

# arginine + H<sub>2</sub>O => ornithine + urea [ARG1]

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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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Reactome database release: 88

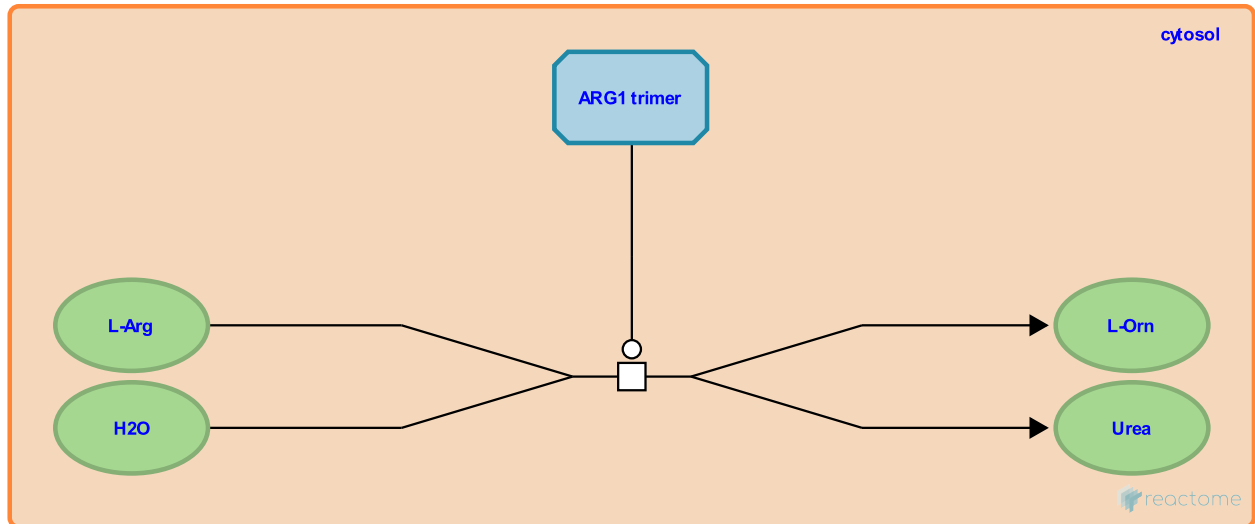
This document contains 1 reaction ([see Table of Contents](#))

**arginine + H2O => ornithine + urea [ARG1]** ↗

**Stable identifier:** R-HSA-70569

**Type:** transition

**Compartments:** cytosol



Cytosolic Arginase 1 (ARG1) trimer catalyzes the hydrolysis of arginine to yield ornithine and urea (DiCostanzo et al. 2005). Patients expressing mutated forms of the enzyme with diminished in vitro arginase activity can accumulate arginine to pathogenic levels in the blood (e.g., Uchino et al. 1995).

### Literature references

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Shapira, SK., Matsuda, I., Uchino, T., Lambert, M., Smit, LM., Qureshi, IA. et al. (1995). Molecular basis of phenotypic variation in patients with argininemia. *Hum Genet*, 96, 255-60. ↗

### Editions

|            |                  |                 |
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