RXRA:PPARD binds FABP5:atRA

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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

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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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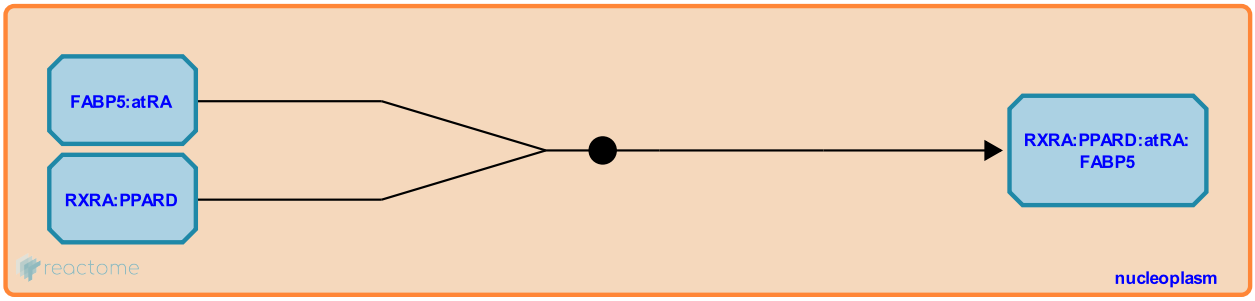
Stable identifier: R-HSA-5422942

Type: binding

Compartments: nucleoplasm



In the nucleus, all-trans-retinoic acid (atRA), bounds to epidermal fatty acid-binding protein (FABP5), is transferred to the heterodimeric complex of retinoic acid receptor alpha RXRA) and peroxisome proliferator-activated receptor delta (PPARD). When bound to PPARD, atRA can significantly increase the expression of proteins involved in fatty acid oxidation and energy metabolism via its induction of PPARD (Wolf 2010, Amengual et al. 2012, Noy 2013).

Literature references

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Editions

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