

1. Personal information

Emilio Mármol Sánchez, PhD.

Email: emilio.marmol.sanchez@gmail.com

ORCID: [0000-0002-4393-1740](https://orcid.org/0000-0002-4393-1740)

Social media: [Linkedin](#), [Github](#) & [Google Scholar](#).

Website: emiliomarmol.academicwebsite.com

Languages: Spanish (native) & English (Advance CAE Cambridge, Grade B - 12/10/2015).

2. Research profile

I am a researcher specialized in bioinformatics, biostatistics, genomics and transcriptomics, with **deep expertise in RNA biology, machine learning applied to omics data, and method development for challenging biological samples**. My career bridges academia, biopharma industry and research infrastructure, with experience designing and deploying computational pipelines, supporting data-driven decision making, and translating scientific results into recommendations for both expert and non-expert audiences. I have led method development across diverse contexts: **i)** predicting microRNA genes from sequencing data using machine learning during my Master's ([eMIRNA](#)), **ii)** investigating gene regulatory mechanisms during my PhD at UAB Barcelona ([EISAcompR](#)), **iii)** pioneering ancient and historical RNA recovery during my postdoctoral work at SciLifeLab and Stockholm University, **iv)** supporting cardiometabolic and rare disease portfolios as Senior Data Scientist at AstraZeneca and Senior Staff Bioinformatician at NBIS, Karolinska Institute, and **v)** currently leading the development of multi-omics techniques on archival degraded samples and FFPE human brain tissues at the University of Copenhagen.

3. Working & Academic experience

01/03/2024 – Current

Postdoctoral Fellow. Center for Evolutionary Hologenomics, The Globe Institute, University of Copenhagen (UCPH); Copenhagen, Denmark.

Project title: ‘Ancient RNA: uncovering the missing link to reveal a new era in Paleogenetics’. **Supervisor:** Dr. Tom Gilbert.

Main duties:

- Develop novel techniques for the optimization of RNA and DNA isolation, library preparation, sequencing and data analysis from museum-preserved animal specimens, with a special emphasis on extinct and/or endangered species, as well as from fresh-modern and decades-old FFPE human brain samples to build predictive AI-powered deep learning classifiers for neurological, neurodegenerative and neurodevelopmental disorders.
- Expand the set of omics techniques applicable to museum-preserved specimens beyond bulk DNA and RNA, with the application of 3D structural genomics, epigenetics and spatial transcriptomics techniques adapted to highly degraded nucleic acids.
- Support and advise RNA-seq and small RNA-seq experiments across different national and international collaborative efforts.

11/09/2023 – 23/02/2024

Senior staff Bioinformatician in Applied Biomedicine at DDLS Data Science Node, National Bioinformatics Infrastructure Sweden (NBIS), Karolinska Institute (KI); Stockholm, Sweden.

Main duties:

- Analysis of bulk RNA-seq and single-cell RNA-seq data for stratification and profiling of gene expression and regulation in inflammatory bowel disease (IBD) models.
- Support as research expert in RNA biology for the design and experimental validation of gene expression biomarkers for IBD trials using public and private human data cohorts.

25/08/2022 – 31/08/2023

Senior Data Scientist. AstraZeneca; Gothenburg, Sweden.

Main duties:

- Trial development, data analysis and drug safety counseling supporting transcriptomics and RNA biology experiments for Clinical Pharmacology and Safety Sciences (CPSS) within the Cardiovascular, Renal and Metabolism (CVRM) portfolio & Rare Diseases division (Alexion S.L.).
- Data analysis and integration for Antisense Oligo (ASO) off-target prediction and self-amplifying RNA (saRNA) oligo therapies within the CVRM portfolio.
- Artificial Intelligence liaison linking initiatives involving Machine Learning and Big Data analysis between CPSS and other departments within the CVRM portfolio.

26/08/2020 – 26/07/2022

Postdoctoral Fellow. Department of Molecular Biosciences, SciLifelab. The Wenner-Gren Institute. Stockholm University (SU); Stockholm, Sweden.

Project title: ‘Sequencing ancient RNA molecules from modern and ancient extinct species’. **Supervisors:** Dr. Marc R. Friedländer and Dr. Love Dalén.

Main duties:

- Develop laboratory and computational techniques for the isolation, library preparation, sequencing and data analysis of historical and ancient RNA molecules from extinct species.
- Co-supervision and support of single-cell RNA-seq experiments for the detection, annotation and quantification of microRNA targets in single cells using AGO-TRIBE molecular A-to-I editors.
- Support and advise RNA-seq and small RNA-seq experiments across different national and international collaborative efforts.

