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Classical Nuclear Import Pathway in Plants - Structural Basis for the Interaction between Rice Importin-α and Plant-Specific Nuclear Localisation Sequences

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In the eukaryotic cell, the classical nuclear import pathway is the most common route for proteins to gain access to the nucleus. Although well studied in yeast and mammals, little is known about the classical nuclear import pathway in plants. Here we investigated the interaction between rice Impα with classical and plant-specific NLSs. Surprisingly, we found that, unlike its yeast and mouse counterparts, rice Impα minor site plays a primary role and enables nanomolar-range affinity for cargoes containing plant-specific (ps)NLSs. High-resolution co-crystal structures of mouse and rice Impα in complex with psNLSs revealed the structural basis for this unexpected binding mode. Moreover, the structure of full-length rice Impα reveals that the autoinhibitory mechanism seen in mammal Impα also operates in plants. Nevertheless, in rice Impα the NLS-mimicking sequences from the protein IBB domain bind to both minor and major sites, whereas in the mammal Impα the equivalent autoinhibitory region only interacts with the protein major site. In conclusion, our studies shed new light into the molecular basis of plant-specific features of nuclear import pathway.

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