

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	A comprehensive analysis of protein-protein interactions in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2000, 403, 623-627.	27.8	4,490
2	The Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2005, 3, e196.	5.6	895
3	Haplotype Variation and Linkage Disequilibrium in 313 Human Genes. <i>Science</i> , 2001, 293, 489-493.	12.6	768
4	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
5	Improved reference genome for the domestic horse increases assembly contiguity and composition. <i>Communications Biology</i> , 2018, 1, 197.	4.4	148
6	A Bioinformatics Approach to Identifying Tail-Anchored Proteins in the Human Genome. <i>Traffic</i> , 2007, 8, 1687-1694.	2.7	122
7	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. <i>BMC Genomics</i> , 2017, 18, 565.	2.8	116
8	A MicroRNA gene is hosted in an intron of a schizophrenia-susceptibility gene. <i>Schizophrenia Research</i> , 2009, 109, 86-89.	2.0	102
9	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
10	SNPs for Parentage Testing and Traceability in Globally Diverse Breeds of Sheep. <i>PLoS ONE</i> , 2014, 9, e94851.	2.5	88
11	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
12	Reduced Lentivirus Susceptibility in Sheep with TMEM154 Mutations. <i>PLoS Genetics</i> , 2012, 8, e1002467.	3.5	78
13	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
14	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
15	Prevalence of the prion protein gene E211K variant in U.S. cattle. <i>BMC Veterinary Research</i> , 2008, 4, 25.	1.9	46
16	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
17	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	6.4	46
18	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

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19	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
20	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
21	Annotation of the Protein Coding Regions of the Equine Genome. <i>PLoS ONE</i> , 2015, 10, e0124375.	2.5	29
22	Genetic Testing for TMEM154 Mutations Associated with Lentivirus Susceptibility in Sheep. <i>PLoS ONE</i> , 2013, 8, e55490.	2.5	28
23	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
24	Using diverse U.S. beef cattle genomes to identify missense mutations in EPAS1, a gene associated with high-altitude pulmonary hypertension. <i>F1000Research</i> , 2016, 5, 2003.	1.6	27
25	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
26	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
27	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021, 112, 184-191.	2.4	25
28	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
29	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
30	Computational and biological inference of gene regulatory networks of the LINE-1 retrotransposon. <i>Genomics</i> , 2007, 90, 176-185.	2.9	22
31	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
32	Using diverse U.S. beef cattle genomes to identify missense mutations in EPAS1, a gene associated with pulmonary hypertension. <i>F1000Research</i> , 2016, 5, 2003.	1.6	21
33	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
34	Equine Arteritis Virus Uses Equine CXCL16 as an Entry Receptor. <i>Journal of Virology</i> , 2016, 90, 3366-3384.	3.4	19
35	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
36	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

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37	Characterization of the placental transcriptome through mid to late gestation in the mare. PLoS ONE, 2019, 14, e0224497.	2.5	15
38	Validation of a Mathematical Model of Gene Transcription in Aggregated Cellular Systems: Application to L1 Retrotransposition. Journal of Computational Biology, 2007, 14, 339-349.	1.6	14
39	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. Journal of Virology, 2018, 92, .	3.4	14
40	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . Journal of Heredity, 2021, 112, 174-183.	2.4	14
41	Observations on macrolide resistance and susceptibility testing performance in field isolates collected from clinical bovine respiratory disease cases. Veterinary Microbiology, 2016, 192, 186-193.	1.9	13
42	Coding RNA Sequencing of Equine Endometrium during Maternal Recognition of Pregnancy. Genes, 2019, 10, 749.	2.4	13
43	Inflamed synovial fluid induces a homeostatic response in bone marrow mononuclear cells in vitro: Implications for joint therapy. FASEB Journal, 2020, 34, 4430-4444.	0.5	13
44	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. F1000Research, 2013, 2, 244.	1.6	13
45	Ovine reference materials and assays for prion genetic testing. BMC Veterinary Research, 2010, 6, 23.	1.9	12
46	Transcriptomic analysis of equine placenta reveals key regulators and pathways involved in ascending placentitis. Biology of Reproduction, 2021, 104, 638-656.	2.7	9
47	Parental bias in expression and interaction of genes in the equine placenta. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	9
48	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. F1000Research, 2013, 2, 244.	1.6	9
49	Next generation sequencing analysis of soy glyceollins and 17- β estradiol: Effects on transcript abundance in the female mouse brain. Molecular and Cellular Endocrinology, 2018, 471, 15-21.	3.2	8
50	Landscape of Overlapping Gene Expression in the Equine Placenta. Genes, 2019, 10, 503.	2.4	8
51	Non-Coding RNA Sequencing of Equine Endometrium During Maternal Recognition of Pregnancy. Genes, 2019, 10, 821.	2.4	8
52	MC1R and KIT Haplotypes Associate With Pigmentation Phenotypes of North American Yak (Bos) Tj ETQq0 0 0 rgBTJ Overlock 10 Tf 50	2.4	8
53	Successful ATAC-Seq From Snap-Frozen Equine Tissues. Frontiers in Genetics, 2021, 12, 641788.	2.3	8
54	Transcriptomic analysis of equine chorioallantois reveals immune networks and molecular mechanisms involved in nocardioform placentitis. Veterinary Research, 2021, 52, 103.	3.0	8

