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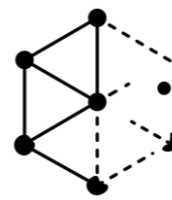
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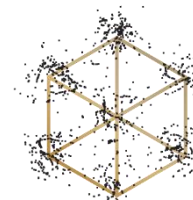
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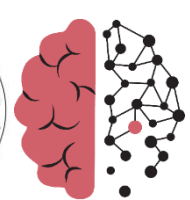
K.G. Jebsen Centre for
Alzheimer's Disease



Kavli Institute for
Systems Neuroscience



NO-Age



NO-AD



MIT-AD

The NO-Age and NO-AD Seminar Series 061

Integrated epigenomics reveal dysregulated chromatin landscapes in aged hematopoietic stem cells underlying aberrant transcription

by

Prof. Isabel Beerman

Translational Gerontology/Epigenetics and Stem Cell Aging Unit, NIA, US

at

13:00-14:15 (CET), Tuesday, 6th Sep. 2022

Room B203.006, Ahus

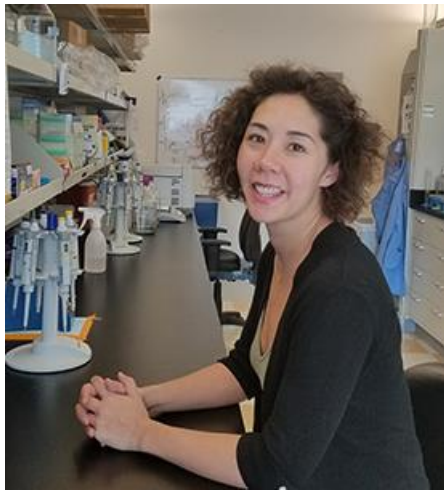
Register in advance:

https://uio.zoom.us/webinar/register/WN_39mctqKCQ12ePBpgYR5OgA

Evandro F. Fang (UiO), Jon Storm-Mathisen (UiO), Lene Juel Rasmussen (KU), W.Y. Chan (CUHK)

Queries: e.f.fang@medisin.uio.no

Previous recorded talks are available here: <https://noad100.com/videos-previous-events/>



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Speaker: Prof. Isabel Beerman

Title: Integrated epigenomics reveal dysregulated chromatin landscapes in aged hematopoietic stem cells underlying aberrant transcription

Abstract: Age-associated hematopoietic stem cell (HSC) phenotypes contribute to myeloid lineage skewing, loss of reconstitution potential, and elevated risk of cancer transformation. To define editable alterations associated with changed potential using updated methodologies, we profiled transcriptomes, histone modifications, chromatin accessibility, and chromatin interactions of HSCs purified with a consistent phenotype from young and aged mice. Aged HSCs had globally decreased levels of active, permissive, and repressive histone modifications, though specific loci displayed age-associated increases. Around twenty percent of bivalent HSC promoters were altered, with half corresponding to transcriptional changes. More open chromatin allowed for increased accessibility to functionally relevant transcription factor binding, aberrant expression of transposable elements, and enrichment of H3K27ac at enhancer regions. HI-C data showed enriched short-range and decreased long-range interactions in mostly heterochromatin in aged HSCs. These epigenomic data provide a consensus library of changes associated with aging and define critical targets for restoration of youthful potential.

Biography:

Prof. Isabel Beerman is a stadtmann investigator in the Epigenetics and Stem Cell Aging Unit, where is focused on understanding mechanisms that underlie age-associated functional decline, with a focus on adult tissue-specific stem cells. By establishing the mechanisms leading to dysregulation of stem cells, we can begin to target these alterations to restore potential to the aging stem cell compartments. As the tissue-specific stem cells are responsible for maintaining overall tissue homeostasis, reestablishing the full potential to these aged cells could mitigate many aged associated phenotypes.