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INDUSTRY PARTNERSHIPS & LICENSING OPPORTUNITIES

Translational Oncology Innovation Portfolio

2026

INDEX

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LICENSABLE TECHNOLOGIES

Selected Deal-Ready Assets

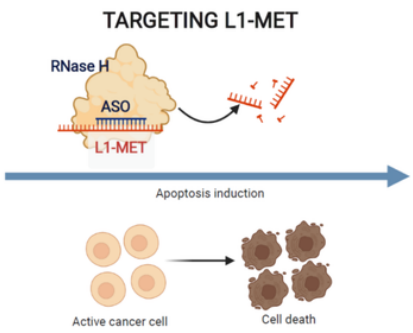
Antisense Oligonucleotides Targeting the LINE1-Derived L1-MET Transcript for Cancer Therapy

Clinical Need

Current targeted therapies are limited by tumor heterogeneity and rapid resistance. The LINE1-derived L1-MET transcript is aberrantly activated in multiple cancers, absent from normal tissues, and associated with oncogene addiction, representing a highly selective therapeutic vulnerability.

Solution

We developed LNA-modified antisense oligonucleotides specifically targeting the L1-MET transcript. L1-MET silencing induces strong apoptosis and loss of tumor cell viability while sparing normal cells, through coordinated downregulation of MET and EGFR and suppression of downstream AKT/ERK signaling.



Advantages

- Tumor-restricted target (no expression in normal tissues)
- Dual MET and EGFR pathway suppression
- Effective across multiple oncogenic backgrounds
- Bypasses resistance to kinase inhibitors
- Clinically validated ASO modality

Applications

Broad applicability in solid tumors, including lung, gastric, and breast cancers. Strongest effects observed in MET-amplified and EGFR-activated tumors, with activity also in cancers with steady-state oncogene expression.
First-in-class therapeutic strategy targeting the LINE1-derived L1-MET oncogenic transcript with potential applications across MET-driven tumors.

Development Stage

TRL 3–4
Validated in multiple cancer cell models with mechanistic confirmation. In vivo evaluation ongoing in patient-derived organoids and PDX models to support preclinical advancement.

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Publication

IP / Patent

"Antisense oligonucleotide sequences to silence human L1-MET transcript in tumors."

Application
IT201900021327A1

Status
Granted: IT, US, JP, CN
Pending: EP, CA, IN, AU, HK

Keywords

L1-MET, chimeric transcript, LINE-1, modified antisense oligonucleotide, apoptosis, gene reprogramming, oncogene down-regulation

In Vitro Evaluation of the Immune Response after Vaccination with an mRNA Vaccine

Clinical Need

mRNA vaccines have demonstrated high efficacy, but current immune monitoring relies largely on antibody titers, which do not fully reflect protective or durable immunity. In particular, the contribution of $CD8^+$ T-cell memory is poorly captured, limiting the ability to distinguish high and low responders, optimize booster strategies, and evaluate therapeutic mRNA vaccines. Robust, scalable methods to assess immune quality and persistence are urgently needed, especially for immunocompromised and high-risk populations.

Solution

We developed a novel in vitro immunomonitoring method that integrates humoral immunity with memory $CD8^+$ T-cell profiling. By measuring CD25 and CD27 expression on $CD8^+$ T cells, the method enables stratification of individuals into high and low responders following mRNA vaccination. This approach provides a biologically meaningful assessment of immune protection that goes beyond antibody measurements alone.

Advantages

- Integrated evaluation of humoral and cellular immunity
- Discriminates high vs. low vaccine responders
- Captures long-term immune memory
- Applicable to infectious and therapeutic mRNA vaccines
- Supports personalized booster and vaccination strategies

Applications

Immune response profiling in mRNA vaccine clinical trials, optimization of vaccination and booster protocols, monitoring of immunocompromised populations, public health immunosurveillance, and evaluation of therapeutic mRNA vaccines, including in oncology and infectious diseases.

Development Stage

TRL 3–4

Validated in subjects vaccinated with SARS-CoV-2 mRNA vaccines, demonstrating clear discrimination between high and low responders based on $CD8^+$ T-cell markers and antibody levels. Long-term immune response assessment has been demonstrated. Extension to additional populations and other mRNA vaccine indications is ongoing.

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Publication

IP / Patent

"Method for in vitro evaluation of the immune response after vaccination with a mRNA vaccine"

Application
IT202200011111A1

Status
Granted: IT

Keywords

Immunomonitoring, Personalized Vaccination, Immune Response Profiling, Therapeutic mRNA Vaccines, Public Health Optimization

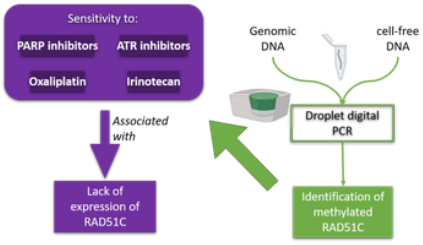
Method for Predicting Cancer Patient Sensitivity to DNA Damage Response–Targeting Therapies

Clinical Need

Precision oncology requires reliable biomarkers to guide treatment selection and avoid ineffective therapies. Alterations in DNA damage repair pathways represent emerging therapeutic vulnerabilities, yet patient stratification remains limited. Identifying robust predictors of response to DNA damage–targeting agents is critical for more rational and effective treatment decisions.

