# ONE4ALL - Valorizzazione dell’Infrastruttura di Ricerca MIRRI-IT a supporto della Bioindustria e della Bioeconomia per uno sviluppo sostenibile con approccio “One Health".

**Proposta progettuale in risposta all’Avviso MUR DECRETO DIRETTORIALE N. 310 DEL 18-03-2025 PN RIC 2021-2027 - MANIFESTAZIONE DI INTERESSE PER IL POTENZIAMENTO DELLE INFRASTRUTTURE DI RICERCA (IR) PUBBLICHE CHE OPERANO IN AMBITO S3 FINALIZZATO ALL’AVANZAMENTO TECNOLOGICO DELLE IMPRESE.**

**CATALOGO OFFERTA Infrastrutture di Ricerca**

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|  | IR | Mission and Offer | website |
| 1 | MIRRI-IT | Based on its partner organisations’ state-of-the-art facilities/equipments and top-level expertise, MIRRI makes available for its users a vast, diverse portfolio of high-quality services. MIRRI’s services and expertise can help researchers and bioindustries delivering the maximum value and impacts from their projects, technologies and products. Services commonly provided by MIRRI’s partner organisations, e.g., supply, deposit or identification of microbial resources by gene sequencing, as well as advanced services, e.g., genomics, screening of metabolites, phylogenetic analysis, consultancy, up to 95 services. General Service of MIRRI include: Supply of microbial resources in different delivery forms or physiological conditions. You can consult the catalogue of MIRRI; Deposit of microbial resources the microbiological material to be deposited is cultivated and preserved following the depositor’s instructions or using optimised conditions when necessary; Identification of microbial isolates up to the genus or species level. The service includes consultancy to define the most suitable method considering the taxonomic group of the strain of interest. Multiphasic approach to identify and diagnose viruses; Characterisation based on the DNA/RNA sequence of molecular markers (housekeeping, rRNA, virulence, drug-resistance genes, etc.). Analysis of several markers (Multi-Locus Sequence Analysis/Typing, MLSA/MLST) allowing strain typing; Strain typing based on differences in the DNA sequence of the isolates or environmental samples. Used, for example, for strain typing/differentiation, for phylogenetic analysis or to study the microbial diversity of environmental samples; MALDI-TOF MS protein profiles: High-throughput dereplication screening using MALDI-TOF MS to group isolates that represent the same taxon. Used to reduce a large number of isolates to a smaller, non-redundant set for further characterization; Karyotyping: Separation of intact chromosomal DNAs by pulsed field gel electrophoresis (PFGE) to type at inter- and intra-specific level; Phenotypic characterization of the strains: structural analysis, metabolic and physiological analysis, enzymatic production ect; Metabolomic profiles of microorganisms: target and untarget metabolites analysis with HRMS-MS, Volatilome, etc; NGS and related services: High-throughput genomic sequencing of a strain including quality assessment, scaffolding and assembly to obtain the draft/complete genome sequence; Metagenomic: High-throughput genomic sequencing of environmental samples or mixed communities; Advanced genome and metagenome analyses: Analysis of the genomic sequences to make a deep characterisation of the strain/sample (strain typing, genome mining, overall genome relatedness indexes, taxonomic composition, etc; Customised optimisation of cultivation and fermentation conditions of microbial cultures to enhance growth rates and productivity; Growth promoting / antimicrobial / antiviral bioassays: Test the effect of different types of agents (e.g. compounds, extracts, soil, etc.) on the growth, replication or yield of a particular microbial strain, virus or plant; Characterisation of technological abilities of microbial strains: A variety of tests to assess the capacity of microbial strains to be used in different industrial applications; Detection of contaminants in raw materials and products : Detection of the presence or absence of viable microorganisms in raw materials and products; Material resistance testing: Analysis of the capacity of microbial strains to grow on certain materials; Taxonomic database tools: Access to a series of database tools for Taxonomic information or analysis; Miscellaneous characterisation analyses, such as Mycovirus detection, assessment of the metabolic status of a culture, assessment of the metabolic status of a culture, DNA extraction or construction and characterisation of intraspecific hybrids, etc; Support and consultancy on legal and regulatory frameworks (such as Nagoya protocol compliance, MTA, MDA, ABS, etc); Data integration via digital platform between OMICS, phenotypic and environmental datasets and AI-driven researches. | Sito Mirri-IT <https://susmirri-mbrc.di.unito.it/>  Sito MIRRI-ERIC  <https://www.mirri.org/>  https://www.mirri.org/services/ |
| 2 | IBISBA-IT | Based on the state-of-the-art facilities and high-level expertise of its partner organisations, IBISBA offers users a broad and integrated portfolio of high-quality services supporting innovation in industrial biotechnology. IBISBA’s capabilities enable researchers and bioindustries to accelerate the development of sustainable bioprocesses, from early-stage discovery to process validation and scale-up, thereby maximizing the scientific, technological and economic impact of their projects and products. Services commonly provided by IBISBA-IT include early-stage discovery and engineering of enzymes and biocatalysts, protein expression, bioactive molecules identification and analysis, development and optimization of microbial production systems, advanced ‘omics’ analyses, metabolic and fermentation engineering, and support for process scale-up and industrial translation. General Services of IBISBA-IT include: Environmental metagenomics, including in geothermal environments, for the identification of novel microorganisms and their enzymes. Identification, biochemical characterization and engineering of innovative proteins and biocatalysts, including those from organisms growing in extreme environments, with particular emphasis on Carbohydrate Active Enzymes, especially from (hyper)thermophilic microorganisms, and of plastic-degrading enzymes for their exploitation in lignocellulosic biomasses and waste products hydrolysis and valorisation Lab-scale microwave pretreatment of lignocellulosic biomasses In