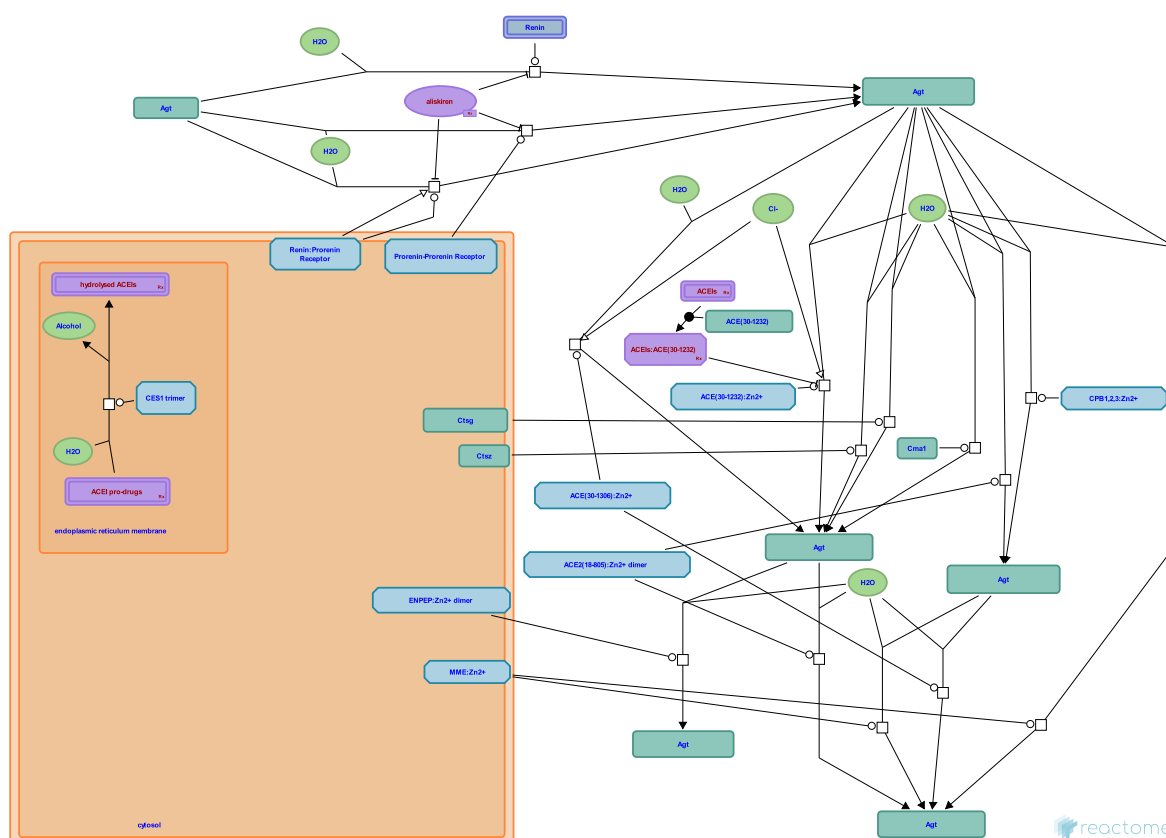


# Metabolism of Angiotensinogen to Angiotensins



European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the [Reactome Textbook](https://reactome.org/faq).

18/05/2024

## 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

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)

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: 88

This document contains 1 pathway and 17 reactions ([see Table of Contents](#))



