

Rachael Thomas

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

4,998
citations

172457
29
h-index

206112
48
g-index

51
all docs

51
docs citations

51
times ranked

5713
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	27.8	2,215
2	Chromosome-Specific Single-Locus FISH Probes Allow Anchorage of an 1800-Marker Integrated Radiation-Hybrid/Linkage Map of the Domestic Dog Genome to All Chromosomes. <i>Genome Research</i> , 2001, 11, 1784-1795.	5.5	236
3	Distinct B-Cell and T-Cell Lymphoproliferative Disease Prevalence among Dog Breeds Indicates Heritable Risk. <i>Cancer Research</i> , 2005, 65, 5654-5661.	0.9	160
4	A mutation in the canine BHD gene is associated with hereditary multifocal renal cystadenocarcinoma and nodular dermatofibrosis in the German Shepherd dog. <i>Human Molecular Genetics</i> , 2003, 12, 3043-3053.	2.9	157
5	Reciprocal Chromosome Painting Reveals Detailed Regions of Conserved Synteny between the Karyotypes of the Domestic Dog (<i>Canis familiaris</i>) and Human. <i>Genomics</i> , 1999, 61, 145-155.	2.9	152
6	Genome-wide analyses implicate 33 loci in heritable dog osteosarcoma, including regulatory variants near CDKN2A/B. <i>Genome Biology</i> , 2013, 14, R132.	9.6	132
7	Gene Profiling of Canine B-Cell Lymphoma Reveals Germinal Center and Postgerminal Center Subtypes with Different Survival Times, Modeling Human DLBCL. <i>Cancer Research</i> , 2013, 73, 5029-5039.	0.9	118
8	ORIGINS AND EVOLUTION OF A TRANSMISSIBLE CANCER. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 2340-2349.	2.3	113
9	An integrated 4249 marker FISH/RH map of the canine genome. <i>BMC Genomics</i> , 2004, 5, 65.	2.8	107
10	Alterations of the p53 and PIK3CA/AKT/mTOR pathways in angiosarcomas. <i>Cancer</i> , 2012, 118, 5878-5887.	4.1	103
11	Molecular cytogenetic characterization of canine histiocytic sarcoma: A spontaneous model for human histiocytic cancer identifies deletion of tumor suppressor genes and highlights influence of genetic background on tumor behavior. <i>BMC Cancer</i> , 2011, 11, 201.	2.6	96
12	The miRâ€17â€92 cluster and its target <i>THBS1</i> are differentially expressed in angiosarcomas dependent on <i>MYC</i> amplification. <i>Genes Chromosomes and Cancer</i> , 2012, 51, 569-578.	2.8	96
13	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. <i>Genome Research</i> , 2015, 25, 1634-1645.	5.5	96
14	Refining tumor-associated aneuploidy through "genomic recoding" of recurrent DNA copy number aberrations in 150 canine non-Hodgkin lymphomas. <i>Leukemia and Lymphoma</i> , 2011, 52, 1321-1335.	1.3	89
15	<i>SETD2</i> Is Recurrently Mutated in Whole-Exome Sequenced Canine Osteosarcoma. <i>Cancer Research</i> , 2018, 78, 3421-3431.	0.9	76
16	Influence of genetic background on tumor karyotypes: Evidence for breed-associated cytogenetic aberrations in canine appendicular osteosarcoma. <i>Chromosome Research</i> , 2009, 17, 365-377.	2.2	74
17	Comparative Genomics Reveals Shared Mutational Landscape in Canine Hemangiosarcoma and Human Angiosarcoma. <i>Molecular Cancer Research</i> , 2019, 17, 2410-2421.	3.4	72
18	Mutations of Phosphatase and Tensin Homolog Deleted from Chromosome 10 in Canine Hemangiosarcoma. <i>Veterinary Pathology</i> , 2005, 42, 618-632.	1.7	71