Solution

We identified loss of RAD51C expression as a biomarker of heightened sensitivity to PARP inhibitors, ATR inhibitors, oxaliplatin, and irinotecan. We developed a molecular assay based on droplet digital PCR (ddPCR) to detect RAD51C deficiency in cancer samples, enabling accurate prediction of drug response in colorectal cancer and other tumors with homologous recombination defects.



Advantages

- Actionable predictive biomarker for DNA damage response–targeting therapies
- High sensitivity and specificity enabled by ddPCR technology
- Applicable across multiple drug classes (PARPi, ATRi, chemotherapy)
- Extends beyond colorectal cancer to other HR-deficient tumors
- Compatible with liquid biopsy–based workflows

Applications

The assay enables identification of tumors likely to respond to PARP inhibitors, ATR inhibitors, oxaliplatin, and irinotecan. It is suitable for patient stratification in colorectal cancer and has potential application in breast, ovarian, prostate, and pancreatic cancers, supporting personalized treatment selection without reliance on tumor tissue availability.

Development Stage

TRL 3

Validated using genomic DNA from colorectal cancer cell lines and organoids, as well as circulating tumor DNA. Next steps include validation in clinical samples, including FFPE tissues and plasma from cancer patients, to support translational and clinical deployment.

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Publication

IP / Patent

"Method for predicting sensitivity to chemotherapeutic agents and/or drugs targeting the dna damage response pathway in a tumour affected individual"

Application
IT202200007535A1

Status
Granted: IT

Keywords

precision oncology, predictive biomarker, DNA damage response, RAD51C deficiency, ddPCR, liquid biopsy, patient stratification

PETsign: A Prognostic Molecular Signature for Breast Cancer

Clinical Need

Breast cancer remains a highly heterogeneous disease, and prognostic uncertainty continues to complicate treatment decisions. Current classification systems do not reliably identify patients at higher risk of poor outcome, particularly within luminal subtypes. Improved prognostic tools are needed to guide treatment intensity and optimize patient management.

Solution

PETsign is a molecular prognostic signature derived from transcriptomic profiling of breast cancer patients. It stratifies tumors based on metabolic activity, as reflected by FDG-PET uptake, and identifies patients with aggressive disease biology. PETsign predicts poor prognosis and complements existing clinical and pathological markers.

Advantages

- Independent prognostic value across multiple breast cancer cohorts
- Particularly informative in luminal breast cancer, where current markers are limited
- Biologically grounded in tumor metabolic state
- Robust and reproducible, validated across independent datasets

Applications

PETsign enables prognostic stratification of breast cancer patients to support risk-adapted treatment decisions. It may identify luminal breast cancer patients who could benefit from more intensive therapeutic strategies and can support clinical decision-making and translational research focused on tumor metabolism.
Companion diagnostic and prognostic test for breast cancer risk stratification.

Development Stage

TRL 4

Developed and validated across multiple independent breast cancer cohorts using transcriptomic datasets. Ready for clinical validation studies and integration into diagnostic and prognostic workflows.

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Publication

IP / Patent

"Method for prognosis of breast cancer"

Application
EP4621073A1

Status
Pending: EP

Keywords
breast cancer, prognostic signature, tumor metabolism, FDG-PET, transcriptomics, risk stratification, precision oncology

Method for Tumor Subtype Prediction Using Tumor-Intrinsic Transcriptional Profiles

Clinical Need

Tumor subtyping is essential for prognosis and treatment selection, yet current classification systems are largely cohort-based and poorly suited for single-patient analysis. Tumor heterogeneity and stromal contamination further limit the clinical applicability of transcriptomic classifiers. There is a clear need for robust methods that enable accurate, patient-level tumor stratification.

Solution

We developed a computational method that predicts intrinsic tumor subtypes from transcriptomic data by isolating tumor-specific gene expression and accounting for stromal contribution. The approach enables classification of individual patient samples and assigns quantitative association scores to one or multiple tumor subtypes, reflecting intra-tumor heterogeneity.

Advantages

- Patient-level tumor subtyping, not dependent on cohort-based classification
- Tumor-intrinsic signal extraction, minimizing stromal bias
- Multi-label classification, capturing tumor heterogeneity
- Quantitative subtype association scores, supporting nuanced clinical interpretation
- Algorithm-agnostic framework, compatible with multiple supervised models

Applications

The method supports molecular stratification of solid tumors, with demonstrated applicability in colorectal cancer and potential extension to other tumor types. It can be used for patient stratification in clinical research, biomarker development, and precision oncology workflows where accurate subtype assignment informs prognosis and therapeutic decision-making.

Development Stage

TRL 3-4

Method developed and validated using large transcriptomic datasets, including tumor-intrinsic and canonical profiles. Demonstrated ability to identify known and novel molecular subtypes and to classify individual patient samples. Ready for further clinical validation and translational integration.

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Publication
In Preparation

IP / Patent
"Method for estimating tumor subtyping of a patient"

Application
N/A

Status
Pending: IT

Keywords
tumor subtyping, precision oncology, transcriptomics, tumor heterogeneity, patient stratification, molecular classification, machine learning

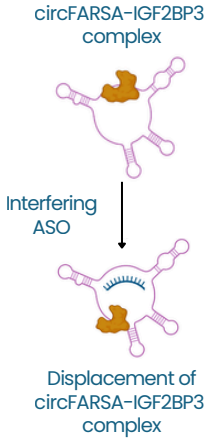
Antisense Oligonucleotide Targeting the circFARSA–IGF2BP3 Complex for Anti-Metastatic Cancer Therapy

Clinical Need

Metastatic disease remains the leading cause of cancer mortality, and effective therapeutic options to prevent tumor dissemination are limited. Current treatments often fail to directly target the molecular mechanisms driving cell migration and invasion. Novel, highly specific strategies are needed to inhibit metastasis while minimizing toxicity to healthy tissues.

