Genomics and Molecular Biology (GMB)

Description

Established in 2002, this core continues to evolve to meet the changing needs of its basic, translational, and clinical researchers for genetics and genomics support. GMBSR is a highly collaborative resource and provides Dartmouth researchers with access to cutting edge instrumentation and expertise, with rapid turnaround times and cost-effective solutions. Technologies are available for DNA and RNA sequencing, and DNA methylation analysis using whole genome and targeted approaches. A comprehensive suite of services supports single cell and spatial omics applications, including tissue processing, QC, library preparation and sequencing, as well as tissue staining and imaging in collaboration with the Pathology and Microscopy Shared Resources. GMBSR also provides DNA fragment analysis, qPCR, Sanger sequencing, and NanoString technologies. Integration with Genomic Data Science Core provides dedicated analysis solutions for all GMBSR workflows.

Staff


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Research Scientist

Services and Instrumentation

Service	Instrument(s)	Applications Supported
Plasmid/Amplicon Seq	Oxford Nanopore	Automated plasmid/amplicon assembly, 2x per week
DNA-seq (WGS, WES) RNA-seq (3', Ribo(-), PolyA) TCR/BCR-seq	EpMotion 5075t Liquid Handler Fragment Analyzer Qubit	SNV Detection Differential Gene Expression Immune Repertoire Profiling Metagenomics
Single Cell RNA / V(D)J / Protein / ATAC	10x Genomics Chromium X K2 Automated Cell Counter	Cell phenotyping T/B-cell clonality Single Cell Lineage Tracing
Next Generation Sequencing	Illumina NextSeq2000 Illumina MiniSeq Oxford Nanopore MinION Illumina NovaSeq6000 (via PSR)	Whole Genome/Exome Sequencing Single Cell / Spatial Omics Metagenomics
Spatial Transcriptomics (FFPE and Frozen)	10x Genomics CytAssist 10x Genomics Xenium	Whole transcriptome (55um res.) Targeted *in situ* (50nM res., 500 genes)
Illumina Infinium Arrays	Illumina iScan	Methylation (Human/Mouse) Consortium SNP Panels
Bioinformatics	Discovery/Andes/Polaris High Performance Computing Clusters	DNA/RNA/ATAC-seq Single Cell / Spatial Omics

Location and Acknowledgements

Rubin 6th Floor
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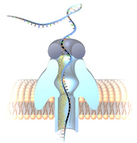
CCSG: 5P30CA023108
COBRE: P20GM130454
S10 (Illumina): 1S10OD030242
RRID: SCR_021293

Sequencing and Array Technologies for DNA, RNA and Methylation Profiling

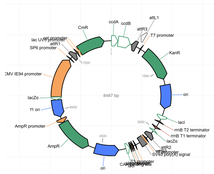
Sample Types: Biofluids, tissues, cells, frozen and FFPE samples can be used for most assays

- **DNA-seq:** Short and long read whole genomes and exomes; amplicon sequencing
- **RNA-seq:** 3'-end, Poly-A and Ribodepletion; smRNA/miRNA
- **Microarray:** Targeted DNA methylation and SNP profiling


Illumina Short Reads

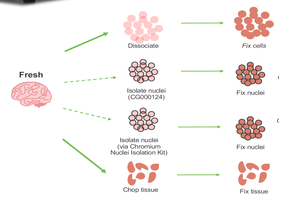

Oxford Nanopore Long Reads

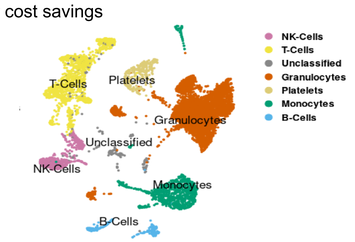

Illumina Infinium Arrays


Weekly Whole Plasmid Sequencing

Single Cell Genomics- Chromium X

- Profile single cells from fresh and fixed tissues, including FFPE, using 10X Genomics Chromium
- Flexible workflows for cell/tissue fixation
- Built-in multiplexing for cost savings



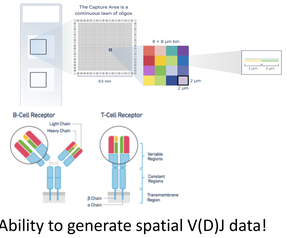


- Flexible workflows for tissue processing and storage
- RBC-depleted whole blood fixed and stored at -80C for 1mo

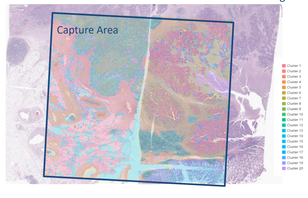
Spatial Genomics- CytAssist

- Generate spatial transcriptomcs data from FFPE tissues on standard histology slides using 10X Genomics Visium
- Leverage existing workflows in pathology for H&E staining and whole slide imaging at 40X
- Whole transcriptome profiling of tissues up to 11cm²

Visium HD
2um resolution



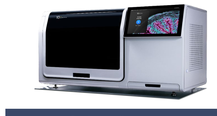
H&E Whole Slide Image



NEW - Ability to generate spatial V(D)J data!

