

LUNA ZEA-REDONDO

Summary

I am a **postdoctoral researcher** in Systems Biology with **+10 years of experience** working in leading **international institutes** across Europe and the US, combining **computational and experimental approaches** to elucidate gene regulatory mechanisms in **health and disease**. My current work investigates dynamic molecular changes in midbrain dopamine neurons following a single drug exposure to identify transient and persistent regulatory programs underlying **drug-induced (mal)adaptations**. My long-term scientific goal is to apply integrative data analysis to support **data-informed decisions** in **biomedical research** and therapeutic development.

Education

- 2025** **Ph.D. Molecular Biology; Humboldt University of Berlin (HU); *summa cum laude***
Berlin, Germany | Supervisor: Prof. Dr. Ana Pombo
Thesis: Molecular mechanisms of cellular memory following a single drug exposure in dopaminergic neurons
- 2017** **M.Sc. in Bioinformatics; Autonomous University of Barcelona (UAB)**
Barcelona, Spain – New York, USA | Supervisor: Prof. Ioannis Aifantis
Thesis: The role of MED12 in Chronic Lymphocytic Leukemia
- 2015** **B.Sc. in Biochemistry and Molecular Biology; University of Cordoba (UCO);**
Cordoba, Spain | Supervisor: Prof. Rafael Rodriguez Ariza
Thesis: Computational analysis and characterization of a new DNA glycosylase/lyase from the HhH-GPD superfamily.

Research Experience

- Oct 2025 – present** **Postdoctoral fellow (bridging)**
Berlin Institute for Medical Systems Biology (MDC-BIMSB), Berlin, Germany
Laboratory of Prof. Ana Pombo (Epigenetic Regulation and Chromatin Architecture)
 - Preparing a first-author manuscript based on PhD work for submission to a peer-reviewed journal.
 - Providing scientific and analytical leadership in two collaborative projects extending my PhD on cocaine-induced Polycomb de-repression and temporal changes on other VTA cell types.
- Jan 2019 – Oct 2025** **Ph.D. student**
Berlin Institute for Medical Systems Biology (MDC-BIMSB), Berlin, Germany
Laboratory of Prof. Ana Pombo (Epigenetic Regulation and Chromatin Architecture)

- Competitively recruited through the DFG-funded IRTG 2403 program, an International Training Research Group between the Humboldt University, Berlin, Germany, and Duke University, Durham, NC, US.
- Conducted experimental and computational work on single-cell data for a co-first-author study on cell-type specialization and chromatin topology in brain cells, published in *Nature* in 2021.
- Designed and executed my main PhD project on the temporal dynamics of gene regulation following single drug exposure; manuscript in preparation for *Neuron*.
- First authorship of a literature review on enhancer function in neuronal systems, and co-authorships on four other manuscripts.
- Mentored MSc and PhD students on computational data analysis strategies.

Feb 2017 – Predoctoral fellow

Aug 2018 New York University Medical School (NYUMS), New York, US

Laboratory of Prof. Ioannis Aifantis (Pathology Department)

- Conducted genomic experiments (ChIP-seq, RNA-seq, ATAC-seq) and computational analyses on patient blood samples and cell lines to investigate the role of MED12 mutations in the onset of chronic lymphocytic leukemia.
- Performed computational genomics analyses contributing to studies on inflammation and leukemic transformation published in *Nature Immunology* and *Cell Stem Cell*.
- Contributed to writing and figure preparation for an NIH-funded R01 grant.

Apr 2016 – Visiting Researcher

Sept 2016 European Molecular Biology Laboratory (EMBL), Rome, Italy

Laboratory of Prof. Phil Avner (Dynamics of Epigenetic Regulation)

- Gained expertise in histological and imaging techniques, including embryo embedding, paraffin sectioning, staining, and immunohistochemistry/immunofluorescence on paraffin-embedded tissues.
- Cultured and genetically manipulated mouse embryonic stem (ES) cells under serum and 2i conditions.
- Processed single-cell RNA-seq samples using the Wafergen platform.
- Maintained laboratory stocks and performed genotyping of mouse lines.