Solution

We developed a chemically modified antisense oligonucleotide (ASO) that selectively disrupts the interaction between the circular RNA circFARSA and the RNA-binding protein IGF2BP3. By sterically blocking this ribonucleoprotein complex, the ASO inhibits tumor cell migration and invasion without affecting circFARSA or linear FARSA expression levels.



Advantages

- First-in-class strategy targeting a circRNA–protein oncogenic complex
- High molecular specificity for circFARSA over linear transcripts
- Anti-migratory and anti-invasive activity demonstrated in cancer cell models
- Minimal impact on healthy cell viability, supporting therapeutic selectivity
- Chemically stabilized ASO design with reduced immunogenicity

Applications

The technology enables development of targeted anti-metastatic therapies for circFARSA-expressing tumors. Primary applications include non-small cell lung cancer, with potential extension to other solid tumors where the circFARSA–IGF2BP3 axis drives invasive behavior. The approach is suitable for further preclinical and translational therapeutic development.
Novel RNA-protein interaction target enabling development of anti-metastatic therapeutics.

Development Stage

TRL 3
Validated in vitro in multiple cancer cell lines, demonstrating selective disruption of the circFARSA–IGF2BP3 complex and significant inhibition of migration and invasion. Next steps include in vivo efficacy and tolerability studies to support translational development.

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Publication
In Preparation

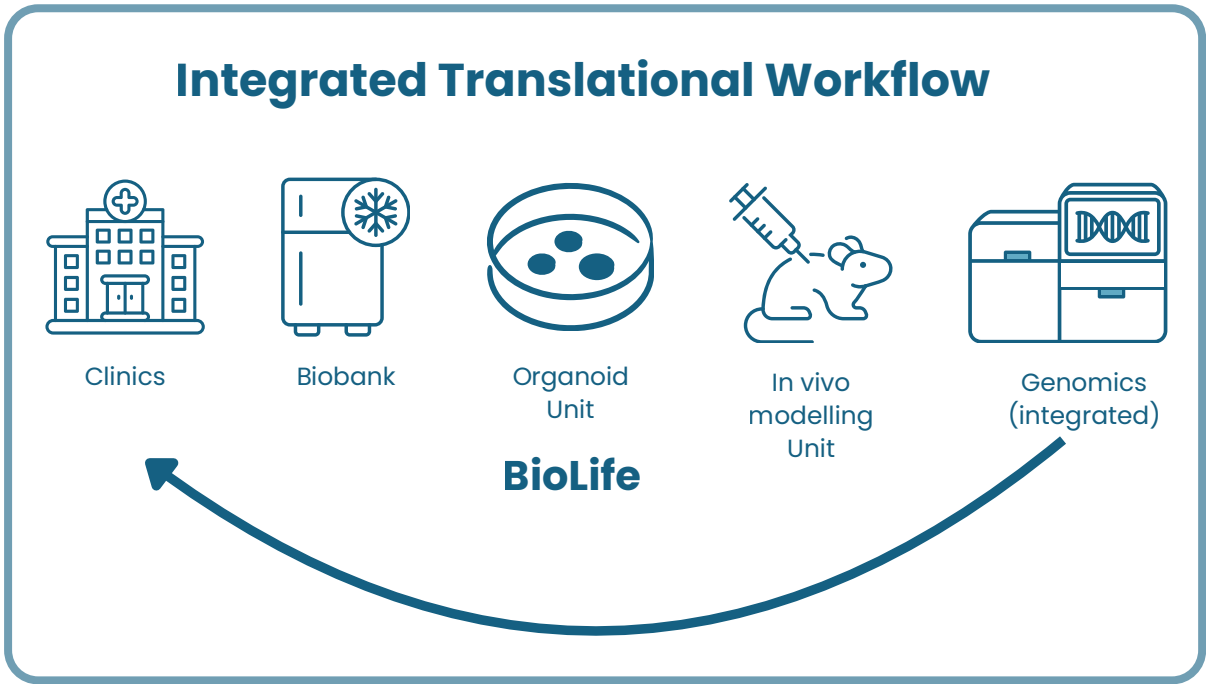
IP / Patent
"Nucleic acid molecule targeting the circFARSA–IGF2BP3 complex"

Application
N/A

Status
Pending: IT

Keywords
antisense oligonucleotide, circular RNA, metastasis inhibition, RNA-protein interaction, precision oncology, targeted therapy

INOC'S TRANSLATIONAL ENGINE



INOC integrates clinically annotated patient-derived biospecimens with a translational research platform.