- H&E-stained colorectal cancer specimens imaged at 40x with Visium on 11cm² area. Colors represent transcriptional similarity.

Spatial Genomics- Xenium



- Platform for *in situ* analysis from 10X Genomics
- Characterize 100s–1,000s of genes in cells and tissues with ultra precise single cell spatial imaging
- Leverage existing workflows for H&E staining or IF

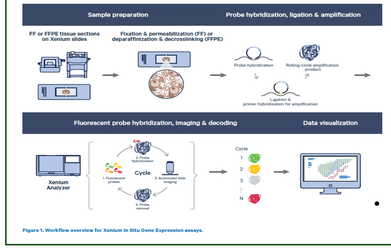
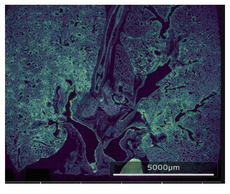


Figure 1. Workflow overview for Xenium In Situ Gene Expression assays.



- 50nm resolution (subcellular) using pre-made panels or custom designs

CD8+ T Cell Clonotypes and Fate Commitment Bias

PIs: Turk, Shirai, Huang, Curiel, Phillips, Usherwood, Wong

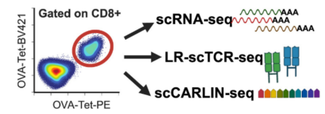
Publication: Abdullah, *Immunity,* 2025

Services Used: scRNA-seq; Illumina and Nanopore sequencing

Key Findings:

- Simultaneous recovery of mRNA, paired TCR sequences and lineage barcodes from single cells (A).
- Single cell phenotyping of T cell subsets (B)
- Many TCR clones show bias toward Memory (C) or Effector (D) phenotypes.

A.



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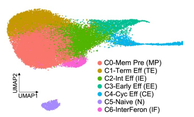

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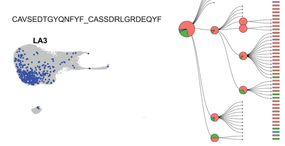
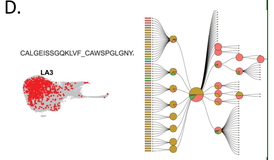


D.



Role of Resident and Recruited Macrophages in Tumor Progression

PIs: Claudia Jakubzick

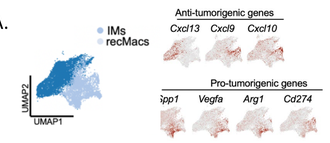
Publication: Gosh, *Nat. Immuno.,* 2026

Services Used: scRNA-seq; Xenium Spatial Transcriptomics; Illumina sequencing

Key Findings:

- Interstitial Macs (Ims) express anti-tumorigenic genes, while recruited Macs (recMacs) are pro-tumorigenic (A).
- Lung mets are identifiable by Acta2 expression and are highly innervated (B).
- Ccl2-expressing IMs are required for recMac recruitment and tumor suppression (C).
- Lung draining lymph node shows B-cell (Cd19) and T-cell zones (Cd3e), and well as Ccl-5 expressing DCs that recruit macrophages responsible for immunosuppression.

A.



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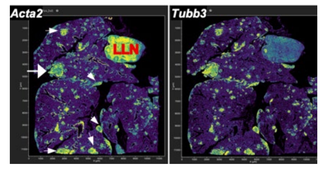
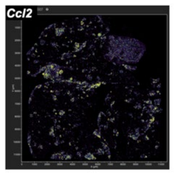
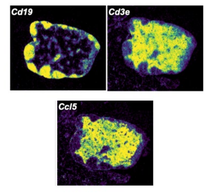


C.



D.



Metagenomics in Cystic Fibrosis

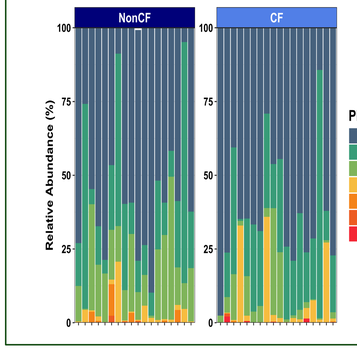
PI: O'Toole

Services Used: DNA-seq; Illumina sequencing, genomic data science core for analysis

Key Findings:

- DNA isolated from fecal samples from patients with cystic fibrosis or healthy controls
- Metagenomics analysis revealed differential abundance of phyla in CF vs non-CF samples (A,B)

A.



B.