ISGylation of IRF3

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26/02/2021

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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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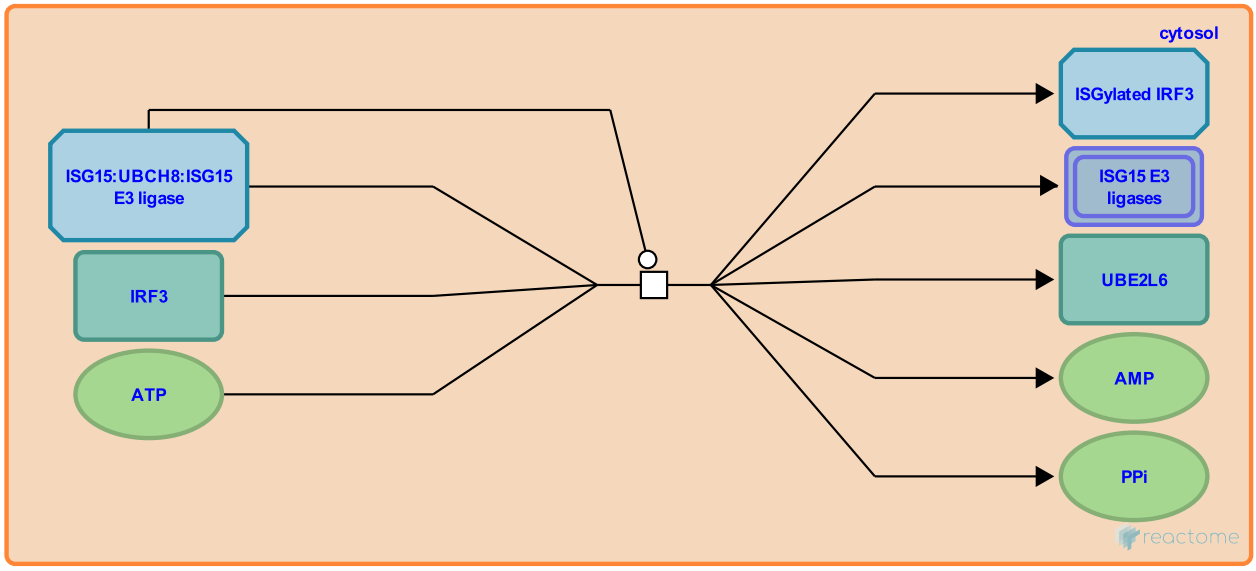
Stable identifier: R-HSA-1169394

Type: transition

Compartments: cytosol



The transcription factor IRF3 is a target for ISGylation. Conjugation of ISG15 positively regulates IRF3 and thereby promotes induction of type I interferons. ISGylation of IRF3 prevents the binding of PIN1, a protein that promotes IRF3 ubiquitination and subsequent degradation.

Literature references

Lu, G., Reinert, JT., Pitha-Rowe, I., Okumura, A., Kellum, M., Knobeloch, KP. et al. (2006). ISG15 enhances the innate antiviral response by inhibition of IRF-3 degradation. *Cell Mol Biol (Noisy-le-grand), 52*, 29-41.

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Editions

2011-01-18	Authored, Edited	Garapati, P V.
2011-02-11	Reviewed	Zhang, DE.