Dissociation of PERK:BiP Heterodimer

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references

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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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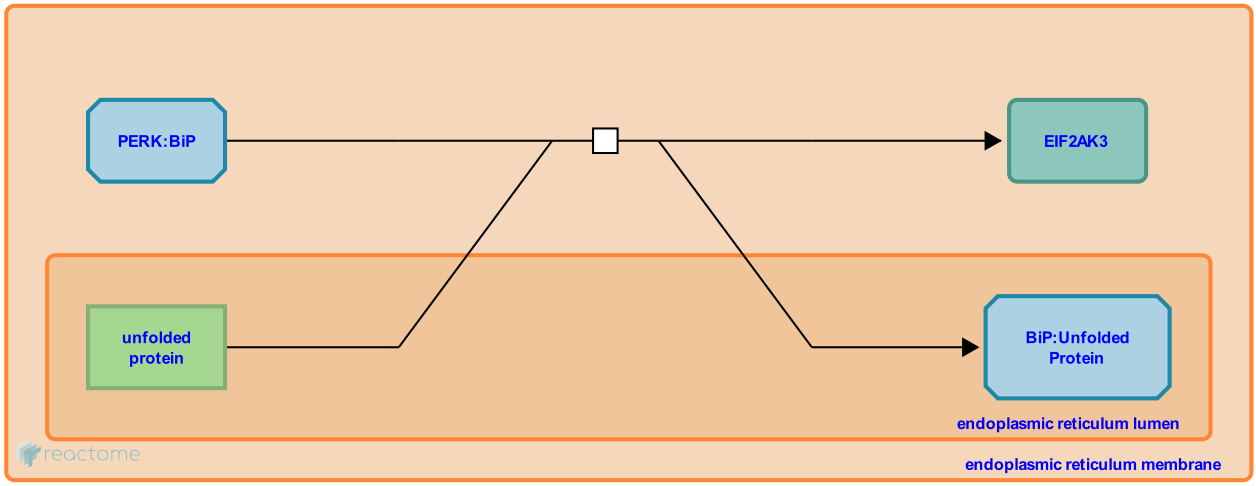
Stable identifier: R-HSA-381086

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen



PERK (EIF2AK3) is a single-pass transmembrane protein located in the Endoplasmic Reticulum (ER) membrane. PERK has an N-terminal luminal domain and a C-terminal cytosolic domain. It is maintained in an inactive state by association of its luminal domain with BiP, a chaperone in the ER. Because BiP also binds unfolded proteins, BiP dissociates from PERK when unfolded proteins exceed chaperone activity in the ER.

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Editions

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