Oct 2015 – Visiting Researcher

Mar 2016 Max-Planck-Institute for Molecular Genetics (MPIMG), Berlin, Germany

Laboratory of Dr. Heinrich Schrewe (Developmental Genetics)

- Gained hands-on experience in molecular and cell biology techniques, including ES-cell culture, transfection, gene targeting, and CRISPR/Cas9 genome editing.
- Generated and characterised Mediator (Med12/Med12-like) mutant embryonic stem-cell lines using both classical and CRISPR-based approaches.
- Performed Southern and western blotting, PCR, plasmid construction, bacterial transformation, and DNA sequencing for cell-line validation.

Publications

First author publications:

1. **Zea-Redondo, L.**, Franke, V., Paul, E. J., Kukalev, A., Haghverdi, L., Bouman, B. J., Arguedas Jimenez, L., Braeuning, C., Marín, O., Akalin, A., Ungless, M. A., Winick-Ng, W., & Pombo, A. **Gene regulatory mechanisms of cellular memory of a single cocaine exposure in VTA dopaminergic neurons.** *Manuscript in preparation for submission to Neuron.*

As the sole first author, I led the conceptualization and design of this project. I optimized and established single-cell experiments and performed static and time series analyses across a comprehensive time course to identify short-term and persistent gene-regulatory signatures induced by cocaine exposure. I integrated these data with published datasets to advance the understanding of the underlying molecular mechanisms. I was responsible for all data analyses, interpretation, figure preparation, and manuscript writing, with conceptual input from supervisors, and coordinated project management and collaboration among co-authors.

Code: Full computational pipeline and analysis scripts available at:

github.com/red-moonx/10X-multiome_DNs_drug_exposure

Data generated and contributed: archived in GEO (GSE307071) and Zenodo (record 16994739), to be released upon publication.

2. Winick-Ng, W.*, Kukalev, A.*, Harabula, I.*, **Zea-Redondo, L.***, Szabó, D.*, Meijer, M., Serebreni, L., Zhang, Y., Bianco, S., Chiariello, A. M., Irastorza-Azcarate, I., Thieme, C. J., Sparks, T. M., Carvalho, S., Fiorillo, L., Musella, F., Irani, E., Torlai Triglia, E., Kolodziejczyk, A. A., Abentung, A., Apostolova, G., Paul, E. J., Franke, V., Kempfer, R., Akalin, A., Teichmann, S. A., Dechant, G., Ungless, M. A., Nicodemi, M., Welch, L., Castelo-Branco, G., & Pombo, A. (2021). **Cell-type specialization is encoded by specific chromatin topologies.** *Nature*, 599, 684–691, <https://doi.org/10.1038/s41586-021-04081-2> (Shared first authorship).

As co-first author, I optimized and generated bulk and single-cell ATAC-seq libraries from murine midbrain, and integrated single-cell RNA-seq, ATAC-seq, and 3D chromatin topology datasets across different brain cell types. I performed data processing and analysis, provided conceptual input and interpretation, prepared figures, and contributed to manuscript revision.

Data generated and contributed: available at GEO (GSE174024, GSE148792).

Literature review

3. **Zea-Redondo, L.**, & Pombo, A. (2023). **Mechanisms of enhancer function in neuronal systems in health and disease.** *Current Opinion in System Biology* (32-33), <https://doi.org/10.1016/j.coisb.2022.100443>.

I wrote the initial draft of this invited review, contributed to the literature review, manuscript structure, and figure design. I also participated in editing and revision in collaboration with the senior author.

Other publications

4. Carvalho, S., **Zea-Redondo, L.**, Tang, T. C. C., Stachel-Braum, P., Miller, D., Caldas, P., Kukalev, A., Diecke, S., Grosswendt, S., Grosso, A. R., & Pombo, A. (2024). **SRRM2 splicing factor modulates cell fate in early development.** *Biology Open*, 13(4), <https://doi.org/10.1242/bio.060415>.

I processed and analyzed single-cell RNA-seq data, performing mapping, quality control, filtering, clustering, and differential expression analyses within and across cell clusters. I also advised the lead author on computational strategy, data visualization, and interpretation of single-cell results.

Data generated and contributed: available at GEO (**GSE243429**).

