

Thomas DERRIEN, PhD

- Scientific CV -

CNRS Research Associate (CRCN) at the [IGDR \(Institute de Génétique et Développement de Rennes\)](#), Rennes, France.

- Lab : [Canine Genetics Team](#) led By Catherine André
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Research Experience

2012 – 2018	Associate Researcher (CRCN) CNRS (IGDR) - Canine genetics team (Dr C.André). => Identification and characterization of long non-coding RNAs from NGS data.	Rennes, FRANCE
2010 – 2011	Postdoctoral reasearcher at IRISA/INRA - Genscale team (Pr. D Lavenier , J-C Simon) => Improving the assembly of the aphid genomes.	Rennes, FRANCE
2008 – 2010	Postdoctoral reasearcher at CRG (Centre de Regulacio Genomica) - (Pr. R. Guigó) => Analysis of functional elements of the human genome within the ENCODE consortium.	Barcelona, SPAIN
2004 – 2007	PhD at Institute for Genetics and Development of Rennes – Dog genetics team (Dr C. Hitte). => Comparative genomics: Applications to the identification of novel canine genes.	Rennes, FRANCE

Research Interests

Long non-coding RNAs annotation ([FEELnc program](#)), evolution and functions, Transcriptome sequencing, Canine genomics, Cancer genomics, bioinformatic...

Publications (n=33 in Oct, 2018)

1. Le Béguec C, Wucher V, Lagoutte L, Cadieu E, Botharel N, Hédan B,... **Derrien, T.*** and Hitte C*. Characterisation and functional predictions of canine long non-coding RNAs. *Sci Rep.* (2018);8:13444.
2. Wucher, V., Legeai, F., Hédan, B., Rizk, G., Lagoutte, L., Leeb, T., ... **Derrien, T.*** (2017). FEELnc: A tool for long non-coding RNA annotation and its application to the dog transcriptome. *Nucleic Acids Research*, 45(8), 1–12. <https://doi.org/10.1093/nar/gkw1306>

3. Muret, K., Klopp, C., Wucher, V., Esquerré, D., Legeai, F., Lecerf, F., ... , **Derrien, T***., Lagarrigue, S*. (2017). Long noncoding RNA repertoire in chicken liver and adipose tissue. *Genetics Selection Evolution*, 49(1), 6. <https://doi.org/10.1186/s12711-016-0275-0>
4. Djebali, S., Wucher, V., Foissac, S., Hitte, C., Corre, E., & **Derrien, T***. (2017). Bioinformatics Pipeline for Transcriptome Sequencing Analysis. *Methods in molecular biology (Clifton, N.J.)*, 1468, 201–19. https://doi.org/10.1007/978-1-4939-4035-6_14
5. Ulvé, R., Rault, M., Bahin, M., Lagoutte, L., Abadie, J., De Brito, C., ... , André, C. (2017). Discovery of Human-Similar Gene Fusions in Canine Cancers. *Cancer Research*, 77(21), 5721–5727. <https://doi.org/10.1158/0008-5472.CAN-16-2691>
6. Broeckx, B. J. G., **Derrien, T.**, Mottier, S., Wucher, V., Cadieu, E., Hédan, B., ... Hitte, C. (2017). An exome sequencing based approach for genome-wide association studies in the dog. *Scientific reports*, 7(1), 15680. <https://doi.org/10.1038/s41598-017-15947-9>
7. Cormier, A., Avia, K., Sterck, L., **Derrien, T.**, Wucher, V., Andres, G., ... Cock, J. M. (2017). Re-annotation, improved large-scale assembly and establishment of a catalogue of noncoding loci for the genome of the model brown alga *Ectocarpus*. *New Phytologist*, 214(1), 219–232. <https://doi.org/10.1111/nph.14321>
8. Mathers, T. C., Chen, Y., Kaithakottil, G., Legeai, F., Mugford, S. T., Baa-Puyoulet, P., ... Hogenhout, S. A. (2017). Rapid transcriptional plasticity of duplicated gene clusters enables a clonally reproducing aphid to colonise diverse plant species. *Genome Biology*, 18(1), 27. <https://doi.org/10.1186/s13059-016-1145-3>
9. Plassais, J., Lagoutte, L., Correard, S., Paradis, M., Guaguère, E., Hédan, B., ... , **Derrien, T.**, André, C. (2016). 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*, 12(12), 1–21. <https://doi.org/10.1371/journal.pgen.1006482>
10. Schmid, M., Smith, J., Burt, D. W., Aken, B. L., Antin, P. B., Archibald, A. L., ... Zhou, H. (2015). Third Report on Chicken Genes and Chromosomes 2015: *Cytogenetic and Genome Research*, 145(2), 78–179. <https://doi.org/10.1159/000430927>
11. Broeckx, B. J. G., Hitte, C., Coopman, F., Verhoeven, G. E. C., De Keulenaer, S., De Meester, E., ... Deforce, D. (2015). Improved canine exome designs, featuring ncRNAs and increased coverage of protein coding genes. *Scientific Reports*, 5, 1–10. <https://doi.org/10.1038/srep12810>
12. Legeai, F., & **Derrien, T.** (2015). Identification of long non-coding RNAs in insects genomes. *Current Opinion in Insect Science*, 7, 37–44. <https://doi.org/10.1016/j.cois.2015.01.003>
13. Steijger, T., Abril, J. F., Engström, P. G., Kokocinski, F., Akerman, M., Alioto, T., ... Zhang, M. Q. (2013). Assessment of transcript reconstruction methods for RNA-seq. *Nature Methods*, 10(12), 1177–1184. <https://doi.org/10.1038/nmeth.2714>
14. **Derrien, T.**, Johnson, R., Bussotti, G., Tanzer, A., Djebali, S., Tilgner, H., ... Guigó, R. (2012). The GENCODE v7 catalogue of human long non-coding RNAs : Analysis of their structure , evolution and expression. *Genome Research*, 22, 1775–1789. <https://doi.org/10.1101/gr.132159.111>
15. Dunham, I., Kundaje, A., Aldred, S. F., Collins, P. J., Davis, C. A., Doyle, F., ... Lochovsky, L. (2012). An integrated encyclopedia of DNA elements in the human genome. *Nature*, 489(7414), 57–74. <https://doi.org/10.1038/nature11247>

