## **Thomas Derrien**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6325044/publications.pdf

Version: 2024-02-01

26 papers

16,033 citations

16 h-index

26 g-index

32 all docs 32 docs citations

times ranked

32

27909 citing authors

#	Article	lF	Citations
1	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	13.7	4,484
2	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
3	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	2.4	4,217
4	Long Noncoding RNAs with Enhancer-like Function in Human Cells. Cell, 2010, 143, 46-58.	13.5	1,664
5	Identification of Genomic Regions Associated with Phenotypic Variation between Dog Breeds using Selection Mapping. PLoS Genetics, 2011, 7, e1002316.	1.5	339
6	FEELnc: a tool for long non-coding RNA annotation and its application to the dog transcriptome. Nucleic Acids Research, 2017, 45, gkw1306.	6.5	281
7	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. BMC Biology, 2019, 17, 108.	1.7	109
8	Transcriptome profiling of mouse samples using nanopore sequencing of cDNA and RNA molecules. Scientific Reports, 2019, 9, 14908.	1.6	90
9	Long noncoding RNA repertoire in chicken liver and adipose tissue. Genetics Selection Evolution, 2017, 49, 6.	1.2	59
10	Identification of long non-coding RNAs in insects genomes. Current Opinion in Insect Science, 2015, 7, 37-44.	2.2	39
11	Characterisation and functional predictions of canine long non-coding RNAs. Scientific Reports, 2018, 8, 13444.	1.6	32
12	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
13	Coat colour in dogs: identification of the merle locus in the Australian shepherd breed. BMC Veterinary Research, 2006, 2, 9.	0.7	28
14	Long-read assembly of a Great Dane genome highlights the contribution of GC-rich sequence and mobile elements to canine genomes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
15	Natural and human-driven selection of a single non-coding body size variant in ancient and modern canids. Current Biology, 2022, 32, 889-897.e9.	1.8	23
16	Discovery of Human-Similar Gene Fusions in Canine Cancers. Cancer Research, 2017, 77, 5721-5727.	0.4	22
17	Identification of a Missense Variant in MFSD12 Involved in Dilution of Phaeomelanin Leading to White or Cream Coat Color in Dogs. Genes, 2019, 10, 386.	1.0	20
18	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. Scientific Reports, 2020, 10, 20457.	1.6	20

#	Article	IF	CITATIONS
19	Bioinformatics Pipeline for Transcriptome Sequencing Analysis. Methods in Molecular Biology, 2017, 1468, 201-219.	0.4	19
20	Genome-Wide Analysis of Long Non-Coding RNA Profiles in Canine Oral Melanomas. Genes, 2019, 10, 477.	1.0	18
21	Identification of common predisposing loci to hematopoietic cancers in four dog breeds. PLoS Genetics, 2021, 17, e1009395.	1.5	16
22	PTPN11 mutations in canine and human disseminated histiocytic sarcoma. International Journal of Cancer, 2020, 147, 1657-1665.	2.3	14
23	An exome sequencing based approach for genome-wide association studies in the dog. Scientific Reports, 2017, 7, 15680.	1.6	10
24	LncRNAs in domesticated animals: from dog to livestock species. Mammalian Genome, 2022, 33, 248-270.	1.0	10
25	Prognostic value of somatic focal amplifications on chromosome 30 in canine oral melanoma. Veterinary and Comparative Oncology, 2020, 18, 214-223.	0.8	9
26	Canine Oral Melanoma Genomic and Transcriptomic Study Defines Two Molecular Subgroups with Different Therapeutical Targets. Cancers, 2022, 14, 276.	1.7	3