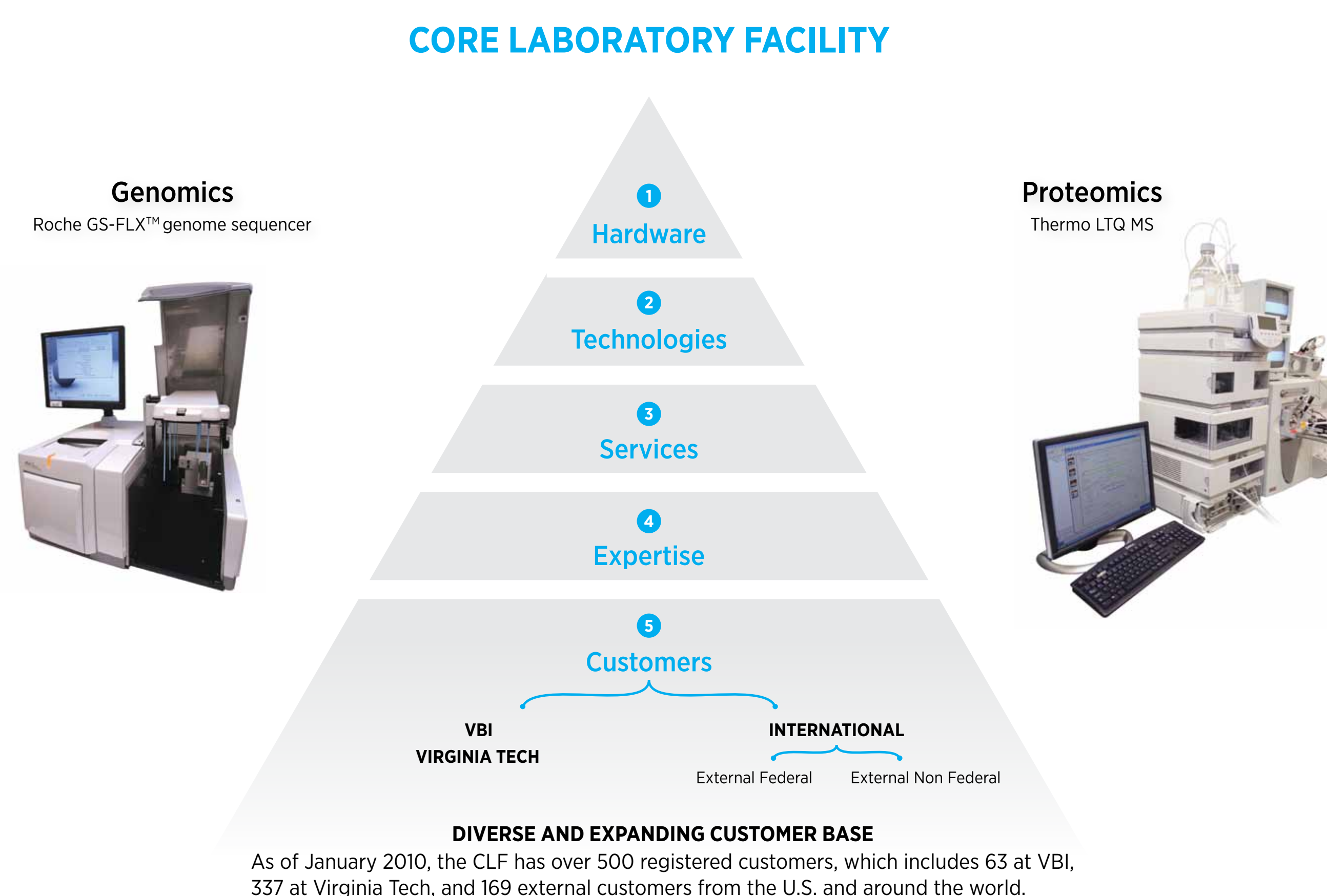


Core Laboratory Facility (CLF)

Developing and expanding its impressive portfolio of high-throughput technologies for diverse clients in the global life science community.

Providing life science customers worldwide with access to best-in-class technologies for discovery and analysis.

The Core Laboratory Facility (CLF) at the Virginia Bioinformatics Institute (VBI) is a dedicated multi-user resource for the development and application of state-of-the-art high-throughput technologies. By offering researchers access to these services and the support of its experienced laboratory staff, the CLF strives to provide high quality data, analysis, and experimental design assistance in a timely fashion while maintaining excellent customer service.



CLF HIGHLIGHTS

NAMED AN AFFYMETRIX NATIONAL CUSTOM ARRAY CENTER



In 2006, under an agreement with Affymetrix Inc., the CLF was designated a National Custom Array Center for custom microarray design, sample processing and analytical services. Affymetrix custom microarrays offer researchers the flexibility to design arrays that can analyze the gene expression profile of any organism. The custom arrays use the same high-quality design and manufacturing technologies used to create GeneChip catalog arrays.

ADDITION OF ROCHE GS-FLX™ GENOME SEQUENCER IN 2007

The CLF officially launched its genome sequencing services for the Roche GS-FLX™ in 2007 and was the first institution to have the sequencer installed. The Roche GS-FLX is a next-generation genome sequencing system that takes advantage of 454 Life Sciences™ revolutionary sequencing technology and allows researchers to go from genome to sequence in record time. The sequence of a typical bacterial genome can be obtained in days with one person and one instrument without the need for cloning and colony picking.

