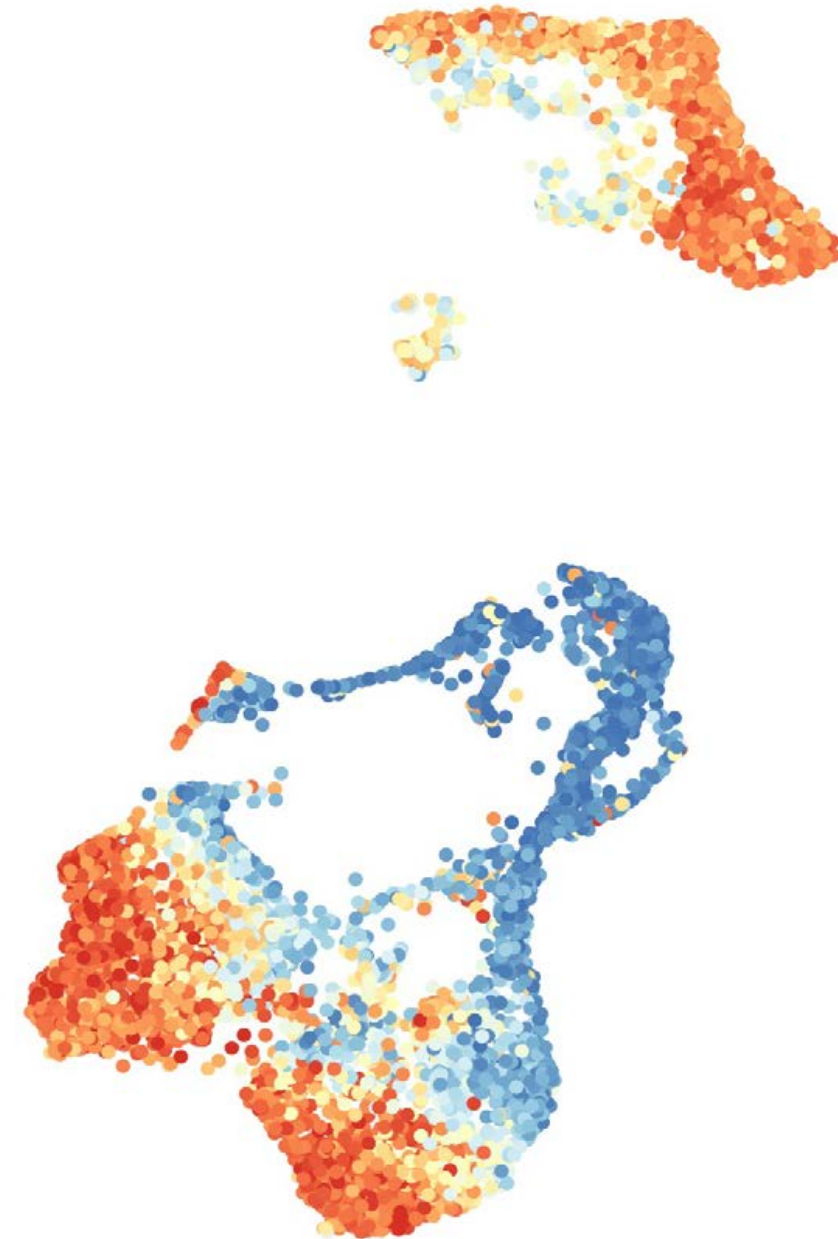
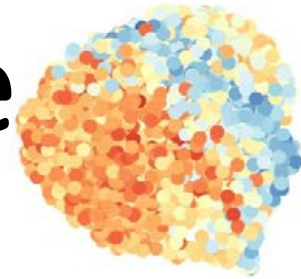




# Deling av sekvensdata frå titusenvis av humane enkeltceller



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Institutt for medisinske basalfag

Avdeling for Molekylærmedisin

Det Medisinske Fakultet

Universitetet i Oslo

QualiFAIR 28.03.2023

Eskeland 2023



Foto:colourbox

Alle cellene i  
kroppen har  
same DNA



# Den genetiske koden fyller ei bokhylle

3 milliardar basepar koder for oppskrifta til alle molekyl som dannar kroppens celler, vev og organ.

