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# Anamaria Elek

## Computational Biologist

linkedin.com/in/anamaria-elek  
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scholar.google.com/citations

### SUMMARY

I study gene regulation and cell type-specific expression changes across evolution, development, and disease. I have extensive experience in biological data analysis and machine learning, with a track record of developing data-driven analysis approaches and visualizations that drive meaningful biological discoveries.

### SKILLS

<b>Coding</b>	Python, R, Bash, Docker, HPC, Git, Markdown, Shiny
<b>Analysis</b>	Statistical analysis, Machine Learning, Deep Learning
<b>Languages</b>	Croatian (native), English (proficient), Spanish (intermediate), German (basic)

### EXPERIENCE

**Postdoctoral Researcher in Kaessmann and Sasse labs** July 2025 — Present  
Center for Molecular Biology of Heidelberg University (ZMBH); Heidelberg, Germany

- Using deep learning to study tissue- and cell-type-specific regulatory logic of alternative splicing
- Modeling alternative splicing in vertebrates, across organs and development.

**Bioinformatician at Biodiversity Cell Atlas** April 2024 — July 2025  
Centre for Genomic Regulation (CRG); Barcelona, Spain

- Processing, analysis, integration and comparisons of single cell RNA-seq atlases, including data generated using different technologies, as well as curation of public datasets.

**Visiting PhD Student in Computational biology lab (Stein Aerts lab)** January 2024 — March 2024  
Center for AI & Computational Biology, VIB-KU Leuven; Leuven, Belgium

- Regulatory sequence analysis using convolutional neural network models.

**PhD Student in Comparative regulatory genomics group (Arnau Sebé-Pedrós lab)** November 2019 — April 2024  
Centre for Genomic Regulation (CRG); Barcelona, Spain

- Analysis and integration of multiomics data (single cell RNA-seq and single cell ATAC-seq, ChIP-seq, DAP-seq).
- Training machine learning models for analysis of gene expression and regulation (e.g. gene regulatory networks modeling, sequence based cell type classifiers).
- Developing interactive web applications for visualization, exploration and summary of single cell datasets.

**Bioinformatician in Genomics Facility (former Tumor Profiling Unit)** March 2019 — November 2019  
The Institute of Cancer Research (ICR); London, UK

- Developing computational pipelines for processing and analysis of next-generation sequencing data (RNA-seq, WGS and WES).

### EDUCATION

<b>PhD in Biomedicine</b> , Universitat Pompeu Fabra; Barcelona, Spain	2019 — 2024
<b>Master's degree in Molecular Biology</b> , University of Zagreb; Zagreb, Croatia	2017 — 2018
<b>Bachelor's degree in Molecular Biology</b> , University of Zagreb; Zagreb, Croatia	2013 — 2017

### PUBLICATIONS

ORCID: 0000-0002-3938-2494

Elek, A.\*, Iglesias, M.\*, Mahieu, L., Zolotarov, G., Grau-Bové, X., Aerts, et al. (2025). "Decoding cnidarian cell type gene regulations". *Nature Ecology Evolution*. doi: [10.1038/s41559-025-02906-1](https://doi.org/10.1038/s41559-025-02906-1).

Levy, S.\*, Elek, A.\*, Grau-Bové, X., Menéndez-Bravo, S., Iglesias, M., Tanay, A., et al. (2021). "A stony coral cell atlas illuminates the molecular and cellular basis of coral symbiosis, calcification, and immunity". *Cell* 184.11, 2973–2987.e18. doi: [10.1016/j.cell.2021.04.005](https://doi.org/10.1016/j.cell.2021.04.005).

Kim, I. V., Navarrete, C., Grau-Bové, X., Iglesias, M., Elek, A., Zolotarov, G., et al. (2025). "Chromatin loops are an ancestral hallmark of the animal regulatory genome". *Nature* 642.8069, pp. 1097–1105. ISSN: 1476-4687. doi: [10.1038/s41586-025-08960-w](https://doi.org/10.1038/s41586-025-08960-w).

Grau-Bové, X.\*, Subirana, L.\*, Meister, L.\*, Soubigou, A., Neto, A., Elek, A., et al. (2024). "An amphioxus neurula stage cell atlas supports a complex scenario for the emergence of vertebrate head mesoderm". *Nature Communications* 15.1, p. 4550. doi: [10.1038/s41467-024-48774-4](https://doi.org/10.1038/s41467-024-48774-4).

