. <i>PLoS Genetics</i> , 2012, 8, e1002467.	3.5	78
57	Differential expression of microRNA expression in tamoxifen-sensitive MCF-7 versus tamoxifen-resistant LY2 human breast cancer cells. <i>Cancer Letters</i> , 2011, 313, 26-43.	7.2	68
58	Genome Assembly Has a Major Impact on Gene Content: A Comparison of Annotation in Two <i>Bos Taurus</i> Assemblies. <i>PLoS ONE</i> , 2011, 6, e21400.	2.5	65
59	Assessment of genetic variation for the LINE-1 retrotransposon from next generation sequence data. <i>BMC Bioinformatics</i> , 2010, 11, S12.	2.6	7
60	Ovine reference materials and assays for prion genetic testing. <i>BMC Veterinary Research</i> , 2010, 6, 23.	1.9	12
61	Interaction among variant vascular endothelial growth factor (VEGF) and its receptor in relation to prostate cancer risk. <i>Prostate</i> , 2010, 70, 341-352.	2.3	42
62	Epigenetic control of mammalian LINE-1 retrotransposon by retinoblastoma proteins. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2009, 665, 20-28.	1.0	88
63	A MicroRNA gene is hosted in an intron of a schizophrenia-susceptibility gene. <i>Schizophrenia Research</i> , 2009, 109, 86-89.	2.0	102
64	Prevalence of the prion protein gene E211K variant in U.S. cattle. <i>BMC Veterinary Research</i> , 2008, 4, 25.	1.9	46
65	Computational and biological inference of gene regulatory networks of the LINE-1 retrotransposon. <i>Genomics</i> , 2007, 90, 176-185.	2.9	22
66	Service-Oriented Laboratory Information Management System for Life Sciences Research. , 2007, , .		6
67	Validation of a Mathematical Model of Gene Transcription in Aggregated Cellular Systems: Application to L1 Retrotransposition. <i>Journal of Computational Biology</i> , 2007, 14, 339-349.	1.6	14
68	A Bioinformatics Approach to Identifying Tailâ€Anchored Proteins in the Human Genome. <i>Traffic</i> , 2007, 8, 1687-1694.	2.7	122
69	A stochastic model of gene transcription: An application to L1 retrotransposition events. <i>Journal of Theoretical Biology</i> , 2006, 242, 101-116.	1.7	21
70	The Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2005, 3, e196.	5.6	895
71	Haplotype Variation and Linkage Disequilibrium in 313 Human Genes. <i>Science</i> , 2001, 293, 489-493.	12.6	768
72	A comprehensive analysis of proteinâ€protein interactions in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2000, 403, 623-627.	27.8	4,490

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73	Untangling the physical contributions to instantaneous normal mode approximations: Inhomogeneous broadening, motional narrowing, and energy relaxation. <i>Journal of Chemical Physics</i> , 1998, 108, 7375-7383.	3.0	25
74	An instantaneous normal mode analysis of solvation: Methyl iodide in high pressure gases. <i>Journal of Chemical Physics</i> , 1996, 105, 7034-7046.	3.0	39
75	A molecular dynamics study of electronic absorption line broadening in high-pressure nonpolar gases. <i>Journal of Chemical Physics</i> , 1995, 103, 7673-7684.	3.0	25
76	Association of ARRDC3 and NFIA variants with bovine congestive heart failure in feedlot cattle. <i>F1000Research</i> , 0, 11, 385.	1.6	6