

Expression of Asns

Bruhat, A., Chen, JJ., May, B., Staschke, KA.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

16/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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

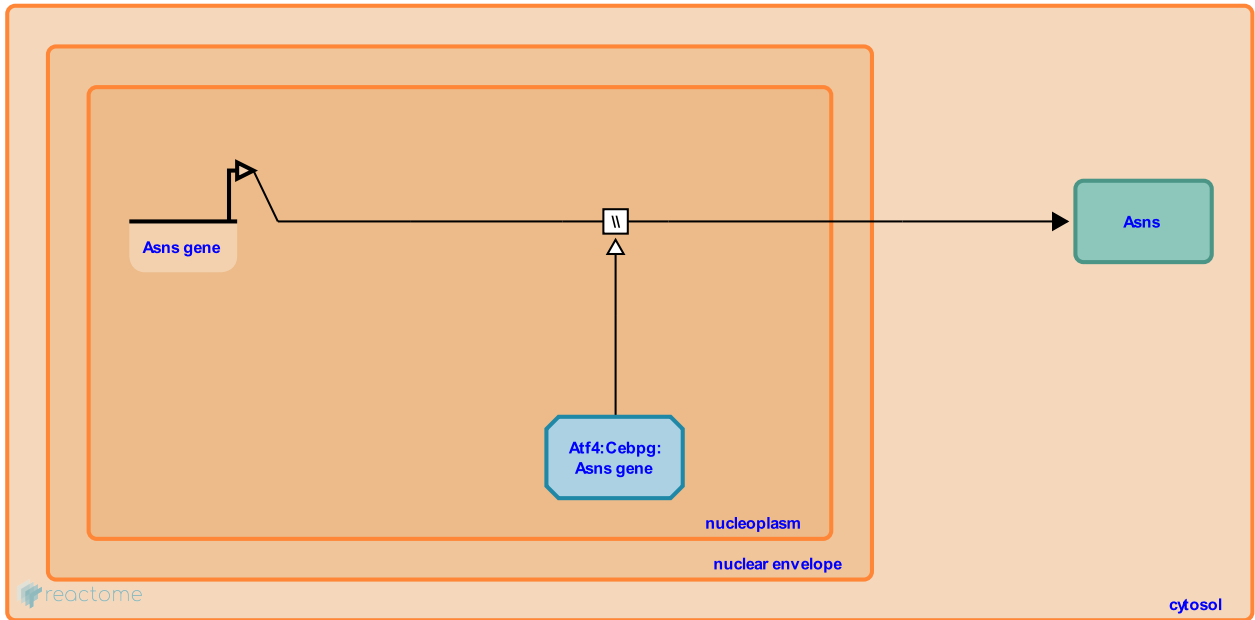
This document contains 1 reaction ([see Table of Contents](#))

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

Macias-Garcia, A., Zhang, S., Butty, VL., Levine, SS., Sankaran, VG., Velazquez, J. et al. (2019). HRI coordinates translation necessary for protein homeostasis and mitochondrial function in erythropoiesis. *Elife*, 8. [↗](#)

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

Editions

2019-04-12	Authored, Edited	May, B.
2019-09-15	Reviewed	Bruhat, A.
2019-10-22	Reviewed	Chen, JJ.
2019-11-20	Reviewed	Staschke, KA.