Expression of CHAC1

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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.

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
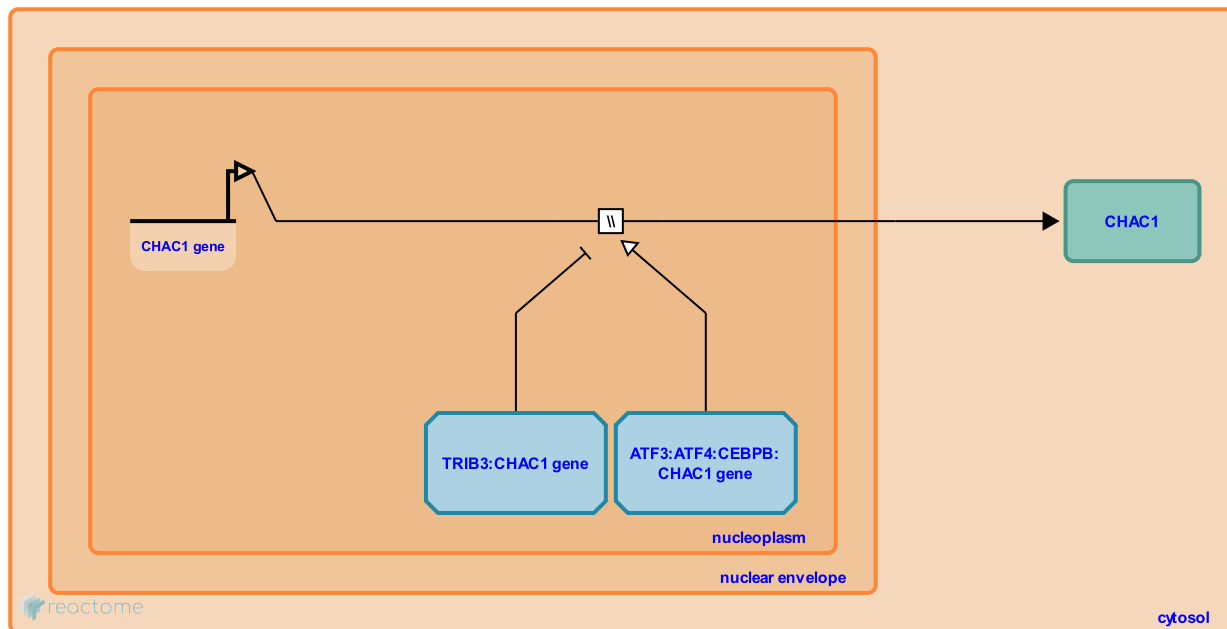
This document contains 1 reaction (see Table of Contents)

Expression of CHAC1 ↗

Stable identifier: R-HSA-9653894

Type: omitted

Compartments: nucleoplasm, cytosol

Inferred from: Expression of Chac1 (Mus musculus)

The CHAC1 gene is transcribed to yield mRNA and the mRNA is translated to yield CHAC1 protein (Crawford et al. 2015, and inferred from the mouse homolog). The transcription factors ATF4, ATF3, and CEBPB (full length) bind ATF/CRE and ACM elements in the CHAC1 promoter and activate transcription of CHAC1 in response to endoplasmic reticulum stress (Crawford et al. 2015). Expression of CHAC1 is also activated by heme deficiency via EIF2AK1 (HRI) and ATF4 (inferred from the mouse homologs). TRIB3 binds the CHAC1 promoter and represses transcription of CHAC1 which leads to decreased cell death during oxidative stress (inferred from mouse homologs).

Literature references

Mungrue, IN., Kilberg, MS., Shan, J., Sylvester, CF., Higdon, AN., Crawford, RR. et al. (2015). Human CHAC1 Protein Degrades Glutathione, and mRNA Induction Is Regulated by the Transcription Factors ATF4 and ATF3 and a Bipartite ATF/CRE Regulatory Element. *J. Biol. Chem., 290*, 15878-91. ↗

Editions

2019-07-15	Authored, Edited	May, B.
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