

List of posters

Session no. 1 – December 5, during lunch break and coffee breaks (morning and afternoon)

P1	A Graph Neural Network deep learning model for the analysis of metabolomics profiles Massimo La Rosa, Antonino Fiannaca, Laura La Paglia, Alfonso Urso
P2	From Correlation to Causation: Differential Causal Networks Pietro Hiram Guzzi, Annamaria Defilippo, Sivia Pugliese, Pierangelo Veltri, Federico Manuel Giorgi
P3	Text Mining in Bioinformatics: Advancements and Future Prospects Maria Chiara Martinis, Mario Cannataro
P4	Data-Driven Nutrigenetics: Crafting and mining a Curated Repository of Nutritional Genomic Polymorphisms Giovanni Maria De Filippis, Maria Monticelli, Alessandra Pollice, Tiziana Angrisano, Bruno Hay Mele, Viola Calabrò
P5	The TIGEM Bioinformatics Core Xavier Bujanda Cundin, Diego Carrella, Rossella De Cegli, Eugenio Del Prete, Diego di Bernardo
P6	Advanced Technologies for Biodiversity Monitoring: A Data Pipeline for Flower Detection, Counting and Tracking Mirella Sangiovanni, Willem-Jan van den Heuvel
P7	Analysis of genetic variants in Finnish prostate cancer patients Dhanaprakash Jambulingam, Samuel Heron, Neha Goel, Vidal Fey, Csilla Sipeky, Johanna Schleutker
P8	A database about the activity of food components and their interaction with human proteins Deborah Giordano, Angelo Facchiano
P9	A draft genome assembly of <i>Agroathelia rolfsii</i> aetiological agent of southern blight disease on industrial hemp Davide D'Angelo, Roberto Sorrentino, Ernesto Lahoz, Domenico Cerrato, Maurizio Viscardi, Loredana Cozzolino, Giovanna Fusco, Nunzio D'Agostino
P10	Comparative transcriptomics to identify RNA Writers and Erasers in microalgae Alessia Riccardi, Luca Ambrosino, Chiara Lauritano
P11	Molecular characterization of mosquito larvae response to <i>Bacillus thuringiensis</i> var. <i>israelensis</i> Gaetano Aufiero, Maria Carmen Valoroso, Silvia Caccia, Nunzio D'Agostino
P12	OMICS approaches to search orthologous genes in two crustacean models: <i>Hippolyte inermis</i> Leach and <i>Idotea balthica basteri</i> Pallas Amalia Amato, Roberta Esposito, Francesca Glaviano, Giulia Di Meglio, Emanuele Somma, Maurizio Lorenti, Giovanni Libralato, Maria Costantini, Valerio Zupo

Session no. 2 – December 6, lunch break and coffee breaks (morning and afternoon)

P13	Prediction of cancer biomarkers by salivary proteomics data Veronica Remori, Lorenzo Azzi, Mauro Fasano
P14	Analysis of the role of the nuclear lamina in genomic stability Anna Noviello, C. Caiazza, S. Ambrosio, G. Scala, S. Amente, B. Majello
P15	Computational approaches for MS-based yeast metabolomics-centric multi-omics data integration: critical survey and perspectives Luca De Martino, Fabrizio Mastrorocco, Clara Musicco, Ernesto Picardi, Graziano Pesole, Sergio Giannattasio
P16	Analyzing nicotine protection mechanism against amyloid toxicity by NMR-metabolomics: an exploratory study Enza Napolitano, Carmen Marino, Michela Buonocore, Angelo Santoro, Manuela Grimaldi, Anna Maria D'Ursi
P17	nf-core/sammyseq: a bioinformatics pipeline for Sequential Analysis of MacroMolecules accessibility sequencing Lucio Di Filippo, Emanuele Di Patrizio Soldateschi, Giovanni Lembo, Cristiano Petrini, Eva Pinatel, Alexia Rabec, Elisa Salviato, Ilario Tagliaferri, Francesco Ferrari, Chiara Lanzuolo, Margherita Mutarelli
P18	Our Results as Scorers in the CASP15-CAPRI Experiment Tiziana Ricciardelli, Didier Barradas-Bautista, Mohit Chawla, Luigi Cavallo and Romina Oliva
P19	Study of lipoxygenases from diatoms exploiting bioinformatics methodologies Bonora Simone, Ilenia D'Orsi, Deborah Giordano, Domenico D'Alelio, Angelo Facchiano
P20	A novel system biology approach to prioritize ASD-genes Veronica Remori, Heather Bondi, Manuel Airoidi, Lisa Pavinato, Diana Carli, Alfredo Brusco, Mauro Fasano
P21	Co-clustering matrix tri-factorization with spatial constraints to detect latent patterns in mass spectrometry imaging Giulia Capitoli, Francesco Denti, Stefania Galimberti, Davide Risso, Vanna Denti, Andrea Sottosanti
P22	Intracellular cross-talk in breast cancer: a case study Alice Chiodi, Paride Pelucchi, Andrea Manconi, Ettore Mosca
P23	Reconstruction of the Yeast Cell Cycle transcriptome expression atlas Maria Chiara Langella and Maria Luisa Chiusano
P24	Variant-driven early warning via unsupervised machine learning analysis of spike protein mutations for COVID-19 Marika D'Avanzo, Francesco Cirotto, Francesco Conventi, Elvira Rossi