## Renin hydrolyzes Angiotensinogen to Angiotensin-(1-10) ↗

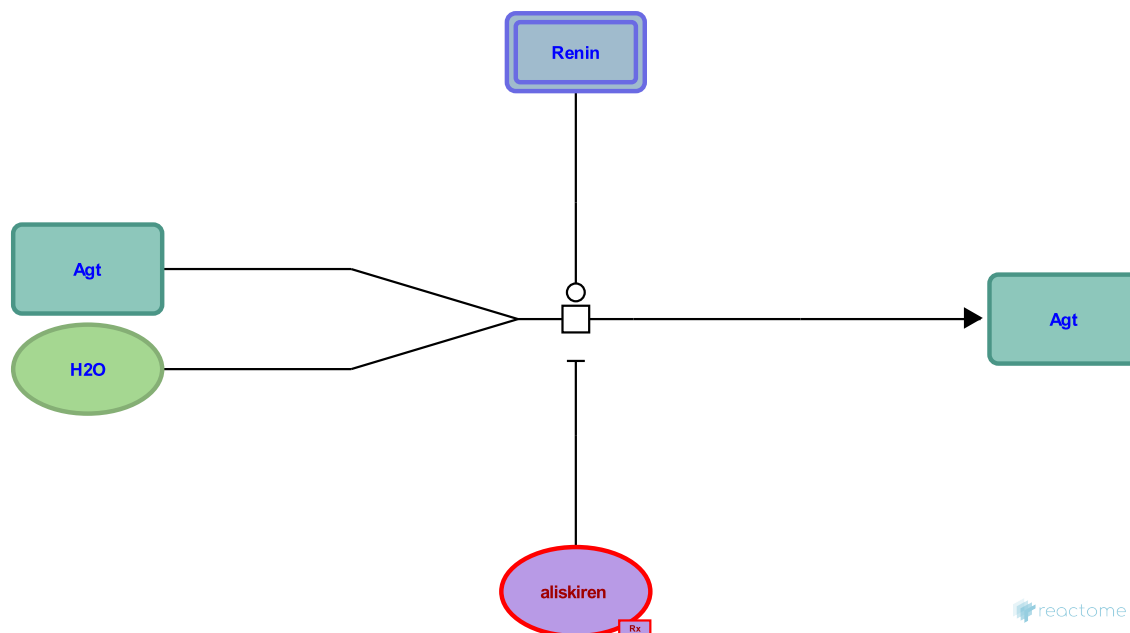
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022412

**Type:** transition

**Compartments:** extracellular region

**Inferred from:** [Renin hydrolyzes Angiotensinogen to Angiotensin-\(1-10\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [Mast Cell Carboxypeptidase hydrolyzes Angiotensin-\(1-10\) to Yield Angiotensin-\(1-9\)](#), [MME:Zn2+ \(Neprilysin\) hydrolyses AGT\(34-43\)](#), [Cathepsin G hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Cathepsin Z \(Cathepsin X\) hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Chymase hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [ACE2\(18-805\):Zn2+ hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-9\)](#), [ACE:Zn2+ hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Secreted ACE:Zn2+ hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#)

## Renin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-(1-10) ↗

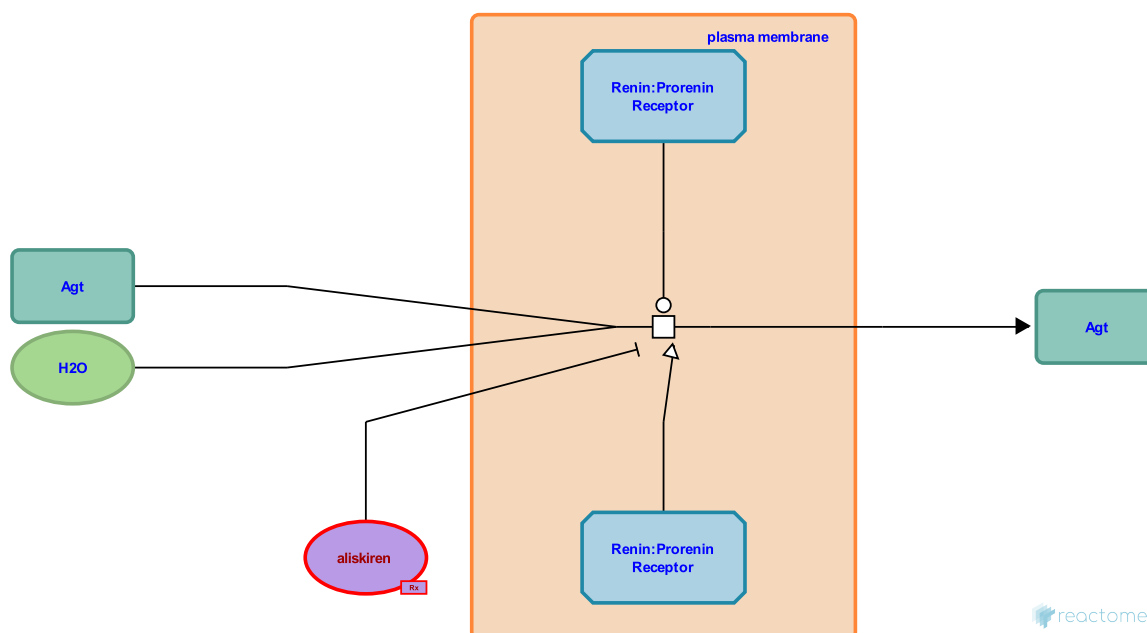
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022403