15/03/2016 – 15/07/2020

PhD in Animal Production. Center for Research in Agricultural Genomics (CRAG). Universitat Autònoma de Barcelona (UAB); Barcelona, Spain.

Thesis title: ‘Modulation of porcine production and molecular phenotypes by nutrition and genetics’. **Supervisor:** Dr. Marcel Amills Eras. **Grade:** Excellent *Cum Laude*.

Main duties:

- Dissect gene regulatory networks using bulk small RNA-seq and RNA-seq data in response to feed intake in muscle and adipose tissue using the pig as a model.
- Determine the effect of deleterious mutations in gene expression phenotypes using eGWAS in a commercial porcine population.
- Analyze the distribution of microRNA-linked mutations in different pig breeds and populations worldwide.
- Develop a bioinformatics pipeline to disentangle post-transcriptional regulation from other sources of gene expression variation using bulk RNA-seq data.

15/09/2016 – 13/07/2018

Master of Science in Bioinformatics and Biostatistics. Universitat Oberta de Catalunya and Universitat de Barcelona (UOC-UB); Barcelona, Spain.

Thesis title: ‘Annotation of new microRNAs in the porcine genome by using a Machine Learning approach’. **Supervisor:** Dr. Albert Pla Planas. **Grade:** 9.1/10.

Main duties:

- Develop an end-to-end pipeline to detect and annotate novel microRNA genes from small RNA-seq data, combining semi-supervised machine

learning classifiers and RNA structural inference with mRNA-microRNA interaction *in silico* prediction.

- 15/10/2016 – 14/07/2017 **Specialization Diploma in Advanced Bioinformatics.** Universidad Pablo de Olavide (UPO, online); Sevilla, Spain. **Grade:** 8.5/10.
- 15/09/2008 – 18/12/2014 **Bachelor's Degree in Veterinary Medicine.** Faculty of Veterinary Medicine, Universidad de Córdoba (UCO); Córdoba, Spain. **Grade:** 8.47/10 (2.62/4).

4. Funded projects

- 01/03/2024 – 01/03/2026 **Project title:** 'Ancient RNA: uncovering the missing link to reveal a new era in Paleogenetics (grant no. 57875)'. **Funding agency:** VILLUM FONDEN. **Budget:** DKK 2 million. **Start:** 01/03/2024. **Duration:** 2 years. **Principal Researcher:** Emilio Mármol Sánchez.

5. Data science skills

I have an extensive range of computational and bioinformatics skills, which make my research profile **highly autonomous**. Moreover, I can **quickly adopt and apply new methods in computational analysis**, as well as efficiently provide outputs and innovative approaches for ongoing or new research projects involving transcriptomics, genomics, RNA biology, evolutionary biology, network inference and machine learning.

- Antisense oligo off-target prediction and self-amplifying RNA sequencing data analysis.
- Analysis of next-generation sequencing, other omics and integrative analyses (RNA-Seq, scRNA-Seq, small RNA-Seq, PacBio & ONT-seq, Hi-C, ChIP-Seq, ATAC-Seq Microarrays, Exon-Intron Split Analysis, Alternative Splicing, Allelic Imbalance).
- Ancient DNA and RNA sequence analysis for validation and evolutionary comparison.
- 3D genomics analysis using Hi-C technology from modern and ancient sequencing data.
- Genome-wide association studies (GWAS), imputation and population statistics approaches (PLINK, GEMMA, GCTA, BEAGLE) for QTL and eQTL mapping and polymorphism segregation studies.
- Non-coding gene (miRNAs and lncRNAs) prediction using supervised, semi-supervised and unsupervised clustering and Machine Learning approaches (SVM, RF, KNN, ANN, Graph theory, Bayesian Inference, XGBoost, LightGBM, t-SNE, UMAP, PCA).
- Gene Regulatory Network analysis (WGCNA, PCIT, RIF, ARACNE, MRNET).
- Whole-Genome and Transcriptome SNP calling analysis (GATK, VCFtools, BCFtools, SAMtools, BEDtools).
- Copy Number Variant detection (PennCNV, ParseCNV).
- UNIX System and Cluster environment management (BASH, AWK, SLURM).
- Programming and algorithm development in R and UNIX (daily basis scripting expertise), Perl and Python (intermediate knowledge).
- Software developing and version control with GitHub (<https://github.com/emarmolsanchez>).

