

## Master project 2020-2021

### Personal Information

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<b>Website</b>	<a href="http://www.ibmb.csic.es/groups/chromatin-regulation-of-human-and-viral-gene-expression">http://www.ibmb.csic.es/groups/chromatin-regulation-of-human-and-viral-gene-expression</a>
<b>Group</b>	Chromatin regulation of human and viral gene expression

### Project

## Computational genomics

### Project Title:

Occupancy of histone H1 variants genome-wide and consequences of altering H1 levels on human chromatin organization.

### Keywords:

Chromatin, histones, genomics, 3D nuclear structure, ChIP-seq

### Summary:

We focus our research on the control of gene expression in human cells by chromatin organization, components and modifications. We investigate the role and specificity of histone H1 variants in chromatin organization and gene expression control. By RNA interference of the different human H1 variants we have found that they have different involvement in cellular processes such as cell cycle progression and gene expression. We have also described a differential role of H1 variants in pluripotency and differentiation. Currently, we are investigating the occupancy of H1 variants genome-wide by ChIP-seq (NGS) and the consequences of altering H1 levels on chromatin organization (ATAC-seq, DNA methylation, hiC, etc), with an extensive use of Genomics and Bioinformatics. Additionally, we are performing proteomics of H1 variant specific protein complexes in chromatin and nucleoplasm.

### References:

▲ Izquierdo-Bouldstridge A\*, Bustillos A\*, Bonet-Costa C, Aribau P, Garcia D, Dabad M, Esteve-Codina A, Pascual L, Peiro S, Esteller M, Murtha M, Millán-Ariño LI, Jordan A (2017) Histone H1 depletion triggers an interferon response in cancer cells via activation of heterochromatic repeats. *Nucleic Acids Research* 45(20): 11622-42. ▲ Millán-Ariño LI, Izquierdo-Bouldstridge A, Jordan A (2016) Specificities and genomic distribution of somatic mammalian histone H1 subtypes. *BBA Gene Regulatory Mechanisms* 1859(3): 510-19. ▲ Mayor R\*, Izquierdo-Bouldstridge A\*, Millán-Ariño LI, Bustillos A, Sampaio C, Luque N, Jordan A (2015) Genome distribution of replication-independent histone H1 variants shows H1.0 associated with nucleolar domains and H1X associated with RNA polymerase II-enriched regions. *Journal of Biological Chemistry* 290(12):7474-91. ▲ Millán-Ariño LI, Islam A, Izquierdo-Bouldstridge A, Mayor R, Terme JM, Luque N, Sancho M, López-Bigas N, Jordan A (2014) Mapping of six somatic linker histone H1 variants in human breast cancer cells uncovers specific features of H1.2. *Nucleic Acids Research*. doi: 10.1093/nar/gku079 ▲ Terme JM\*, Sesé B\*, Millán-Ariño L, Mayor R, Izpisua-Belmonte JC, Barrero MJ, Jordan A (2011) Histone H1 variants are differentially expressed and incorporated into chromatin during differentiation and reprogramming to pluripotency. *Journal of Biological Chemistry* 286(41):35347-57 ▲ Sancho M, Diani E, Beato M, Jordan A (2008) Depletion of human histone H1 variants uncovers specific roles in gene expression and cell growth. *PLOS Genetics*- Oct;4(10):e1000227.

**Expected skills::**

Strong motivation for research. Background or interest in Biology/Biomedicine and Epigenetics. The student will work in analyzing high-throughput genomic data such as ChIP-seq, RNA-seq, ATAC-seq and hi-C. To do so, experience in handling aligners, peak calling softwares, differential gene expression analysis and statistics tests will be an advantage. In addition, programming skills in R, Python and/or Perl are also necessary.

**Possibility of funding::**

No

**Possible continuity with PhD: :**

To be discussed

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