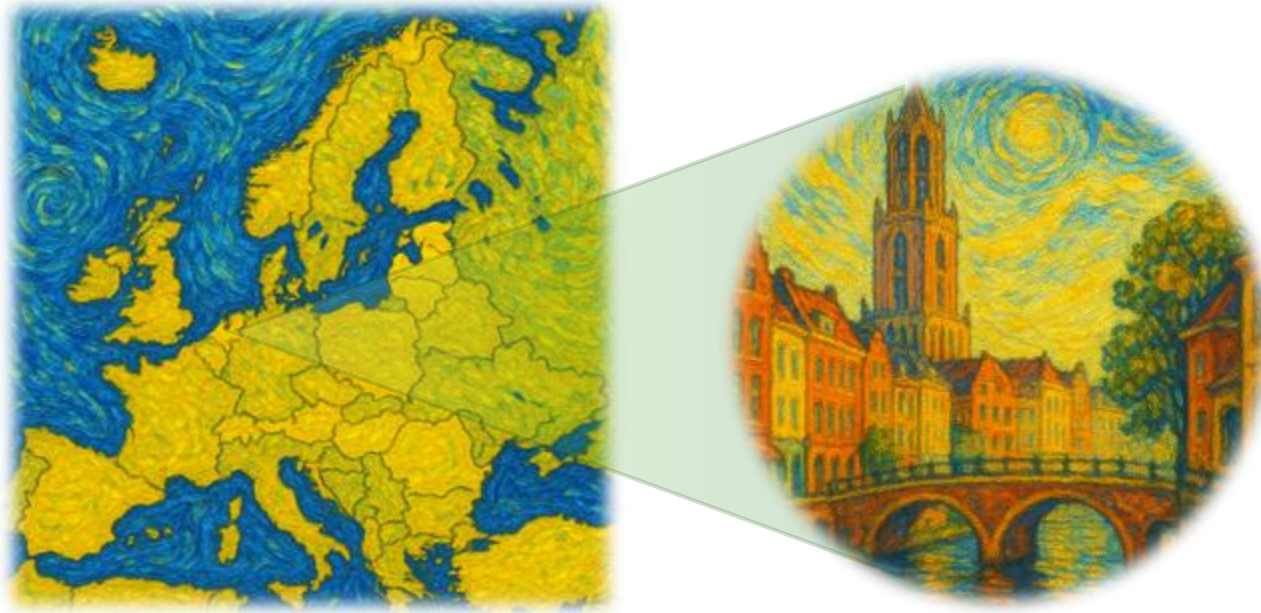




Computational Cancer Biology Lab

Asst. Prof. Dr. Stefan Prekovic, group leader





“Well, in our country,” said Alice, still panting a little, “you’d generally get to somewhere else — if you run very fast for a long time, as we’ve been doing.”