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [Renin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [Mast Cell Carboxypeptidase hydrolyzes Angiotensin-\(1-10\) to Yield Angiotensin-\(1-9\)](#), [MME:Zn2+ \(Neprilysin\) hydrolyses AGT\(34-43\)](#), [Cathepsin G hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Cathepsin Z \(Cathepsin X\) hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Chymase hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [ACE2\(18-805\):Zn2+ hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-9\)](#), [ACE:Zn2+ hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Secreted ACE:Zn2+ hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#)

## Prorenin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-(1-10) ↗

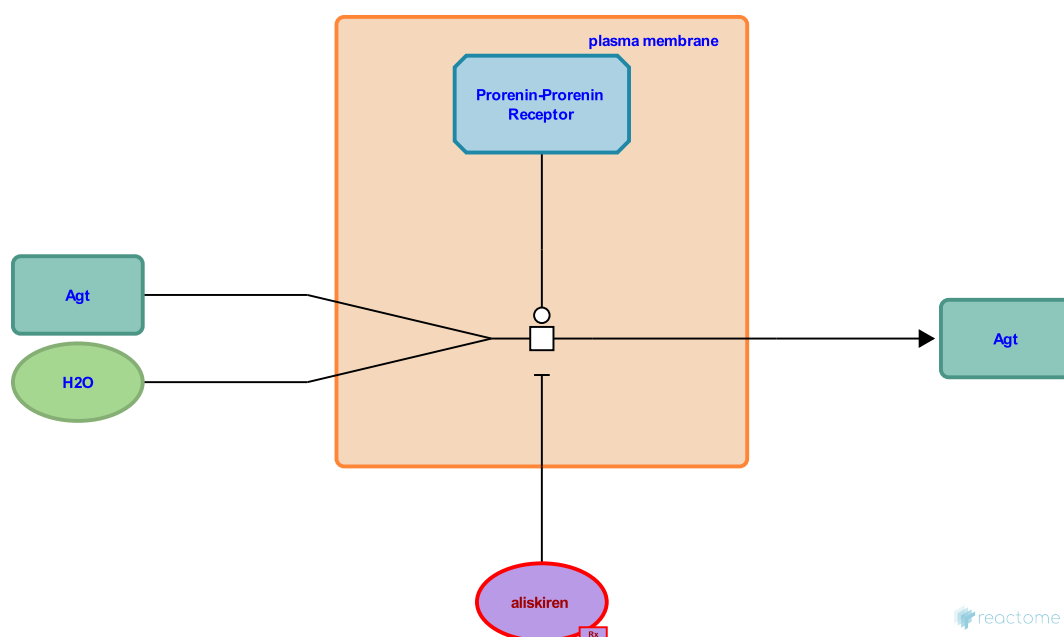
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2065357

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [Prorenin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [Mast Cell Carboxypeptidase hydrolyzes Angiotensin-\(1-10\) to Yield Angiotensin-\(1-9\)](#), [MME:Zn<sup>2+</sup> \(Neprilysin\) hydrolyses AGT\(34-43\)](#), [Cathepsin G hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Cathepsin Z \(Cathepsin X\) hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Chymase hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [ACE2\(18-805\):Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-9\)](#), [ACE:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Secreted ACE:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#)

