The Ralph N. Adams Institute Microfabrication Facility is a 2400 ft² ISO Class 5 and 6 facility that specializes in the manufacture of microfluidic devices. Our equipment versatility can also be utilized for the manufacture and evaluation of a variety of micro-scale devices and materials. We offer our services to KU research groups, as well as research groups from other universities and private institutions.

**Services Offered**

- Microfluidic Device Fabrication
  - Material availability: soda-lime and borosilicate glass, PMMA, and PDMS
  - Embedded electrodes: carbon, platinum, nickel, copper, chromium
- Device and material evaluation: step profiling, ellipsometry, image capture
- Consultation
- Photomask design
- Limited open access
  - Includes training and support
  - Multiple rates available to suit users’ needs

**Core Equipment**

- Amray 1810 Tungsten Filament Scanning Electron Microscope
- Thermionics VE-100 E-beam evaporator
- Lesker DC magnetron sputterer with three Torus guns
- Oxford Plasmalab 80 Plus Plasma-Enhanced Chemical Vapor Deposition System: Silicon Dioxide and Silicon Nitride deposition currently available
- Oxford Plasma Plasmalab System 100 Inductively-Coupled Plasma Reactive Ion Etch System
- HORIBA Jobin Yvon UVISEL Spectroscopic Elipsometer
- ABM, Inc. i-line UV flood source and mask aligner
- WABECO 3-Axis CNC Mill

supported by the National Institute Of General Medical Sciences of the National Institutes of Health under Award Number P20GM103638

http://cmadp.cobre.ku.edu
The MPC provides researchers with access to a wide variety of commercially-available and custom-synthesized fluorescent probes as well as microscopy-based analysis of fluorescent small molecules and proteins in the model organisms *Caenorhabditis elegans* (nematode worm) and *Danio rerio* (zebrafish).

**Services Offered**

- Design, synthesis, and evaluation of novel fluorescent probes
- Fluorescent probes for studies of biology and models of disease
- Housing, care, and cryopreservation of *C. elegans* and *D. rerio* animals
- Access to models of human disease in *C. elegans* and *D. rerio*
- High-resolution video microscopy imaging of fluorescent probes *in vivo*
- Qualitative and quantitative image and video data analysis
- Structure-activity studies and genotype vs. distribution relationships *in vivo*
- Microinjection for probe administration and generation of transgenic organisms
- Digital archiving of images and video microscopy data

**Core Equipment**

- Zeiss AxioZoom V16 stereoscope fitted with a Hamamatsu ORCA-Flash4.0 sCMOS camera and Sutter DG5 fast filter switching excitation source
- Pentair Aquatic Habitats ZF0601 zebrafish habitat system

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**GENOME SEQUENCING CORE**

1030 Haworth Hall  
1200 Sunnyside Avenue, Lawrence, KS 66045  
Erik A. Lundquist, Ph.D., Core Leader, erikl@ku.edu (785) 864-5853  
Jennifer Hackett, M.S., Core Director, jhackett@ku.edu, (785) 864-7023  
Melinda Branin, Assistant Core Director, mbranin@ku.edu, (785) 864-7023

http://gsc.ku.edu

The GSC offers next generation DNA sequencing services for researchers at KU and other institutions. As opposed to “standard” Sanger sequencing, next generation sequencing has astronomically higher throughput (billions of reads and hundreds of Gbs of data), allowing whole genome sequencing in a single run and allowing deep, quantitative analysis of genome-wide gene expression (transcriptomics), among others.

**Services Offered**

- Genome re-sequencing:
  - Mutant identification (model organisms, human syndromes)
  - Evolutionary comparisons
  - Disease tissue sequencing (e.g. cancer)
- Genotyping: single nucleotide polymorphisms (SNPs), copy number variations (CNVs), genome-wide association studies (GWAS), & linkage analysis
- De novo genome assembly: new un-sequenced species
- Expression analysis (transcriptomics): cDNA sequencing (RNA-Seq) for deep and quantitative analysis of genome-wide gene expression
- Epigenomic & gene regulation analyses
  - Chromatin immunoprecipitation sequencing (ChIP-Seq) to find binding sites of transcription factors or other DNA-interacting proteins
  - Methylated DNA sequencing (Methyl-Seq) to identify methylated regions of the genome
  - Small RNA discovery and analysis

**Core Equipment**

**Illumina Hiseq 2500**

**Next Generation Sequencer**

- Normal mode (more data, more time)
  - 3-6 billion reads of 100 bp per run of two eight-lane flow cells (600Gb data)
  - Single reads or paired end reads (both ends of the DNA fragment)
  - ~5-11 day run time
- Rapid Mode (less data, less time)
  - 1.2 billion reads of 150 bp per run on two two-lane flow cells (120 Gb data)
  - ~27 hour run time

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**MOLECULAR PROBES CORE**

1053 Structural Biology Center (SBC)  
2034 Becker Drive, Lawrence, KS 66047  
Blake Peterson, Ph.D., Core Leader, brpeters@ku.edu, (785) 864-8156  
Chamani Perera, Ph.D., Core Director, chamani@ku.edu, (785) 864-6193

http://mpc.ku.edu

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*MPNS tumor*

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*Posterior acidity*  
*C. elegans*  
$t = 0$ s  
250 µm

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*Anterior acidity*  
*D. rerio* (p53/p53)  
$t = 4$ s

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*FF*