

# Formation of PPARG:RXRA heterodimer (ARF6 complex)

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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., 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

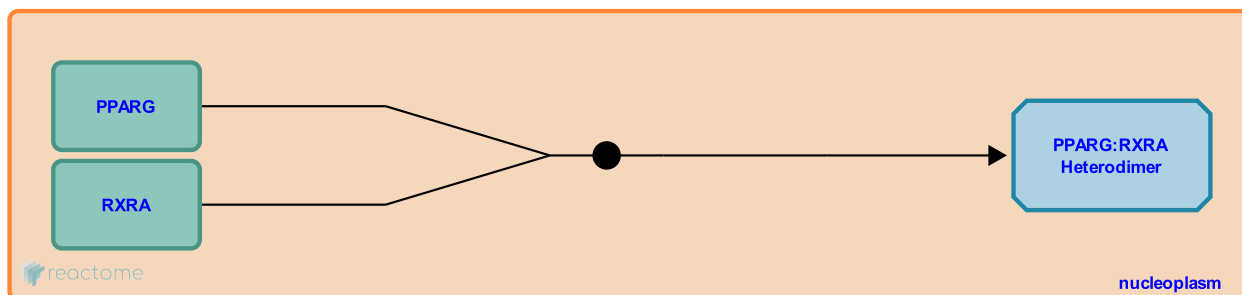
This document contains 1 reaction ([see Table of Contents](#))

## Formation of PPARG:RXRA heterodimer (ARF6 complex) [↗](#)

**Stable identifier:** R-HSA-381262

**Type:** binding

**Compartments:** nucleoplasm



PPARG binds the Retinoic acid X Receptor RXRA to form a heterodimer that has transcriptional activation activity. The complex was initially called ARF6 when discovered. PPARG binds RXRA via the C-terminus and AF-2 regions of PPARG.

### Literature references

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### Editions

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