5. Harabula, I., Speakman, L., Musella, F., Fiorillo, L., **Zea-Redondo, L.**, Kukalev, A., Beagrie, R. A., Morris, K. J., Fernandes, L., Irastorza-Azcarate, I., Fernandes, A. M., Carvalho, S., Szabó, D., Ferrai, C., Nicodemi, M., Welch, L., & Pombo, A. (2025). **Specialised super-enhancer networks in stem cells and neurons.** *bioRxiv*. <https://doi.org/10.1101/2025.08.13.670083> (Under revision in *Genome Research*)

I optimized and generated bulk ATAC-seq datasets from ESC and in vitro differentiated neurons, performed data preprocessing, and integrated ATAC-seq with ChIP-seq data to identify and curate enhancer and super-enhancer regions in stem cells and neurons.

Data generated and contributed: archived in GEO (**GSE304720**) and Zenodo (**record 16780836**), to be released upon publication.

6. Loof, G., Szabó, D., Garg, V., Kukalev, A., **Zea-Redondo, L.**, Kempfer, R., Sparks, T. M., Zhang, Y., Thieme, C. J., Carvalho, S., Weise, A., Balachandran, M., Liehr, T., Welch, L. R., Hadjantonakis, A.-K., & Pombo, A. (2022). **3D genome topologies distinguish pluripotent epiblast and primitive endoderm cells in the mouse blastocyst.** *bioRxiv*. <https://doi.org/10.1101/2022.10.19.512781>

I generated bulk ATAC-seq libraries, performed ATAC-seq data processing and analysis, and optimized peak calling to refine chromatin accessibility profiles distinguishing pluripotent epiblast and primitive endoderm cells in the mouse blastocyst.

Data generated and contributed: archived in GEO (**GSE196080**), to be released upon publication.

7. Szabó, D., Franke, V., Bianco, S., Batiuk, M. Y., Paul, E. J., Kukalev, A., Pfisterer, U. G., Irastorza-Azcarate, I., Chiariello, A. M., Demharter, S., **Zea-Redondo, L.**, Lopez-Atalaya, J. P., Nicodemi, M., Akalin, A., Khodosevich, K., Ungless, M. A., Winick-Ng, W., & Pombo, A. (2024). **A single dose of cocaine rewires the 3D genome structure of midbrain dopamine neurons.** *bioRxiv*. <https://doi.org/10.1101/2024.05.10.593308>

I supported data interpretation, critically reviewed the manuscript before submission, and provided datasets and analyses for rebuttal preparation during the revision process.

Contributions before PhD:

8. Muto, T., Guillaumot, M., Yeung, J., Fang, J., Bennett, J., Nadorp, B., Lasry, A., **Zea-Redondo, L.**, Choi, K., Gong, Y., Walker, C. S., Hueneman, K., Bolanos, L. C., Barreyro, L., Lee, L. H., Greis, K. D., Vasylyev, N., Khodadadi-Jamayran, A., Nudler, E., Lujambio, A., Lowe, S. W., Aifantis, I., & Starczynowski, D. T. (2022). **TRAF6 functions as a tumor suppressor in myeloid malignancies by**

directly targeting MYC oncogenic activity. *Cell Stem Cell*, 29(2), 298–314.e9, <https://doi.org/10.1016/j.stem.2021.12.007>

9. Guillaumot, M., Ouazia, D., Dolgalev, I., Yeung, S. T., Kourtis, N., Dai, Y., Corrigan, K., **Zea-Redondo, L.**, Saraf, A., Florens, L., Washburn, M. P., Tikhonova, A. N., Malumbres, M., Gong, Y., Tsirigos, A., Park, C., Barbieri, C., Khanna, K. M., Busino, L., & Aifantis, I. (2019). **The E3 ubiquitin ligase SPOP controls resolution of systemic inflammation by triggering MYD88 degradation.** *Nature Immunology*, 20, 1196–1207, <https://doi.org/10.1038/s41590-019-0454-6>.

Data generated and contributed: available at GEO (GSE112542).

10. Oliveira, T. Í. S., **Zea-Redondo, L.**, Moates, G. K., Wellner, N., Cross, K., Waldron, K. W., & Azeredo, H. M. C. (2016). **Pomegranate peel pectin films as affected by montmorillonite.** *Food Chemistry*, 198, 107–112, <https://doi.org/10.1016/j.foodchem.2015.09.109>

Expertise and training

Biological Data Analysis: Processing, analyzing, and interpreting bulk and single-cell RNA-seq, ATAC-seq, ChIP-seq, and multi-omics datasets. Managing large biological datasets. Proficient in programming with R, Python and shell.