silico design, enzyme engineering, and morphological analysis of enzymatic activity Production and characterization of recombinant proteins Optimization of protein expression and secretion in eukaryotic hosts. Design and development of protein biosensors. Production of sustainable nanoplatforms for enzyme immobilization, also cascade-based and with orientation control Production of bio-inks, bio-fillers, and functional materials Isolation and identification of bioactive molecules from natural sources Characterization of bioactive molecules in mammalian cells Rational genetic engineering for increasing the production of specialized metabolites System biocatalysis: set-up of novel metabolic pathways Targeted metabolic analysis System biology: Metabolic engineering, quantitative microbial physiology Proteomic, Transcriptomic, Metabolomic analyses, and screening for secondary metabolites Genetic improvement of microbial strains Design and validation of fermentation processes Selection and characterization of microbial communities for sustainable biorefineries agro-industrial and urban wastes and surplus Valorization of microbial cultures for functional foods and fermentation processes | [www.ibisba.it](http://www.ibisba.it) |
| 3 | ITACA.SB | The main objective of the ITACA.SB IR (Potentiating the Italian Capacity for Structural Biology Services in Instruct-ERIC) is to strengthen Italy's capacity in the strategic field of structural biology. Through the creation of a dedicated research infrastructure, ITACA.SB makes available to the scientific community, Italian and non-Italian, tools and skills for the study of (macro)molecules at different levels of complexity and their mechanisms of action. In this way, the project consolidates, with an immediately perceptible impact, Italy's role within the European Instruct-ERIC network, effectively increasing the quality and visibility of Italian research and aligning our country with what has been happening for some time in the international field in the field of structural biology and modern technologies used. With the acquisition of a fleet of high-tech tools, the project aims to stimulate innovation and technology transfer by connecting the world of research and that of business, especially in the biotechnology, agrifood, and pharmaceutical sectors, stimulating the birth of new ideas and the development of new products in the pharmaceutical sector (drugs and diagnostics), nutraceuticals and functional foods. Also, ITACA.SB aims to contribute significantly to the development of society through the continuous training of researchers, including those from the industrial world, equipping them with a wide spectrum of skills essential for their future academic or industrial careers.  **Service Description of ITACA.SB**  High Performance Computing cluster designed to provide support to the scientific community for CryoEM, BioSAXS, X-Ray data storage and processing, as well as to enhance theoretical and computational research in Structural Biology and Drug Discovery  BioSAXS - Small Angle X-Ray Scattering analysis on biological macromolecules in solution: Characterization of biological specimens under native-like conditions to assess oligomeric states and conformational changes as a function of time, pH, ionic strength, and temperature:  BioSAXS data analysis (Offline). Extensive analysis of BioSAXS data collected either at the ITACA.SB BioSAXS Operative Unit or other centres.  Large scale protein expression (recombinant in E. coli) and purification for X-ray studies. Protein production and biophysical characterization services Protein Production in E. coli with Isotope Labelling for NMR Protein Production in Mammalian Cells for in-cell NMR  CryoEM sample preparation and data collection – Comprehensive characterization of vitreous biological specimens, encompassing sample vitrification, screening, and data collection.  CryoEM - Data Analysis Single Particle Analysis (SPA) of cryoEM data (up to electron density map)  Mass Spectrometry- Matrix - Identify and separate a wide variety of compounds ranging from chemical to biological entities, Peptide characterization, Analysis of Polysaccharides and Glycoproteins and Glycopeptides: MS/MS analysis for Metabolomics  High-throughput crystallization of soluble and membrane proteins - Screening of crystallization conditions to produce highly diffracting crystals of proteins amenable to X-ray crystallography  Crystal optimization. Optimization of crystallization conditions based on 2D gradients, cross-matrix optimization, additive scatter optimization and matrix microseeding  *Surface Plasmon Resonance*- Determination of binding constants for protein-protein and protein-small ligands (>200 Da) interactions  Mass Photometry - Label-free characterization of macromolecule samples (sample homogeneity, protein aggregation and oligomerization, biomolecular interactions, macromolecular complex assembly), measurement of the light scattered by individual particles.  Magnetic Resonance Services:  - Atomic-level characterization of structure and dynamics of proteins  - Atomic-level characterization of the interaction of these proteins with partners, host proteins and nucleic acids including when transient or fuzzy  - Quick structural screening of the variants addressing differences in interaction mode with drugs and biologics  - Druggability of intrinsically disordered or heterogenous proteins, not addressable by other techniques  - Characterization of the structural properties of the candidate vaccine antigen  - NMR interaction studies of candidate vaccine antigen with different antibodies  - Acquisition of NMR spectra at 1.2 GHz NMR spectrometer in order to structurally characterize the therapeutic mAb at the atomic level.  - Acquisition of high-field solid-state NMR spectra in order to structurally characterize high molecular weight therapeutics and vaccine viral vectors.  - Fast fingerprinting/profiling via NMR metabolomics on blood (serum, plasma) and urine  - NMR metabolomics on food  - Map of local dynamic and structural features of biomolecules via EPR  - Exploration of different modes of biomolecule-ligand interaction via EPR  - Study of long-range structural restraints via EPR  - Investigation of coordination in metal-ion-binding sites via EPR  - Measurements of nuclear relaxation at various magnetic fields with a Fast Field Cycling Relaxometry | [www.itaca-sb.it](http://www.itaca-sb.it) |