

# Expression of Asns

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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

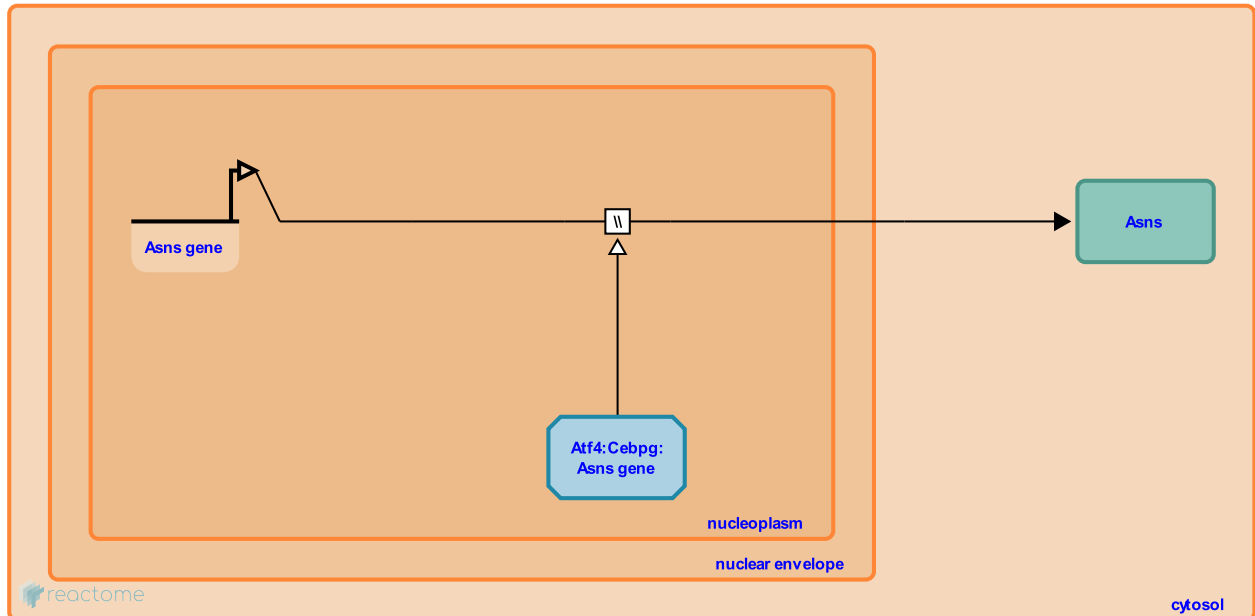
This document contains 1 reaction ([see Table of Contents](#))

## Expression of Asns [↗](#)

**Stable identifier:** R-MMU-9644315

**Type:** omitted

**Compartments:** nucleoplasm, cytosol



The Asns gene is transcribed to yield mRNA and the mRNA is translated to yield protein (Huggins et al. 2015). Expression of Asns is increased in response to amino acid deficiency (Huggins et al. 2015) and heme deficiency (Zhang et al. 2019).

## Literature references

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Haines, DC., Jailwala, P., Saylor, KL., Huggins, CJ., Quiñones, OA., Johnson, PF. et al. (2015). C/EBP $\gamma$  Is a Critical Regulator of Cellular Stress Response Networks through Heterodimerization with ATF4. *Mol. Cell. Biol.*, 36, 693-713. [↗](#)

## Editions

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