## ACE:Zn<sup>2+</sup> hydrolyzes Angiotensin-(1-10) to Angiotensin-(1-8) ↗

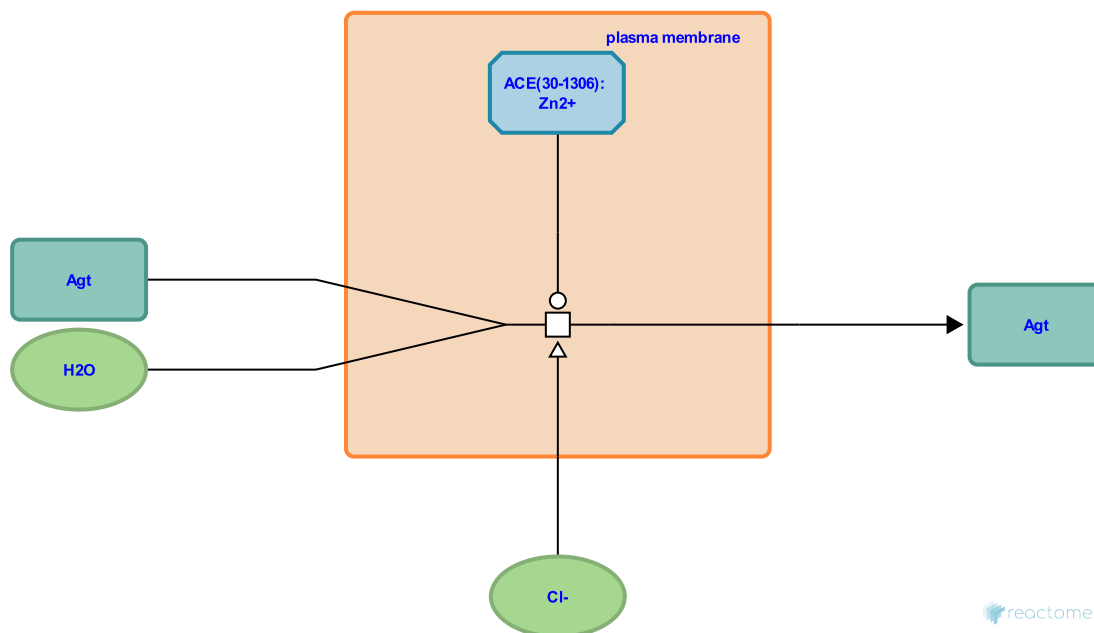
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022405

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [ACE:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Prorenin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#)

**Followed by:** [ACE2\(18-805\):Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(1-7\)](#), [ENPEP:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(2-8\)](#)

## Secreted ACE:Zn<sup>2+</sup> hydrolyzes Angiotensin-(1-10) to Angiotensin-(1-8) ↗

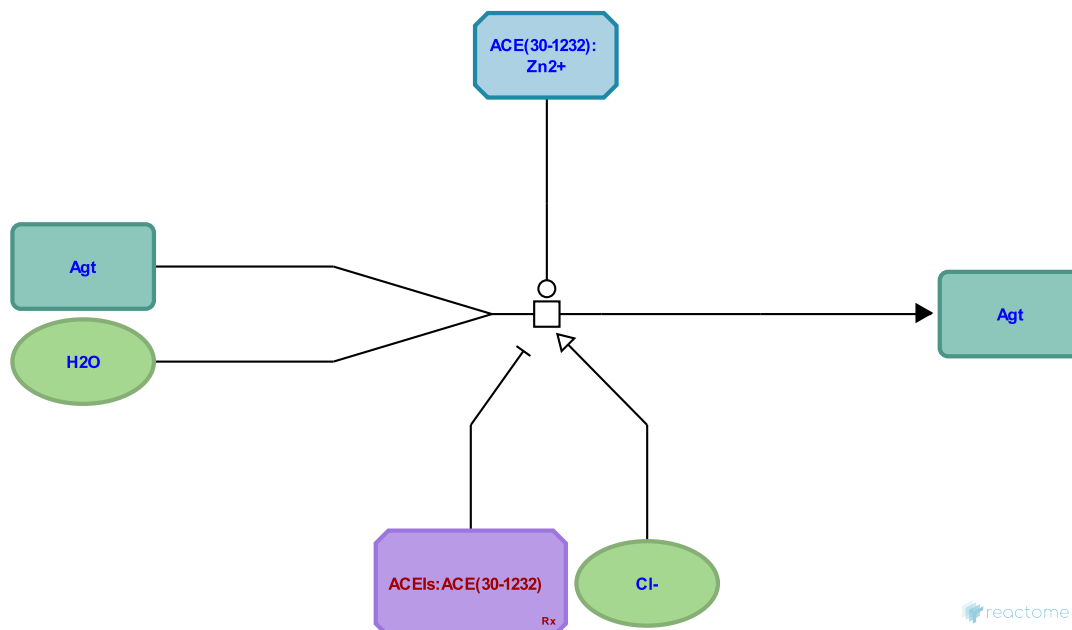
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2065355

