ANNEX 1 - NOA ELIXIRxNextGenIT service catalogue

The following analysis and services will be carried out by the following service installations.

Facility at O.U. CNR-IBIOM.

The Omics facility of ELIXIR-IT, funded by the CNRBiomics and ElixirNextGenIT projects, provides access to the most advanced technologies for genomics, proteomics and metabolomics data production.
The Genomics platform provides access to second and third generation sequencing platforms for high-quality and high- throughput sequencing, for generating massive genomic and transcriptomic data.
The proteomics and metabolomics platforms, through advanced high-resolution, accurate mass spectrometry-based instruments allow biomarkers discovery and validation as well as targeted and untargeted metabolomics analyses.

Institution
CNR, Istituto di Biomembrane, Bioenergetica e Biotecnologie Molecolari (IBIOM).

Services list at CNR-IBIOM

Amplicon sequencing

- Service ID: AMS1
- Analysis type: DNA sequencing
- Analysis description: Amplicon sequencing allows to sequence amplified fragments of different genetic origin (e.g. DNA metabarcoding Sequencing) up to 2 x 300 bp reads.
- Equipment: Illumina® MiSeq, Illumina NextSeq2000

Whole Genome Sequencing (WGS)

- Service ID: WGS30
- Analysis type: DNA sequencing
- Analysis description: Complete genome sequencing, 2 x 150 bp reads – coverage 30X. Applications: Genome resequencing or de novo-sequencing; Genome assembly; Genotyping; Structural variants.
- Equipment: Illumina® NovaSeq6000,

Whole Exome Sequencing (WES)

- Service ID: WES100
- Analysis type: DNA sequencing
- Analysis description: human exome sequencing, 2 x 150 bp reads – coverage 100X
- Equipment: Illumina® NextSeq2000, Illumina® NovaSeq6000

totalRNA-Seq

- Service ID: TRS100
- Analysis type: RNA sequencing
- Analysis description: total stranded RNA sequencing - 100M Read paired Ends 2 x100 bp
- Equipment: Illumina® NextSeq2000, Illumina® NovaSeq6000

mRNA-Seq

- Service ID: MRS50

- Analysis type: RNA sequencing
- Analysis description: polyadenylated RNA sequencing - 50M Read paired Ends 2 x 100 bp
- Equipment: Illumina® NextSeq2000, Illumina® NovaSeq6000

Small RNA-Seq

- Service ID: SRS20
- Analysis type: RNA sequencing
- Analysis description: Small Noncoding RNA Sequencing – 20M reads 2 x 50 bp
- Equipment: Illumina® NextSeq2000

Metabolomics Untargeted Profiling.

- Service ID: MUP1
- Analysis type: metabolomics, LC-MS/MS2/MS3 profiling
- Analysis description: sample collection, method development, metabolites extraction; metabolites separation using UHPLC with RP and HILIC chromatography; High-resolution MS analyses (positive and negative mode) with MS2 and MS3 fragmentation; raw files analysis using Compound Discoverer™ 3.3.0.5 software (Thermo Fisher Scientific) with metabolites annotation and statistical analyses.
- Equipment: : Vanquish™ Flex UHPLC system (Thermo Fisher Scientific), Orbitrap Fusion™ Tribrid™ mass spectrometer (Thermo Fisher Scientific), Attune™ NxT Flow Cytometer (INVITROGEN/Thermo Fisher Scientific), Optima™ MAX-XP tabletop ultracentrifuge (BECKMAN COULTER)

Metabolomics Targeted Profiling.

- Service ID: MTP1
- Analysis type: metabolomics, LC-MS/MS2/MS3 analysis with appropriate standards
- Analysis description: sample collection, method development, metabolites extraction, ; metabolites separation using UHPLC with RP or HILIC chromatography; High-resolution MS analyses (positive and negative mode) with MS2 and MS3 fragmentation; raw files analysis using Compound Discoverer™ 3.3.0.5 software (Thermo Fisher Scientific) with metabolites annotation and statistical analyses.
- Equipment: Vanquish™ Flex UHPLC system (Thermo Fisher Scientific), Orbitrap Fusion™ Tribrid™ mass spectrometer (Thermo Fisher Scientific), Attune™ NxT Flow Cytometer (INVITROGEN/Thermo Fisher Scientific), Optima™ MAX-XP tabletop ultracentrifuge (BECKMAN COULTER).

