Translocation of ERBB4s80:YAP1 complex to the nucleus

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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. ↗

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. ↗
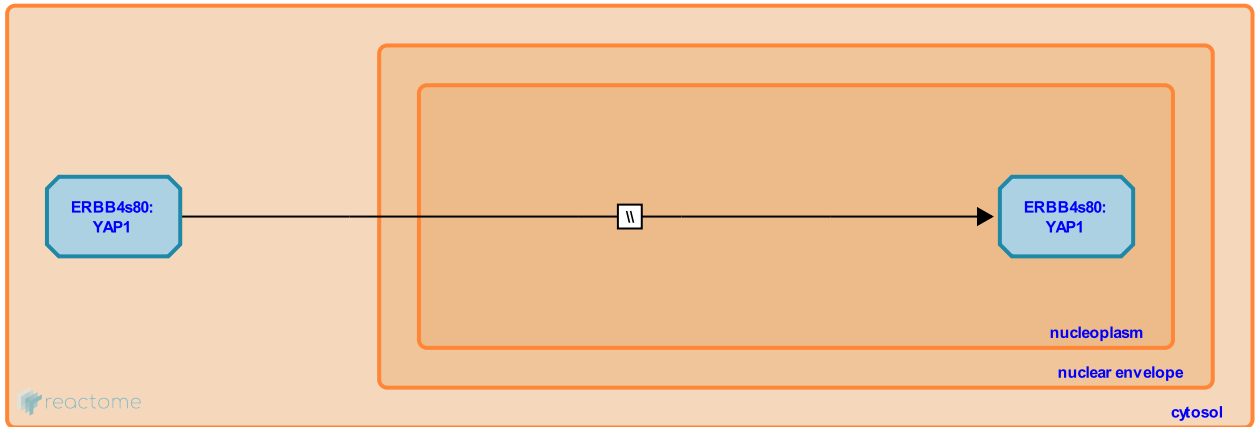
Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

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Stable identifier: R-HSA-1254248

Type: omitted

Compartments: cytosol, nucleoplasm

Upon formation of ERBB4s80:YAP1 complex in the cytosol, the complex translocates to the nucleus, where it may act as a regulator of transcription (Komuro et al. 2003, Omerovic et al. 2004, Aqeilan et al. 2005).

Literature references

Navin, NE., Sudol, M., Komuro, A., Nagai, M. (2003). WW domain-containing protein YAP associates with ErbB-4 and acts as a co-transcriptional activator for the carboxyl-terminal fragment of ErbB-4 that translocates to the nucleus. *J Biol Chem, 278*, 33334-41. ↗

Trapasso, F., Kaou, M., Pekarsky, Y., Donati, V., Aqeilan, RI., Croce, CM. et al. (2005). WW domain-containing proteins, WWOX and YAP, compete for interaction with ErbB-4 and modulate its transcriptional function. *Cancer Res , 65*, 6764-72. ↗

Fraioli, R., Frati, L., Puggioni, EM., Gulino, A., Alimandi, M., Omerovic, J. et al. (2004). Ligand-regulated association of ErbB-4 to the transcriptional co-activator YAP65 controls transcription at the nuclear level. *Exp Cell Res, 294*, 469-79. ↗

Editions

2011-11-04	Authored	Orlic-Milacic, M.
2011-11-07	Edited	Matthews, L.
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