Foto: privat

Frå wellcomecollection

Eskeland 2023





Foto:colourbox

# Epigenetikk fungerer som kjemiske brytarar

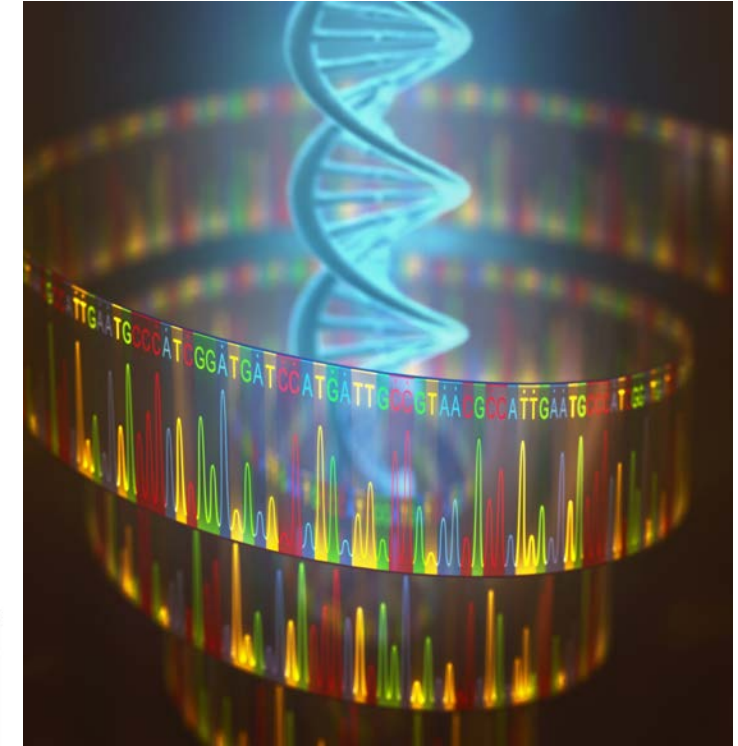
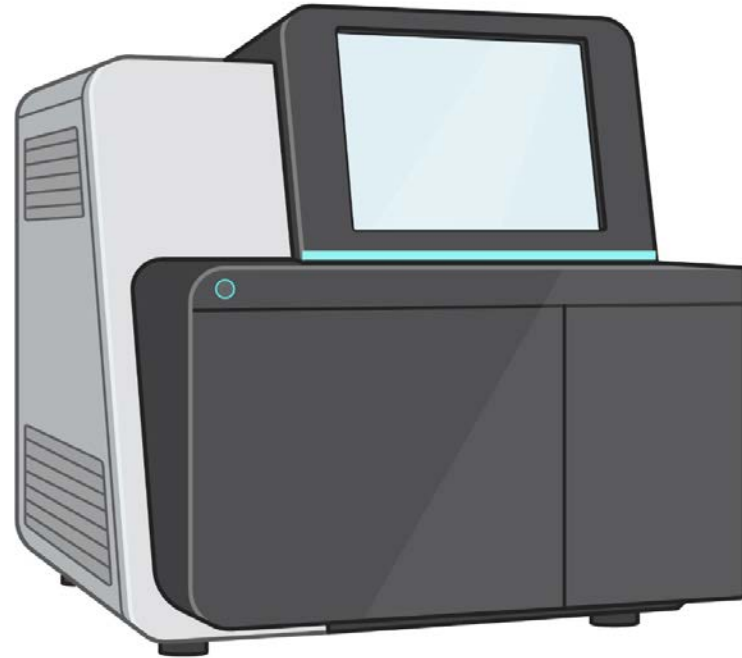
Kan skru av, på eller "dimme" genene sin aktivitet

"Epi" – betyr oppå/over



# Sekvenseringsteknologi er nøkkelen

- Forskjellen på celletypene, epigenetiske landskapet, er kva gener som er skrudd på eller av.
- Sekvensering av arvematerialet eller RNA kan identifisere nye celletypar.



RNA

DNA

# Genomet vårt



Human Genom Prosjekt: 1990- 2006

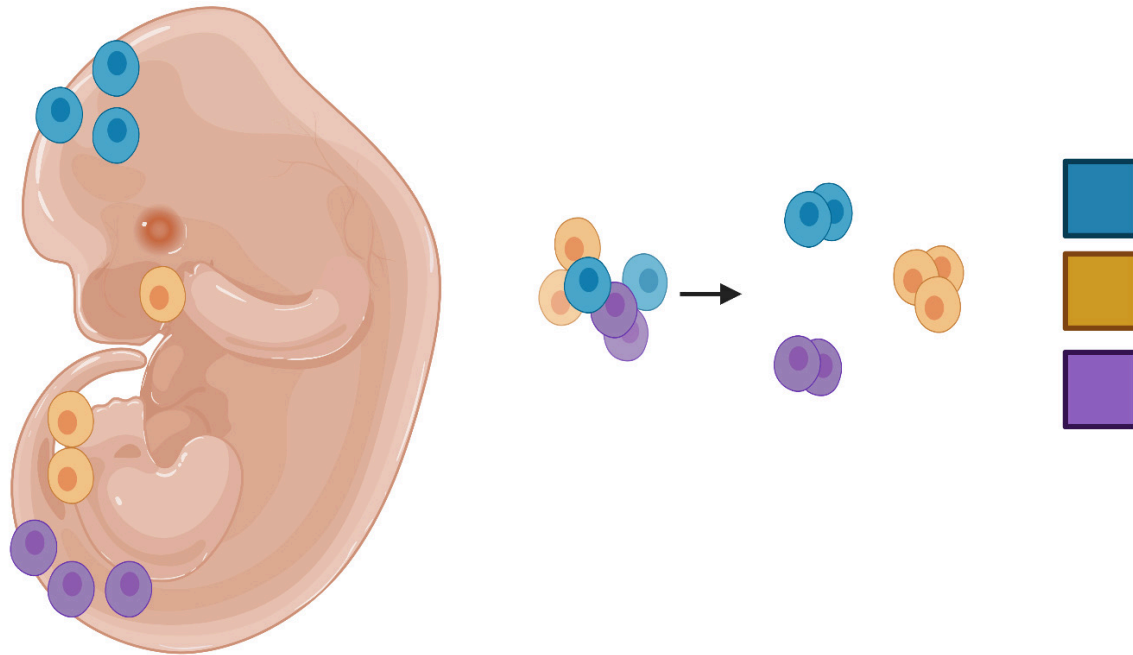


=



Menneskets genom tilsvarar 2x 750 MB

# Sekvensering av enkeltceller har vore banebrytande for celleidentifiseringa



## Method of the Year 2013

*Nature Methods* 11, 1 (2014) | [Cite this article](#)

32k Accesses | 46 Citations | 133 Altmetric | [Metrics](#)

**Methods to sequence the DNA and RNA of single cells are poised to transform many areas of biology and medicine.**

Editorial | [Published: 06 January 2020](#)