**Type:** transition

**Compartments:** extracellular region

**Inferred from:** [Secreted ACE:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Prorenin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#)

**Followed by:** [ACE2\(18-805\):Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(1-7\)](#), [ENPEP:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(2-8\)](#)



## Chymase hydrolyzes Angiotensin-(1-10) to Angiotensin-(1-8) ↗

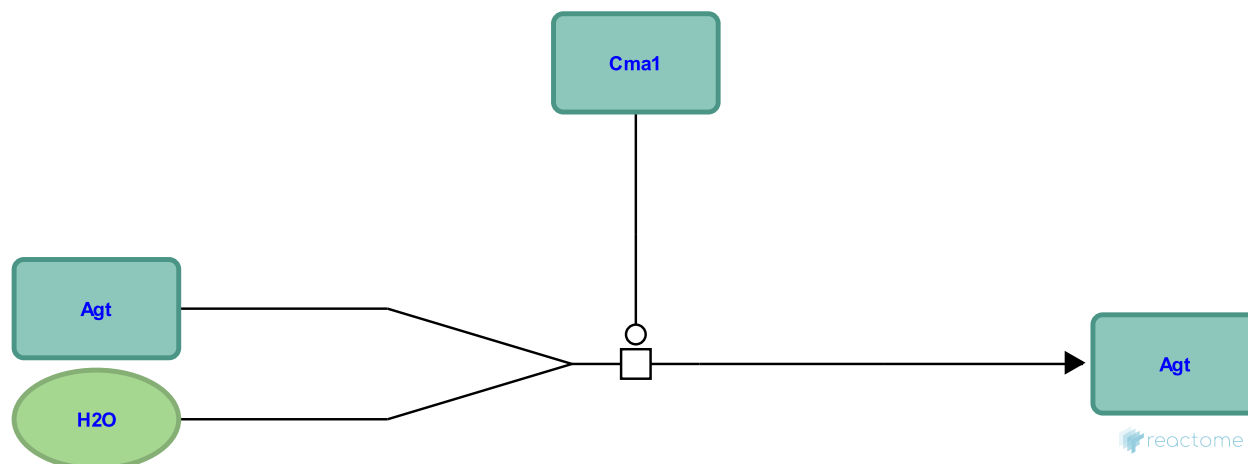
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022383

**Type:** transition

**Compartments:** extracellular region

**Inferred from:** [Chymase hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Prorenin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#)

**Followed by:** [ACE2\(18-805\):Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(1-7\)](#), [ENPEP:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(2-8\)](#)

