

Project in Multi-Omics and Project in Simulation

final presentation seminar

Friday, March 1st 2024, ITQB NOVA Auditorium

13h50	Welcome remarks
14h00	André Simão <i>Assess the transcriptome alterations mediated by FOXO1 activation using different mutations</i> Host: Ana Rita Grosso, Paulo Caldas — FCT NOVA
14h15	Nuno Bragança <i>Filter selection of de novo protein designs</i> Host: Casper Goverde, Bruno Correia — EPFL
14h30	Beatriz Val <i>Identificação e caracterização de células imunes associadas a Síndrome de Sjögren usando sequenciação de resolução celular</i> Host: Tomás Gomes — IMM
14h45	Sara Vitória <i>Protein-ligand interaction dynamics: Validating a Martini 3 model of estradiol</i> Host: Tâmega Madaloz, Manuel N. Melo — ITQB NOVA
15h00	Maria Inês Gomes <i>Unveiling differential gene expression in the yeast, Wickerhamiella versatilis: A comparative RNA-seq study between different growth conditions</i> Host: Patrícia Brito — FCT NOVA
15h15	Grigore Platon <i>Evaluation of different hybrid models to predict aromatic amino acid overproduction in Escherichia coli</i> Host: Leslie Avendaño, Sofia Ferreira, Isabel Rocha — ITQB NOVA
15h30	Andrea Duque <i>Multi-omics for drug discovery: Finding novel toxins from marine Invertebrates</i> Host: Pedro Costa — FCT NOVA
15h45	Coffee-break
16h15	Raquel Domingues <i>Docking study of affinity ligands</i> Host: Arménio Barbosa, Cecília Roque — FCT NOVA
16h30	Daniela Holdych <i>Estimating differentially expressed genes in Starmerella bombicola</i> Host: Patrícia Brito — FCT NOVA
16h45	Drosoula Nikolopoulou <i>NSP10-binding mini-protein design</i> Host: Pedro Moreira, Diana Lousa, Cláudio Soares — ITQB NOVA
17h00	Beatriz Infante <i>Compare single-cell transcriptome profiles obtained from zAvatars model from breast cancer with different protocols</i> Host: Ana Rita Grosso — FCT NOVA
17h15	Constança Ilunga <i>Giving Alamethicin more freedom in coarse-grain molecular dynamic simulations</i> Host: Ana Carolina Borges-Araújo, Manuel N. Melo — ITQB NOVA
17h30	Manuel Mantas <i>Generation of virtual datasets for the optimization of metagenomics data analysis pipelines</i> Host: João Dourado Santos — INSA
17h45	Inês Pacheco <i>Visualizing Phosphorylation Sites: A Novel Tool for Mass Spectrometry Phosphoproteomics Data</i> Host: Rune Matthiesen — NOVA MS