

# GSAF

GENOME SEQUENCING and ANALYSIS FACILITY



THE UNIVERSITY OF TEXAS AT AUSTIN

College of Natural Sciences



The University of Texas at Austin

WHAT STARTS HERE CHANGES THE WORLD

The **ICMB Genomic Sequencing and Analysis Facility (GSAF)** provides next-generation sequencing (NGS) services including sample preparation and sequencing for a wide variety of applications.

**VISION:** The GSAF's vision is to be a world-class genomic analysis center in terms of data quality, breadth of available methods, and productivity. We strive to provide the best quality analytical results with the best value to life science researchers.

**EQUIPMENT:** We have two Illumina HiSeq 2500's and two Illumina MiSeq sequencers, and have operated other next-generation DNA sequencing systems in the past. We have a variety of quality control tools to test library quality and support users who create their own libraries or who wish to outsource this service to the GSAF.

**SUPPORT STAFF:** The GSAF has a staff of experienced technicians capable of performing many RNA and DNA library preps including directional RNA-seq libraries, small RNA libraries, normalized cDNA libraries, whole genome DNA libraries, enriched DNA libraries (e.g. exome capture libraries), and many other more specialized library types.

**BIG DATA:** Our data systems are integrated with the Texas Advanced Computing Center (TACC) supercomputer resources, and we work closely with the CCBB/CSSB Bioinformatics Consulting Group who consult and analyze NGS data.



**1 University Station A4800, 2500 Speedway, MBB 3.210, Austin, TX 78712 512-475-9725**

## GRADUATE STUDENT SPOTLIGHT

"My project focuses on the epigenetic regulation of vertebrate eye development. Specifically, I am interested in how DNA methylation orchestrates differentiation events during the lens epithelial to fiber transition and during retinal neurogenesis, when progenitor cells are actively reprogrammed and the DNA methylation pattern is likely dynamic. To test this, I utilize genome engineering approach to target genes involved in DNA methylation, and genome-wide approaches to profile the methylation and transcription statuses of progenitor and differentiated cell types." - *Pawat Seritrakul, 4th year Cell & Molecular Biology PhD student*

"Thanks for pushing the sequencing forward so fast. I have used at least 5 different sequencing centers over the last 5 years, and you all are by far the best to work with. More projects will be coming your way this spring."

## TESTIMONIAL

# SUMMER SCHOOL FOR BIG DATA IN BIOLOGY

MAY 26 - 29, 2015

With the advent of data-intensive technologies in modern biology, computational and bioinformatic approaches are quickly becoming essential parts of every biologist's toolkit.

Are you looking to obtain or hone skills for the design, analyze, and interpret complex large-scale experiments? If so, check out the 2015 Summer School for Big Data in Biology here at UT Austin. The Summer School is hosted by the Center for Computational Biology & Bioinformatics, the Center for Systems & Synthetic Biology, and the Genome Sequencing & Analysis Facility. Visit our website for more information on courses and to

**Offering intensive, hands-on, 4-day workshops for trainees with all levels of experience**  
**PROTEOMICS • NEXT-GEN SEQUENCING • BIOLOGICAL NETWORKS • PROGRAMMING & SOFTWARE**

## BYTE CLUB

The Byte Club is intended to bring the UT Bioinformatics community together to share tricks and tips and to help resolve Bioinformatics issues we may all face. The meetings will include a short research talk followed by general discussions about new tools, pipelines, publications, etc.

During the 2015 spring semester, Byte will occur on **the third Wednesday of every month from 3-4 pm at NHB 1.720.**

