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Advancing RBP Research: Scalable Tools for Protein-RNA Interaction Analysis

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RNA-binding proteins (RBPs) are key regulators of gene expression, with implications for a range of diseases, particularly neurological disorders. Despite their importance, out of approximately 4,000 RBPs encoded in the human genome, less than 10% have been thoroughly characterized. The Yeo laboratory is at the forefront of developing innovative technologies that facilitate the large-scale mapping of protein-RNA interactions, which is crucial for understanding not only RNA processing but also complex regulatory roles of RBPs within diseases. We will detail our cutting-edge methods, including STAMP (Systematic Transcriptome-wide Analysis of Multifactorial Post-transcriptional Regulation), eCLIP (enhanced Crosslinking and Immunoprecipitation), and Antibody-Conjugation CLIP, which collectively enable the precise identification and study of RBP targets. To define the impact of RBPs on their cognate targets, binding site data must be combined with functional assays to characterize how these proteins regulate RNA. Integrating these methods with machine learning models, we have begun to develop a computational framework that can predict of how disrupting binding sites affects RNA processing pioneering how we design RNA therapeutics. Our work not only expands the catalog of known RBP and RBP interactions but also provides essential tools for the scientific community to uncover the multifaceted roles of RBPs in gene regulation and disease.