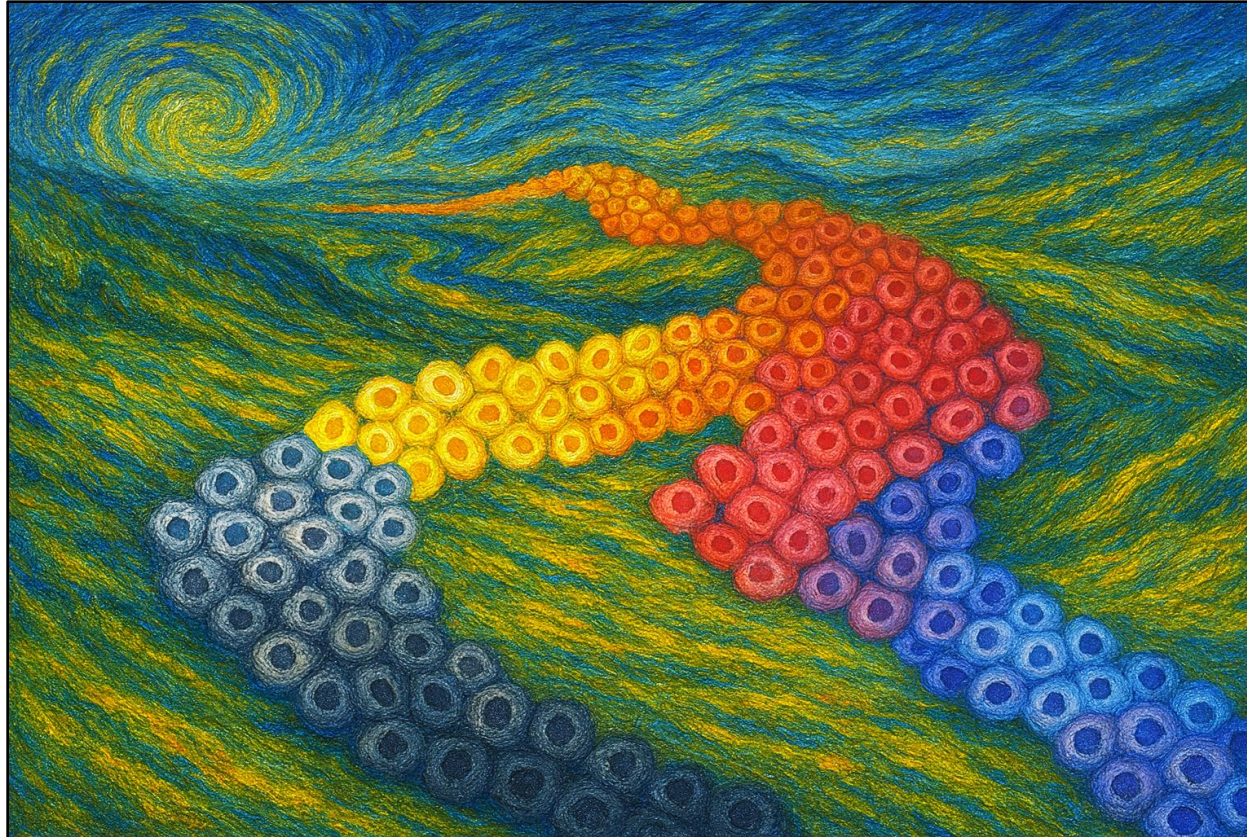
“A slow sort of country!” said the Queen. “Now, here, you see, it takes all the running you can do, to keep in the same place. If you want to get somewhere else, you must run at least twice as fast as that!”

— Lewis Carroll, *Alice through the Looking Glass*

Red Queen Hypothesis



Cancer Progression



Cancer Cell Evolution



Vendramin, Roberto, Kevin Litchfield, and Charles Swanton. "Cancer evolution: Darwin and beyond." *The EMBO Journal* 40.18 (2021): e108389.