6. Laboratory skills

I have experience in genomics laboratory techniques both with fresh and ancient tissues working with RNA and DNA molecules using commercial and in-house protocols and dedicated machinery for sequencing and PCR amplification.

- RNA/DNA extraction tailored for fresh-modern and historic/ancient tissue samples.
- Hi-C and 6-base methylation library preparation from both fresh-modern and historic/ancient tissue samples.
- Library preparation protocols tailored for RNA sequencing.
- Safety procedures for historic/ancient laboratory work.
- PCR and RT-qPCR laboratory techniques for nucleic acid amplification and quantification.
- Qubit and Nanodrop for nucleic acids concentration protocols.

- Bioanalyzer and TapeStation profiling for nucleic acids integrity analysis.
- Sequencing equipment management (Illumina & Oxford NanoPore).

7. Consulting experience

01/06/2021 – 01/06/2022	Bioinformatics data analysis and scientific consulting for small RNA-Seq datasets in clinical trials. Department of Veterinary Clinical and Animal Science, Animal Genetics, Bioinformatics and Breeding. Faculty of Health and Medical Sciences, University of Copenhagen (UCPH); Copenhagen, Denmark. Collaborator: Dr. Susanna Cirera.
01/11/2021 – 28/02/2022	Bioinformatics data analysis and scientific consulting for RNA-Seq datasets as external consultant. Collaborator: DataOmics S.L.

8. Supervision experience

So far, I have **officially supervised** 2 bachelor students and 1 MSc student.

25/08/2025 – 06/02/2026	Program: Master of Biology (Faculty of Science, University of Copenhagen). Project title: ‘MicroRNA profiles in serum and bronchoalveolar lavage for equine asthma’. Student: Emilie Rudolph Røgild. Supervisor: Dr. Emilio Mármol Sánchez. Co-supervisors: Dr. Susanna Cirera & Dr. Sanni Hansen.
25/08/2025 – 13/01/2026	Program: Bachelor thesis from the Bioanalytical Degree at Copenhagen University College (Bioanalytikeruddannelsen, Københavns Professionshøjskole). Project title: ‘The Danish Brain Collection: Genomic and transcriptomic applications’. Students: Caroline Robinson Christiansen & Emily Hansen Firoozfard. Supervisor: Dr. Emilio Mármol Sánchez & Dr. Christina Kjær. *Awarded prize for best bachelor thesis presented in the Bioanalytical Degree course 2025/2026.
01/04/2025 – 26/06/2025	Program: Bachelor practicum from the Bioanalytical Degree at Copenhagen University College (Bioanalytikeruddannelsen, Københavns Professionshøjskole). Project title: ‘RNA Degradation in Pig Skeletal Muscle and Liver Tissue: Implications for Handling of Future Museum Specimens’. Students: Caroline Robinson Christiansen & Emily Hansen Firoozfard. Supervisor: Dr. Emilio Mármol Sánchez & Dr. Christina Kjær.

I will be the **main supervisor** of a MSc student from September 2026 to June 2027 hosted by Vrije Universiteit (VU) Amsterdam in collaboration with UCPH Copenhagen, Globe Institute, where I currently sit. The project will revolve around extracting structural patterns of RNA preservation using degraded sequencing data.

I have also hosted 2 bachelor students during summer 2026 for their external internships under Erasmus+ funding schemes and **co-supervised** 2 MSc students (2017/2018 and 2018/2019) and 1 undergrad student (2022) under the main supervision of Dr. Marcel Amills and Dr. Marc R. Friedländer.

9. Teaching portfolio

Since 2018 I have accumulated **161h of teaching experience** across Bachelor, MSc and undergraduate levels in three institutions: University of Copenhagen (UCPH), Stockholm University (SU) and Universitat Autònoma de Barcelona (UAB). This includes **expert lectures** in official MSc and Bachelor courses, and **practical teaching** in modules covering bioinformatics analysis (RNA-seq and small RNA-seq) and biomolecular laboratory techniques (DNA and RNA extraction, PCR, qPCR, library preparation, gel electrophoresis, and restriction enzyme digestion). Subjects taught include genomics and laboratory methods in modern domestic species, ancient DNA and RNA biomolecules, comparative mammalian genomics, and paleogenetics.

