

TFAP2C translocates to the nucleus

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01/05/2024

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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.

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

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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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Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

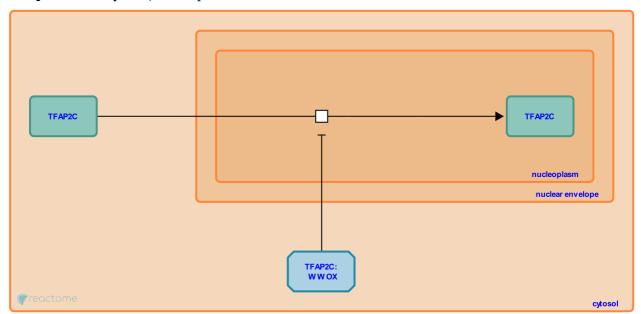
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TFAP2C translocates to the nucleus **↗**

Stable identifier: R-HSA-8864577

Type: transition

Compartments: cytosol, nucleoplasm



Like other AP-2 (TFAP2) transcription factor family members, TFAP2C (AP-2 gamma) mainly localizes to the nucleus. WWOX inhibits nuclear translocation of TFAP2C (Ageilan et al. 2004).

Literature references

Weigel, RJ., Palamarchuk, A., Herrero, JJ., Aqeilan, RI., Croce, CM., Pekarsky, Y. (2004). Physical and functional interactions between the Wwox tumor suppressor protein and the AP-2gamma transcription factor. *Cancer Res.*, 64, 8256-61.

Editions

| 2016-03-14 | Authored, Edited | Orlic-Milacic, M. |
|------------|------------------|----------------------------|
| 2016-05-04 | Reviewed | Dawid, IB., Zarelli, VE. |
| 2016-05-17 | Reviewed | Weigel, RJ., Bogachek, MV. |