

# Dimerization of p-IRF7

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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. [↗](#)
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Reactome database release: 88

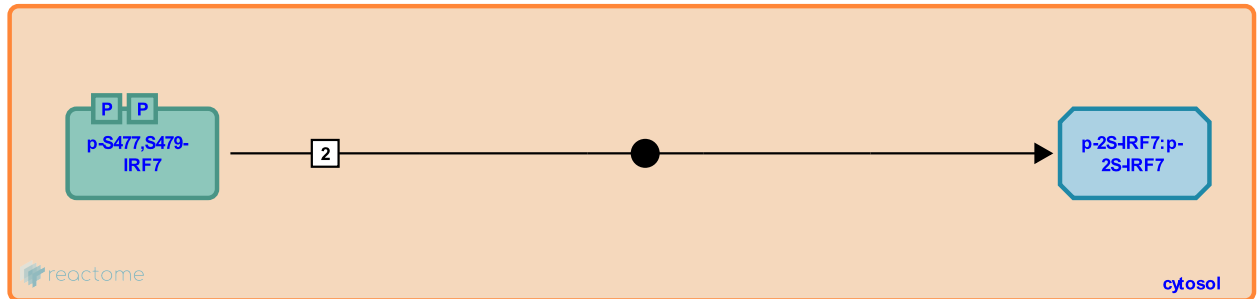
This document contains 1 reaction ([see Table of Contents](#))

## Dimerization of p-IRF7 [↗](#)

**Stable identifier:** R-HSA-933533

**Type:** binding

**Compartments:** cytosol



Phosphorylation stimulates the C-terminal autoinhibitory domain of IRF7 to attain a highly extended conformation triggering dimerization through extensive contacts to a second IRF7 subunit.

### Literature references

Marié, I., Prakash, A., Smith, E., Levy, DE. (2000). Phosphorylation-induced dimerization of interferon regulatory factor 7 unmasks DNA binding and a bipartite transactivation domain. *Mol Cell Biol*, 20, 8803-14. [↗](#)

Chen, W., Royer WE, Jr. (2010). Structural insights into interferon regulatory factor activation. *Cell Signal*, 22, 883-7. [↗](#)

### Editions

2010-08-02	Authored, Edited	Garapati, P V.
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