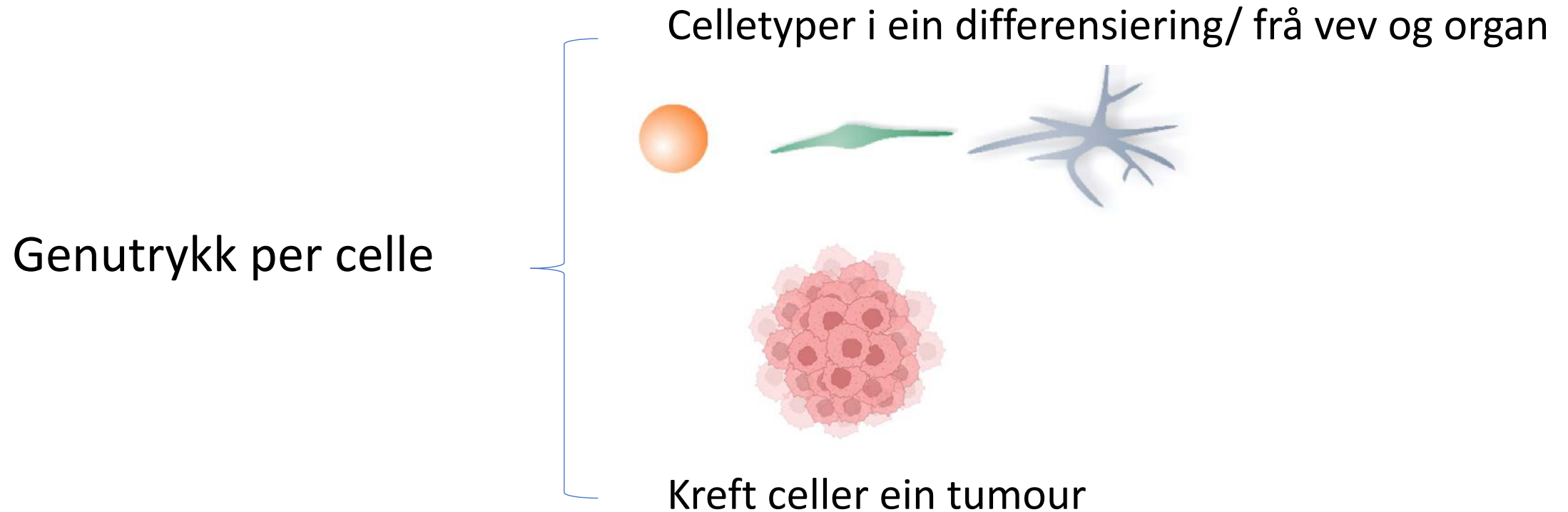
## Method of the Year 2019: Single-cell multimodal omics

*Nature Methods* 17, 1 (2020) | [Cite this article](#)

38k Accesses | 48 Citations | 128 Altmetric | [Metrics](#)

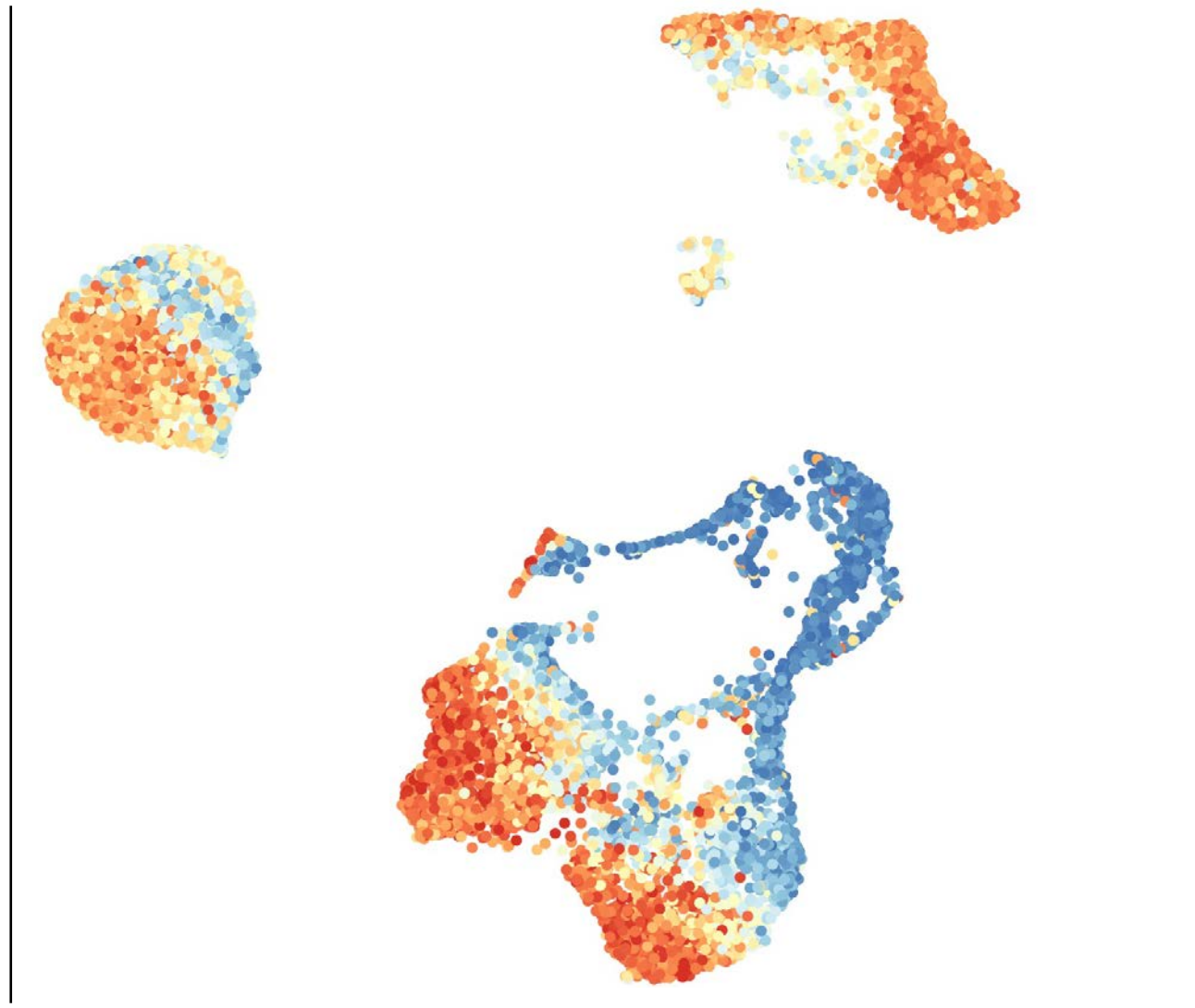
**Multimodal omics measurement offers opportunities for gaining holistic views of cells one by one.**