Main teacher (lecturer in MSc and Bachelor courses, 2021 to 2026):

- *Mammalian Genomics: Comparative genomics & genome evolution* (UCPH): ‘Ancient DNA and other old molecules to study mammalian evolution’ (**2h** each 2024, 2025, 2026); ‘Genetic variation, chromosomal abnormalities & Causal mutations’ (**3h** each 2025, 2026).
- *Ancient DNA & Evolution* (UCPH): ‘Ancient RNA: The missing link in paleogenetics beyond DNA and proteins’ (**3h** each 2024, 2025).
- *Palaeogenetics and Historical Genetics* (SU): ‘From aDNA to aRNA and beyond’ (**4h**, 2021).

Assistant teacher (practical modules, 2018 to 2022):

- *Bioinformatics for Molecular Biology* (SU): RNA-seq and small RNA-seq practical module (**12.5h** each 2021 and 2022).
- *Molecular Genetics applied to domestic species* (UAB): Veterinary Medicine Bachelor’s Degree, laboratory practices module (**39h** each 2018 to 2020).

10. Awards and scholarships

29/08/2025	Award for the ‘Best Archaeozoology talk’ on behalf of the International Council for Archaeozoology (ICAZ). ISBA 2025.
24/09/2024	Award for significant scientific contribution of the year by the Gizmodo Science Fair 2024 .
15/07/2020	Extraordinary Award course 2019/2020 for best PhD from the Animal and Food Science Department at Universitat Autònoma de Barcelona (UAB).
01/07/2019 – 31/08/2019	International Research Scholarship funded by the National Spanish Research Programme (FPU). Department of Animal Genetics and Integrative Biology (GABI) at the National Institute for Agronomic Research (INRAE), Université Paris-Saclay; Jouy-en-Josas, France. Budget: €3,700
01/09/2018 – 30/11/2018	International Research Scholarship funded by the National Spanish Research Programme (FPU). Department of Veterinary Clinical and Animal Science, Animal Genetics, Bioinformatics and Breeding. Faculty of Health and Medical Sciences, University of Copenhagen (UCPH); Copenhagen, Denmark. Budget: €5,150
15/03/2016 – 15/03/2020	PhD Fellowship funded by the National Spanish Research Programme (FPU). Spanish Ministry of Education. Budget: €65,688.
18/12/2014	Extraordinary Award course 2013/2014 for best grades obtained in the Faculty of Veterinary Medicine, University of Córdoba (UCO); Córdoba, Spain.
15/09/2013 – 15/07/2014	Erasmus Scholarship for international exchange . Università degli Studi di Torino (UNITO); Turin, Italy.

11. Academic leadership and management

29/04/2024 – 30/04/2024	Co-organizer of the 1 st Ancient RNA workshop funded by Carlsbergfondet. Budget: DKK 72,000. University of Copenhagen (UCPH); Copenhagen, Denmark.
01/06/2017 – 01/08/2019	PhD Union representative . Center for Research in Agricultural Genomics (CRAG). Universitat Autònoma de Barcelona (UAB); Barcelona, Spain.
11/03/2018 – 12/03/2018	Team leader in the Organization committee responsible for the Annual Congress of Young Researchers (ACYR) 2018. Center for Research in Agricultural Genomics (CRAG); Barcelona, Spain.

12. Invited talks and outreach

09/05/2026	Title: ‘From ancient DNA to ancient RNA and beyond: Toward a multi-omics future in Paleogenetics’. Organizer: Warsaw Society of Biotechnology (Symbioza) 2026. Keynote Speaker.
27/03/2026	Title: ‘Ancient RNA expression profiles from the extinct woolly mammoth’. Organizer: Bionordika & SciLifeLab.
16/02/2026	Title: ‘Ancient RNA: Unlocking the Lost Ark of palaeogenetics’. Organizer: Copenhagen RNA Club.
12/11/2025	Title: ‘Ancient RNA: a new era for palaeogenetics research’. Organizer: Ancient Genomics Colloquium Series. American Museum of Natural History (AMNH). <u>Online talk.</u>
26/07/2024	Title: ‘Ancient RNA expression profiles from the extinct woolly mammoth’. Organizer: Animal aDNA Research Community (AaRC). <u>Online talk.</u>
13/05/2024	Title: ‘How close are we to resurrecting the woolly mammoth?’. Organizer: Pint of Science Copenhagen 2024.
08/11/2023	Title: ‘Historical RNA expression profiles from the extinct Tasmanian tiger’. Organizer: LUOMUS Research Seminars. Finnish Museum of Natural History. <u>Online talk.</u>

13. Academic service

Frequent reviewer for academic journals for specialized and broad audiences such as: *Science Advances*, *BMC Genomics*, *BMC Bioinformatics*, *Genome Research*, *Scientific Reports*, *RNA*, *Journal of Animal Science and Biotechnology*, *Animal Genetics*, *Genetics*, *Selection & Evolution* etc.

