IOWA INSTITUTE OF HUMAN GENETICS – NEXT GENERATION SEQUENCING INTEREST GROUP

Developing DEEPN as a Powerful New Approach to Study Protein-Protein Interactions Based on Yeast Two-Hybrid Analysis and Next Generation Sequencing

Wednesday, December 16
2pm-3pm
283 EMRB (Seebohm Conference Room)

Dynamic Enrichment for Evaluation of Protein Networks (DEEPN) was developed to expand the power of yeast two-hybrid analysis to uncover many transient and static protein-protein interactions within a single screen. DEEPN improves upon yeast two-hybrid analysis by allowing the detection of relatively low-affinity binding interactions and by allowing candidate binding domains or motifs to be discerned quickly from sequence information. We show that applying DEEPN, using the small GTP-binding protein rab5 as bait, leads to the identification of both known and previously unknown conformation-specific direct-rab5-binding partners.

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