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Protein Folding Pathways Across Physiology & Therapy

Advanced computational methods have allowed us to define a novel drug discovery paradigm, called PPI-FIT, to suppress protein expression by acting on folding pathways. To translate such a conceptual framework to physiological contexts, we assessed the solvent accessibility of 87,138 modified residues in the human proteome and discovered that one-third of phosphorylated proteins have phosphosites buried within their core. These cryptic phosphosites likely become exposed during folding, influencing protein expression. Our findings re-define the intricate regulatory landscape of protein folding and open up possibilities for therapeutic interventions.



Thursday
January 23, 2025



BIOS-U3 building
room U3-07



4.30 pm
to 5.30 pm



host
Francesco Peri



seminar webpage



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