## Cathepsin G hydrolyzes Angiotensin-(1-10) to Angiotensin-(1-8) ↗

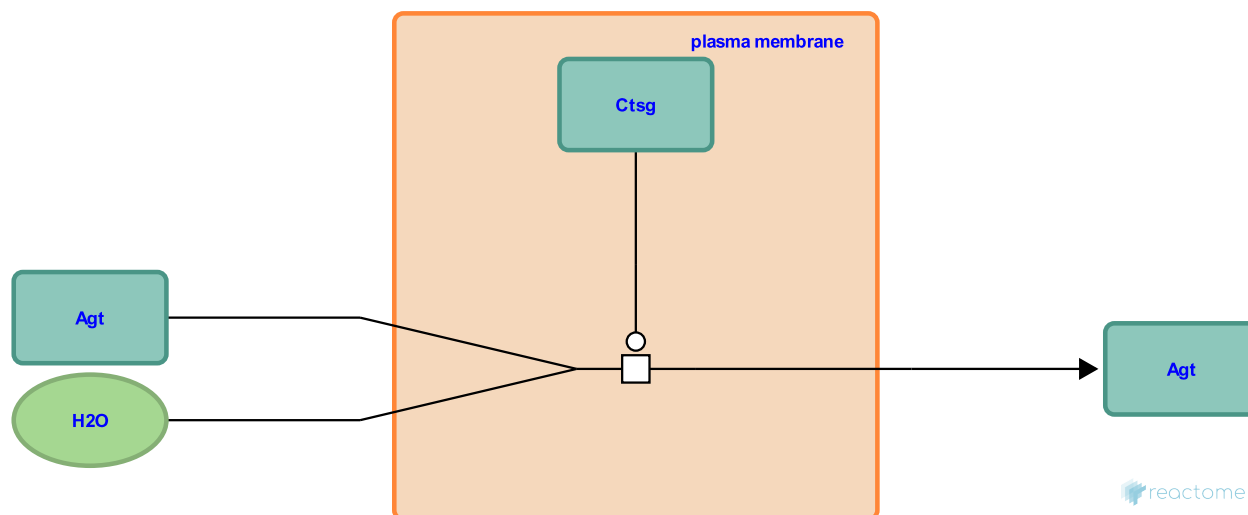
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022411

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [Cathepsin G hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Prorenin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#)

**Followed by:** [ACE2\(18-805\):Zn2+ hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(1-7\)](#), [ENPEP:Zn2+ hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(2-8\)](#)

## Cathepsin Z (Cathepsin X) hydrolyzes Angiotensin-(1-10) to Angiotensin-(1-8) ↗

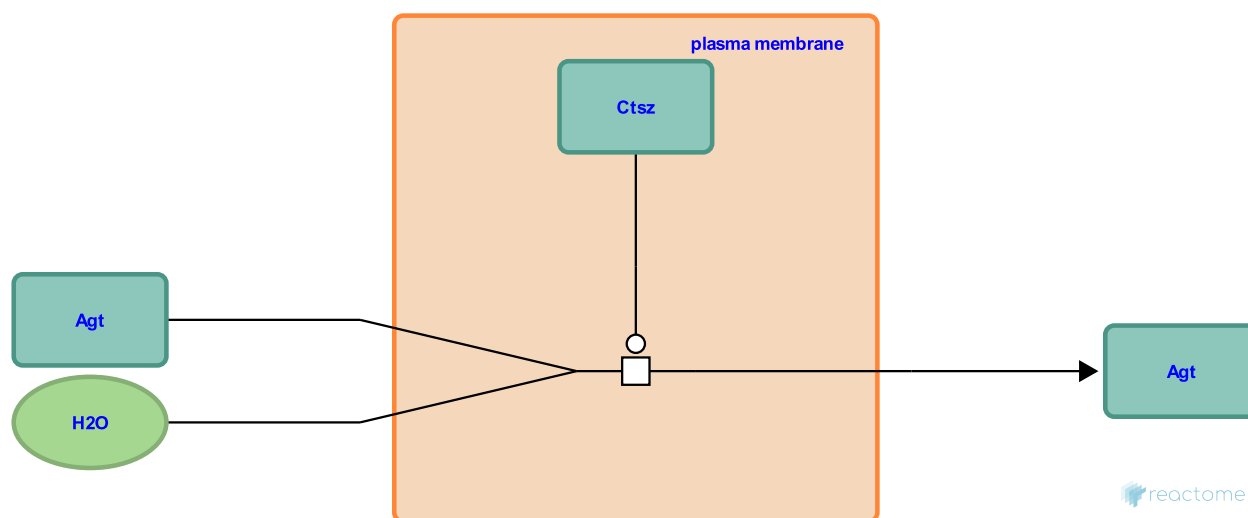
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022381

