

## SUPPORT INSTRUMENTATION



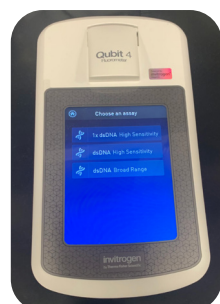
FLx800 Microplate  
Fluorescence Reader



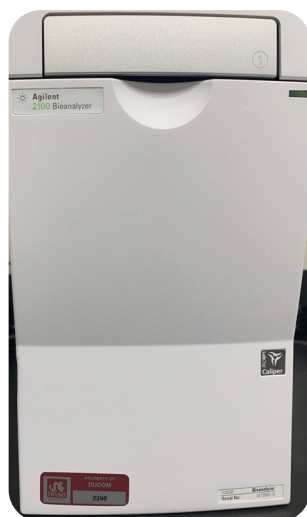
NanoDrop 2000



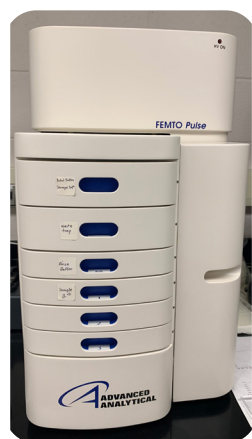
Blue Pippin



Qubit 4 Fluorometer



Agilent 2100 Bioanalyzer



Femto Pulse System

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DREXEL UNIVERSITY  
**Genomics Core  
Facility**  
*College of Medicine*

A comprehensive, academic shared resource facility for laboratory and informatic based genomic, epigenomic and transcriptomic analyses of prokaryotes and eukaryotes employing both next generation and third/fourth generation long-read, error correcting sequencing technologies.

<https://bit.ly/genomicscore>

## Benefits of Analyses Performed at the Genomics Core Facility

- Pacific Biosciences Certified Service Provider
- Wide variety of projects accepted – both large and small:
  - Choice of instrumentation platforms including Pacific Biosciences, Illumina and Nanopore for nucleic acid analyses, sequencing, and transcriptomic studies
  - DNA-based: amplicon; microbiome; metagenomic; whole genome; epigenetic
  - RNA-based: nanoString (counting method); RNAseq (illumina); IsoSeq (PacBio)
  - Nucleic acid analyses: quantitation; integrity; size analyses and selection
  - Normalization capabilities: ensure uniform concentrations of starting templates for multiplex analyses – including droplet digital PCR
- Most specimens handled according to validated SOPs to ensure reliable and reproducible results
- Rigorous analyses of nucleic acids before sequencing to minimize run failure due to inadequate starting materials
- Professional Informaticians on staff to assist with analyses
- Trial runs available
- Return of unused samples upon request

## Specialties of the Facility Scientists

### Species-specific pan-domain microbiome assays

- Full length 16S provides for quantitative analyses of all bacterial species present in any complex microbiota (*Earl et al 2018*); useful for biomarker discovery (*Greathouse et al 2018*); and pathogenesis studies (*Mone et al 2022*)



- (Coming in 2023) 18S-23S long-read trans-pan-domain eukaryotic microbiome studies covering fungi, apicomplexan parasites, alveolates and trypanosomes

### Whole Genome Sequencing

- Single contig bacterial genomes – provides for high resolution comparative genomic studies and pangenome analyses (*Moleris et al 2018*; *Krol et al 2019*; *Majer et al 2021*)

### RNA Sequencing

- Specialized for RNA sequencing on Illumina platforms, but IsoSeq-based full-length transcript sequencing by PacBio is available

## Our Projects

- Sequenced several thousands of bacterial genomes – many at the single contig level
- Performed thousands of microbiome analyses for a wide variety of tissue and sample types
- Performed dozens of large-scale comparative RNAseq studies
- Sequenced thousands of SARS\_CoV2 isolates

## Professional Help with Experimental Design – Including Nonstandard Projects

- Short vs. long read sequencing
- Error corrected or non-error corrected long read sequencing (PacBio vs Nanopore)
- Read depth considerations: RNAseq, microbiome, metagenomic sequencing

## Main Platforms

