

Expression of Ebf1

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https://reactome.org

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)

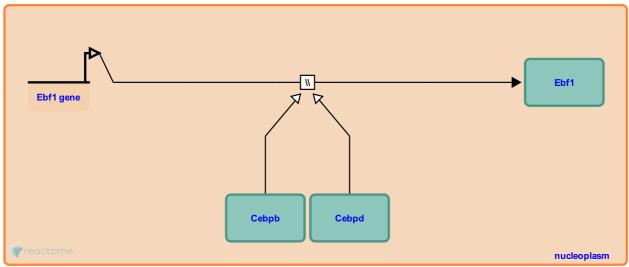
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Expression of Ebf1

Stable identifier: R-MMU-977286

Type: omitted

Compartments: nucleoplasm



The gene encoding Ebf1 is transcribed to yield mRNA and translated to yield protein in adipocytes (Jimenez et al. 2007).

Literature references

Rosen, ED., Akerblad, P., Sigvardsson, M., Jimenez, MA. (2007). Critical role for Ebf1 and Ebf2 in the adipogenic transcriptional cascade. *Mol Cell Biol*, 27, 743-57.

Editions

2010-10-18	Authored, Edited	May, B.
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