2026 Physician Scientist Call

AVAILABLE POSITIONS

Principal Investigator	BACHI ANGELA
Institute of Affiliation	IFOM - Istituto Fondazione di Oncologia Molecolare, ETS
Title of the proposed project:	Proteomic profiling of epithelioid sarcoma to identify diagnostic markers and clinically actionable pathways
Short description of the project	Epithelioid sarcoma (ES) is a rare soft tissue malignancy characterized by aggressive behavior, local recurrence, and distant metastasis. It accounts for less than 1% of all soft tissue sarcomas and predominantly affects young adults, causing significant morbidity and reduced quality of life. Current diagnostic approaches rely on histopathological criteria and loss of SMARCB1/INI1 expression, yet these markers lack sensitivity and specificity for early or equivocal cases. Therapeutic options remain limited and the molecular landscape driving ES progression is incompletely characterized, highlighting an urgent need for novel biomarker discovery. Membrane and global proteomic profiling was performed on patient-derived ES tumor tissues and matched healthy counterparts using state-of-the-art mass spectrometry. Analysis revealed distinct proteomic signatures discriminating neoplastic from non-neoplastic tissues, identifying differentially expressed proteins enriched at the cell surface - a compartment particularly relevant for diagnosis and therapeutic targeting. These findings motivate expanding the analytical framework to include metabolomic profiling for a more comprehensive molecular characterization. Building on these preliminary data, the project will develop along four interconnected tasks: 1.Biomarker identification. Candidate proteins from the proteomic discovery phase will be validated as diagnostic markers via immunohistochemistry on tissue microarrays and targeted mass spectrometry on an expanded patient cohort. 2.Bioinformatic analysis. Pathway enrichment, protein-protein interaction mapping, and integration with transcriptomic and metabolomic datasets will prioritize clinically relevant candidates and key dysregulated networks. 3.Orthogonal validation. Selected candidates will be confirmed using immunohistochemistry, targeted mass spectrometry, and flow cytometry, with attention to subcellular localization and surface accessibility. 4. Functional studies. Top candidates will be assessed through in vitro loss- and gain-of-function experiments, evaluating their role in proliferation, invasion, and pharmacological response. The student will gain hands-on competence across the full analytical pipeline, from sample preparation and data acquisition to statistical analysis and biological interpretation, with focus on proteomics and metabolomics.
Main research area for the project	Cancer biology
3 key words for the project	Proteomics, Sarcoma, Biomarkers

LAB INFO

PHYSICIAN SCIENTIST
LA MEDICINA INCONTRA LA RICERCA
promosso da: AIRC Fondazione CARIPLO | con il supporto di: SIFMM European School of Molecular Medicine | UNIVERSITÀ DEGLI STUDI DI MILANO

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Main topic/s of the lab	Molecular crosstalk in the tumor microenvironment, cancer metabolism
Short description of the lab activity	The laboratory focuses on understanding how tumor cells sense and reshape their surrounding microenvironment to facilitate growth, invasion, and metastatic spread. Two central questions guide our research: how do cancer cells communicate with neighboring cells and stromal components, and how do they both sense and actively modify the microenvironment to their advantage? To address these questions the lab adopts a global, untargeted, multi-omic point of view, as this is representative of what happens in vivo, where multiple signals are simultaneously conveyed and integrated to establish a functional tumor–microenvironment crosstalk. Indeed, A key focus of the laboratory is the study of the tumor-derived secretome — the ensemble of proteins, metabolites, and lipids actively released by cancer cells into the extracellular space. By characterizing secretomic profiles in tumors with different degrees of aggressiveness, we aim to identify specific molecular signatures that distinguish more invasive from less invasive phenotypes, and to elucidate which secreted molecules act on neighboring cells, potentially reprogramming them to support tumor progression. By combining proteomics, metabolomics, and lipidomics, we gain insights into how changes in nutrient availability or utilization modulate cancer cell responses. Studying how cancer cells interact with their surrounding environment is not always easy in a standard lab dish. That is why we have created scaffolds that replicate the real extracellular matrix organization and we have adopted 3D models such as organoids and spheroids that preserve cell–cell and cell–matrix interactions.
Recent bibliography	- SMARCA5 interacts with NUP98-NSD1 oncofusion protein and sustains hematopoietic cells transformation. J EXP CLIN CANC RES 2022 Jan; 41: 34 - SP140 represses specific loci by recruiting polycomb repressive complex 2 and NuRD complex. NUCLEIC ACIDS RES 2025 Feb; 53: - BACE2 tunes lipid uptake through lipid transporters shedding supporting cancer cell proliferation. J EXP CLIN CANC RES 2026 Jan; 45: 36 - Unveiling the mechanistic link between extracellular amyloid fibrils, mechano-signaling and YAP activation in cancer. Cell Death Dis 2024 Jan; 15: 28 - Mismatch Repair-Proficient Colorectal Cancer can evade Immune Surveillance Through an Intrinsic Suppressive Program. CANCER DISCOV 2026 May; :
Group composition	2 staff scientists, 3 PhD students, 2 Master students
Institutional page link	https://www.ifom.eu/en/
Lab website link	https://www.ifom.eu/en/cancer-research/research-labs/research-lab-bachi.php