

Activation and dimerization of c-JUN in the nucleus

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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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- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 82

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

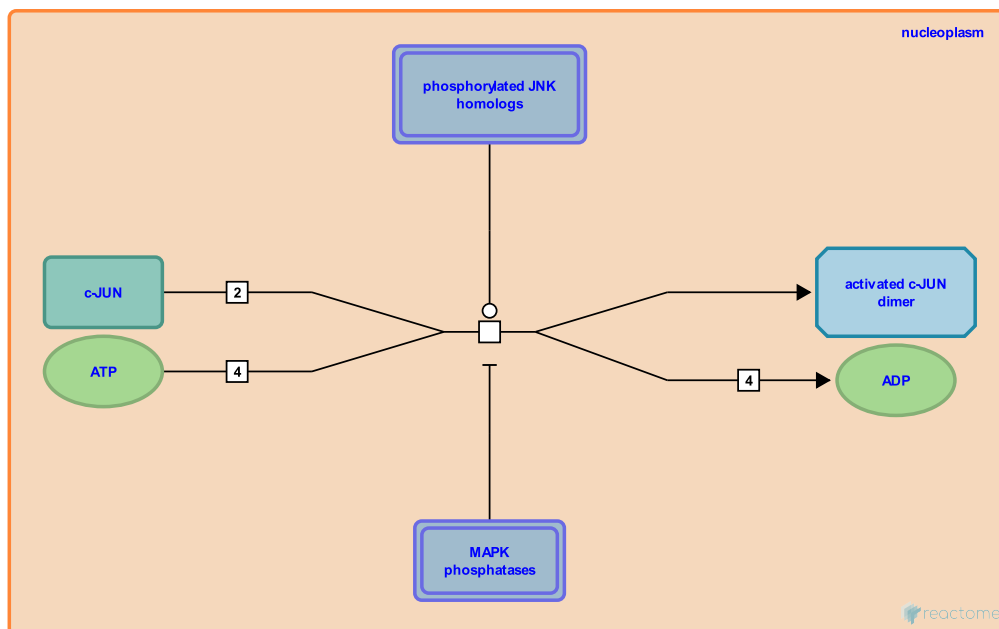
Activation and dimerization of c-JUN in the nucleus ↗

Stable identifier: R-GGA-438026

Type: transition

Compartments: nucleoplasm

Inferred from: [Activated JNKs phosphorylate c-JUN \(Homo sapiens\)](#)



Shortly after phosphorylation JNKs are translocated to nucleus where they associate and activate their target transcription factors.

Literature references

Raivich, G. (2008). c-Jun expression, activation and function in neural cell death, inflammation and repair. *J Neurochem*, 107, 898-906. ↗

Editions

2009-09-22	Authored	Shamovsky, V.
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