



“Combining targeted AP-MS with phosphoproteomics maps the TOR interactome”

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The target of rapamycin (TOR) kinase is a central regulatory hub that translates environmental and nutritional information into permissive or restrictive growth decisions. Although the TOR pathway is conserved across eukaryotes, plants developed unique adaptations to this pathway to cope with their autotrophic and sessile nature. Overall, compared to other eukaryotic model species, the current knowledge of TOR signaling in plants is still scarce. Only few TOR pathway components are known and no phosphoproteome or interactome screens targeted to the TOR kinase have been performed. To fill this gap, we combined a systematic phosphoproteome screen with an extensive state of the art protein complex analysis, generating for the first time a comprehensive TOR signaling network in plants. Integration of both networks significantly increased our understanding of plant TOR signaling, elucidating both evolutionarily conserved as well as novel plant-specific links, covering a broad range of biological processes such as protein and nucleotide biosynthesis, autophagy, auxin signaling, chloroplast development, lipid metabolism, and senescence.