16. Djebali, S., Davis, C. A., Merkel, A., Dobin, A., Lassmann, T., Mortazavi, A., ... Gingeras, T. R. (2012). Landscape of transcription in human cells. *Nature*, 489(7414), 101–108. <https://doi.org/10.1038/nature11233>
17. **Derrien, T.**, Vaysse, A., André, C., & Hitte, C. (2012). Annotation of the domestic dog genome sequence: Finding the missing genes. *Mammalian Genome*, 23(1-2), 124–131. <https://doi.org/10.1007/s00335-011-9372-0>
18. **Derrien, T***, Estellé, J., Sola, S. M., Knowles, D. G., Raineri, E., Guigó, R., ... Ribeca, P*.. (2012). Fast Computation and Applications of Genome Mappability. *PLoS ONE*, 7(1). <https://doi.org/10.1371/journal.pone.0030377>
19. **Derrien, T.**, Guigó, R., & Johnson, R. (2012). The long non-coding rnas: A new (p)layer in the « dark matter ». *Frontiers in Genetics*, 2(JAN), 2007–2012. <https://doi.org/10.3389/fgene.2011.00107>
20. Howald, C., Tanzer, A., Chrast, J., Kokocinski, F., **Derrien, T.**, Walters, N., ... Reymond, A. (2012). Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. *Genome Research*, 22(9), 1698–1710. <https://doi.org/10.1101/gr.134478.111>
21. **Derrien, T***, & Guigó, R. (2011). De longs ARN non codants activateurs de la transcription des gènes. *Medecine/Sciences*, 27(4), 359–361. <https://doi.org/10.1051/medsci/2011274009>
22. Vaysse, A., Ratnakumar, A., **Derrien, T.**, Axelsson, E., Pielberg, G. R., Sigurdsson, S., ... Webster, M. T. (2011). Identification of genomic regions associated with phenotypic variation between dog breeds using selection mapping. *PLoS Genetics*, 7(10). <https://doi.org/10.1371/journal.pgen.1002316>
23. Mudge, J. M., Frankish, A., Fernandez-Banet, J., Alioto, T., **Derrien, T.**, Howald, C., ... Harrow, J. (2011). The origins, evolution, and functional potential of alternative splicing in vertebrates. *Molecular biology and evolution*, 28(10), 2949–59. <https://doi.org/10.1093/molbev/msr127>
24. Myers, R. M., Stamatoyannopoulos, J., Snyder, M., Dunham, I., Hardison, R. C., Bernstein, B. E., ... Risk, B. (2011). A user's guide to the Encyclopedia of DNA elements (ENCODE). *PLoS Biology*, 9(4). <https://doi.org/10.1371/journal.pbio.1001046>
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26. Ørom, Ulf Andersson, **Derrien, T.**, Beringer, M., Gumireddy, K., Gardini, A., Bussotti, G., ... Shiekhattar, R. (2010). Long noncoding RNAs with enhancer-like function in human cells. *Cell*, 143(1), 46–58. <https://doi.org/10.1016/j.cell.2010.09.001>
27. **Derrien, T.**, Thézé, J., Vaysse, A., André, C., Ostrander, E. A., Galibert, F., & Hitte, C. (2009). Revisiting the missing protein-coding gene catalog of the domestic dog. *BMC Genomics*, 10(1), 62. <https://doi.org/10.1186/1471-2164-10-62>
28. **Derrien, T.**, André, C., Galibert, F., & Hitte, C. (2007a). Analysis of the Unassembled Part of the Dog Genome Sequence: Chromosomal Localization of 115 Genes Inferred from Multispecies Comparative Genomics. *Journal of Heredity*, (5), 461–467. <https://doi.org/10.1093/jhered/esm027>
29. **Derrien, T.**, André, C., Galibert, F., & Hitte, C. (2007b). AutoGRAPH: An interactive web server for automating and visualizing comparative genome maps. *Bioinformatics*, 23(4), 498–499. <https://doi.org/10.1093/bioinformatics/btl618>