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19	“Putting our heads together”™: insights into genomic conservation between human and canine intracranial tumors. <i>Journal of Neuro-Oncology</i> , 2009, 94, 333-349.	2.9	71
20	Characterization of canine osteosarcoma by array comparative genomic hybridization and RT-qPCR: Signatures of genomic imbalance in canine osteosarcoma parallel the human counterpart. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 859-874.	2.8	69
21	Genome-wide Association Study Identifies Shared Risk Loci Common to Two Malignancies in Golden Retrievers. <i>PLoS Genetics</i> , 2015, 11, e1004922.	3.5	66
22	Genomic profiling reveals extensive heterogeneity in somatic DNA copy number aberrations of canine hemangiosarcoma. <i>Chromosome Research</i> , 2014, 22, 305-319.	2.2	54
23	Construction of a 2-Mb resolution BAC microarray for CGH analysis of canine tumors. <i>Genome Research</i> , 2005, 15, 1831-1837.	5.5	51
24	Anchoring the dog to its relatives reveals new evolutionary breakpoints across 11 species of the Canidae and provides new clues for the role of B chromosomes. <i>Chromosome Research</i> , 2011, 19, 685-708.	2.2	49
25	Growth Requirements and Chromosomal Instability of Induced Pluripotent Stem Cells Generated from Adult Canine Fibroblasts. <i>Stem Cells and Development</i> , 2013, 22, 951-963.	2.1	49
26	A novel canine lymphoma cell line: A translational and comparative model for lymphoma research. <i>Leukemia Research</i> , 2007, 31, 1709-1720.	0.8	47
27	Inactivation of the p16 Cyclin-Dependent Kinase Inhibitor in High-Grade Canine Non-Hodgkin's T-Cell Lymphoma. <i>Veterinary Pathology</i> , 2007, 44, 467-478.	1.7	45
28	A Cytogenetically Characterized, Genome-Anchored 10-Mb BAC Set and CGH Array for the Domestic Dog. <i>Journal of Heredity</i> , 2007, 98, 474-484.	2.4	32
29	Canine prostate cancer cell line (Probasco) produces osteoblastic metastases in vivo. <i>Prostate</i> , 2014, 74, 1251-1265.	2.3	30
30	IDH1 and IDH2 hotspot mutations are not found in canine glioma. <i>International Journal of Cancer</i> , 2010, 127, 245-246.	5.1	29
31	Molecular cytogenetic analysis of a novel high-grade canine T-lymphoblastic lymphoma demonstrating co-expression of CD3 and CD79a cell markers. <i>Chromosome Research</i> , 2001, 9, 649-657.	2.2	26
32	Genomic profiling of canine mast cell tumors identifies DNA copy number aberrations associated with KIT mutations and high histological grade. <i>Chromosome Research</i> , 2017, 25, 129-143.	2.2	24
33	FLT3 mutations in canine acute lymphocytic leukemia. <i>BMC Cancer</i> , 2011, 11, 38.	2.6	22
34	Extensive conservation of genomic imbalances in canine transmissible venereal tumors (CTVT) detected by microarray-based CGH analysis. <i>Chromosome Research</i> , 2009, 17, 927-934.	2.2	19
35	The Establishment of the Pfizer-Canine Comparative Oncology and Genomics Consortium Biospecimen Repository. <i>Veterinary Sciences</i> , 2015, 2, 127-130.	1.7	19
36	CD40 ligand is necessary and sufficient to support primary diffuse large B-cell lymphoma cells in culture: a tool for <i>in vitro</i> preclinical studies with primary B-cell malignancies. <i>Leukemia and Lymphoma</i> , 2012, 53, 1390-1398.	1.3	17

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37	Molecular prevalence of Bartonella, Babesia, and hemotropic Mycoplasma species in dogs with hemangiosarcoma from across the United States. PLoS ONE, 2020, 15, e0227234.	2.5	16
38	Microarray-based cytogenetic profiling reveals recurrent and subtype-associated genomic copy number aberrations in feline sarcomas. Chromosome Research, 2009, 17, 987-1000.	2.2	14
39	Cytogenomics of Feline Cancers: Advances and Opportunities. Veterinary Sciences, 2015, 2, 246-258.	1.7	13
40	Canine Histiocytic Malignancies—Challenges and Opportunities. Veterinary Sciences, 2016, 3, 2.	1.7	13
41	Genomically Complex Human Angiosarcoma and Canine Hemangiosarcoma Establish Convergent Angiogenic Transcriptional Programs Driven by Novel Gene Fusions. Molecular Cancer Research, 2021, 19, 847-861.	3.4	12
42	An integrated cytogenetic, radiation-hybrid, and comparative map of dog Chromosome 5. Mammalian Genome, 2001, 12, 371-375.	2.2	11
43	Generation and characterization of novel canine malignant mast cell line CL1. Veterinary Immunology and Immunopathology, 2009, 127, 114-124.	1.2	10
44	Genome-wide DNA copy number analysis and targeted transcriptional analysis of canine histiocytic malignancies identifies diagnostic signatures and highlights disruption of spindle assembly complex. Chromosome Research, 2019, 27, 179-202.	2.2	7
45	Naturally occurring canine cancers: powerful models for stimulating pharmacogenomic advancement in human medicine. Pharmacogenomics, 2013, 14, 1929-1931.	1.3	4
46	Evaluation of gene expression and DNA copy number profiles of adipose tissue-derived stromal cells and consecutive neurosphere-like cells generated from dogs with naturally occurring spinal cord injury. American Journal of Veterinary Research, 2017, 78, 371-380.	0.6	4
47	Development of a Genome-Wide Oligonucleotide Microarray Platform for Detection of DNA Copy Number Aberrations in Feline Cancers. Veterinary Sciences, 2020, 7, 88.	1.7	4
48	A high-resolution comparative map of canine Chromosome 5q14.3?q33 constructed utilizing the 1.5x1/2 canine genome sequence. Mammalian Genome, 2004, 15, 544-51.	2.2	3
49	Addendum: Mazcko, C., et al. The Establishment of the Pfizer-Canine Comparative Oncology and Genomics Consortium Biospecimen Repository. Vet. Sci. 2015, 2, 127-130. Veterinary Sciences, 2015, 2, 406-406.	1.7	0