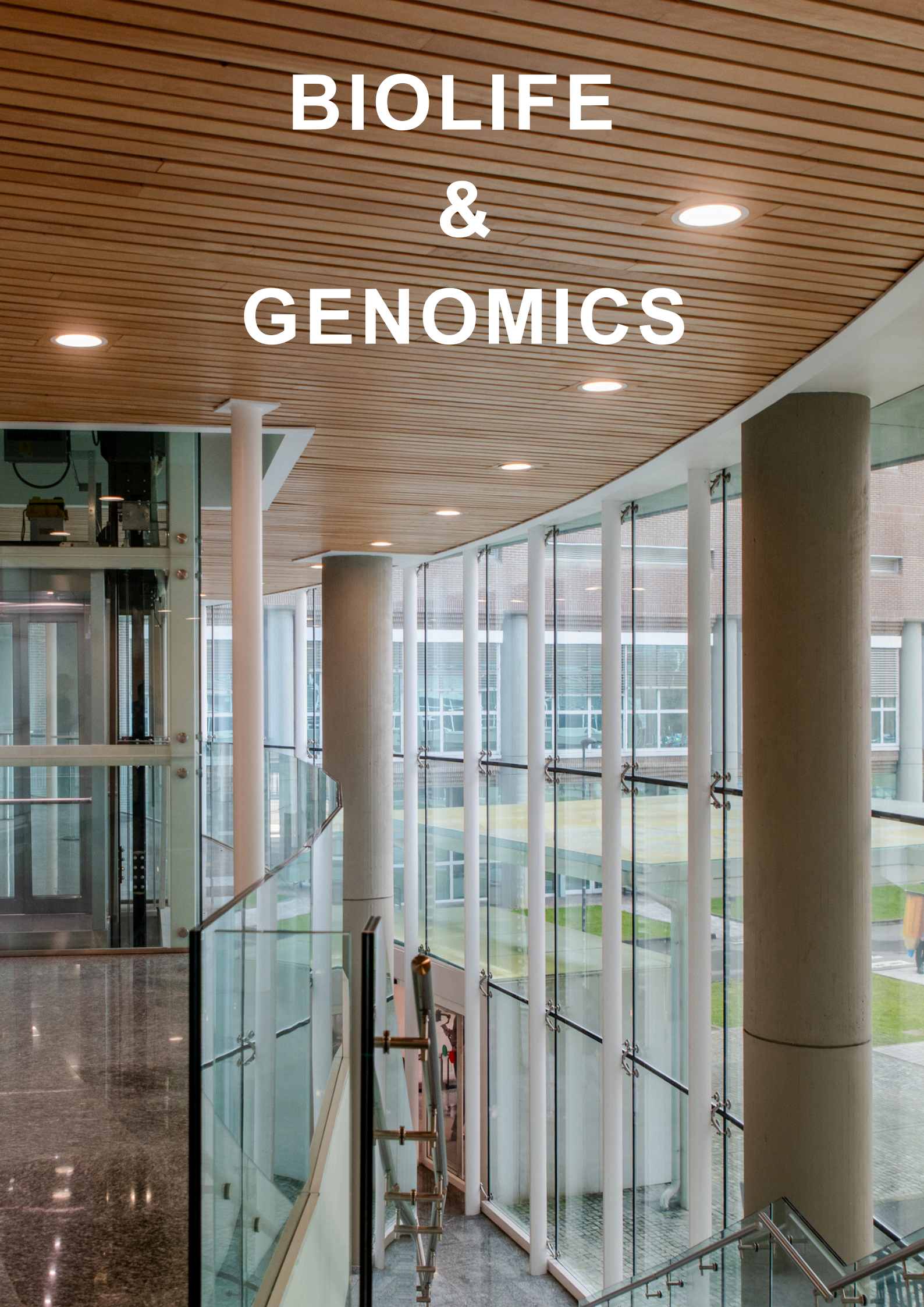
Our biological models and licensable technologies are developed and validated within BioLife, an integrated translational research platform that comprises three main pillars:

- Biobank (patient-derived biospecimens)
- Organoid Unit (*in vitro* models)
- In vivo Modelling Unit (*in vivo* validation)

With strong ties to the Candiolo Genomics Centre (molecular characterization)

This integration enables end-to-end workflows from discovery to preclinical validation, accelerating translational research and partnership opportunities.

BIOLIFE & GENOMICS



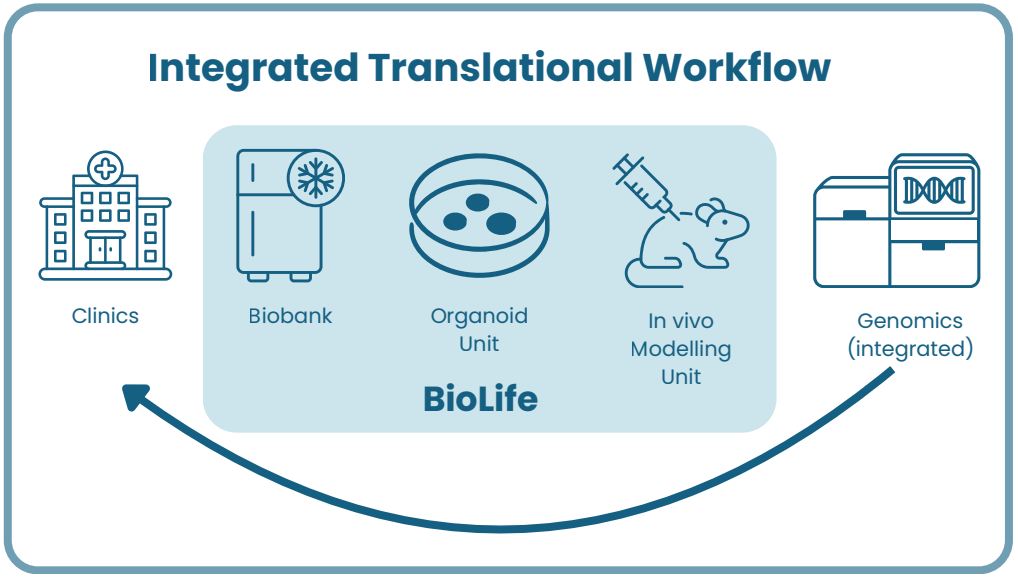
BioLife
Integrated Translational Research Platform

Overview

BioLife is a fully integrated translational research platform at INOC, designed to interface patient-derived biospecimens and data with advanced preclinical modelling and downstream molecular profiling.

