

Expression of AGT

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27/01/2023

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. [↗](#)
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Reactome database release: 83

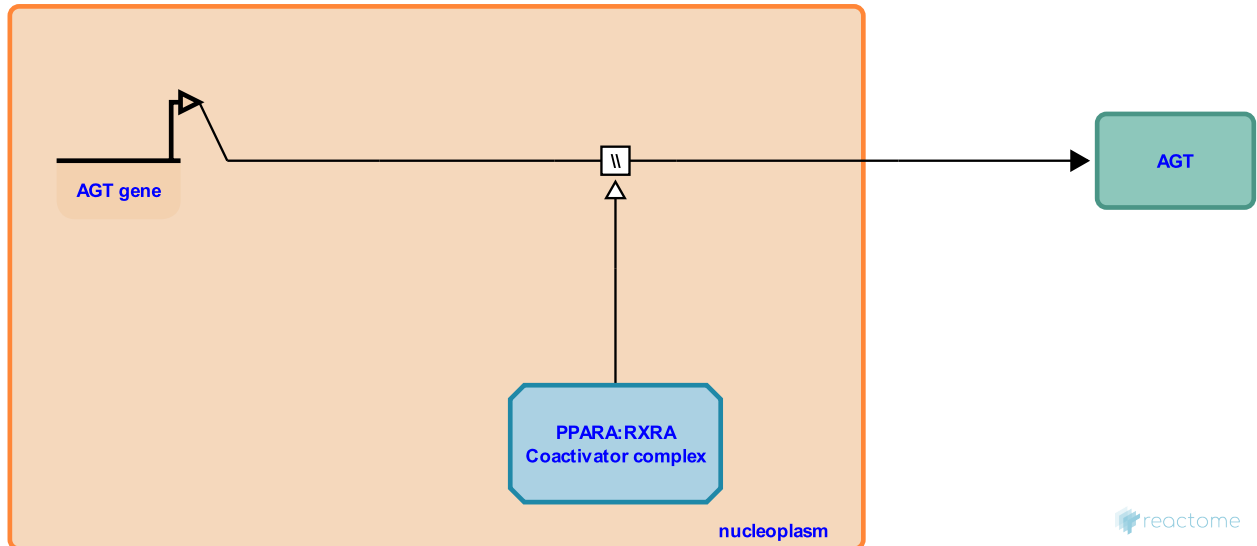
This document contains 1 reaction ([see Table of Contents](#))

Expression of AGT [↗](#)

Stable identifier: R-HSA-1989774

Type: omitted

Compartments: nucleoplasm, extracellular region



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

Literature references

Fukamizu, A., Hirota, K., Shimamoto, Y. (2004). Effect of peroxisome proliferator-activated receptor alpha on human angiotensinogen promoter. *Int J Mol Med*, 13, 729-33. [↗](#)

Editions

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