# Sekvensering av genuttrykk i individuelle celler





# Titusenvis av celler blir sekvensert



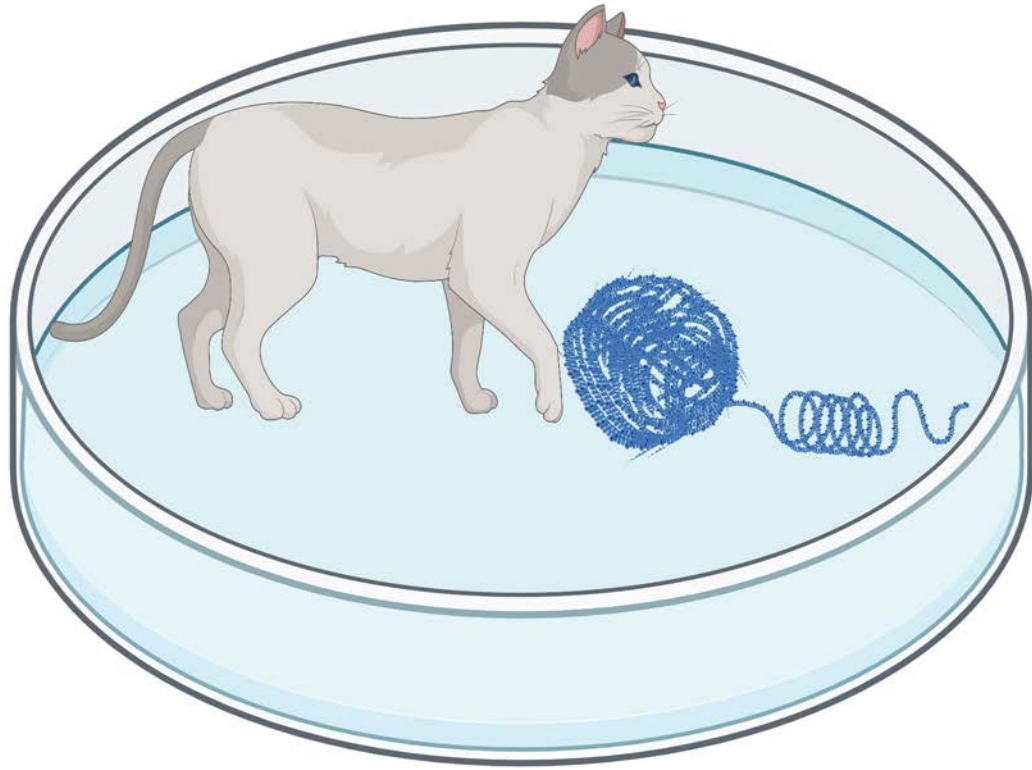
UMAP plot

Nervedifferensiering frå human embryonale stamceller

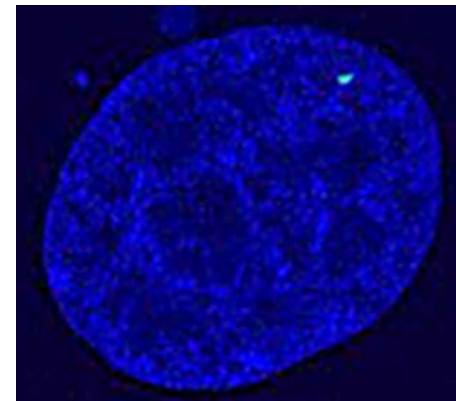
Kvar prikk representerer ei enkelt celle

Samara et al., 2022, iScience

# Katten og eit DNA garnnøste



Måling av åpne DNA områder i enkeltceller gjev informasjon om det epigenetiske landskapet og celletypen.