Najle, S. R.\*, Grau-Bové, X.\*, Elek, A., Navarrete, C., Cianferoni, D., Chiva, C., et al. (2023). "Stepwise emergence of the neuronal gene expression program in early animal evolution". *Cell* 186.21, 4676–4693.e29. ISSN: 0092-8674. doi: [10.1016/j.cell.2023.08.027](https://doi.org/10.1016/j.cell.2023.08.027).

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- Li, Y., Slavik, K. M., Toyoda, H. C., Morehouse, B. R., Oliveira Mann, C. C. de, Elek, A., et al. (2023). "cGLRs are a diverse family of pattern recognition receptors in innate immunity". *Cell* 186.15, 3261–3276.e20. ISSN: 0092-8674. DOI: [10.1016/j.cell.2023.05.038](https://doi.org/10.1016/j.cell.2023.05.038).
- Miguel-Escalada, I., Maestro, M. Á., Balboa, D., Elek, A., Bernal, A., Bernardo, E., et al. (2022). "Pancreas agenesis mutations disrupt a lead enhancer controlling a developmental enhancer cluster". *Developmental Cell* 57.16, 1922–1936.e9. ISSN: 1534-5807. DOI: [10.1016/j.devcel.2022.07.014](https://doi.org/10.1016/j.devcel.2022.07.014).
- García-Castro, H., Kenny, N. J., Iglesias, M., Álvarez-Campos, P., Mason, V., Elek, A., et al. (2021). "ACME dissociation: a versatile cell fixation-dissociation method for single-cell transcriptomics". *Genome Biology* 22.1. ISSN: 1474-760X. DOI: [10.1186/s13059-021-02302-5](https://doi.org/10.1186/s13059-021-02302-5).
- Roje, B.\*, Elek, A.\*, Palada, V., Bom, J., Iljazovic, A., Simic, A., et al. (2020). "Microbiota alters urinary bladder weight and gene expression". *Microorganisms* 8.3. DOI: [10.3390/microorganisms8030421](https://doi.org/10.3390/microorganisms8030421).
- Elek, A., Kuzman, M., and Vlahovicek, K. (2018). *coRdon: codon usage analysis and prediction of gene expressivity*. DOI: [10.18129/B9.BIOC.CORDON](https://doi.org/10.18129/B9.BIOC.CORDON).

\* These authors contributed equally.

## PRESENTATIONS

- EMBO Meeting: The evolution of animal genomes** Sevilla, Spain September 2023  
Regulatory characterization of cell types in *Nematostella vectensis*. (poster)
- Single Cell Biology** Wellcome Trust Campus, Hinxton, UK June 2022  
Integration of whole-organism single cell atlases for comparative studies of animal cell types. (poster)
- Single Cell Genomics Symposium** Barcelona, Spain March 2022  
Single cell approaches for comparative and regulatory characterization of animal cell types. (presentation)
- BCN Single Cell Club** online July 2021  
Coral cell atlas and a quest to understand cell type evolution. (presentation)
- EMBO Meeting: The Identity and Evolution of Cell Types** online May 2021  
A stony coral cell atlas illuminates the molecular and cellular basis of coral symbiosis, calcification, and immunity. (poster)

## AWARDS

- EMBO Postdoctoral Fellowship** 2026 — 2027
- SSC Fellows Program** Scientific Software Center, Heidelberg University 2025
- FPI Severo Ochoa PhD Scholarship** Spanish Ministry of Science 2019 — 2024
- Best Poster Award** EMBO meeting: The Identity and Evolution of Cell Types May 2021
- Vienna Biocenter Summer School Fellowship** July — August 2017

## TEACHING AND OUTREACH

- Deep Learning for Regulatory Genomics: Modeling Sequence-to-Function** course at the Heidelberg University January 2026  
This was a project course for the Molecular Biosciences Master's degree programme. I contributed to preparing course content and teaching materials, and held a lecture with practical workshop on TF-MoDISco. I also mentored a group of students working on 10-weeks-long project.
- UBDS3**, data science summer school; Uzhorod, Ukraine August 2024  
I prepared and conducted workshops on clustering and supervised machine learning.
- NGSchool**, bioinformatics summer school; Warsaw, Poland and online 2021 — 2022  
I was a member of the organizing committee and developed [NGSchool website](#).  
I was teaching machine learning and programming in R, and mentored a hackathon team working on a week long RNA-seq analysis project.
- Introduction to Machine Learning**, CRG internal training course; Barcelona, Spain May 2021  
I gave a lecture on feature selection and dimensionality reduction, with a hands-on session using scikit-learn.