

# BDR SEMINAR in Kobe

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**Thursday, January 16, 2020**

14:00-15:00, 7<sup>th</sup> Floor Seminar Room, DB Building A

## Data-driven and technical approaches to understand spatial gene regulation

### Summary

Gene expression is precisely regulated by transcription factors (TFs) and chromatin structures, but their combinatorial actions for cell type-specific expression are not fully understood. Here, I developed a database designated ChIP-Atlas (<https://chip-atlas.org>), which integrates all of public ChIP-seq data including more than 120,000 experiments. The integrated data were further analyzed to identify TFs associated with tissue-specific gene expression and disease risk. In addition, I established a high-resolution spatial genomics technology, named photo-isolation chemistry, which allows to isolate gene expression profiles only from photo-irradiated regions out of whole tissues. This chemistry has a potential to be applied for other genomics technologies such as ATAC-seq and Bisulfite-seq. Combination of those data-driven and technical approaches will accelerate to gain deeper insight into the mechanisms of spatial gene regulation.

1) Shinya OKi\*, et al., ChIP-Atlas: a data-mining suite powered by full integration of public ChIP-seq data. *EMBO Rep*, 19:e46255 (2018)

2) Shinya OKi\*, et al., Integrative analysis of transcription factor occupancy at enhancers and disease risk loci in noncoding genomic regions. *bioRxiv Rep*, 262899



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