sequencingcenter

Providence Saint John's Health Center
John Wayne Cancer Institute

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The John Wayne Cancer Institute Sequencing Center is equipped with state-of-the-art next generation sequencing technology and offers a variety of innovative assays that support a wide range of research applications. Our mission is to provide research support for cancer and other diseases, develop novel sequencing methodologies, and ultimately drive advances in precision medicine.

contact

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sequencing

Whole Genome Sequencing
All-inclusive whole genome sequencing covers both coding and non-coding regions allowing for the examination of SNVs, CNVs, and indels across the entire genome.

Human Exome Sequencing
Captures coding regions encompassing over 20,000 genes from blood, frozen tissue, saliva, cell lines, and FFPE. Standard coverage from ~50-200X depending on specimen type and can be scaled to meet project objectives.

RNA-seq
mRNA-focused sequencing from blood, frozen tissue, cell lines, FFPE and other low-quality samples. Standard coverage from ~20-50 million reads and can be scaled to meet project objectives.

Targeted Deep Sequencing
Isolating genomic regions of interest allows for cost-effective, focused detection of germline and somatic mutations with deep coverage. Custom gene panels can be designed to meet project objectives.

miRNA Whole Transcriptome Assay
Extraction-free direct assay of 2,083 miRNA from plasma, serum, FFPE, and cell lines. Low-input requirements make this assay ideal for precious specimens. Standard coverage from ~0.5-2 million reads and can be scaled to meet project objectives.

Human DNA Methyl-seq
Highly sensitive DNA methylation detection for 3.7 million CpG sites from a variety of specimen sources. Standard coverage from ~50-200X and can be scaled to meet project objectives.

DNA Methylation Arrays
Quantitatively interrogate DNA methylation level for >850K CpG sites from a variety of specimen sources, including FFPE. We also offer expertise in methylation analysis.

ChIP-seq (Chromatin Immunoprecipitation Sequencing)
Analyze interactions between protein and DNA to identify binding-sites for transcription factors and other proteins. Standard coverage from ~20-50 million reads per cell line and can be scaled to meet project objectives. Expertise in data analysis is also available.

ATAC-seq (Assay for Transposase-Accessible Chromatin Sequencing)
Explore chromatin accessibility and identify open/closed regions of DNA with only 50K cells. Standard coverage from ~20-50 million reads and can be scaled to meet project objectives. Expertise in data analysis is also available.

Expedited rapid turnaround is available, subject to project size.

The Sequencing Center is certified by the **Illumina Propel Certification for Core and Service Labs**

Illumina PROPEL certified™

Please contact us for pricing details, sample submission guidelines, or to schedule a consultation to discuss specific needs for your research project.