14. Publications

I have published a total of **36 peer-reviewed papers** so far, of which I am first author or co-first author in 15 of them (42.8%), and corresponding author in 5 of them (14.3%). **Total citations:** 747 (2018-2026, as of 26/08/2026); **H-index:** 15; **i10-index:** 19 ([Google Scholar](#)). *: equal contribution. †: corresponding author.

A full list of all the **36 peer-reviewed papers and available preprints** is described in the following link: emiliomarmol.academicwebsite.com

Selected publications (**10 most relevant**):

- 1. Mármol-Sánchez E[†]**, Fromm B, Oskolkov N, Pochon Z, Dehasque M, Bozlak E, Brown K, Aslanzadeh M, van der Valk T, Chacón-Duque CJ, Kalogeropoulos P, Biryukova I, Heintzman PD, Furugård C, Plotnikov V, Protopopov A, Andersson B, Ersmark E, Peterson KJ, Friedländer MR, Dalén L. Ancient RNA expression profiles from the extinct woolly mammoth. *Cell* 2026; 189(1):52-69.e22. <https://doi.org/10.1016/j.cell.2025.10.025>. **Contribution:** I led the project where I performed and/or supervised all laboratory work, sequencing and data analysis. With this, I generated, for the first time, ancient transcriptional profiles from the extinct woolly mammoth using skeletal muscle and skins preserved in the permafrost for thousands of years (10,000-50,000 YBP).
- 2. Mármol-Sánchez E[†]**, Fromm B, Oskolkov N, Pochon Z, Kalogeropoulos P, Eriksson E, Biryukova I, Sekar V, Ersmark E, Andersson B, Dalén L, Friedländer MR. Historical RNA expression profiles from the extinct Tasmanian tiger. *Genome Research* 2023; 3(8):1299-1316. <https://doi.org/10.1101/gr.277663.123>. **Contribution:** I led the project performing all laboratory work, sequencing and data analysis. With this, I generated, for the first time, historic transcriptional profiles from the extinct Tasmanian tiger using skeletal muscle and skins preserved at room temperature in desiccation. It has been recognized as a significant scientific contribution of the year by the [Gizmodo Science Fair 2024](#).
- 3. Sekar V, Mármol-Sánchez E**, Kalogeropoulos P, Stanicek L, Sagredo EA, Widmark A, Doukoumopoulos E, Bonath F, Biryukova I, Friedländer MR. Detection of transcriptome-wide microRNA-target interactions in single cells with agoTRIBE. *Nature Biotechnology* 2023; 42(8):1296-1302. <https://doi.org/10.1038/s41587->

[023-01951-0](#). **Contribution:** I co-supervised, revised and actively participated as senior postdoc in the development of the computational pipeline for the detection of TRIBE-derived editing signatures in miRNA targets using single cell and bulk RNA-seq.

4. Mármol-Sánchez E, Heidemann PL*, Gredal H, Cirera S. MicroRNA profiling of cerebrospinal fluid from dogs with steroid responsive meningitis-arteritis and meningoencephalitis of unknown origin. *Frontiers in Veterinary Science* 2023; 10:1144084. <https://doi.org/10.3389/fvets.2023.1144084>. *Shared first co-authorship. **Contribution:** I performed all computational analyses of small RNA-seq and qPCR data, and contributed to data visualization, manuscript writing and editing.

5. Mármol-Sánchez E[†], Cirera S, Zingaretti LM, Jacobsen MJ, Ramayo-Caldas Y, Jørgensen CB, Fredholm M, Cardoso TF, Quintanilla R, Amills M. Modeling microRNA-driven post-transcriptional regulation using exon-intron split analysis in pigs. *Animal Genetics* 2022; 53(5):613-626. <https://doi.org/10.1111/age.13238>. **Contribution:** I led the development of a publicly available pipeline for modelling post-transcriptional regulatory signals using bulk RNA-seq data ([EISAcompR](#)). With this, I run the pipeline to generate exon-intron split profiles using porcine RNA-seq data, and integrated it with small RNA-seq data from the same experiment jointly with qPCR validation.

