

Theodore Kalbfleisch

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

74
papers

6,932
citations

21
h-index

80
g-index

80
ext. papers

7,789
ext. citations

5.4
avg. IF

4.58
L-index

#	Paper	IF	Citations
74	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> , 2021 ,	4.4	2
73	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	3.9	2
72	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	6.9	7
71	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,	11.5	2
70	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	5.8	11
69	Successful ATAC-Seq From Snap-Frozen Equine Tissues. <i>Frontiers in Genetics</i> , 2021 , 12, 641788	4.5	0
68	Transcriptomic analysis of equine placenta reveals key regulators and pathways involved in ascending placentitis <i>Biology of Reproduction</i> , 2021 , 104, 638-656	3.9	3
67	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021 , 112, 184-191	2.4	4
66	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021 , 112, 174-183	2.4	3
65	Transcriptomic analysis of equine chorioallantois reveals immune networks and molecular mechanisms involved in nocardioform placentitis. <i>Veterinary Research</i> , 2021 , 52, 103	3.8	2
64	Transcriptional and Histochemical Signatures of Bone Marrow Mononuclear Cell-Mediated Resolution of Synovitis.. <i>Frontiers in Immunology</i> , 2021 , 12, 734322	8.4	0
63	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	0.9	7
62	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020 , 9,	7.6	18
61	Using triallelic SNPs for determining parentage in North American yak () and estimating cattle () introgression. <i>F1000Research</i> , 2020 , 9, 1096	3.6	1
60	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	3.6	1
59	MC1R and KIT Haplotypes Associate With Pigmentation Phenotypes of North American Yak (<i>Bos grunniens</i>). <i>Journal of Heredity</i> , 2020 , 111, 182-193	2.4	2
58	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	1.9	1

57	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,	7.1	2
56	Coding RNA Sequencing of Equine Endometrium during Maternal Recognition of Pregnancy. <i>Genes</i> , 2019 , 10,	4.2	6
55	Non-Coding RNA Sequencing of Equine Endometrium During Maternal Recognition of Pregnancy. <i>Genes</i> , 2019 , 10,	4.2	3
54	Landscape of Overlapping Gene Expression in the Equine Placenta. <i>Genes</i> , 2019 , 10,	4.2	7
53	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	7.6	12
52	Characterization of the placental transcriptome through mid to late gestation in the mare. <i>PLoS ONE</i> , 2019 , 14, e0224497	3.7	5
51	Exclusion of adrenoceptor alpha 2 variants in a horse insensitive to medetomidine. <i>Animal Genetics</i> , 2018 , 49, 141	2.5	0
50	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,	6.6	9
49	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	4.4	3
48	A SNP resource for studying North American moose. <i>F1000Research</i> , 2018 , 7, 40	3.6	3
47	A bovine CD18 signal peptide variant with increased binding activity to leukotoxin. <i>F1000Research</i> , 2018 , 7, 1985	3.6	1
46	Improved reference genome for the domestic horse increases assembly contiguity and composition. <i>Communications Biology</i> , 2018 , 1, 197	6.7	74
45	Ruling out BGN variants as simple X-linked causative mutations for bilateral corneal stromal loss in Friesian horses. <i>Animal Genetics</i> , 2018 , 49, 656-657	2.5	6
44	Generation of an equine biobank to be used for Functional Annotation of Animal Genomes project. <i>Animal Genetics</i> , 2018 , 49, 564-570	2.5	19
43	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. <i>BMC Genomics</i> , 2017 , 18, 565	4.5	66
42	Molecular cloning and functional expression of the K channel K7.1 and the regulatory subunit KCNE1 from equine myocardium. <i>Research in Veterinary Science</i> , 2017 , 113, 79-86	2.5	3
41	Using sheep genomes from diverse U.S. breeds to identify missense variants in genes affecting fecundity. <i>F1000Research</i> , 2017 , 6, 1303	3.6	12
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	3.3	11

