

קטלוג שירותים המרכז לחקר הסרטן, שיבא

היחידה לטכנולוגיות מתקדמות שבמרכז לחקר הסרטן בשיבא מתמחה בשירותי פרוטאומיקה, NGS, וציפים ומספקת פתרונות מקיפים לאנליזות פרוטאומיות, גנומיות ולאפיין מתילציות. שרות הפרוטאומיקה שלנו מתבסס על מערכת מס-ספקטרומטריה וכולל טכניקות שונות לזיהוי ולכימות חלבונים ממגוון סוגי דגימות. שרות ה-NGS שלנו עושה שימוש בפלטפורמות שונות של מכשירים (אילומינה ו-PACBIO) המאפשרות ריצופים קצרים וארוכים לצורך ביצוע יישומים שונים, החל מרמת הגן הבודד ועד ריצוף גנומי מלא. כמו כן אנו מבצעים קביעת פרופיל מתילציות באמצעות ציפים וכן באמצעות ריצוף.

לפרטים נוספים:

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Next Generation Sequencing

The Wohl Institute provides NGS (Next-Generation Sequencing) services on PacBio Sequel IIe and Illumina® sequencing platforms.

Ready-to-run libraries on Illumina® sequencing platforms:

We provide the most advanced and powerful sequencing platforms with different capacities and read lengths to fit the project scale and budget. Our QC library service ensures optimal cluster generation and maximal data output for each run. Different samples can be multiplexed and sequenced together as long as they have the same read length. We also offer FREE PhiX spike-in and demultiplexing (FASTQ) of the results.

PacBio Sequel IIe Platform:

PacBio Sequel IIe is an advanced sequencing platform that generates long-read length DNA and cDNA sequences, allowing the generation of high-quality single-molecule sequences (HiFi) of genomic DNA (~10-15kbp), full-length cDNA (up to 10 kbp long), and amplicons up to 10 kbp long. This technology offers additional benefits including uniform coverage of typically inaccessible regions, single-molecule resolution, and direct detection of epigenetic modifications. Applications include de novo assembly, variant and structural variant detection, full-length transcript sequencing for whole transcriptome, which can identify alternatively spliced isoforms.

We offer Pacbio library preparation and sequencing for: DNA, RNA, and amplicons.

Mass Spectrometry-Based Proteomics

The Proteomics Unit offers protein profiling services which include sample preparation and analysis using liquid chromatography (LC, Nano Easy NLC 1200 System) coupled to mass spectrometry (MS, Q-Exactive HF) to identify and quantify the protein content in the sample (using by MaxQuant and Perseus softwares). **We provide the following services:**

Single shot proteomics

Label-free proteome identification and quantitation of ~4,000 proteins from cell extracts/ tissue lysates. Sample preparation includes in-solution digestion, peptide extraction, and LC/MS analysis of 2hr chromatography gradient.

Affinity proteomics

Analysis of samples after affinity purification (such as co-IP or pull down experiments). Sample preparation includes on-bead digestion, peptide extraction, and LC/MS analysis of 2hr chromatography gradient.

Secretome / extracellular vesicles (EVs)

Proteomics analysis of secreted proteins. Sample preparation includes digestion, peptide extraction, and LC/MS analysis of 2hr chromatography gradient.

Service include Project planning, sample preparation, data acquisition, analysis and basic statistical analyses.

Infinium MethylationEPIC Array Service

The Infinium MethylationEPIC Array is a genome-wide DNA methylation analysis technique based on bisulfite conversion and Illumina Bead Array technology. It allows to quantitatively detect the total methylation level of over 935,000 CpG sites in the most biologically significant regions of the human methylome. Infinium array chemistry employs many bead replicates for each CpG site queried, each with thousands of probes attached to it. As a result, the Infinium methylation assay provides highly precise methylation measurements.

Infinium MethylationEPIC Array is an 8-samples BeadChip that is processed following the Infinium HD Methylation Assay and scanned on the NextSeq 550 systems. It is compatible a wide range of sample types including fresh/frozen tissues, whole blood, cell lines, and FFPE (with additional mandatory QC and DNA Restoration step).

10x Genomics Single Cell Services

The Chromium System of 10X Genomics provides for the massive partitioning and barcoding of single cells/nuclei using unique barcodes. This technology creates a unique reagent delivery system that partitions single cells or nuclei in the presence of barcoded gel beads and oil to create GEMs (Gel Bead in Emulsions). This allows the encapsulation of up to 10,000 cells per sample, with each barcode per cell/nucleus. Resulting libraries are compatible with Illumina sequencing platforms.