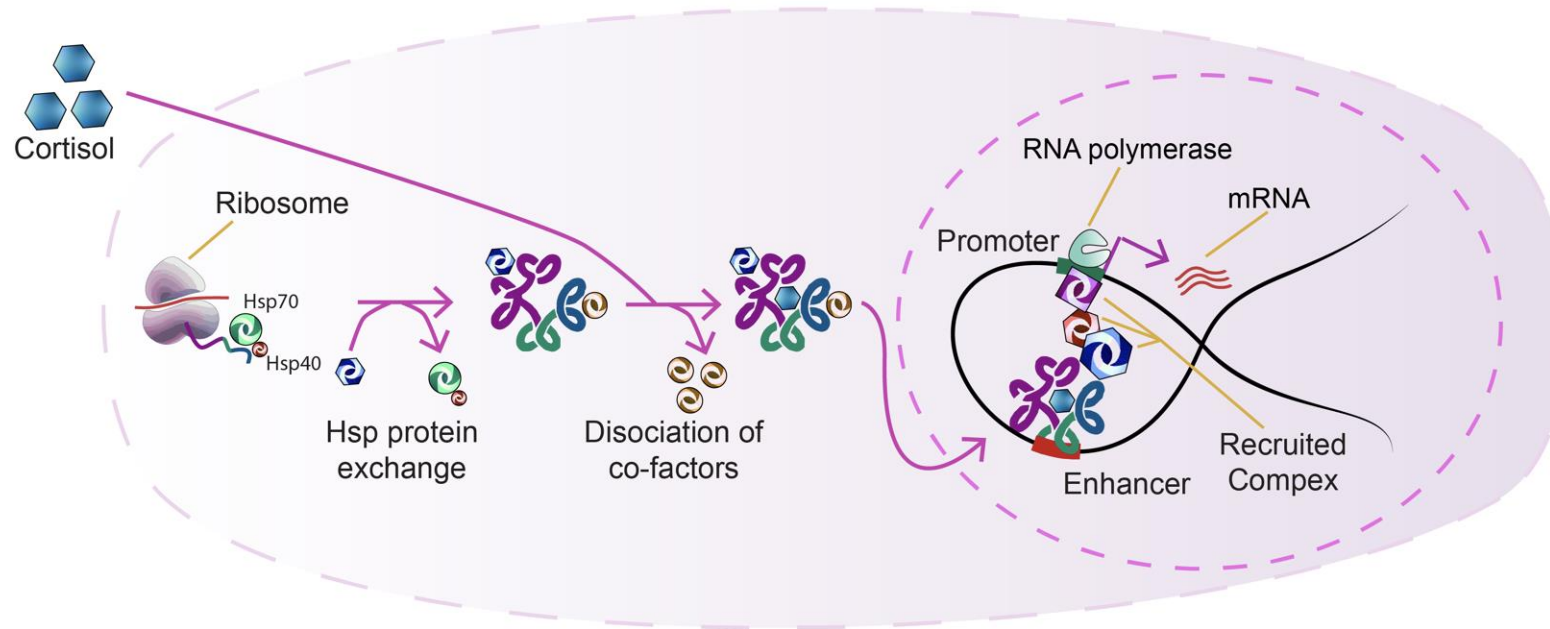
Prekovic Lab



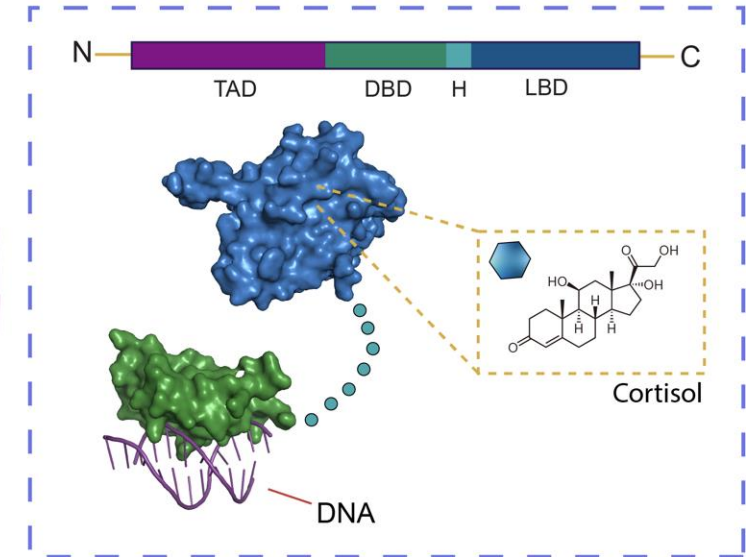
Cancer Cell Transdifferentiation



Transcription Factors



GR Structure



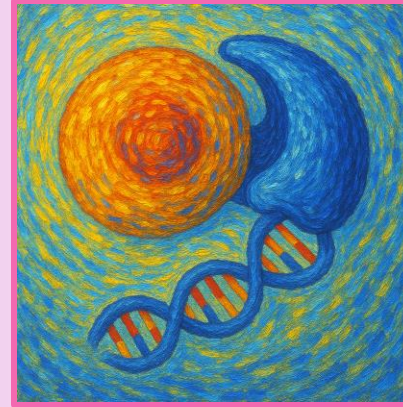
To understand how transcription factors support cancer cell identity switching to discover novel biomarkers and therapeutic routes.