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31. Hédan, B., Corre, S., Hitte, C., Dréano, S., Vilboux, T., **Derrien, T.**, ... André, C. (2006). Coat colour in dogs: Identification of the Merle locus in the Australian shepherd breed. *BMC Veterinary Research*. <https://doi.org/10.1186/1746-6148-2-9>
32. Hitte, C., Madeoy, J., Kirkness, E. F., Priat, C., Lorentzen, T. D., Senger, F., ... Galibert, F. (2005). Facilitating genome navigation: survey sequencing and dense radiation-hybrid gene mapping. *Nature reviews. Genetics*, 6(8), 643–8. <https://doi.org/10.1038/nrg1658>
33. Hitte, C., **Derrien, T.**, André, C., Ostrander, E. A., & Galibert, F. (2004). CRH_Server: an online comparative and radiation hybrid mapping server for the canine genome. *Bioinformatics (Oxford, England)*, 20(18), 3665–7. <https://doi.org/10.1093/bioinformatics/bth411>

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Publications in conference proceedings

- Céline Le Béguet, Valentin Wucher, Lætitia Lagoutte, Edouard Cadieu, Nadine Botherel, Benoît Hédan, Catherine André, Thomas Derrien, Christophe Hitte. . **The 9th Advances in Feline and Canine Genomics**. Saint Paul, Minnesota, USA, May 21-24 2017
- **Derrien T**, André C, Hitte C. FEELnc: Fast and Effective Extraction of Long non-coding RNAs. Communication avec actes *In Journées Ouvertes Biologie Informatique Mathématique*. Edited par Christine Gaspin 2013
- **Derrien T**, Vaysse A, Hennuy B, Coppieters W, Hédan B, André C, **Hitte C**. Computational detection and expression profiling of conserved long non-coding RNAs in the domestic dog. Communication avec actes *In Journées Ouvertes Biologie Informatique Mathématique*. Edited par François Coste et Denis Tagu, 2012, p115-121.
- Vaysse A, Ratnakumar A, **Derrien T**, Lindblad-Toh K, André C, Webster, Hitte C. Differentiation of allelic frequencies analysis identifies short genomic regions with signatures of artificial selection between canine breeds., **JOBIM-2010**. Edited by Marie-France Sagot and Olivier Gascuel, 2010.
- Vaysse A, **Derrien T**, André C, Galibert F, Hitte C. Lineage-specific pseudogenes identification through selective constraints analysis in the canine genome. **JOBIM-2009**. Edited by Eric Rivals and Irina Rusu, 2009, p145-146.
- **Derrien T**, André C, Ostrander EA, Galibert F, Hitte C. Identification de gènes et prédiction de pertes de gènes par génomique comparative : application au génome canin. **JOBIM-2008**. Edited by Jacques van Helden and Yves Moreau, 2008, p23-29.
- Guyon R., Kirkness E.F, Lorentzen T.D et al. Building comparative maps using 1.5x sequence coverage: human chromosome 1p and the canine genome. **Cold Spring Harb Symp Quant Biol**. 2003.

Book chapter

1. Djebali S, Wucher Va, Foissac S, Hitte C, Corre E, **Derrien T**. Bioinformatics pipeline for transcriptome sequencing analysis. *Methods in Molecular Biology*, 2017.

Oral Communications (selection)

1. Muret K, (...) , Derrien T and Lagarrigue S. Long-Non Coding RNAs Repertoire in Liver and Adipose Tissue in Chicken. **Plant and Animal Genome conference**. San Diego, USA, 8-13 Jan 2016.
2. Derrien T et al. FEELnc : FIExible Extraction of LncRNAs. **LncRNAs hackaton**. Hinxton, UK, Dec 2015.
3. Derrien T et al. An extended repertoire of long-non coding RNAs in the domestic dog. **The 8th Advances in Feline and Canine Genomics**. Cambridge, UK, June 2015.
4. Derrien T. Non-coding RNAs in the human ENCODE project: perspectives for "non-model" organisms. **FR-AgENCODE – SeedENCODE** joint kick-off meeting. Paris. 2014
5. Derrien T. FEELnc : Fast and Effective Extraction of Long non-coding RNAs. **Workshop AVIESAN « ARN non codants » (ITMO CMN et GGB)**. Paris. Décembre 2013
6. Derrien T. FEELnc : Fast and Effective Extraction of Long non-coding RNAs. **LBBE seminar**. Lyon. January 2013
7. Derrien T. Human long non-coding RNAs in ENCODE data. **Symbiose seminar**. Rennes, France. June 2010.
8. Derrien T. Characterization of human long non-coding RNAs from ENCODE data. **PRBB Computational seminar**, 7 Mai 2009. Barcelona, Espagne.