# Genom sekvenser deles via NCBI GEO

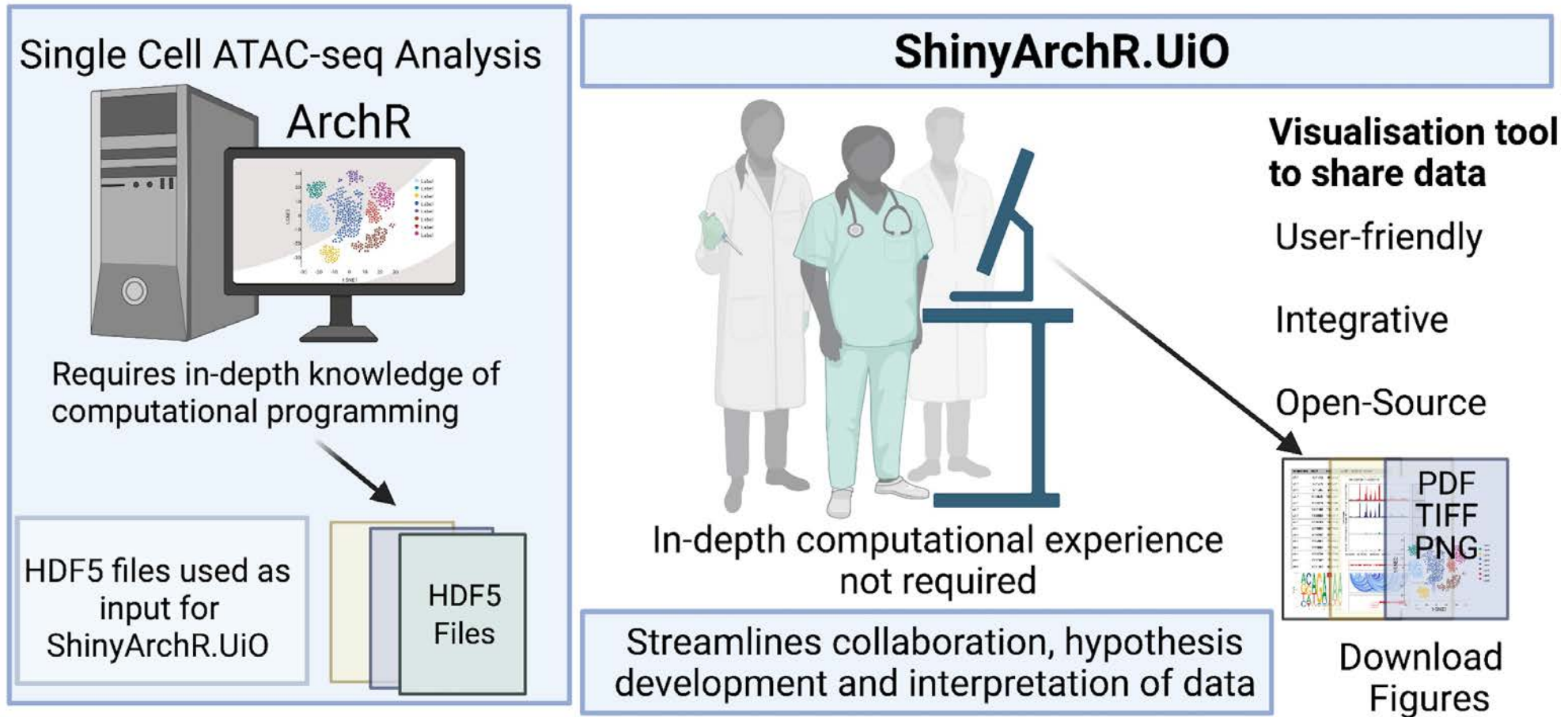
The screenshot displays the NCBI GEO website interface. At the top, it identifies itself as an official website of the United States government, part of the National Library of Medicine (NIH) National Center for Biotechnology Information. A search bar contains the term 'Eskeland'. The search results are displayed in a list format, showing three items. The first item is titled 'Epigenome analysis and Gene expression analysis of hESCs undergoing neuronal differentiation' and includes details such as organism (Homo sapiens), type (Methylation profiling by genome tiling array; Expression profiling by high throughput sequencing; Genome binding/occupancy profiling by high throughput sequencing), platforms (GPL21145 GPL27644 51 Samples), and accession numbers (GSE192858 ID: 200192858). The second item is 'Gene expression analysis of hESCs undergoing neuronal differentiation [scRNA-seq]' and the third is 'Single-cell ATAC-seq analysis of hESCs undergoing neuronal differentiation [scATAC-seq]'. The interface also includes navigation options like 'First', 'Prev', 'Page 1 of 2', 'Next', and 'Last', as well as filters and related data sections.



2018: GDPR for Humane data  
TSD UiO Sikker analyse og lagring  
Eskeland 2023

UiO : Institute of Basic Medical Sciences  
University of Oslo

# Open deling av enkeltcelle landskap



Sharma et al.,2021, Bioinformatics

Eskeland 2023



# ShinyArchR.UiO

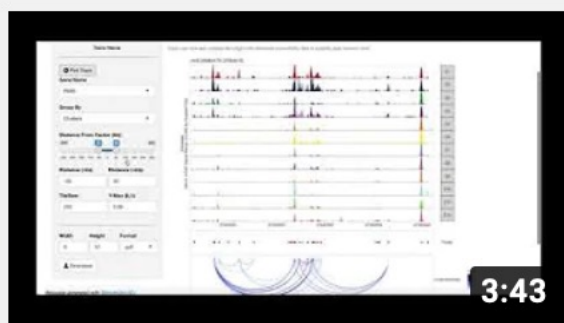
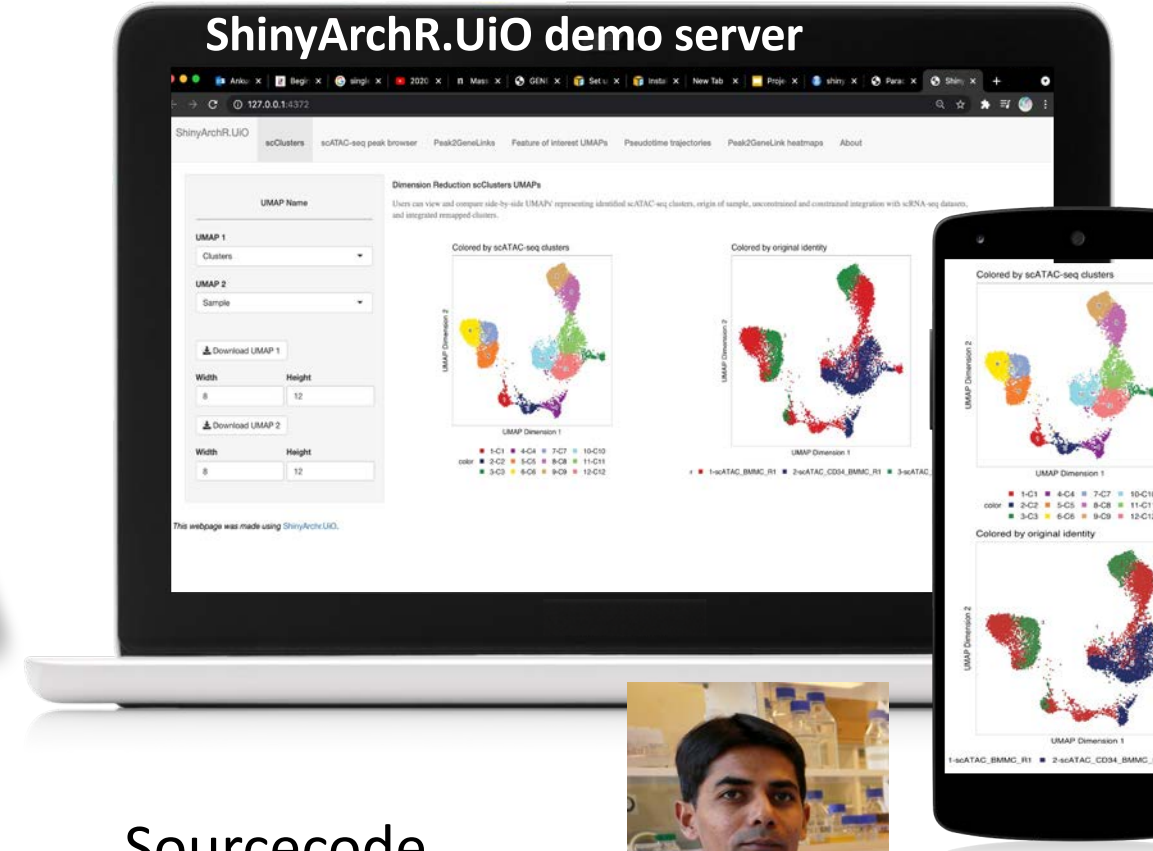
OXFORD ACADEMIC

