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High-quality domain-based protein interaction mapping: application for drug discovery

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Protein interaction mapping has proven instrumental for the delineation and understanding of cancer signaling pathways, both in *Homo sapiens* and model organisms. We previously published a *drosophila* protein interaction map centered on fly orthologs of human cancer-related and signaling proteins¹. We now report the completion of the cognate human interaction map using the same high-quality, domain-based yeast two-hybrid (Y2H) technology. 149 human homologs of the 102 *drosophila* proteins, including 29 human oncogenes and tumor suppressors, were used as entry points to screen at saturation a highly complex, random-primed placenta cDNA library comprised of 10 million independent fragments in yeast. The features of the *drosophila* and human parallel interaction maps were compared. Orthology relationships were combined with Y2H and genetics data to examine the conservation of interaction networks across evolution. We believe that this protein interaction map centered on human cancer signaling pathways will be an invaluable resource for researchers in the field. The same technology was applied to the unbiased identification of the protein targets of bioactive compounds, using a “chemical three-hybrid” approach. Example of target deconvolution for compounds initially selected in phenotypic screens will be presented.

Biography

Samy SAKR is a Business Development Manager at Hybrigenics services, a major player in the field of protein interactions with landmark contributions and achievements. He has done a PhD on PcG proteins and their implication in cancer at the Human Genetics Institute (University of Montpellier, FRANCE) and a MBA at the Grenoble Business School FRANCE.

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