

# Thomas Derrien

## 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.

27  
papers

12,261  
citations

13  
h-index

32  
g-index

32  
ext. papers

14,718  
ext. citations

9.6  
avg, IF

4.8  
L-index

#	Paper	IF	Citations
27	LncRNAs in domesticated animals: from dog to livestock species. <i>Mammalian Genome</i> , <b>2021</b> , 1	3.2	2
26	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> , <b>2021</b> , 118,	11.5	6
25	Identification of common predisposing loci to hematopoietic cancers in four dog breeds. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009395	6	5
24	PTPN11 mutations in canine and human disseminated histiocytic sarcoma. <i>International Journal of Cancer</i> , <b>2020</b> , 147, 1657-1665	7.5	8
23	Prognostic value of somatic focal amplifications on chromosome 30 in canine oral melanoma. <i>Veterinary and Comparative Oncology</i> , <b>2020</b> , 18, 214-223	2.5	4
22	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. <i>Scientific Reports</i> , <b>2020</b> , 10, 20457	4.9	8
21	Identification of a Missense Variant in Involved in Dilution of Phaeomelanin Leading to White or Cream Coat Color in Dogs. <i>Genes</i> , <b>2019</b> , 10,	4.2	10
20	Genome-Wide Analysis of Long Non-Coding RNA Profiles in Canine Oral Melanomas. <i>Genes</i> , <b>2019</b> , 10,	4.2	12
19	Transcriptome profiling of mouse samples using nanopore sequencing of cDNA and RNA molecules. <i>Scientific Reports</i> , <b>2019</b> , 9, 14908	4.9	47
18	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. <i>BMC Biology</i> , <b>2019</b> , 17, 108	7.3	38
17	Characterisation and functional predictions of canine long non-coding RNAs. <i>Scientific Reports</i> , <b>2018</b> , 8, 13444	4.9	21
16	FEELnc: a tool for long non-coding RNA annotation and its application to the dog transcriptome. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e57	20.1	167
15	Long noncoding RNA repertoire in chicken liver and adipose tissue. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 6	4.9	45
14	Discovery of Human-Similar Gene Fusions in Canine Cancers. <i>Cancer Research</i> , <b>2017</b> , 77, 5721-5727	10.1	13
13	An exome sequencing based approach for genome-wide association studies in the dog. <i>Scientific Reports</i> , <b>2017</b> , 7, 15680	4.9	9
12	Bioinformatics Pipeline for Transcriptome Sequencing Analysis. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1468, 201-19	1.4	12
11	A Point Mutation in a lincRNA Upstream of GDNF Is Associated to a Canine Insensitivity to Pain: A Spontaneous Model for Human Sensory Neuropathies. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006482	6	22

10	Identification of long non-coding RNAs in insects genomes. <i>Current Opinion in Insect Science</i> , <b>2015</b> , 7, 37-44	5.1	30
9	GENCODE: the reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , <b>2012</b> , 22, 1760-74	9.7	3142
8	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , <b>2012</b> , 22, 1775-89	9.7	3408
7	Landscape of transcription in human cells. <i>Nature</i> , <b>2012</b> , 489, 101-8	50.4	3544
6	Identification of genomic regions associated with phenotypic variation between dog breeds using selection mapping. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002316	6	249
5	Long noncoding RNAs with enhancer-like function in human cells. <i>Cell</i> , <b>2010</b> , 143, 46-58	56.2	1422
4	Coat colour in dogs: identification of the merle locus in the Australian shepherd breed. <i>BMC Veterinary Research</i> , <b>2006</b> , 2, 9	2.7	16
3	Long-read assembly of a Great Dane genome highlights the contribution of GC-rich sequence and mobile elements to canine genomes		3
2	Transcriptome and chromatin structure annotation of liver, CD4+ and CD8+ T cells from four livestock species		12
1	Transcriptome profiling of mouse samples using nanopore sequencing of cDNA and RNA molecules		4