Bioinformatics

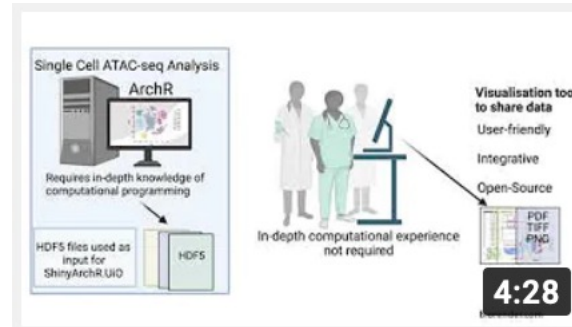
Genome Analysis

**ShinyArchR.UiO: user-friendly, integrative and open-source tool for visualization of single-cell ATAC-seq data using ArchR**

Ankush Sharma <sup>1,2,3,4,5,\*</sup>, Akshay Akshay <sup>6</sup>, Marie Rogne <sup>3,5</sup> and Ragnhild Eskeland <sup>3,4,5,\*</sup>



Introduction to ShinyArchR.UiO for single-...



Setup ShinyArchR.UiO

## Sourcecode

<https://github.com/EskelandLab/ShinyArchRUiO>

<https://cancell.medisin.uio.no>



Ankush Sharma

<https://www.youtube.com/watch?v=gIUggJWIWCw>  
<https://www.youtube.com/watch?v=diyySkVfmks>

Eskeland 2023

# Open sharing of single-cell datasets

Findability, accessibility, interoperability, and reusability

FAIR@uio

Både UiO og eksterne finansiører stiller krav til økt åpenhet i forskning, med større grad av gjenbruk og deling av data. For at det skal være mulig i praksis trengs rike metadata, slik at data i seg selv blir FAIR (Findable, Accessible, Interoperable, Reusable). Dagens satsning rundt FAIR data – Open Science og data management kombinert med arbeid rundt datahåndteringsplaner og kursing innen datahåndtering bør fortsettes ved UiO.

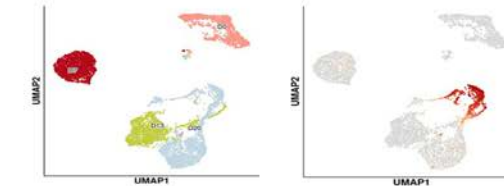
- Deling av ikke sensitive data
- Legg alle data tilgjengelig frå publisering av preprint
- Lisenser for videre bruk i nye publikasjoner

<https://cancell.medisin.uio.no>

## Single-Cell Projects

Welcome to Chromatin Biology group Single-Cell Data server. Here users are able to visualize and explore our single-cell datasets. All scripts are made available in <https://github.com/EskelandLab>.

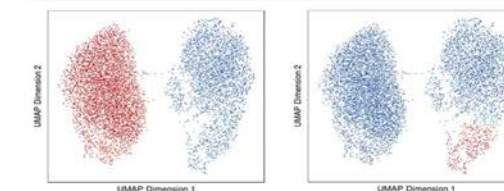
### Human ESC Neuronal differentiation scRNA-seq



We have developed a neuronal differentiation protocol and studied gene expression by single-cell RNA-seq at four time points: From Human Embryonic Stem Cells (Day 0), and Days 7, 13 and 20 of neuronal differentiation. Here we present a searchable interactive web-tool utilising ShinyCell that allows users to explore expression of their favourite genes in individual cells and annotated cell populations during the timeline of the differentiation.

For more details read our preprint, Samara et al., "A multi-omics approach to visualize early neuronal differentiation in 4D" at [bioRxiv.org](https://doi.org/10.1101/2021.03.18.437888).

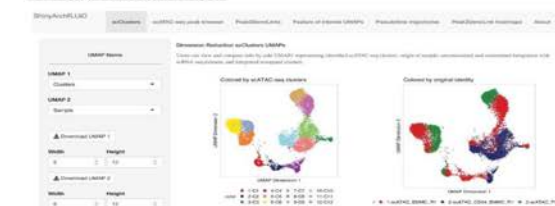
### Human ESC Neuronal differentiation scATAC-seq



Utilizing our new neuronal differentiation protocol, we have performed scATAC-seq to explore chromatin accessibility landscapes in the cells in the beginning (ESC, Day 0) and at differentiation endpoint (Day 20). The data has been analyzed using ArchR and is openly available for the user in a web tool based on our in house ShinyArchR.UIO. Take a tour into the epigenetic landscape of these cells and utilize different functionalities to learn more about gene regulation during differentiation.

