

**Project Title:**

**Predicting 3D structure of the human genome**

**Name:**

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1. Background and purpose of the project, relationship of the project with other projects

Viral infection alters the transcriptome landscape of the infected cells, which may result from changes in their promoter-enhancer regulatory network. For our project, we are using the three-dimensional structure of the genome to identify the potential changes in the regulatory elements network due to viral infection due to different viral strains.

2. Specific usage status of the system and calculation method

The server was used to identify the variation in chromatin interaction as the infection progress in the human cell line.

3. Result/Conclusion

We found the variation in the genomic interaction as infection progress. Many of these changes overlap with the enhancers expressed as result of the infection.

4. Schedule and prospect for the future

We will use the server in the next FY for downstream analysis of the explore the processed Hi-C data.

5. If no job was executed, specify the reason.

Not applicable