Bio-Imaging

- Service ID: IMG1
- Analysis type: Confocal Imaging of different biological samples
- Analysis description: : Confocal imaging with the possibility to excite the fluorophore in the sample choosing any specific wavelength between 485 nm and 685 nm.
- Equipment: Leica® Stellaris 5 White Light Laser Confocal Microscope.

Facility at O.U. University of Bari.

The Omics facility of ELIXIR-IT, funded by the CNRBiomics and ElixirNextGenIT projects, provides access to the most advanced technologies for genomics, proteomics and metabolomics data production.
The Genomics platform provides access to second and third generation sequencing platforms for high-quality and high- throughput nucleotide sequencing, for generating massive genomic and transcriptomic data and to the microarray platform for genotyping and methylome profiling.

Institution
Università di Bari Aldo Moro - Dipartimento di Bioscienze, Biotecnologie e Ambiente (DBBA).

Services list at University of Bari

Nanopore Human Whole Genome Re-sequencing

- Service ID: ONTHSWGS30
- Analysis type: DNA sequencing
- Analysis description: Re-sequencing of human genome from High Molecular Weight DNA (HMW-DNA), long reads, min coverage 30X
- Equipment: ONT PromethION 24

Nanopore de-novo Genome sequencing

- Service ID: ONTDNWGS
- Analysis type: DNA sequencing with Oxford Nanopore Technology (ONT) for long read production; possible High Molecular Weight DNA (HMW-DNA) extraction from animal tissues
- Analysis description: Complete genome sequencing from HMW-DNA, long reads, min coverage not guaranteed
- Equipment: ONT PromethION 24 or GridION

Amplicon sequencing

- Service ID: AMS1-1
- Analysis type: DNA sequencing
- Analysis description: Amplicon sequencing allows to sequence amplified fragments of different genetic origin (e.g. DNA metabarcoding Sequencing) up to 2 x 300 bp reads.
- Equipment: Illumina® MiSeq

Whole Genome Sequencing (WGS)

- Service ID: WGS30-1
- Analysis type: DNA sequencing
- Analysis description: Complete genome sequencing, 2 x 150 bp reads – coverage 30X. Applications: Genome resequencing or de novo-sequencing; Genome assembly; Genotyping; Structural variants.
- Equipment: Illumina NovaSeqX Plus

Whole Exome Sequencing (WES)

- Service ID: WES100-1
- Analysis type: DNA sequencing
- Analysis description: human exome sequencing, 2 x 150 bp reads – coverage 100X
- Equipment: Illumina NovaSeqX Plus

totalRNA-Seq

- Service ID: TRS100-1
- Analysis type: RNA sequencing
- Analysis description: total stranded RNA sequencing - 100M Read paired Ends 2 x100 bp
- Equipment: Illumina NovaSeqX Plus

Genotyping analysis on Array

- Service ID: GAAV3.0
- Analysis type: human genotyping
- Analysis description: human genotyping with Infinium Global Screening Array-48 v3.0
- Equipment: Illumina® iScan

Genotyping analysis on Array

- Service ID: GAAV1.0
- Analysis type: human genotyping
- Analysis description: human genotyping with Infinium Global Diversity Array-8 v1.0
- Equipment: Illumina® iScan

Methylome Profiling on Array

- Service ID: METV2.0
- Analysis type: human methylome profiling
- Analysis description: human methylome profiling with Infinium MethylationEPIC v2.0
- Equipment: Illumina® iScan

ELIXIR-IT - OASI Metabolomics Facility at O.U. CNR-IBSBC.

The metabolomics infrastructure offers a whole setup of advanced and complementary technologies for mass-spectrometry and other services, providing high data quality and versatile packages for metabolic profiling to suit your needs.