Experimental Techniques: bulk genomic (RNA-, ATAC- and ChIP-seq) library construction, single-cell 10X multiome library construction, cell culture, in situ hybridization, experience with CRISPR/Cas9 editing, transfection, histology, and general molecular biology methods.

Project Management and Conceptualization: Designing large genomic projects and allocating resources. Coordinating multidisciplinary teams to ensure effective collaboration across various project stages.

Communication: Authoring peer-reviewed scientific articles. Presenting research findings through selected talks and posters, at international conferences and seminars.

Academic services

Outreach and Organization: Organizer, *Pombo Lab Winter Retreat* (2021) and Co-organizer, *Pombo Lab Online Journal Club Series with Invited Speakers* (2020–2021).

Mentoring: Advised MSc (2025, Derek Hui) and PhD students (2022–2023, Silvia Carvalho) on single-cell transcriptomic analyses, including data pre-processing, integration, biological interpretation, and effective result presentation.

Reviewing Activities: Served as co-reviewer (2020–present) for *Nature Methods*, *Nature Biotechnology*, *Genome Biology*, *Cell Reports*, and *Molecular Systems Biology*.

Conferences

- **2024:** Spatial Omics and complexities of human diseases: Resolve and Solve (*Rome, Italy*): poster.
- **2024:** FENS forum Vienna | International Neuroscience Conference (*Vienna, Austria*): poster.
- **2023:** 16th BIMS Summer Meeting (*Berlin, Germany*): poster.
- **2022:** 14th Aegean International Conference on Genomes, Pathways and Systems Medicine (*Rhodes, Greece*): **selected talk**.
- **2022:** Abcam conference Epigenetics in the Nervous System: Development and disease (*Berlin, Germany*): poster.
- **2022:** Keystone Symposium on Single Cell Biology: Pushing New Frontiers in the Life Sciences (*Florence, Italy*): **selected talk**.

- **2019:** 4DN Annual meeting (Washington, US): poster.

Awards and Honors

- **2022:** Aegean Conference Travel Award “In recognition of an excellent research contribution” at 14th International Conference on Genomes, Pathways and Systems Medicine.
- **2022:** Selected Short-Talk at Keystone Symposium on Single Cell Biology.
- **2022:** Travel Fellowship to attend Keystone Symposium on Single Cell Biology.
- **2019:** PhD studentship; DFG-funded international training group IRTG2403.
- **2017:** *Programa Propi Pràctiques*, (UAB, Spain): awarded funding for an international research placement.
- **2015:** Erasmus+ Scholarship funded by the European Commission (Brussels, Belgium).
- **2014:** Erasmus+ Scholarships for international exchange; Institute of Food Research (UK)

Summer schools and workshops

- **2025:** Helmholtz Career and Leadership Development, (Hofgeismar, Germany; 6-18 September).
- **2025:** iNAMES summer school training course: Mixed Models (online, 29-30 April and 6-7 May).
- **2025:** Computational Genomics Course: AI-assisted data analysis (online, 3-9 March).
- **2024:** Good Scientific Practice workshop for PhD researchers (BIMSB, Berlin, 3 March).
- **2019:** SCOG workshop and hackathon “Computational single-cell genomics” (Munich, Germany; 26-28 March).
- **2019:** SCOG workshop and hackathon “Advances in single-cell epigenomics” (Linslerhof, Überherrn/Saarlouis, Germany; 4-6 November).
- **2019:** Berlin and London Joint School “Epigenetics in single cells” (MDC, Berlin - MRC LMS, London; 3rd-10th April).
- **2019:** Adobe Illustrator - Basic and Intermediate (1+1 day course, MDC, Berlin).

Resources

- **GitHub:** <https://github.com/red-moonx>: Personal repository containing code developed for the manuscript *Zea-Redondo et al., in preparation for Neuron*.
- **GEO:** [GSE307071](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE307071): 10x Genomics single-cell ATAC and gene expression datasets generated for *Zea-Redondo et al., in preparation*.
- **Zenodo:** <https://zenodo.org/records/16994739>: Repository hosting supplementary datasets associated with the manuscript *Zea-Redondo et al., in preparation*.

Languages:

English (full professional proficiency) | German (B1 level) | Spanish (native proficiency).