

Resource Sharing Plan(s)

1) Data Sharing Plan:

We will comply with the NIH Grant Policy on data sharing and release of final research data in a timely manner in peer-reviewed publications and presentations. All research resources, e.g. plasmids, vectors and cell lines will be made readily available to the scientific community.

2) Sharing Model Organisms:

As for our plan to share materials and our management of intellectual property, we will adhere to the NIH Grant Policy on Sharing of Unique Research Resources including the Sharing of Biomedical Research Resources Principles and Guidelines for Recipients of NIH Grants and Contracts issued in December, 1999 <http://www.ott.nih.gov/policies-reports>. There will be no new model organisms generated by this project. The p53 mutant mouse model used in this project was received from Dr. Brian Schutte at Michigan State University. We have to get his permission first before we can make it available to the broader research community. In addition, we will provide relevant protocols, and in vitro and in vivo data upon request. Material transfers will be made with no more restrictive terms than in the Simple Letter Agreement (SLA) or the Uniform Biological Materials Transfer Agreement (UBMTA) and without reach through requirements. Should any intellectual property arise which requires a patent, we will ensure that the technology (materials and data) remains widely available to the research community in accordance with the NIH Principles and Guidelines document.

3) Next Generation Sequencing and Analysis (ChIP-Seq and RNA-Seq data):

The proposed project will generate high-throughput sequencing data from ChIP-Seq and RNA-Seq experiments. According to the NIH grant policy on data sharing, we will make readily available all data released for publications and all raw high-throughput generated data once published to the scientific community for research purposes. Particularly, the genome annotation for CisOMs, CisOMs target genes generated from the ChIP-Seq and RNA-seq experiments in this proposal and the SNPs within CisOMs from UCSC and TCGA database will be deposited into the repositories (e.g. GEO-NCBI and UCSC) that are accessible to the research community.

4) Computational models and data:

We will make all publications and related code documentation available on the co-PIs' laboratory websites to the scientific community. Analysis software will be provided as open-source packages where feasible, and deposited in the GitHub code and/or R library repositories. We also develop user-friendly interfaces for our code packages and interactive data visualization portals (e.g., <https://pipeline.rice.edu/dream9/dream9.html>) to disseminate high-dimensional datasets.

The lab's open-source data analysis tools are currently stored and run on Rice's DAVinCi and SPICE servers. We have streamlined our computational programs and optimized them for computing time. This permits us to offer access to collaborators and other academic researchers, for non-commercial purposes.