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [Cathepsin Z \(Cathepsin X\) hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Prorenin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#)

**Followed by:** [ACE2\(18-805\):Zn2+ hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(1-7\)](#), [ENPEP:Zn2+ hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(2-8\)](#)

## ACE2(18-805):Zn2+ hydrolyzes Angiotensin-(1-10) to Angiotensin-(1-9) ↗

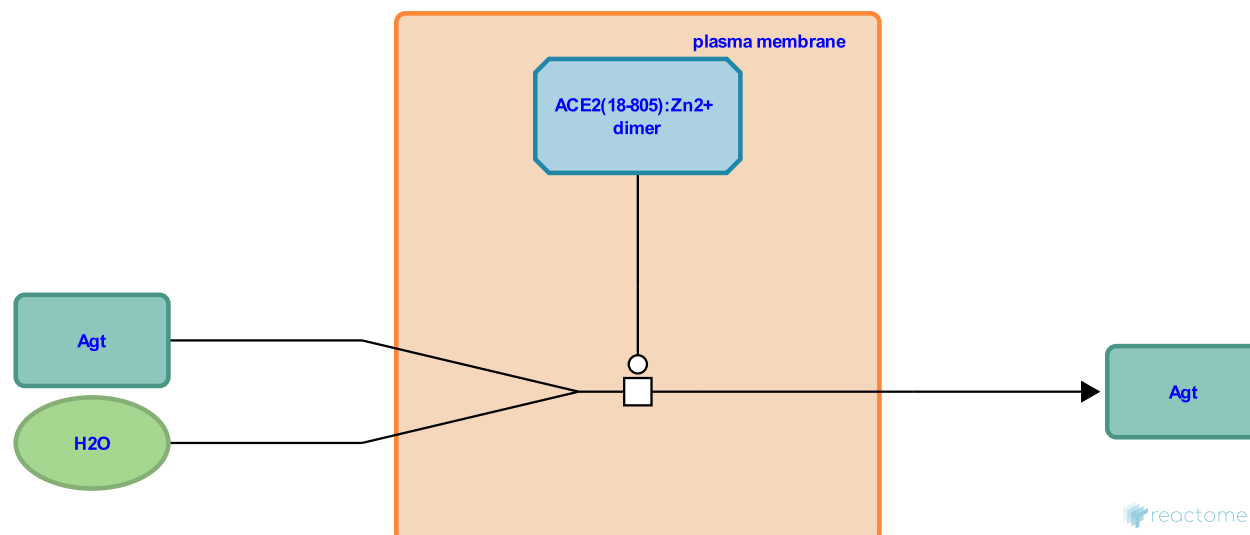
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022378

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [ACE2\(18-805\):Zn2+ hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-9\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Prorenin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#)

**Followed by:** [MME:Zn2+ \(Nepilysin\) hydrolyses AGT\(34-42\)](#), [ACE:Zn2+ hydrolyzes Angiotensin-\(1-9\) to Angiotensin-\(1-7\)](#)