39	Equine Arteritis Virus Uses Equine CXCL16 as an Entry Receptor. <i>Journal of Virology</i> , 2016 , 90, 3366-84	6.6	15
38	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	3.6	20
37	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	6	14
36	Using diverse U.S. beef cattle genomes to identify missense mutations in a gene associated with high-altitude pulmonary hypertension. <i>F1000Research</i> , 2016 , 5, 2003	3.6	18
35	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	4.5	33
34	Interaction between smoking history and gene expression levels impacts survival of breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2015 , 152, 545-56	4.4	22
33	Health status, perceptions and needs of Hispanics in rural Shelbyville, Kentucky. <i>Journal of Immigrant and Minority Health</i> , 2015 , 17, 148-55	2.2	1
32	Annotation of the Protein Coding Regions of the Equine Genome. <i>PLoS ONE</i> , 2015 , 10, e0124375	3.7	17
31	Comparison of the Equine Reference Sequence with Its Sanger Source Data and New Illumina Reads. <i>PLoS ONE</i> , 2015 , 10, e0126852	3.7	6
30	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	3.6	3
29	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	11.5	197
28	SNPs for parentage testing and traceability in globally diverse breeds of sheep. <i>PLoS ONE</i> , 2014 , 9, e94857	5.7	62
27	Characterization of ovine Nectin-4, a novel peste des petits ruminants virus receptor. <i>Journal of Virology</i> , 2013 , 87, 4756-61	6.6	72
26	Genetic testing for TMEM154 mutations associated with lentivirus susceptibility in sheep. <i>PLoS ONE</i> , 2013 , 8, e55490	3.7	19
25	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. <i>F1000Research</i> , 2013 , 2, 244	3.6	11
24	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. <i>F1000Research</i> , 2013 , 2, 244	3.6	9
23	The Intersection of Genetics and Epigenetics: Reactivation of Mammalian LINE-1 Retrotransposons by Environmental Injury. <i>Epigenetics and Human Health</i> , 2013 , 127-160		3
22	Reduced lentivirus susceptibility in sheep with TMEM154 mutations. <i>PLoS Genetics</i> , 2012 , 8, e1002467	6	58

21	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	9.9	66
20	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	3.7	46
19	Assessment of genetic variation for the LINE-1 retrotransposon from next generation sequence data. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 9, S12	3.6	6
18	Ovine reference materials and assays for prion genetic testing. <i>BMC Veterinary Research</i> , 2010 , 6, 23	2.7	9
17	Interaction among variant vascular endothelial growth factor (VEGF) and its receptor in relation to prostate cancer risk. <i>Prostate</i> , 2010 , 70, 341-52	4.2	36
16	Epigenetic control of mammalian LINE-1 retrotransposon by retinoblastoma proteins. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2009 , 665, 20-8	3.3	73
15	A MicroRNA gene is hosted in an intron of a schizophrenia-susceptibility gene. <i>Schizophrenia Research</i> , 2009 , 109, 86-9	3.6	91
14	Prevalence of the prion protein gene E211K variant in U.S. cattle. <i>BMC Veterinary Research</i> , 2008 , 4, 25	2.7	39
13	Validation of a mathematical model of gene transcription in aggregated cellular systems: application to l1 retrotransposition. <i>Journal of Computational Biology</i> , 2007 , 14, 339-49	1.7	12
12	A bioinformatics approach to identifying tail-anchored proteins in the human genome. <i>Traffic</i> , 2007 , 8, 1687-1694	5.7	102
11	Computational and biological inference of gene regulatory networks of the LINE-1 retrotransposon. <i>Genomics</i> , 2007 , 90, 176-85	4.3	18
10	Service-Oriented Laboratory Information Management System for Life Sciences Research 2007 ,		3
9	A stochastic model of gene transcription: an application to L1 retrotransposition events. <i>Journal of Theoretical Biology</i> , 2006 , 242, 101-16	2.3	20
8	The pattern of polymorphism in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2005 , 3, e196	9.7	764
7	Haplotype variation and linkage disequilibrium in 313 human genes. <i>Science</i> , 2001 , 293, 489-93	33.3	685
6	A comprehensive analysis of protein-protein interactions in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2000 , 403, 623-7	50.4	3974
5	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	3.9	23
4	An instantaneous normal mode analysis of solvation: Methyl iodide in high pressure gases. <i>Journal of Chemical Physics</i> , 1996 , 105, 7034-7046	3.9	38

3	A molecular dynamics study of electronic absorption line broadening in high-pressure nonpolar gases. <i>Journal of Chemical Physics</i> , 1995 , 103, 7673-7684	3.9	25
2	EquCab3, an Updated Reference Genome for the Domestic Horse		11
1	Association of ARRDC3 and NFIA variants with bovine congestive heart failure in feedlot cattle. <i>F1000Research</i> , 11, 385	3.6	1