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List of articles citing

Comparative RNA-Seq and microarray analysis of gene expression changes in B-cell lymphomas of *Canis familiaris*

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#	Paper	IF	Citations
46	The transcriptional landscape of <i>Campylobacter jejuni</i> under iron replete and iron limited growth conditions. <i>PLoS ONE</i> , 2013 , 8, e79475	3.7	33
45	RNA sequencing analysis and atrial natriuretic peptide production in patients with dilated and ischemic cardiomyopathy. <i>PLoS ONE</i> , 2014 , 9, e90157	3.7	17
44	A comparison of RNA-seq and exon arrays for whole genome transcription profiling of the L5 spinal nerve transection model of neuropathic pain in the rat. <i>Molecular Pain</i> , 2014 , 10, 7	3.4	68
43	RNA-sequencing analysis reveals new alterations in cardiomyocyte cytoskeletal genes in patients with heart failure. <i>Laboratory Investigation</i> , 2014 , 94, 645-53	5.9	27
42	Gene Expression Profiling in Pancreatic Cancer. 2014 , 151-167		
41	Pollen-specific activation of <i>Arabidopsis</i> retrogenes is associated with global transcriptional reprogramming. <i>Plant Cell</i> , 2014 , 26, 3299-313	11.6	22
40	Genomics of pancreatic ductal adenocarcinoma. <i>Hepatobiliary and Pancreatic Diseases International</i> , 2014 , 13, 381-5	2.1	2
39	Detecting and correcting systematic variation in large-scale RNA sequencing data. <i>Nature Biotechnology</i> , 2014 , 32, 888-95	44.5	125
38	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. <i>Nature Biotechnology</i> , 2014 , 32, 926-32	44.5	323
37	A multistep screening method to identify genes using evolutionary transcriptome of plants. <i>Evolutionary Bioinformatics</i> , 2014 , 10, 69-78	1.9	3
36	Generation of a de novo transcriptome from equine lamellar tissue. <i>BMC Genomics</i> , 2015 , 16, 739	4.5	10
35	Gene profiling of bone around orthodontic mini-implants by RNA-sequencing analysis. <i>BioMed Research International</i> , 2015 , 2015, 538080	3	6
34	The importance of comparative oncology in translational medicine. <i>Cancer Immunology, Immunotherapy</i> , 2015 , 64, 137-48	7.4	24
33	Transcriptome sequencing reveals thousands of novel long non-coding RNAs in B cell lymphoma. <i>Genome Medicine</i> , 2015 , 7, 110	14.4	50
32	Transcriptome profiling of expression changes during neuronal death by RNA-Seq. <i>Experimental Biology and Medicine</i> , 2015 , 240, 242-51	3.7	6
31	Altered microglial phagocytosis in GPR34-deficient mice. <i>Glia</i> , 2015 , 63, 206-15	9	46
30	A comparative analytical assay of gene regulatory networks inferred using microarray and RNA-seq datasets. <i>Bioinformatics</i> , 2016 , 12, 340-346	1.1	8

29	Transcriptomic analysis identified up-regulation of a solute carrier transporter and UDP glucuronosyltransferases in dogs with aggressive cutaneous mast cell tumours. <i>Veterinary Journal</i> , 2016 , 212, 36-43	2.5	9
28	Application of post-genomic techniques in dog cancer research. <i>Molecular BioSystems</i> , 2016 , 12, 2665-79		5
27	Distant eQTLs and Non-coding Sequences Play Critical Roles in Regulating Gene Expression and Quantitative Trait Variation in Maize. <i>Molecular Plant</i> , 2017 , 10, 414-426	14.4	89
26	Use of RNA-seq to determine variation in canine cytochrome P450 mRNA expression between blood, liver, lung, kidney and duodenum in healthy beagles. <i>Journal of Veterinary Pharmacology and Therapeutics</i> , 2017 , 40, 583-590	1.4	3
25	Transcriptome Analysis of Canine Cutaneous Melanoma and Melanocytoma Reveals a Modulation of Genes Regulating Extracellular Matrix Metabolism and Cell Cycle. <i>Scientific Reports</i> , 2017 , 7, 6386	4.9	17
24	Meta-analysis of microarray and RNA-Seq gene expression datasets for carcinogenic risk: An assessment of Bisphenol A. <i>Molecular and Cellular Toxicology</i> , 2017 , 13, 239-249	1.6	12
23	Comprehensive gene expression analysis of canine invasive urothelial bladder carcinoma by RNA-Seq. <i>BMC Cancer</i> , 2018 , 18, 472	4.8	30
22	Machine learning approaches to predict lupus disease activity from gene expression data. <i>Scientific Reports</i> , 2019 , 9, 9617	4.9	31
21	Compendiums of cancer transcriptomes for machine learning applications. <i>Scientific Data</i> , 2019 , 6, 194	8.2	8
20	Suitability of ultrasound-guided fine-needle aspiration biopsy for transcriptome sequencing of the canine prostate. <i>Scientific Reports</i> , 2019 , 9, 13216	4.9	5
19	Identification of two molecular subtypes in canine mast cell tumours through gene expression profiling. <i>PLoS ONE</i> , 2019 , 14, e0217343	3.7	5
18	Novel Treatments for Lymphoma. <i>Veterinary Clinics of North America - Small Animal Practice</i> , 2019 , 49, 903-915	2.4	10
17	BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019 , 10,	4.2	12
16	New molecular and therapeutic insights into canine diffuse large B-cell lymphoma elucidates the role of the dog as a model for human disease. <i>Haematologica</i> , 2019 , 104, e256-e259	6.6	23
15	Gene Expression Analysis in the Age of Mass Sequencing: An Introduction. <i>Methods in Molecular Biology</i> , 2016 , 1381, 67-73	1.4	2
14	Compendiums of Cancer Transcriptome for Machine Learning Applications.		1
13	Transforming RNA-Seq data to improve the performance of prognostic gene signatures. <i>PLoS ONE</i> , 2014 , 9, e85150	3.7	81
12	Systems-based analyses of brain regions functionally impacted in Parkinson's disease reveals underlying causal mechanisms. <i>PLoS ONE</i> , 2014 , 9, e102909	3.7	44

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10	The evolutionary panorama of organ-specifically expressed or repressed orthologous genes in nine vertebrate species. <i>PLoS ONE</i> , 2015 , 10, e0116872	3.7	3
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8	Cross-platform normalization of microarray and RNA-seq data for machine learning applications. <i>PeerJ</i> , 2016 , 4, e1621	3.1	45
7	Consensus-based somatic variant-calling method correlates FBXW7 mutations with poor prognosis in canine B-cell lymphoma.		
6	Machine Learning and Bioinformatics Framework Integration to Potential Familial DCM-Related Markers Discovery.. <i>Genes</i> , 2021 , 12,	4.2	1
5	Gene network profiling in muscle-invasive bladder cancer: A systematic review and meta-analysis.. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2022 ,	2.8	1
4	Developing a novel DNA methylation risk score for survival and identification of prognostic gene mutations in endometrial cancer: a study based on TCGA data.. <i>Japanese Journal of Clinical Oncology</i> , 2022 ,	2.8	
3	A Robust Immuno-Prognostic Model of Non-Muscle-Invasive Bladder Cancer Indicates Dynamic Interaction in Tumor Immune Microenvironment Contributes to Cancer Progression. <i>Frontiers in Genetics</i> , 2022 , 13,	4.5	0
2	Integrative transcriptome-wide analysis of atopic dermatitis for drug repositioning. <i>Communications Biology</i> , 2022 , 5,	6.7	0
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