Translation of ATF5

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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. ↗

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. ↗

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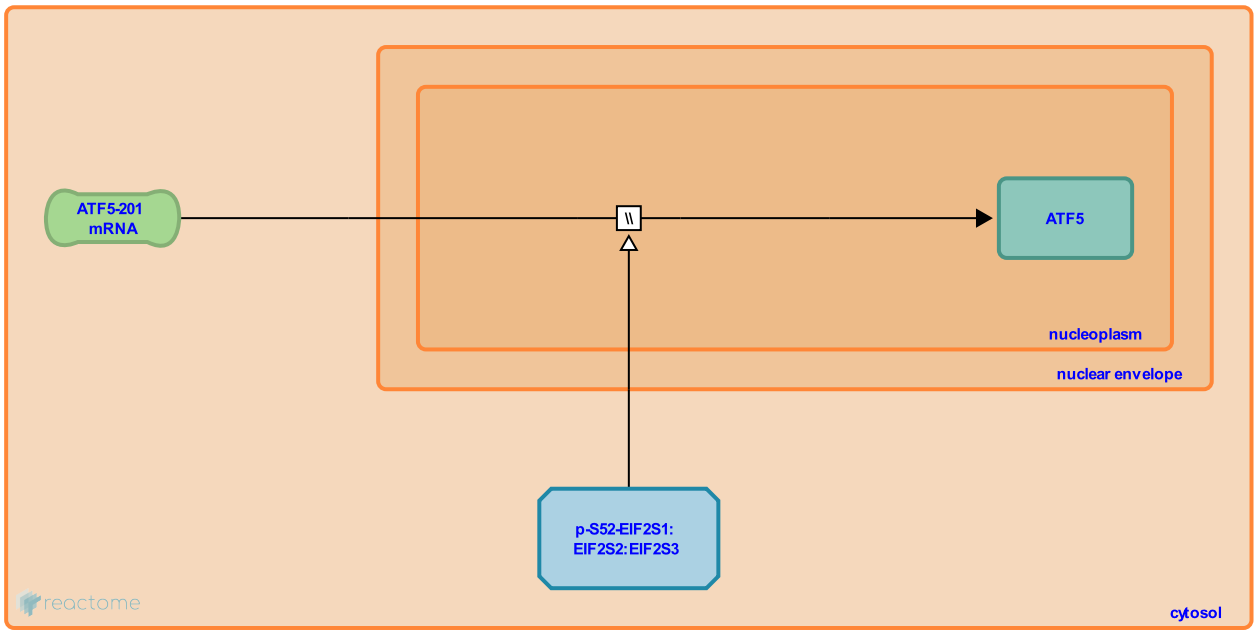
Stable identifier: R-HSA-9653745

Type: omitted

Compartments: cytosol, nucleoplasm

Inferred from: Translation of Atf5 (Mus musculus)



The ATF5 mRNA is translated to yield ATF5 protein (Watatani et al. 2008, and inferred from the mouse homolog) which is then imported into the nucleus. The ATF5 mRNA contains 2 upstream ORFs (uORFs) which inhibit translation of the downstream ATF5 coding region (Watatani et al. 2008). Translation of uORF2 also targets the mRNA for nonsense-mediated decay (Hatano et al. 2013). During stresses such as amino acid limitation and arsenite-induced oxidative stress, EIF2S1 (eIF2-alpha) is phosphorylated, decreasing translation initiation at the uORFs and increasing translation of ATF5 (Watatani et al. 2008, and inferred from the mouse homolog).

Literature references

Yamazaki, T., Takahashi, S., Takeda, H., Hatano, M., Umemura, M., Takahashi, Y. et al. (2013). The 5'-untranslated region regulates ATF5 mRNA stability via nonsense-mediated mRNA decay in response to environmental stress. *FEBS J., 280*, 4693-707.

Takahashi, S., Takeda, H., Ichikawa, K., Nakanishi, N., Hirose, H., Takahashi, Y. et al. (2008). Stress-induced translation of ATF5 mRNA is regulated by the 5'-untranslated region. *J. Biol. Chem., 283*, 2543-53.

Editions

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