By synergising and consolidating the capabilities of its three core pillars: the Biobank, Organoid Unit, and *in vivo* Modelling unit, BioLife serves as an innovative structural and technological hub that supports a comprehensive experimental pipeline, from primary biospecimen procurement to rigorous functional validation

Furthermore, the platform operates in close synergy with the Candiolo Genomics Centre, thereby enabling deep molecular characterization and fostering data-driven translational discovery.



From patient-derived samples to functional validation within a single integrated platform

Core Components

Biobank
Collection, processing, characterisation and annotation of patient-derived biospecimens

Organoid Unit
In vitro patient-derived models for functional assays and drug testing

in vivo Modelling Unit
In vivo PDX models for preclinical validation and co-clinical studies

Applications

Key areas of translational and preclinical application

- End-to-end translational research programs
- Biomarker discovery and validation
- Preclinical drug development and testing
- Co-clinical studies
- Precision oncology research
- Integration of multi-omics and functional data

Collaboration Opportunities

Available partnership and research engagement models

- Access to integrated platform for academic and industrial partners
- Design and execution of translational research programs
- Combination of in vitro and in vivo model systems
- Multi-omics and data-driven project development
- Long-term strategic partnerships

Contact

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Platform Snapshot

1. Integrated translational oncology platform
2. End-to-end workflows from patient to validation
3. Biobank, in vitro and *in vivo* integration, with access to advanced genomics and multi-omics analysis
4. Clinically annotated patient-derived biospecimens
5. Advanced preclinical model systems (organoids, PDX)
6. Multi-omics and bioinformatics capabilities
7. Scalable for academic and industrial partnerships

Keywords

translational oncology
precision medicine
biobank
organoids
PDX models
genomics
multi-omics
drug development
biomarker discovery
co-clinical studies

Biobank
Clinically Integrated Biospecimen and associated data

Overview

The Biobank is a strategic translational research infrastructure that is dedicated to the collection, processing and storage of high-quality biospecimens and clinically annotated data, supporting the development of innovative diagnostics, biomarkers and precision therapies.

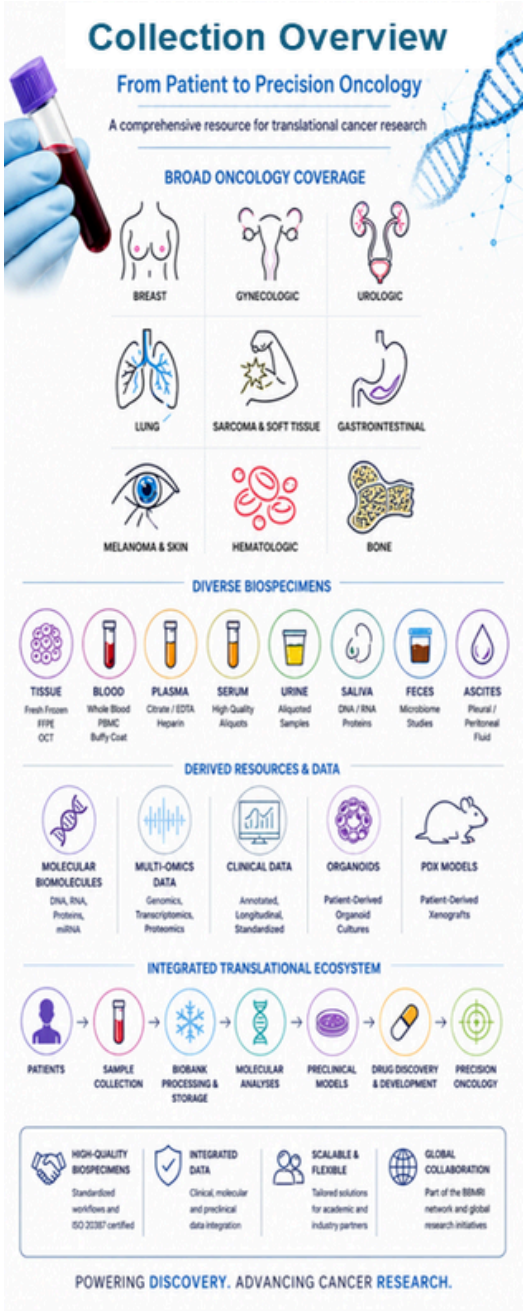
The Biobank is the main pillar of the BioLife translational research platform, already embedded within a comprehensive oncology ecosystem. It seamlessly connects clinical practice, pathology, molecular profiling and advanced preclinical models, transforming patient-derived biospecimens into reliable, research-ready resources.

Through rigorous, ISO 20387-compliant quality standards, comprehensive traceability, and integrated data management, the Biobank supports high-impact collaborations with academic institutions, healthcare organizations, and industry partners—accelerating translational research from discovery to clinical application.