Mass-spectrometry is a well-established technology for studying metabolic changes by detecting the metabolites related to the physio-pathological state of the cell, tissue, or organism within the context of the environmental condition, genetic regulation, altered kinetic activity of enzymes, and changes in metabolic reactions.

Metabolomics profiling identifies thousands of metabolites generated by the enzymatic reactions of specific pathways, providing a snapshot of cell activity such as cell signaling, energy transfer, and cell-to-cell communication. Alternative metabolic pathways due to environmental adaptation or acquired drug resistance may be identified using labeled substrates (stable isotope tracers).

Metabolomics has multiple applications, from novel mechanisms and new biomarkers discovery to food, nutrition, human and animal health, and clinics. Our team of researchers will help you design the strategy to adopt the best approach for your research. Our technology platform can serve multiple industries, including biomedicine, pharmaceuticals, agriculture, animal husbandry, nutrition, and other fields.

See more at : https://oasi.ibsbc.cnr.it/metabolomics/

Institution

CNR, Istituto di Bioimmagini e Sistemi Biologici Complessi (IBSBC).

Services available at CNR-IBSBC Metabolmics Facility

Metabolomics analysis Untargeted Profiling

- Service ID: MUP2
- Analysis type: metabolomics
- Analysis description: Metabolomics analysis -x LC-MS or GCMS Untargeted Profiling. SAMPLE PREPARATION, data collection and data analysis. Untargeted Profiling – DATA ANALYSIS: metabolites annotation, statistical analyses, figures of output.
- Equipment: LCQTOF (The High-Performance Liquid Chromatography (HPLC) of the 1290 Infinity series and the combined Q-TOF 6550 mass spectrometer permit a metabolite detection sensitivity of a few femtograms. The system allows untargeted and stable isotope labeling metabolomic analyses for a wide spectrum of samples and metabolites) GCQTOF (the 7890B Gas Chromatography System combined with the 7250 Q-TOF spectrometer enables robust

untargeted metabolomic and structural analyses of small polar and nonpolar molecules)

Metabolomics analysis Targeted Profiling

- Service ID: MTP2
- Analysis type: metabolomics
- Analysis description: Metabolomics analysis - LC-MS or GC-MS TARGETED Profiling. SAMPLE PREPARATION and data collection, TARGETED Profiling – DATA ANALYSIS: metabolites annotation, statistical analyses, figures of output.
- Equipment: GC-MSD Intuvo 9000 gas chromatography system paired with MSD Inert Plus 5977B mass spectrometer. The system allows small molecules quantification through the Single Ion Monitoring method as well as labeling analyses using stable isotopes.; LCQQQ The 6495D triple quadrupole LC/MS system allows the quantitative analysis of known compounds thanks to Multiple Reaction Monitoring technology. The system is used for targeted analyzes with high sensitivity and specificity; Ion Mobility UHPLC/Q-TOF MS The HPLC system is coupled to the 6560 Ion Mobility (IM) Q-TOF LC/MS mass spectrometer, which includes a new dimension of separation of molecular species in the ion mobility phase. Ion mobility mass spectrometry allows you to create a more complete profile of metabolomic samples, providing access to new information that is difficult to gain from other MS systems, such as isomers identification or chiral molecules.

Metabolomics analysis Targeted Labeling Profiling

- Service ID: MLP1
- Analysis type: metabolomics
- Analysis description: Combining the targeted analysis and specific tracer molecules allows for identifying where metabolites end up in the biological system, opening new possible scenarios of altered metabolic pathways that drive diseases such as cancer, neurodegeneration, cardiomyopathy, diabetes, etc. Metabolomics analysis Targeted Labeling Profiling by liquid chromatography-QTOF or gas chromatography-quadrupole or QTOF mass spectrometry. Metabolomics analysis - Metabolomics Flux: 13C6 and 15N Glutamine. Included sample preparation, data collection and mass isotopomer distribution analysis.
- Equipment: the same instrumentation available used for the service “Metabolomics analysis Targeted Profiling” (MTP2).