

# Expression of ANKRD1

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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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- 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: 82

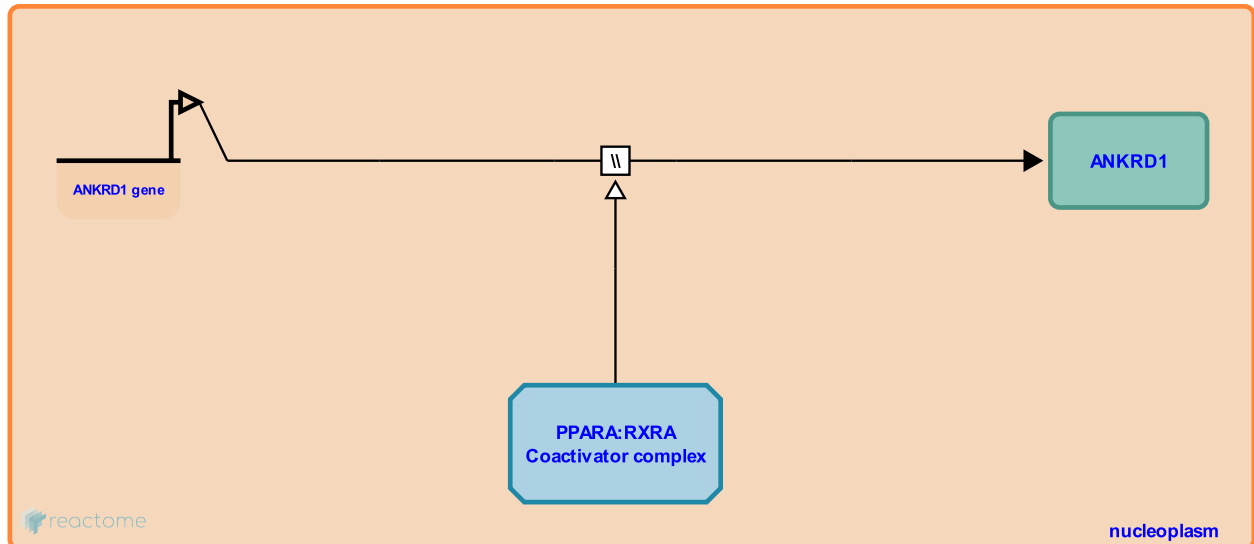
This document contains 1 reaction ([see Table of Contents](#))

## Expression of ANKRD1 [↗](#)

**Stable identifier:** R-HSA-1989779

**Type:** omitted

**Compartments:** nucleoplasm



The ANKRD1 gene is transcribed to yield mRNA and the mRNA is translated to yield protein.

### Literature references

de Groot, P.J., de Vries, S.C., Kersten, S., van der Meer, D.L., Vaisanen, S., Carlberg, C. et al. (2010). Profiling of promoter occupancy by PPAR{alpha} in human hepatoma cells via ChIP-chip analysis. *Nucleic Acids Res.* [↗](#)

### Editions

2009-06-08	Reviewed	Kersten, S.
2011-11-08	Authored, Edited	May, B.