Services

Core functional capabilities of the biobank:

- Collection, processing, characterisation and long-term storage of patient-derived biospecimens
- Cryopreservation of organoids, primary cells, and other biological derivatives
- DNA/RNA extraction with standardized quality control assessment
- Integration with clinical, pathological, and molecular data
- Support for translational research, biomarker discovery, and EU-funded projects.



Biospecimen Portfolio

Biological materials available:

- Tumor resections, matched normal tissues and biopsies
- Fresh-frozen, FFPE and OCT-embedded specimens
- Whole blood, plasma, serum, PBMCs and follow-up longitudinal blood collections
- Urine, saliva and feces
- Patient-derived models: organoids, primary cell cultures and biological derivatives
- Patient-derived xenograft (PDX) tissues and biological samples.

Associated Data

- Clinical and clinicopathological annotations
- Patient demographics, diagnosis, staging and treatment history
- Therapeutic response and longitudinal clinical follow-up
- Standardized pathology review and histopathological annotations
- Complete pre-analytical and sample quality metadata
- Molecular, genomic and multi-omics data (when available).

Collaboration Opportunities

Available partnership and research engagement models:

- Access to high-quality, clinically annotated biospecimens through tailored collaboration models
- End-to-end support for academic, biotech and pharmaceutical R&D programs
- Integration with multi-omics, organoid and PDX facilities
- Biomarker and companion diagnostic co-development
- Prospective collection and longitudinal studies

Applications

Key areas of translational and preclinical application:

- Biomarker discovery and validation
- Comprehensive molecular profiling of human tumors
- Liquid biopsy for disease monitoring and treatment response assessment
- Retrospective, prospective and multicenter clinical studies
- Translational and co-clinical research
- Precision medicine and companion diagnostics

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Snapshot

1. Broad and curated biospecimen collection across oncology indications
2. High-quality, standardized processing and storage workflows
3. Integration with clinical, molecular and preclinical data
4. Access to patient-derived experimental models (organoids, PDXs)
5. Scalable platform for translational and industrial research

Keywords

biobank
biospecimens
clinical data
precision oncology
biomarker discovery
translational research
liquid biopsy
tumor heterogeneity
multi-omics
preclinical models

Organoid Unit
Patient-Derived Organoids for Translational Oncology

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Overview

The Organoid Unit is dedicated to the derivation, expansion, functional characterization, and experimental use of patient-derived organoids. Samples are obtained from patients treated at iNOC - Istituto Nazionale Oncologico Candiolo or from external collaborators.

Integrated within the BioLife platform, it has strong interconnection with the Biobank, Genomics Centre, and In vivo Modelling Unit. The Organoid Unit enables the development of biologically relevant, patient-derived preclinical models.

By combining advanced 3D culture systems, functional assays, and digital data analysis, the centre supports translational oncology research, biomarker discovery, and the development of precision medicine strategies.

The Organoid Unit is designed in a modular, scalable way to enable future progressive expansion toward automated organoid maintenance and high-content phenotypic screening.

Collection Overview

Clinically Annotated Tumor Types of Interest:

- Colorectal cancer
- Gastric cancer
- Breast cancer
- Prostate cancer
- Ovarian cancer
- Pancreatic cancer
- Melanoma
- Lung cancer

Applications

Key areas of translational and preclinical application:

- Therapeutic target identification and validation
- Drug screening and sensitivity testing
- Biomarker discovery and validation
- Mechanisms of resistance
- Precision oncology research
- Support for functional precision oncology studies
- Preclinical evaluation of targeted and combination therapies

Supported Sample Types

Biological materials compatible with the unit:

- Patient-derived organoids (PDOs) (already available)
- Organoids derived from patient-derived xenografts (PDX-derived organoids) (already available)
- Advanced 3D culture systems (coming soon)
- Tumor–stromal and immune co-culture models (coming soon)
- Advanced 3D and co-culture systems (planned).

Collaboration Opportunities

Available partnership and research engagement models:

- Drug testing and functional assays on organoid models
- Support for translational and preclinical research programs
- Integration with genomics and multi-omics datasets
- Co-development of organoid models and workflows

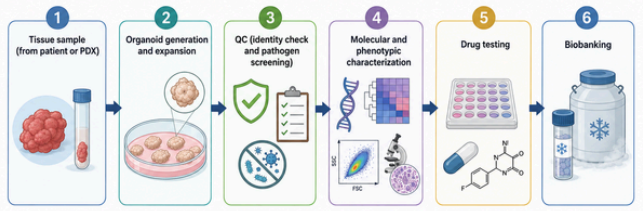
Services

Core functional capabilities:

- Derivation of organoids from clinical samples and preclinical models
- Development and implementation of standardized protocols for advanced 3D culture systems
- Expansion and long-term maintenance of organoid collections
- Cryopreservation of organoid models
- Systematic quality control procedures to ensure genetic fidelity to the original samples and pathogen-free cultures
- Centralized data management system ensuring full sample traceability
- Molecular profiling of organoid models
- Targeted pharmacological response testing on organoids

Strategic Strengths

- Direct access to longitudinal clinical samples through the Biobank
- Integration with genomic, imaging and clinical research units
- Development of living tumor models with high translational relevance
- Scalable infrastructure enabling future high-throughput functional screening
- Strong potential for industrial partnerships and technology transfer



Contact

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Snapshot

1. Patient-derived organoid models across multiple tumor types
2. Standardized derivation, expansion and cryopreservation workflows
3. Functional assays for drug response and tumor heterogeneity
4. Integration with clinical, molecular and genomic data
5. Centralized data management and traceability
6. Scalable platform for translational and industrial applications

Keywords

organoids
patient-derived models
3D cell culture
precision oncology
drug screening
functional assays
tumor heterogeneity
biomarker discovery

In vivo Modelling Unit
Preclinical validation for Translational Oncology

Overview

The In vivo Modelling Unit is a state-of-the-art preclinical facility within the BioLife translational research platform, set up to support translational oncology research.