For more details read our preprint, Samara et al., "A multi-omics approach to visualize early neuronal differentiation in 4D" at [bioRxiv.org](https://doi.org/10.1101/2021.03.18.437888).

### ShinyArchR.UIO



We have created ShinyArchR.UIO, an R-based Shiny app, that promotes scATAC-seq data accessibility and visualisation in a user-friendly, interactive, and open-source web interface. ShinyArchR.UIO is a tool that can streamline collaborative efforts for interpretation of large chromatin accessibility datasets and promote open access data sharing for wider audiences.

Sharma, A., Akshay, A., Rogne, M., and Eskeland, R. (2021). ShinyArchR.UIO: user-friendly, integrative and open-source tool for visualization of single-cell ATAC-seq data using ArchR. *Bioinformatics*.

Learn more about ShinyArchR.UIO in our short Introduction video.

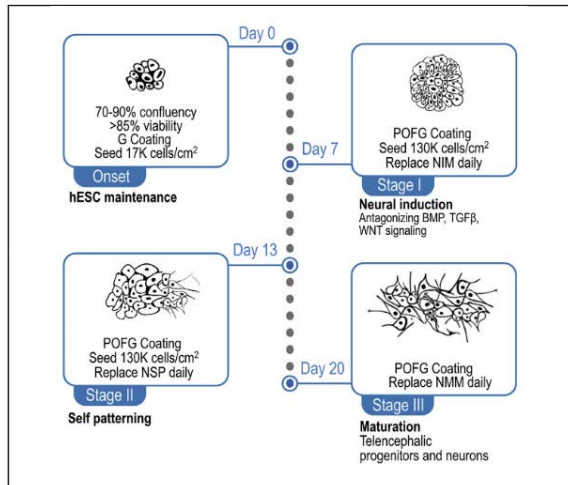
# Neuronal celle differensiering av humane stamceller

## STAR Protocols



### Protocol

Robust neuronal differentiation of human embryonic stem cells for neurotoxicology



Athina Samara,  
 Martin Falck, Mari Spildrejorde,  
 Magnus Leithaug,  
 Ganesh Acharya,  
 Robert Lyle,  
 Ragnhild Eskeland

athina.samara@ki.se (A.S.)  
 ragnhild.eskeland@medisin.uio.no (R.E.)

**Highlights**  
 Day-by-day visual aids to monitor morphological changes during differentiation

Optimized cell numbers and passages for neurotoxicology studies

Web tools available for single-cell omics data

Ideal for early brain development exploration from human embryonic stem cells

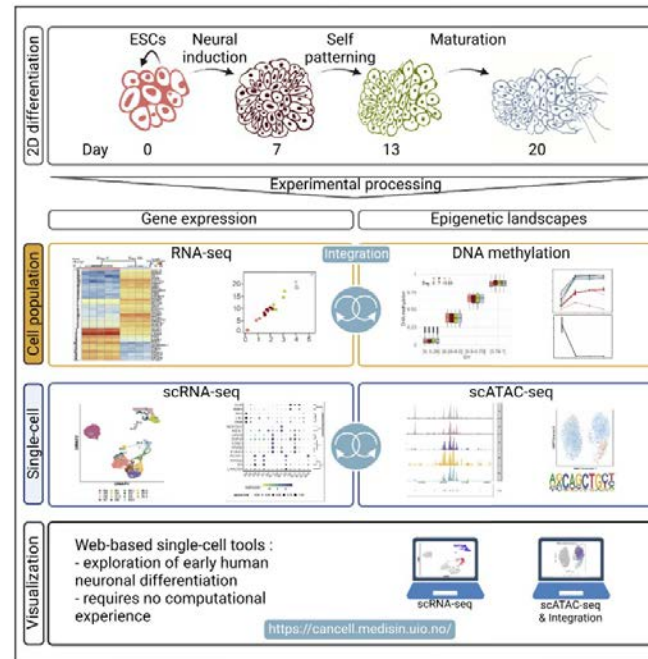
Samara et al., STAR Protocols  
 3, 101533  
 September 16, 2022 © 2022  
 The Author(s).  
<https://doi.org/10.1016/j.xpro.2022.101533>

Here, we describe a protocol for rapid neuronal differentiation from human embryonic stem cells (hESCs) toward a heterogeneous population of telencephalic progenitors, immature and mature neurons, for drug-screening and early-brain differentiation studies. hESC neuronal differentiation depends on adhesion and minimal cell-passaging to avert monolayer cross-connectivity rupture. In this protocol, we detail optimized cell-seeding densities and coating conditions with high cell viability suitable for neurotoxicology and high-resolution single-cell omics studies. Daily media changes reduce compound instability and degradation for optimal screening.

Publisher's note: Undertaking any experimental protocol requires adherence to local institutional guidelines for laboratory safety and ethics.

### Article

A multi-omics approach to visualize early neuronal differentiation from hESCs in 4D



Athina Samara,  
 Mari Spildrejorde,  
 Ankush Sharma,  
 ..., Kristina Gervin,  
 Robert Lyle,  
 Ragnhild Eskeland

athina.samara@ki.se (A.S.)  
 robert.lyle@medisin.uio.no (R.L.)  
 ragnhild.eskeland@medisin.uio.no (R.E.)

**Highlights**  
 Multi-omics charting a new neuronal differentiation protocol for human ES cells

Single-cell analyses reveal marker genes during neuronal differentiation

Identified transcriptional waves similar to early human brain development

Searchable tools to visualize single-cell gene expression and chromatin state

Samara et al., Science 25,  
 105279  
 November 18, 2022 © 2022  
 The Author(s).  
<https://doi.org/10.1016/j.jsci.2022.105279>

Me har utvikla ein modell for tidleg human hjernecelle utvikling.

