Tommer Ravid, Biol Syst Open Access 2017, 6:1(Suppl)
DOI: 10.4172/2329-6577-C1-008

Mapping the landscape of a eukaryotic degronome

Tommer Ravid
Hebrew University of Jerusalem, Israel

The ubiquitin-proteasome system (UPS) for protein degradation has been under intensive study, and yet, we have only partial understanding of mechanisms by which proteins are selected to be targeted for proteolysis. One of the obstacles in studying these recognition pathways is the limited repertoire of known degradation signals (degrons). To better understand what determines the susceptibility of intracellular proteins to degradation by the UPS, we developed an unbiased method for large-scale identification of eukaryotic degrons. Using a reporter-based high-throughput competition assay, followed by deep sequencing, we measured a degradation potency index for thousands of native polypeptides in a single experiment. We further used this method to identify protein quality control (PQC)-specific and compartment-specific degrons. Our method provides an unprecedented insight into the yeast degrome, and it can readily be modified to study protein degradation signals and pathways in other organisms and in various settings.

Biography

Tommer Ravid has completed his PhD from Tel Avi University in 2001 and Post-doctoral studies from the University of California, Davis, School of Medicine and Yale University, School of Medicine. He is a Faculty Member in the Department of Biological Chemistry, Faculty of Life Sciences, the Hebrew University of Jerusalem, since 2007. His research focuses on the mechanisms underlying protein quality control and degradation by the ubiquitin-proteasome system, using the budding yeast *Saccharomyces cerevisiae* as a model organism.

tommer.ravid@mail.huji.ac.il

Notes: