

ATF4 and phospho-ATF2 bind the DDIT3

promoter

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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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

This document contains 1 reaction (see Table of Contents)

ATF4 and phospho-ATF2 bind the DDIT3 promoter 7

Stable identifier: R-HSA-9635804

Type: binding

Compartments: nucleoplasm



The promoter of the DDIT3 (CHOP) gene contains an Amino Acid Response Element (AARE) that binds ATF4 and ATF2. ATF2 and ATF4 are required for full activation of gene transcription in response to amino acid deprivation (Bruhat et al. 2000, Averous et al. 2004). Phospho-ATF2 is essential in the acetylation of histone H4 and H2B (Bruhat et al. 2007). ATF4 recruits PCAF to enhance transcription (Chérasse et al. 2007). ATF4 appears to be a monomer in the absence of DNA and a dimer after binding DNA (Podust et al. 2001).

Literature references

- Bruhat, A., Cherasse, Y., Fafournoux, P., Jousse, C., Jones, N., Maurin, AC. et al. (2007). ATF2 is required for amino acid-regulated transcription by orchestrating specific histone acetylation. *Nucleic Acids Res.*, 35, 1312-21.
- Jousse, C., Carraro, V., Fafournoux, P., Averous, J., Thiel, G., Bruhat, A. (2004). Induction of CHOP expression by amino acid limitation requires both ATF4 expression and ATF2 phosphorylation. *J Biol Chem, 279*, 5288-97.
- Bruhat, A., Cherasse, Y., Fafournoux, P., Chambon, C., Carraro, V., Chaveroux, C. et al. (2007). The p300/CBP-associated factor (PCAF) is a cofactor of ATF4 for amino acid-regulated transcription of CHOP. *Nucleic Acids Res.*, 35, 5954-65.
- Ferrara, M., Carraro, V., Bruhat, A., Fafournoux, P., Jousse, C., Reimold, AM. (2000). Amino acids control mammalian gene transcription: activating transcription factor 2 is essential for the amino acid responsiveness of the CHOP promoter. *Mol. Cell. Biol., 20*, 7192-204.
- Kim, Y., Krezel, AM., Podust, LM. (2001). Crystal structure of the CCAAT box/enhancer-binding protein beta activating transcription factor-4 basic leucine zipper heterodimer in the absence of DNA. J. Biol. Chem., 276, 505-13.

Editions

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