

Thomas Derrien

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

16,033
citations

516561

16
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552653

26
g-index

32
all docs

32
docs citations

32
times ranked

27909
citing authors

#	ARTICLE	IF	CITATIONS
1	LncRNAs in domesticated animals: from dog to livestock species. <i>Mammalian Genome</i> , 2022, 33, 248-270.	1.0	10
2	Canine Oral Melanoma Genomic and Transcriptomic Study Defines Two Molecular Subgroups with Different Therapeutical Targets. <i>Cancers</i> , 2022, 14, 276.	1.7	3
3	Natural and human-driven selection of a single non-coding body size variant in ancient and modern canids. <i>Current Biology</i> , 2022, 32, 889-897.e9.	1.8	23
4	Long-read assembly of a Great Dane genome highlights the contribution of GC-rich sequence and mobile elements to canine genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
5	Identification of common predisposing loci to hematopoietic cancers in four dog breeds. <i>PLoS Genetics</i> , 2021, 17, e1009395.	1.5	16
6	Prognostic value of somatic focal amplifications on chromosome 30 in canine oral melanoma. <i>Veterinary and Comparative Oncology</i> , 2020, 18, 214-223.	0.8	9
7	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. <i>Scientific Reports</i> , 2020, 10, 20457.	1.6	20
8	PTPN11 mutations in canine and human disseminated histiocytic sarcoma. <i>International Journal of Cancer</i> , 2020, 147, 1657-1665.	2.3	14
9	Genome-Wide Analysis of Long Non-Coding RNA Profiles in Canine Oral Melanomas. <i>Genes</i> , 2019, 10, 477.	1.0	18
10	Transcriptome profiling of mouse samples using nanopore sequencing of cDNA and RNA molecules. <i>Scientific Reports</i> , 2019, 9, 14908.	1.6	90
11	Identification of a Missense Variant in MFSD12 Involved in Dilution of Pheomelanin Leading to White or Cream Coat Color in Dogs. <i>Genes</i> , 2019, 10, 386.	1.0	20
12	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. <i>BMC Biology</i> , 2019, 17, 108.	1.7	109
13	Characterisation and functional predictions of canine long non-coding RNAs. <i>Scientific Reports</i> , 2018, 8, 13444.	1.6	32
14	FEELnc: a tool for long non-coding RNA annotation and its application to the dog transcriptome. <i>Nucleic Acids Research</i> , 2017, 45, gkw1306.	6.5	281
15	Long noncoding RNA repertoire in chicken liver and adipose tissue. <i>Genetics Selection Evolution</i> , 2017, 49, 6.	1.2	59
16	Discovery of Human-Similar Gene Fusions in Canine Cancers. <i>Cancer Research</i> , 2017, 77, 5721-5727.	0.4	22
17	An exome sequencing based approach for genome-wide association studies in the dog. <i>Scientific Reports</i> , 2017, 7, 15680.	1.6	10
18	Bioinformatics Pipeline for Transcriptome Sequencing Analysis. <i>Methods in Molecular Biology</i> , 2017, 1468, 201-219.	0.4	19

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19	A Point Mutation in a lincRNA Upstream of GDNF Is Associated to a Canine Insensitivity to Pain: A Spontaneous Model for Human Sensory Neuropathies. PLoS Genetics, 2016, 12, e1006482.	1.5	31
20	Identification of long non-coding RNAs in insects genomes. Current Opinion in Insect Science, 2015, 7, 37-44.	2.2	39
21	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	2.4	4,217
22	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	2.4	4,428
23	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	13.7	4,484
24	Identification of Genomic Regions Associated with Phenotypic Variation between Dog Breeds using Selection Mapping. PLoS Genetics, 2011, 7, e1002316.	1.5	339
25	Long Noncoding RNAs with Enhancer-like Function in Human Cells. Cell, 2010, 143, 46-58.	13.5	1,664
26	Coat colour in dogs: identification of the merle locus in the Australian shepherd breed. BMC Veterinary Research, 2006, 2, 9.	0.7	28