What is Our Approach?

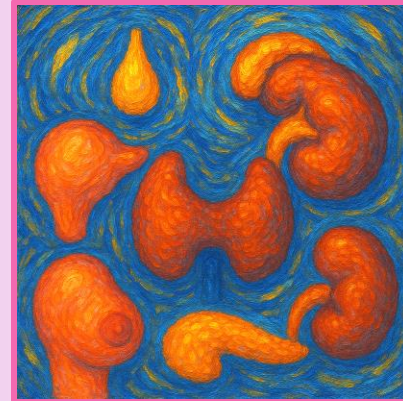


Nucleus



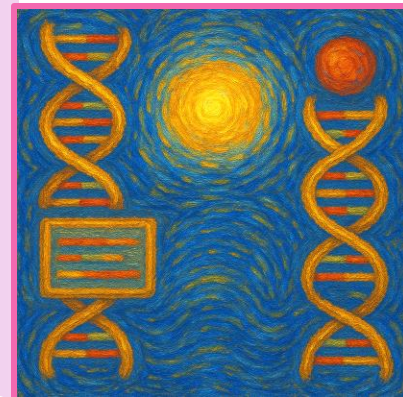
Nuclear Receptors

- Target Gene Selection
- Interactomics
- Regulation of Translation



Endocrine Cancers

- Transcriptional Heterogeneity
- Developing New Models
- Clinical Cohorts



Gene Regulation

- 3D genome integration
- Genetic Drivers
- Methods Development



Wet-Lab

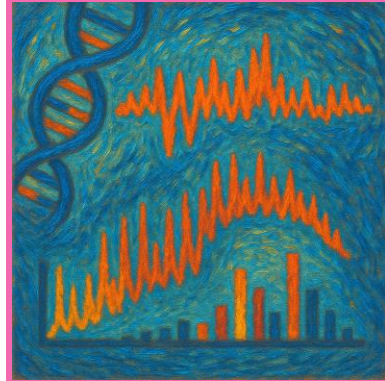
Transcriptomics



ChIP-seq



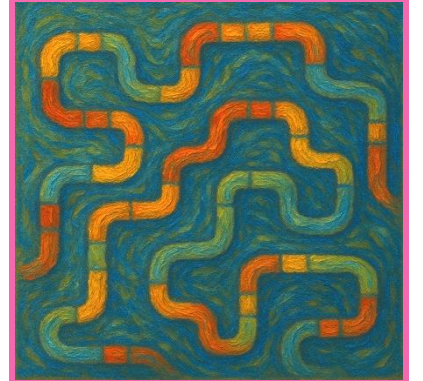
ATAC-seq



CC Techniques



Workflows



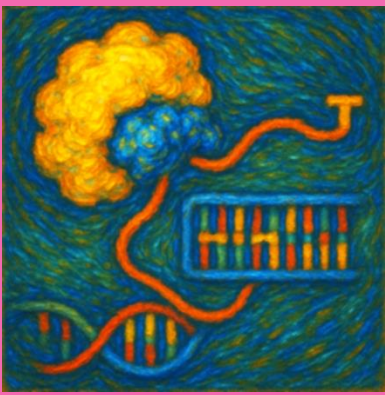
Ribo-Seq



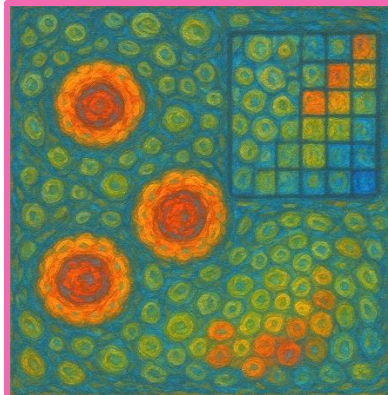
RIME



Screens



Spatial Techniques



Data Integration



Potential Collaborations with Korean Researchers



Korea



Min-Jun Baek



Hong Sook Kim



Joon Ho Kang



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Erasmus+



UMC Utrecht
Center for Molecular Medicine

Strategic Program Cancer

