

## **The three-dimensional genome conformation of *Mycoplasma pneumoniae***

### **Abstract**

A recent study, involving a genome-reduced bacterium, *Mycoplasma pneumoniae*, the smallest self-replicating organism known to date, has revealed impressive transcriptome complexity.

Using recent Hi-C method, enabling purification of ligation products followed by massively parallel sequencing, allows unbiased identification of chromatin interactions across an entire genome.

We are seeking to build a 3D model of the genome conformation of the *Mycoplasma pneumoniae* using Hi-C data.

Indeed direct analysis of this genome-wide library of ligation products reveals numerous features of genomic organization, that change from exponential to stationary phases of growth. Chromatin structure information will allow us identify gene interactions that could affect the supercoiling. All these will hopefully help us to understand the complex transcriptional regulation of prokaryotes.

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