

**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  
Characterizing the function of lncRNAs systematically is challenging due to their low expression, high cell type-specificity and lack of conservation across organisms. Studies have shown non-coding regions of the genome regulate the genes that are in their close proximity in the nuclear three-dimensional space. For our project, we are using three-dimensional structure of the genome in different human cell types to identify the potential target genes of the long non-coding RNAs.

2. Specific usage status of the system and calculation method  
Identifying the genomic interactions using Hi-C data is a computationally intensive process and the supercomputer facility was used extensively to determine these structures. Server was used to process the Hi-C data for different cell types used in the study.

3. Result/Conclusion  
Potential target regions of several lncRNA were identified in different human cell types using Hi-C data. Many of these target genes show enrichment for different regulators including RNA binding proteins.

4. Schedule and prospect for the future  
We are finalizing the results for this project and will use the server for analysis requiring further processing of Hi-C data.

5. If no job was executed, specify the reason.  
Not applicable