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55	Genetics of Thoroughbred Racehorse Performance. Annual Review of Animal Biosciences, 2022, 10, 131-150.	7.4	8
56	Assessment of genetic variation for the LINE-1 retrotransposon from next generation sequence data. BMC Bioinformatics, 2010, 11, S12.	2.6	7
57	Molecular cloning and functional expression of the K + channel K V 7.1 and the regulatory subunit KCNE1 from equine myocardium. Research in Veterinary Science, 2017, 113, 79-86.	1.9	7
58	A SNP resource for studying North American moose. F1000Research, 2018, 7, 40.	1.6	7
59	Service-Oriented Laboratory Information Management System for Life Sciences Research. , 2007, , .		6
60	Comparison of the Equine Reference Sequence with Its Sanger Source Data and New Illumina Reads. PLoS ONE, 2015, 10, e0126852.	2.5	6
61	Ruling out <i><scp>BGN</scp></i> variants as simple Xâ€linked causative mutations for bilateral corneal stromal loss in Friesian horses. Animal Genetics, 2018, 49, 656-657.	1.7	6
62	Comparison of Poly-A+ Selection and rRNA Depletion in Detection of lncRNA in Two Equine Tissues Using RNA-seq. Non-coding RNA, 2020, 6, 32.	2.6	6
63	Delineating the Effects of Passaging and Exposure in a Longitudinal Study of Arsenic-Induced Squamous Cell Carcinoma in a HaCaT Cell Line Model. Toxicological Sciences, 2022, 185, 184-196.	3.1	6
64	Association of ARRDC3 and NFIA variants with bovine congestive heart failure in feedlot cattle. F1000Research, 0, 11, 385.	1.6	6
65	Transcriptional and Histochemical Signatures of Bone Marrow Mononuclear Cell-Mediated Resolution of Synovitis. Frontiers in Immunology, 2021, 12, 734322.	4.8	6
66	Paternally expressed retrotransposon Gag-like 1 gene, RTL1, is one of the crucial elements for placental angiogenesis in horses. Biology of Reproduction, 2021, 104, 1386-1399.	2.7	5
67	Characterization of an APC Promoter 1B deletion in a Patient Diagnosed with Familial Adenomatous Polyposis via Whole Genome Shotgun Sequencing. F1000Research, 2015, 4, 170.	1.6	5
68	Decoding the Equine Genome: Lessons from ENCODE. Genes, 2021, 12, 1707.	2.4	5
69	The Intersection of Genetics and Epigenetics: Reactivation of Mammalian LINE-1 Retrotransposons by Environmental Injury. Epigenetics and Human Health, 2013, , 127-160.	0.2	4
70	A bovine CD18 signal peptide variant with increased binding activity to Mannheimia hemolytica leukotoxin. F1000Research, 2018, 7, 1985.	1.6	4
71	Evaluating Large Spontaneous Deletions in a Bovine Cell Line Selected for Bovine Viral Diarrhea Virus Resistance. Viruses, 2021, 13, 2147.	3.3	4
72	Health Status, Perceptions and Needs of Hispanics in Rural Shelbyville, Kentucky. Journal of Immigrant and Minority Health, 2015, 17, 148-155.	1.6	1

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73	Exclusion of adrenoceptor alpha 2 variants in a horse insensitive to medetomidine. <i>Animal Genetics</i> , 2018, 49, 141-141.	1.7	1
74	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
75	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
76	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