RESEARCH ACTIVITY SHEET

2025 PhD selections

YOUR DETAILS

* Name & Surname Magda Bienko

* Affiliation HT

PHD PROJECT DETAILS

* Title of the proposed project

Unravelling the design principles shaping chromosomal territories

* Short description of the project (up to 300 words)

In eukaryotic cells, the genome is folded into a three-dimensional (3D) structure that is thought to be critical for instructing and regulating gene expression and cell identity. While the 3D genome has been extensively studied at the nanoscale, its higher-order spatial organization at the microscale is much less characterized. For example, individual chromosomes are known to occupy discrete volumes in the nucleus known as chromosomal territories (CTs), but the forces that lead to their formation remain unknown. In this project, we will employ a multitude of functional genomics assays to identify factors critical for the formation of CTs. We will establish an optical pooled screening approach using DNA FISH as the readout to interfere with large numbers of genes and identify those whose activity shapes CTs.

* Indicate the main research area for the project described above Molecular Biology

If needed indicate a second research area for the project described above Computational biology

* Provide up to 3 key words for project:

Genome organization; optical pooled screens; epigenetics

YOUR LABORATORY ACTIVITIES DETAILS

* Main topic/s of the lab

3D genome organization and its interplay with gene expression

* Short description of the lab activity (up to 500 words)

The Bienko Lab at HT aims at understanding the design principles and mechanisms that shape the spatial arrangement of DNA, RNAs and proteins in the nucleus of mammalian cells. We investigate how the three-dimensional (3D) architecture of the genome instructs and/or is instructed by fundamental processes including DNA replication, transcription, and repair. We are particularly interested in understanding how the constituents of chromatin are spatially arranged, and which factors and mechanisms mediate the spatial organization of chromatin in the nucleus. We are also interested in understanding how mutations and genomic alterations associated with prevalent disorders like cancer form in the context of the 3D genome and, in turn, how they perturb the 3D genome structure and function to exert their pathogenic effects. To this end, we go beyond state-of-the art by developing novel (single-cell) sequencing and microscopy methods, as well as novel mathematical modeling approaches. In this way, we put our creativity into developing new technologies, we satisfy our curiosity by addressing fundamental biological questions and we have fun pursuing interdisciplinary research where we can learn from each other’s expertise and do science in a highly synergistic manner.

* Recent bibliography (max 5 references)

1. Cell type-specific intronic RNAs shape genome architecture during neuronal lineage specification. Kang W, Yip WH, Verron Q, Bouwman BAM, Li-Wang X, Abou Yaghi A, Murata M, Stout M, Salviati L, Shu X, Yasuzawa K, Gaviraghi M, Pracana R, Lord J, Ballarino R, Falk A, Shin JW, Kasukawa T, Yip CW, Kato M, Takahashi H, Crosetto N, Carninci P, **Bienko M.** ***bioRxiv*** doi: https://doi.org/10.1101/2025.03.13.641826

2. Deconwolf enables high-performance deconvolution of widefield fluorescence microscopy images. Wernersson E, Gelali E, Girelli G, Wang S, Castillo D, Mattsson Langseth C, Verron Q, Nguyen HQ, Chattoraj S, Martinez Casals A, Blom H, Lundberg E, Nilsson M, Marti-Renom MA, Wu CT, Crosetto N, **Bienko M**. **Nat Methods**. 2024 Jul;21(7):1245-1256. doi: 10.1038/s41592-024-02294-7. Epub 2024 Jun 6.

3. scCircle-seq unveils the diversity and complexity of extrachromosomal circular DNAs in single cells. Chen JP, Diekmann C, Wu H, Chen C, Della Chiara G, Berrino E, Georgiadis KL, Bouwman BAM, Virdi M, Harbers L, Bellomo SE, Marchiò C, **Bienko M***, Crosetto N* **Nat Commun**. 2024 Feb 27;15(1):1768. doi: 10.1038/s41467-024-45972-y.

4. Mota A, Berezicki S, Wernersson E, Harbers L, Li-Wang X, Gradin K, Peuckert C, Crosetto N, **Bienko M**. FRET-FISH probes chromatin compaction at individual genomic loci in single cells. **Nat Commun**. 2022 Nov 5;13(1):6680. doi: 10.1038/s41467-022-34183-y.

5. Girelli G, Custodio J, Kallas T, Agostini F, Spanjaard B, Wernersson E, Mota A, Gelali E, Crosetto N, **Bienko M**. GPSeq reveals radial genome organization at high resolution. **Nat Biotechnol**. 2020 Oct;10.1038/s41587-020-0519-y. doi:10.1038/s41587-020-0519-y

* Group composition: total members, and roles distribution (PhD, postdoc, technician, etc.)

1 staff scientist, 1 senior technician, 4 postdocs, 1 PhD student

Institutional page link

https://humantechnopole.it/en/research-groups/bienko-group/

Lab website link, if any

https://www.bicrolabs.com/

Social media links, if any

@BienkoMagda

If you prepare a video to promote your lab/project, please include the link below