The facility specializes in the generation and application of patient-derived in vivo models, particularly PDX, operating under high microbiological standards, full traceability and regulatory compliance.

Facility Overview

~1,000 sqm
Purpose-built facility

PDX-focused
In vivo oncology models

Clinically integrated
Biobank-derived samples

Applications

Key areas of translational and preclinical application

- Preclinical drug efficacy and proof-of-concept studies
- Translational validation of therapeutic targets
- PDX-based preclinical oncology studies
- Co-clinical study design
- Biomarker-driven in vivo validation

Supported Sample Types

Biological materials compatible with the platform

- Biobank-derived tumor tissues
- Fresh patient tumor samples
- Implantable tumor fragments
- Blood/tissue samples for in vivo analysis

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Snapshot

1. State-of-the-art in vivo oncology facility
2. ~1,000 sqm dedicated space
3. Specialized in PDX models
4. High-barrier housing for immunocompromised mice
5. Integrated with Biobank and Organoid Centre
6. Charles River operational partnership
7. Full traceability via LIMS
8. Flexible industrial collaboration models

Workflow

Capabilities / Expertise

- Established expertise in PDX model development, with activities dating back to 2008 and early scientific outputs since 2011
- Commitment to 3Rs principles (Replacement, Reduction, Refinement) and animal welfare, fully integrated into study design and execution in compliance with regulatory standards
- Experimental surgery and in vivo monitoring
- Management of immunocompromised mouse lines
- Advanced colony and breeding management
- Integrated sample-to-model workflows with Biobank

Services

Core functional capabilities of the platform

- Preclinical in vivo studies (efficacy and proof-of-concept), with optional PK/PD support via Charles River
- Project-specific PDX development and biobanking
- In vivo expansion of established models
- In-house breeding of immunocompromised mouse strains (NOD-SCID)
- Custom SOP development and quality-controlled workflows
- End-to-end data management via integrated LIMS

Collaboration Opportunities

Available partnership and research engagement models

- Preclinical in vivo studies for academic and industrial partners
- PDX model development and co-development programs
- Long-term strategic collaborations with dedicated facility access
- Integration with Biobank, Organoid Centre and Genomics platforms
- Co-clinical and translational research programs

Keywords

PDX models
in vivo studies
preclinical oncology
patient-derived xenografts
drug efficacy
PK/PD
translational research
immunocompromised mice
biomarker validation
co-clinical studies

XENTURION Collection

Clinical Need

Metastatic colorectal cancer (**mCRC**) remains a major cause of cancer mortality. Drug development is limited by the lack of large, clinically annotated model collections capturing tumor heterogeneity.

Solution

The XENTURION translational model collection is a **clinically annotated, population-scale resource of patient-derived preclinical models** generated from **metastatic colorectal cancer patients.**

The collection integrates:

- **Tumoroids (organoids), including:**
  - **PDX-derived tumoroids (PDXTs)**
  - **Patient-derived tumoroids (PDTs)**
- **Matched patient-derived xenografts (PDX)**
- **Genomic, transcriptomic, and pharmacologic characterization**
- **Drug response profiling**

This multidimensional framework enables **parallel *in vitro* and *in vivo* drug testing,** supporting identification of therapeutic vulnerabilities and predictive biomarkers of response.

Key Features

- **130 metastatic CRC tumoroid models (126 PDXTs, 4 PDTs)**
- **High derivation success rate (~77%)**
- Majority of tumoroids derived from **matched PDX models**
- Derived from **metastatic patient samples**
- **Comprehensive molecular profiling**
  - mutational landscape
  - copy number architecture
  - transcriptomics
- **Drug response profiling in PDXT models**

Advantages

- **Population-scale diversity** capturing inter-patient heterogeneity
- **Matched PDX–tumoroid systems** enabling translational validation
- Integration of **genomic, molecular and pharmacologic data**
- Suitable for **biomarker discovery and drug screening**
- Enables **cross-platform validation** of therapeutic targets

Applications

- Therapeutic target identification and validation
- Drug screening and sensitivity testing
- Biomarker discovery
- Mechanisms of resistance
- Precision oncology research
- Preclinical evaluation of targeted and combination therapies

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Publication

Biobank Snapshot

130 tumoroid models
126 PDX-derived (PDXTs)
4 patient-derived (PDTs)
Metastatic CRC models
Multi-omic characterization
Drug response profiling

Keywords
colorectal cancer, tumoroids, patient-derived xenografts, PDX, organoids, metastatic CRC, precision oncology, drug screening, translational models

Gastric Cancer Model Collection

Clinical Need

Gastric cancer remains a major global health burden, characterized by high molecular heterogeneity and limited therapeutic options in advanced disease. Preclinical drug development is hindered by the lack of clinically relevant, well-annotated models that faithfully recapitulate tumor diversity and treatment response.