Enkeltcelle analyser står sentralt i å forstå kva celler me får ved differensiering.



# Epigenetisk studie for å forstå effekten av paracetamol på tidlig hjerneutvikling

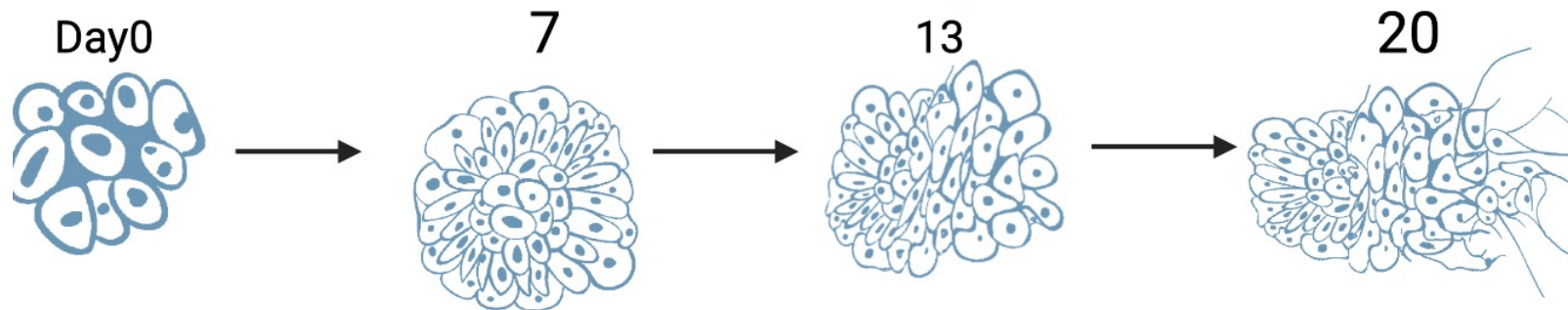
New Results

🔔 [Follow this preprint](#)

## Multi-omics analysis of paracetamol exposure identifies dysregulated genes involved in neurotoxicity and neuronal differentiation of human embryonic stem cells

Mari Spildrejorde,  Athina Samara,  Ankush Sharma, Magnus Leithaug, Martin Falck, Stefania Modafferi,  Arvind Y. M. Sundaram,  Ganesh Acharya,  Hedvig Nordeng,  Ragnhild Eskeland,  Kristina Gervin,  Robert Lyle

doi: <https://doi.org/10.1101/2022.12.08.519620>



Ved å nytte differensieringsmodell for tidlig hjerneutvikling så kan me følge effekten av paracetamol i cellekultur.

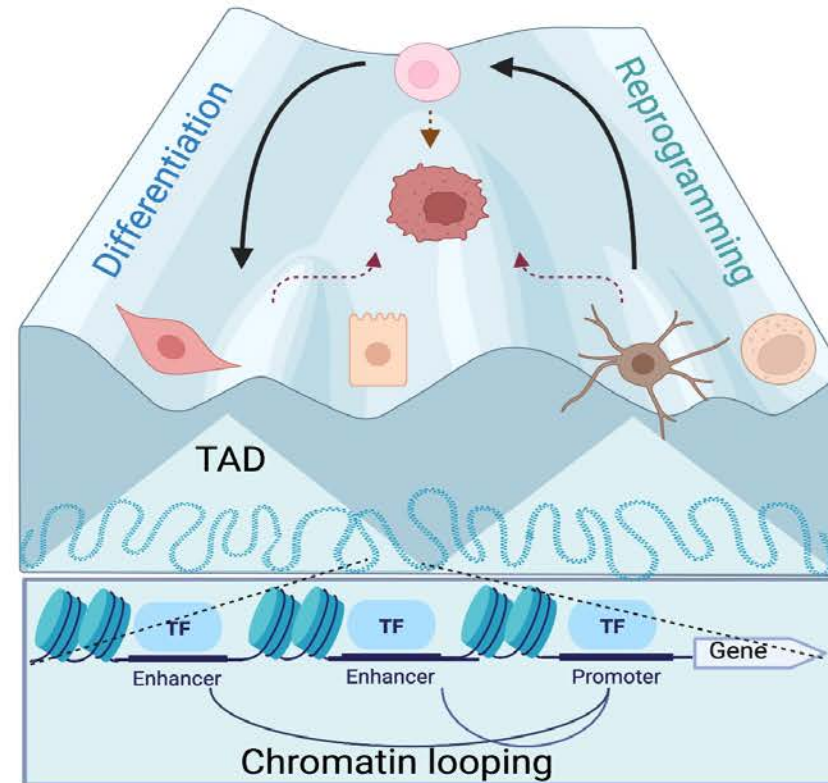


Colourbox.com

 **PharmaTox**  
STRATEGIC RESEARCH INITIATIVE



# Kreftceller deler seg ukontrollert



Created with BioRender.com

## **CanCell Mål:**

*Identifisere Kreftens akilles hel for å kunne reprogrammere den til "ufarlege" celler me kan leve med*

# Takk til...



UiO : **Institute of Basic Medical Sciences**  
University of Oslo

UiO : **CanCell – Centre for Cancer Cell Reprogramming**  
University of Oslo

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Akshay Akshay, UoB

Marie Rogne, UiO

Knut Waagan, USIT

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Hedvig Nordeng, UiO

Kristina Gervin, OUS

Robert Lyle, OUS

Stockholms Medicinska Biobank



The Research Council of Norway



Nansen fond og de forbundne fond

Wedel Jarlsberg Fond

Anders Jahre Fond

Chromatin Biology Group



[www.chromatome.no](http://www.chromatome.no)