6. Fromm B, Høye E, Domanska D, Zhong X, Aparicio-Puerta E, Ovchinnikov V, Umul SU, Chabot P, Kang W, Aslanzadeh M, Tarbier M, **Mármol-Sánchez E**, Urgese G, Johansen M, Hovig E, Hackenberg M, Friedländer MR, Peterson KJ. MirGeneDB 2.1: Toward a complete sampling of all major animal phyla. *Nucleic Acids Research* 2022; 50(D1):D204-D210. <https://doi.org/10.1093/nar/gkab1101>. **Contribution:** I contributed to modeling folding structures for microRNA sequences, data visualization and manuscript editing.

7. Mármol-Sánchez E, Luigi-Sierra MG, Castelló A, Guan D, Quintanilla R, Tonda R, Amills M. Variability in porcine microRNA genes and its association with mRNA expression and lipid phenotypes. *Genetics Selection Evolution* 2021; 53(1):43. <https://doi.org/10.1186/s12711-021-00632-3>. **Contribution:** I led this project where I performed all laboratory work and analyzed all genome-wide sequencing data for the characterization of polymorphic sites in microRNA loci across multiple pig breeds worldwide. I also performed phenotype-genotype association analyses using gene expression data and qPCR validation.

8. Fromm B, Tarbier M, Smith O, **Mármol-Sánchez E**, Dalén L, Gilbert TP, Friedländer MR. Ancient microRNA profiles of 14,300-year-old canid samples confirm taxonomic origin and give glimpses into tissue-specific gene regulation from the Pleistocene. *RNA* 2021;27(3):324-34. <https://doi.org/10.1261/rna.078410.120>. **Contribution:** I contributed performing RNA damage analyses, microRNA quantification, data visualization, manuscript writing and editing.

9. Mármol-Sánchez E, Ramayo-Caldas Y, Quintanilla R, Cardoso TF, González-Prendes R, Tibau J, Amills M. Co-expression network analysis predicts a key role of microRNAs in the adaptation of the porcine skeletal muscle to nutrient supply. *Journal of Animal Science and Biotechnology* 2020; 11:10. <https://doi.org/10.1186/s40104-019-0412-z>. **Contribution:** I led this project where I analyzed all RNA-seq sequencing data, phenotype-genotype association analyses and performed all laboratory work, data visualization, manuscript writing and editing.

10. Mármol-Sánchez E[†], Cirera S, Quintanilla R, Pla A, Amills M. Discovery and annotation of novel microRNAs in the porcine genome by using a semi-supervised learning approach. *Genomics* 2019; 112(3):2107-2118. <https://doi.org/10.1016/j.ygeno.2019.12.005>. **Contribution:** I led the development of a publicly available pipeline for novel microRNA prediction and miRNA-mRNA target prediction using small RNA-seq data ([eMIRNA](#)) and implemented it for predicting novel microRNA candidates in the pig genome, jointly with validation using qPCR, data visualization, manuscript writing and editing.

Most relevant under review or in preparation

1. Robinson Christiansen C*, Hansen Firoozfard E*, Gilbert MTP, Mak ST, Wrenfeldt M, Kjær C, **Mármol-Sánchez E[†]**. Recovering genomic and transcriptomic profiles from decades-old FFPE brain tissues. *Under Review*. <https://www.biorxiv.org/content/10.64898/2026.04.20.719637v1>. **Contribution:** I led this project as the main supervisor of the first authors in collaboration with Dr. Christina Kjær, designed the experiments, acquired funding and contributed to laboratory work, data analysis, visualization, manuscript writing and editing.

3. Mármol-Sánchez E[†], Luigi-Sierra MG, Bardou P, Charlier C, Colli L, Cardoso TF, Crepaldi P, Bionda A, Milanesi M, Lazzari B, VarGoats Consortium, Tosser-Klopp G, Amills M. The variability of goat microRNA genes is strongly shaped by functional constraints. Under Review.

<https://doi.org/10.1101/2025.09.30.679575>. **Contribution:** I am leading this project where I have planned all the implementation and performed all the data analyses. This project involves the analysis of potentially deleterious load within noncoding loci in the goat genome and across multiple breeds world-wide with different population sizes and inbreeding trajectories through time.

4. Hinzke T, Lauber C, Hoff K, Klunk J, Tapson M, Mármol-Sánchez E, Suchard MA, Lemey P, Emslie SD, Calvignac-Spencer S. RNA virus sequences from centuries- to millennia-old Adélie penguin mummies. Under Review. <https://doi.org/10.64898/2025.12.17.693957>. **Contribution:** I contributed analyzing host RNA expression profiles in ancient penguin sequencing data.