

# Expression of DDIT3 (CHOP, GADD153) in response to unfolded protein

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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: 88

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

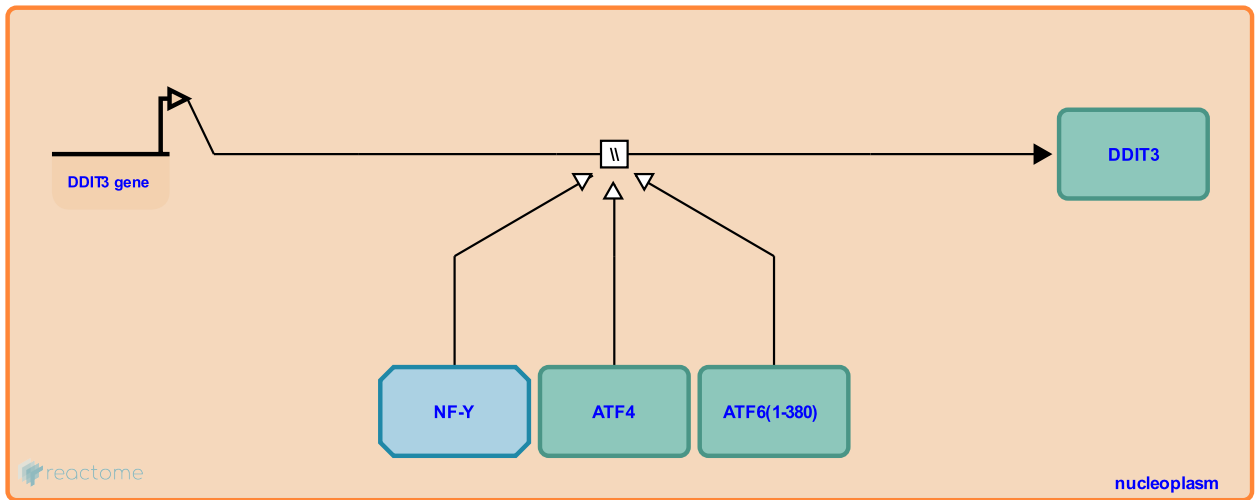
**Expression of DDIT3 (CHOP, GADD153) in response to unfolded protein** ↗

**Stable identifier:** R-HSA-1791107

**Type:** omitted

**Compartments:** nucleoplasm

**Inferred from:** [Expression of Ddit3 \(Rattus norvegicus\)](#), [Expression of DDIT3 \(Cricetulus griseus\)](#)



The DDIT3 (CHOP) gene is transcribed to yield mRNA and the mRNA is translated to yield protein (Bartlett et al. 1992, Carlson et al. 1993, Bruhat et al. 1997, Yoshida et al. 2000, Lee et al. 2008, Sikalidis et al. 2011). In response to amino acid starvation, transcription of DDIT3 is enhanced by ATF4 and phosphorylated ATF2 (Bruhat et al. 2000, Averous et al. 2004, Bruhat et al. 2007). In mouse, expression of Ddit3 is activated by DNA damage and by NF-Y and Atf4 in response to endoplasmic reticulum stress.

**Literature references**

Mori, K., Yoshida, H., Yanagi, H., Negishi, M., Okada, T., Haze, K. et al. (2000). ATF6 activated by proteolysis binds in the presence of NF-Y (CBF) directly to the cis-acting element responsible for the mammalian unfolded protein response. *Mol Cell Biol*, 20, 6755-67. ↗

Tsukada, S., Yoshida, K., Takeuchi, Y., Fukuda, R., Takayanagi, S. (2013). Gene regulatory network of unfolded protein response genes in endoplasmic reticulum stress. *Cell Stress Chaperones*, 18, 11-23. ↗

**Editions**

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