LARGEST AFFYMETRIX GENECHIP® PLANT EXPERIMENT COMPLETED IN AN ACADEMIC INSTITUTE

In 2007, the CLF completed the largest ever Affymetrix GeneChip® microarray study for a plant experimental system in an academic research setting. The 2600-chip experiment explored the counterplay of plant and pathogen genes during infection of soybean with the root-rot pathogen *Phytophthora sojae*, with a focus on mechanisms of long-lasting disease resistance.

SEQUENCING OF THE TURKEY GENOME

In 2009, the CLF completed the genome sequencing of the domesticated turkey, *Meleagris gallopavo*, using the Roche GS-FLX™ sequencer. Turkey is the fourth most economically important source of meat for consumers in the United States. The genome sequence and genomic resources should provide turkey breeders with the tools needed to improve commercial breeds of turkey for production traits such as meat yield and quality, health and disease resistance, fertility and reproduction.

CUSTOM LABORATORY INFORMATION MANAGEMENT SYSTEM

The CLF is supported by a custom Laboratory Information Management System (LIMS) that provides an easy-to-use, secure interface for sample submission and retrieval. LIMS uses a web-based interface to track submissions to the lab and data generated from those samples, providing a comprehensive system that stores, retrieves, and manages: projects; client and sample information; workflow and data management; storage of sample and reagents; equipment management; associated costs; audit trails; and security.

PUBLICATION HIGHLIGHTS

CLF STAFF HAVE CO-AUTHORED 11 SCIENTIFIC PAPERS SINCE 2007, INCLUDING:

A draft genome sequence of *Pseudomonas syringae* pv. *tomato* strain T1 reveals a repertoire of Type III related genes significantly divergent from that of *Pseudomonas syringae* pv. *tomato* strain DC3000. Yan S, Almeida NF, Lindeberg M, et al (2009) *Molecular Plant-Microbe Interactions* 22(1): 52-62.

- Describes a powerful approach to identify differences in gene content between different strains of plant pathogens
- A draft genome sequence of *Pseudomonas syringae* pv. *tomato* T1, which causes disease in tomato but not in *Arabidopsis thaliana*, was obtained and compared with the genome of the closely related *A. thaliana* and tomato model pathogen *P. syringae* pv. *tomato* DC3000.
- Comparative genomics of closely related pathogens with different host specificities represents an excellent approach for identification of genes contributing to host-range determination.
- The overall genetic content of each of the two bacterial genomes appears to be highly similar but the repertoire of disease-causing effectors was found to diverge significantly

Transcriptome Sequencing of the Microarray Quality Control (MAQC) RNA Reference Samples using Next Generation Sequencing Platforms. Mane SP, Evans C, Cooper KL, et al (2009) *BMC Genomics* 10: 264.

- Describes the use of next-generation sequencing (deep sequencing) on the Roche GS-FLX platform to determine the suitability of new state-of-the-art DNA microarray technologies for global gene expression analysis
- Focused on cDNA synthesized from the Microarray Quality Control (MAQC) reference RNA samples. The goal of the Microarray Quality Control (MAQC) project was to identify quality metrics for evaluating gene expression measurement technologies. The MAQC study provided a set of reference RNA samples with large numbers of differentially expressed genes consisting of the commercially available A sample from pooled human cell lines and the B sample from a pooled human brain preparation. These two samples were exhaustively analyzed on a number of different whole genome microarray platforms and Quantitative Real-Time PCR (QRT-PCR)
- In this paper, the deep sequencing analysis of cDNA on the Roche GS-FLX platform confirmed and validated the suitability of the new state-of-the-art DNA microarray technologies (whole genome microarray platforms and Quantitative Real-Time PCR) used in the MAQC study for global gene expression analysis.

The latest, cutting-edge technologies for data generation and analysis

The CLF is a cost-recovery center occupying 6,500 square feet of space. The facility houses \$3.7 million of equipment used to provide the latest genomic, transcriptomic, and proteomic technologies. Equipment used in the lab includes:

GENOMICS

DNA Sequencer, ABI, Prism 3130XL Genetic Analyzer
DNA Sequencer, ABI, Prism 3730 Genetic Analyzer
QpixII Colony Picker
Multiprobe Liquid Handler

2ND GENERATION SEQUENCING

GS-FLX™ Roche Sequencer
GAIIIX Illumina Sequencer

GENE EXPRESSION

BioMek FX
SpectraMAX Plate Reader
Affymetrix Platform with command console
iCycler

PROTEOMICS

2D Gel Service
Gel Scanner and Spot cutter
Finnegan LTQ
Mass Prep

Wide range of technology platforms available for the study of DNA, RNA, and proteins (proteomics)

GENOMICS

Sequence Gap Closures and Assembly
Sanger Sequencing
PCR Products
Plasmids
Microsatellites

2ND GENERATION SEQUENCING

Roche GS-FLX™ Sequencing
Titanium (Shotgun, Amplicon, Transcriptome, Paired-End Runs)
GAIIIX Illumina Sequencing
Shotgun, Amplicon, Transcriptome, Paired-End Runs, Mate Pair Runs

GENE EXPRESSION ANALYSIS

Affymetrix
Real-time PCR

PROTEOMICS

Protein Expression Profiling
Peptide/Protein Sequencing
Peptide/Protein Quantitation

MOLECULAR BIOLOGY APPLICATIONS

PCR
Cloning
Mini Preps
Robotics

BIOINFORMATICS

Experimental Design Assistance
Data Analysis and Interpretation
Access to Biostatistical Help