

Translation of DDIT3

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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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- 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. [↗](#)
- 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](#))

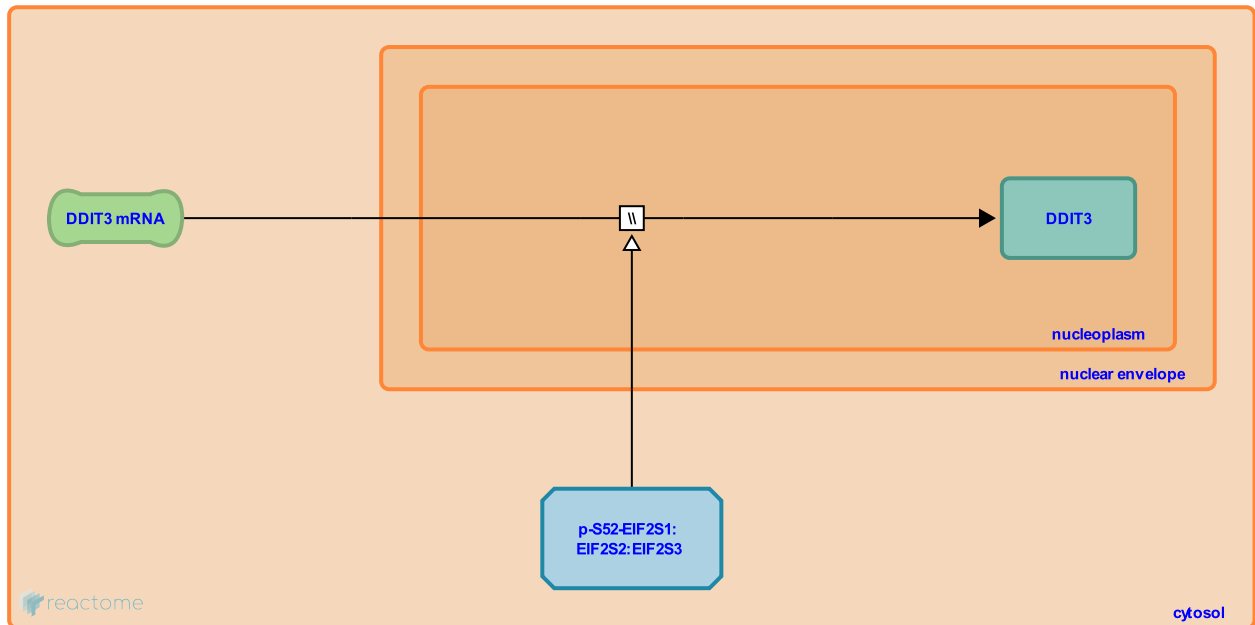
Translation of DDIT3 [↗](#)

Stable identifier: R-HSA-9650722

Type: omitted

Compartments: cytosol, nucleoplasm

Inferred from: [Translation of Ddit3 \(Mus musculus\)](#)



The DDIT3 mRNA is translated to yield DDIT3 (CHOP) protein (Jousse et al. 2001, and inferred from the mouse homolog), which is then imported into the nucleus. The mRNA of DDIT3 contains an upstream ORF (uORF) which has a start codon in an unfavorable context (Jousse et al. 2001, and inferred from the mouse homolog), resulting in low expression of the downstream DDIT3 coding region. When EIF2S1 (eIF2-alpha) is phosphorylated in response to stress, translation of the uORF is suppressed and translation of DDIT3 is increased (inferred from the mouse homolog).

Literature references

Ferrara, M., Carraro, V., Ron, D., Urano, F., Bruhat, A., Fournoux, P. et al. (2001). Inhibition of CHOP translation by a peptide encoded by an open reading frame localized in the chop 5'UTR. *Nucleic Acids Res.*, 29, 4341-51. [↗](#)

Editions

2019-06-15	Authored, Edited	May, B.
2019-09-15	Reviewed	Bruhat, A.
2019-10-22	Reviewed	Chen, JJ.
2019-11-20	Reviewed	Staschke, KA.