MEET THE CBG TEAM

Dr. Yehia Mechref
CBG Director, Paul W. Horn Professor, Chemistry & Biochemistry Department
yehia.mechref@ttu.edu

Shannon Sears, M.A.
Business Manager
shannon.sears@ttu.edu

Dr. Jatindra Tripathy
Graduate Program Coordinator/Advisor
Research Associate Professor
jatindra.n.tripathy@ttu.edu

Dr. Mohamed Fokar
Genomics Core Manager
Research Associate Professor
m.fokar@ttu.edu

Dr. Xiaomei Shu
Genomics Core
Research Assistant Professor
xiaomei.shu@ttu.edu

Dr. Ruwanthi Wettasighe
Genomics Core
Senior Research Associate
ruwanthi.wettasighe@ttu.edu

Dr. Chiquito Crasto
Bioinformatics Core Manager
Research Associate Professor
chiquito.crasto@ttu.edu

Dr. Masoud Zabet
Mass Spectrometry, Proteomics, and Metabolomics Core Manager, Research Associate Professor
masoud.zabet@ttu.edu

Dr. Xiaoxia Gong
Proteomics and Metabolomics Core
Research Associate
xiaoxia.gong@ttu.edu

Parvin Mirzaei, M.S.
Bioinformatics, Proteomics, and Metabolomics Core, Research Associate
parvin.mirzaei@ttu.edu

Shannon Sears, M.A.
Business Manager
shannon.sears@ttu.edu

Dr. Jatindra Tripathy
Graduate Program Coordinator/Advisor
Research Associate Professor
jatindra.n.tripathy@ttu.edu

Dr. Mohamed Fokar
Genomics Core Manager
Research Associate Professor
m.fokar@ttu.edu

Dr. Xiaomei Shu
Genomics Core
Research Assistant Professor
xiaomei.shu@ttu.edu

Dr. Ruwanthi Wettasighe
Genomics Core
Senior Research Associate
ruwanthi.wettasighe@ttu.edu

Dr. Chiquito Crasto
Bioinformatics Core Manager
Research Associate Professor
chiquito.crasto@ttu.edu

Dr. Masoud Zabet
Mass Spectrometry, Proteomics, and Metabolomics Core Manager, Research Associate Professor
masoud.zabet@ttu.edu

Dr. Xiaoxia Gong
Proteomics and Metabolomics Core
Research Associate
xiaoxia.gong@ttu.edu

Parvin Mirzaei, M.S.
Bioinformatics, Proteomics, and Metabolomics Core, Research Associate
parvin.mirzaei@ttu.edu

TEXAS TECH UNIVERSITY CENTER FOR BIOTECHNOLOGY AND GENOMICS

NEXTGEN SEQUENCING/GENOMICS

PROTEOMICS/METABOLOMICS

BIOINFORMATICS

Experimental Sciences Building
Room 101 | Canton & Main
Lubbock, Texas 79409

T: 806.742.6927 | F: 806.742.3788
Email: biotechnology.staff@ttu.edu
Web: http://www.depts.ttu.edu/biotechnologyandgenomics/
**BIOINFORMATICS**

The Bioinformatics core facility at the Center for Biotechnology and Genomics provides services in the domains of genomics, proteomics, and general bioinformatics.

Services include:
- **Nextgen 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

---

**NEXTGENSEQUENCING/ GENOMICS**

The Nextgen Sequencing/Genomics core facility at the Center for Biotechnology and Genomics 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, Miseq, and NovaSeq 6000 platforms, and 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
- Metatranscriptome sequencing after target depletion
- ChiP-sequencing
- Sanger sequencing

---

**PROTEOMICS/ METABOLOMICS**

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 using cutting-edge instrumentation and methods.

**Services offered:**
- Protein IDs by LC-MS/MS and MALDI-TOF/TOF
- Whole proteome profiling from cells, tissue, etc.
- In-gel/in-solution digestion of proteins
- Data analysis using advanced software such as MASCOT, SEQUEST, Compound Discoverer, LipidSearch, and Ingenuity Pathway Analysis (IPA)
- Protein quantification (label-free quantification, tagging)
- Analysis of post-translational modifications in proteins (e.g. phosphorylation)
- Global metabolite/lipid profiling
- Targeted metabolite analysis (identification and quantification)

**Instruments include:**
- Mass Spectrometers: Q-Exactive HF, LTQ Orbitrap Velos, ABI SCIEX 4800 (MALDI-TOF/TOF)
- LC systems: Dionex-Ultimate 3000 Nano-LC, Vanquish UHPLC, Dionex-Ultimate 3000 with fraction collector for peptide fractionation