Solution

The Gastric Cancer Model collection is a **clinically annotated, multilevel platform of patient-derived preclinical models,** derived from biobanked patient samples and integrated within the Candiolo translational ecosystem, designed to capture the biological and molecular heterogeneity of gastric tumors.
The collection integrates:

- Patient-derived xenografts (PDX)
- Patient-derived organoids
- Primary tumor cell lines
- Molecular and transcriptomic characterization
- In vivo and in vitro drug response evaluation

This integrated framework enables translational research and parallel functional studies across model systems.

Key Features

- ~100 gastric cancer PDX models
- ~30–40 primary cell lines
- ~30–40 organoid models
- Clinically annotated patient-derived samples
- Transcriptomic and molecular profiling
- Drug response evaluation in xenograft models

Advantages

- Multilevel model system reflecting tumor complexity
- Large and diverse cohort of gastric cancer models
- Integration of molecular classification (including TCGA subtypes)
- High fidelity to original patient tumors
- Enables cross-validation between in vitro and in vivo systems
- Suitable for biomarker discovery and therapeutic development

Applications

- Therapeutic target identification and validation
- Drug screening and sensitivity testing
- Biomarker discovery
- Mechanisms of resistance
- Precision oncology research
- Preclinical evaluation of targeted and combination therapies

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Publication

Biobank Snapshot
Multilevel gastric cancer models
~100 PDX
~30–40 organoids
~30–40 cell lines
Clinically annotated
Molecularly characterized
Drug response capability

Keywords
gastric cancer, patient-derived xenografts, PDX, organoids, precision oncology, translational models, drug screening, tumor heterogeneity

INOC Genomics Centre

Advanced Sequencing and Bioinformatics Platform for Translational Cancer Research

Overview

The INOC Genomics Centre was established in 2025 as a joint initiative between the FPO – IRCCS (Candiolo Cancer Institute) and the Italian Institute for Genomics Medicine (IIGM).

The Centre integrates cutting-edge sequencing technologies, automation platforms and bioinformatics expertise to support translational cancer research and precision oncology initiatives.

Its mission is to provide high-quality genomic, transcriptomic and single-cell profiling services to research groups within FPO and IIGM, to the Candiolo Biobank, and to external academic and industrial partners.

A key strategic objective of the Centre is to develop and implement innovative sequencing-based assays, particularly for challenging clinical samples such as FFPE tissues, enabling robust genomic analysis in real-world clinical research settings.

Services

A comprehensive portfolio of genomics and bioinformatics services, including:

Core Sequencing Services

- Whole Genome Sequencing (WGS)
- Whole Exome Sequencing (WES)
- Bulk RNA sequencing
- Targeted sequencing panels

Advanced Genomics Applications

- Long-read sequencing
- Single-cell sequencing
- Spatial transcriptomics
- Metagenomic profiling

Bioinformatics Support

- Data processing and quality control
- End-to-end analysis pipelines for genomics and transcriptomics
- Custom bioinformatic analysis for research and clinical projects
- Data storage, management and deposition to public repositories

Applications

Translational and biomedical research applications, including:

- Cancer genomics and transcriptomics
- Biomarker discovery
- Single-cell tumor profiling
- Tumor microenvironment analysis
- Precision oncology studies
- Spatial tumor biology
- Metagenomics and microbiome research

Supports both discovery research and clinically oriented genomic studies.

Supported Sample Types

Compatible with a wide range of biological materials, including:

- Extracted DNA and RNA from any species
- Microbial DNA for metagenomic studies
- Human and mouse cell lines
- Peripheral blood mononuclear cells (PBMCs)
- Organoids
- Fresh-frozen tissues
- FFPE tissues

Specialized workflows are available for low-input and clinically derived samples.

Key Technologies

A diverse portfolio of state-of-the-art sequencing and automation platforms enabling high-throughput, scalable and reproducible genomics workflows.

Illumina sequencing platforms

- NovaSeq 6000
- NextSeq 500
- MiSeq

Oxford Nanopore platforms

- PromethION 24
- GridION

Single-cell and spatial genomics

- 10x Genomics Chromium X
- 10x Genomics CytAssist

Laboratory automation

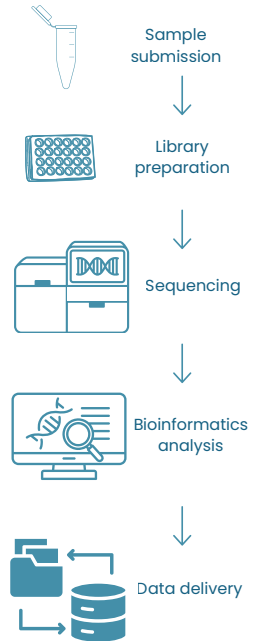
- Beckman Coulter Biomek i7
- Tecan Freedom EVO
- Hamilton robotic systems
- I.DOT liquid handling platform

Collaboration Opportunities

Academic and industrial collaboration opportunities include:

- Genomic profiling of clinical cohorts
- Sequencing support for preclinical research programs
- Multi-omics integration in translational research projects
- Custom assay development for challenging clinical specimens

Workflow



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Snapshot

1. Integrated genomics and bioinformatics platform
2. Short-read and long-read sequencing technologies
3. Single-cell and spatial genomics capabilities
4. High-throughput laboratory automation
5. End-to-end bioinformatics analysis pipelines
6. Support for clinical and FFPE samples

Keywords
genomics
next-generation sequencing
single-cell genomics
spatial transcriptomics
bioinformatics
precision oncology
translational research
multi-omics analysis