SUMO-CRABP2 dissociates from atRA:RAR:RXR

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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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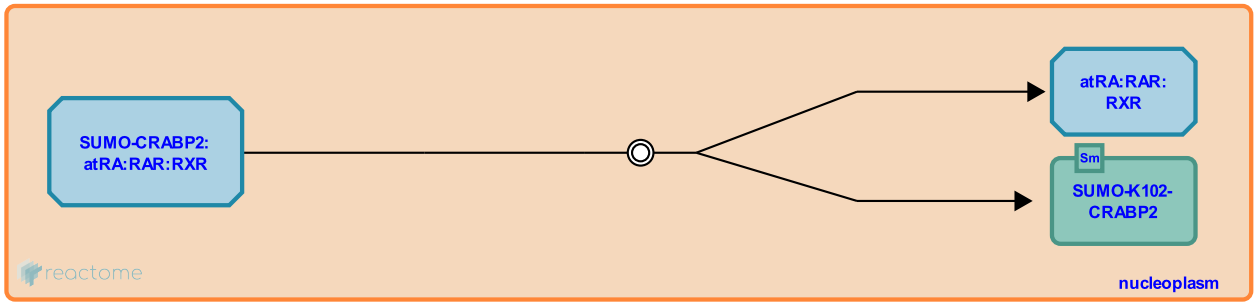
Stable identifier: R-HSA-5634103

Type: dissociation

Compartments: nucleoplasm



In the nucleus, cellular retinoic acid binding protein 2 (CRABP2), bound to all trans retinoic acid (atRA), directly binds to heterodimeric nuclear retinoic acid receptors (RAR:RXR) to form a complex through which atRA is channeled from the binding protein to RAR (Majumdar et al. 2011). The RAR:RXR heterodimer can be formed between any of three receptor isoforms for each; RARA, RARB, or RARG with RXRA, RXRB, or RXRG (Neiderreither and Dolle 2008). RARA requires sumoylation and phosphorylation for ligand binding and nuclear localisation (Zhu et al. 2009, Santos & Kim 2010).

RAR:RXR bind to their RA response elements (RARE, composed of tandem direct repeats of 5'-AGGTCA-3' spaced by either 2 bp or 5 bp (DR2, DR5) in response to their physiological ligand atRA, and regulate gene expression in various biological processes.

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