MEET THE CBG TEAM

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TEXAS TECH UNIVERSITY CENTER FOR BIOTECHNOLOGY AND GENOMICS

Next Generation Sequencing/Genomics

Bioinformatics

Proteomics/Metabolomics
The Nextgen sequencing/Genomics core facility provides sequencing services to the entire TTU community as well as outside customers. These services include sequencing library preparation from DNA/RNA, sequencing on Illumina platform, primary and secondary data analysis. We also standardize new protocols for sequencing library preparation. A major component of our service includes student training in Nextgen sequencing and associated Bioinformatics.

Services offered
► Stranded mRNA-sequencing for both prokaryotes and eukaryotes
► Small RNA sequencing
► Whole genome resequencing
► 16S metagenome sequencing
► Meta-transcriptome sequencing after target depletion
► ChIP-sequencing
► Sanger sequencing


The Bioinformatics Core at the Center for Biotechnology and Genomics offers services in the domains of genomics, proteomics and general bioinformatics. The Services include:

Next-generation Sequencing (NGS)
► RNA-Seq analysis
► Small RNA-Seq analysis
► de novo transcriptome assembly and annotation
► Whole genome assembly
► Metagenome and Metatranscriptome analysis
► Pathway analysis

Proteomics
► Proteome analysis for identification of proteins
► Quantitative proteome analysis
► Pathway analysis
► Analysis of post-translational modifications in proteins
► Computational proteomics
► Protein modeling
► Protein-protein and protein-ligand docking

General Bioinformatics
Software Development

The Proteomics/Metabolomics core facility at the Center for Biotechnology and Genomics provides services to the entire TTU community as well as outside customers for analysis of proteins and metabolites from cells, tissues or other biological samples. These services include sample preparation, instrumentation and method development. We also offer consultation to faculty, students and researchers to help with experimental design.

► Protein IDs by LC-MS/MS and MALDI-TOF/TOF
► In-gel/in-solution digestion of proteins
► Database search (MASCOT, SEQUEST, GPM)
► Protein quantification (Label-free quantification, Tagging)
► Analysis of post-translational modifications in proteins
► Targeted metabolite analyses (identification, quantification and profiling)