





Decoding transcription regulation in regeneration by advanced genomics and computational tools

https://danio-recode.eu/

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Reactivating regeneration in animals beyond natural limits is a key question in regenerative medicine. Can mammals regain lost regenerative abilities of fish and amphibians or is this potential permanently lost? To answer this broader question, we will ask questions such as,

- What are the regulators of genes activated in regeneration in highly regenerative models such as zebrafish?
- · What are the shared genetic components (genes and regulatory elements) that regulate regeneration of different tissues and organs?
- How much do these regulatory components overlap in non-regenerating vertebrates?



Imperial College London



University Hospital Schleswig Holstein



Karlsruhe Institute of Technology



University of Tuebingen











Johannes Kepler University



Institute of Mol Biotechnology



The objective of DANIO-ReCODE is to provide world-class doctoral training to a new generation of early-career researchers. We offer 15 doctoral positions within the multidisciplinary expertise of 12 research laboratories in the EU an UK:

- 1. cis-regulation during *in vivo* and *in vitro* organ development.
- 2. Epigenetic interpretation of cell extrinsic mechanical properties of zebrafish eye organoids.
- 3. Deciphering molecular mechanisms underlying successful brain regeneration in zebrafish.
- 4. Characterization of cis-regulatory networks in cardiac muscle de- and re-differentiation in heart regeneration.
- 5. Promoter architecture and usage during zebrafish, axolotl, and mouse regenerative neurogenesis.
- **6.** Novel approaches to integrate genomic information from model organisms into human regulatory landscapes.
- 7. Identifying the gene regulatory code for regeneration.

- 8. Deciphering molecular programs regulating the reversible quiescence of mammalian neural stem cells.
- 9. Conversational AI for exploring complex data in tissue regeneration research.
- 10. An innovative genome browser to integrate time-resolved single-cell and bulk-cell data.
- 11. Novel solutions for combining multi-omics embeddings and regulatory network visualisations.
- 12. Annotation, characterisation, and conservation of 3D chromatin topology in telencephalon injury.
- **13.** Multi-omic characterisation of transcription initiation regulation in development and injury response.
- **14.** Comparative epigenomics of vertebrate regeneration
- **15.** Cross-species cell atlases for regeneration.