## ACE:Zn<sup>2+</sup> hydrolyzes Angiotensin-(1-9) to Angiotensin-(1-7) ↗

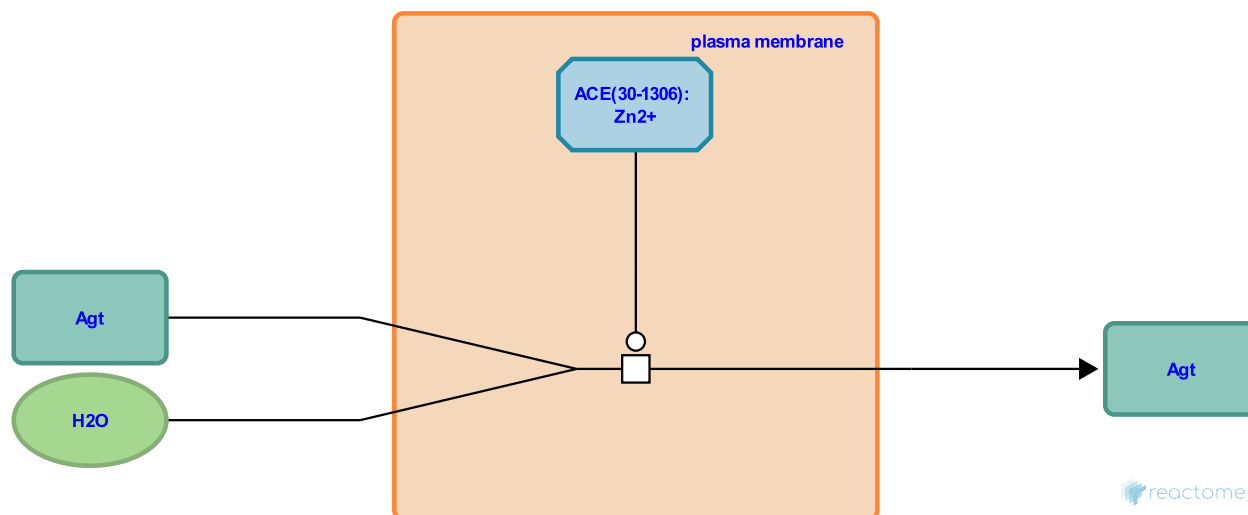
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022398

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [ACE:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-9\) to Angiotensin-\(1-7\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [ACE2\(18-805\):Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-9\)](#)

## MME:Zn<sup>2+</sup> (Neprilysin) hydrolyses AGT(34-42) ↗

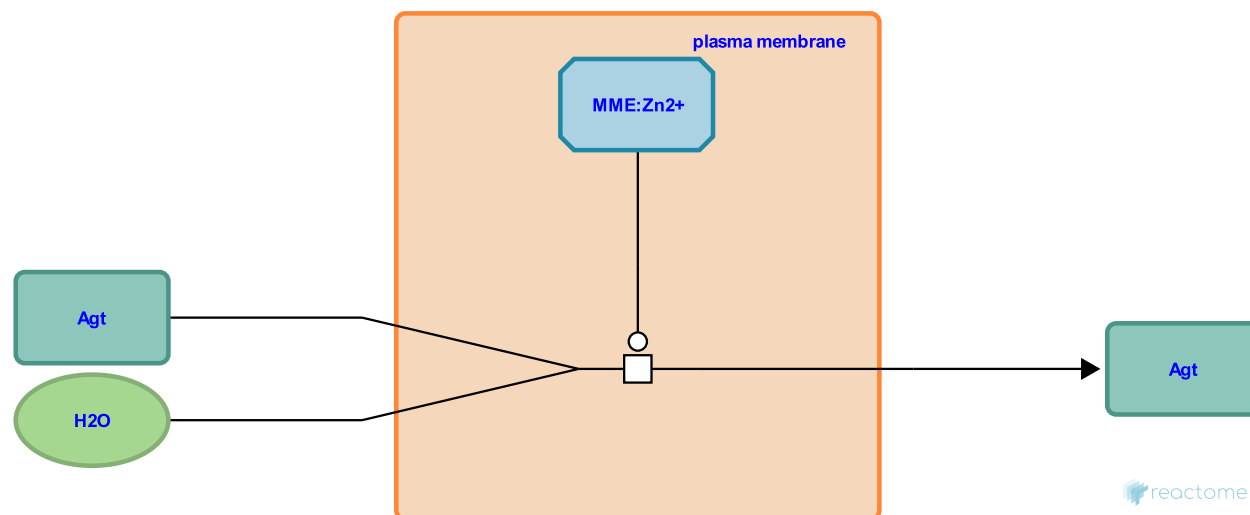
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022368

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [MME:Zn<sup>2+</sup> \(Neprilysin\) hydrolyses AGT\(34-42\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [ACE2\(18-805\):Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-9\)](#)

## MME:Zn<sup>2+</sup> (Neprilysin) hydrolyses AGT(34-43) ↗

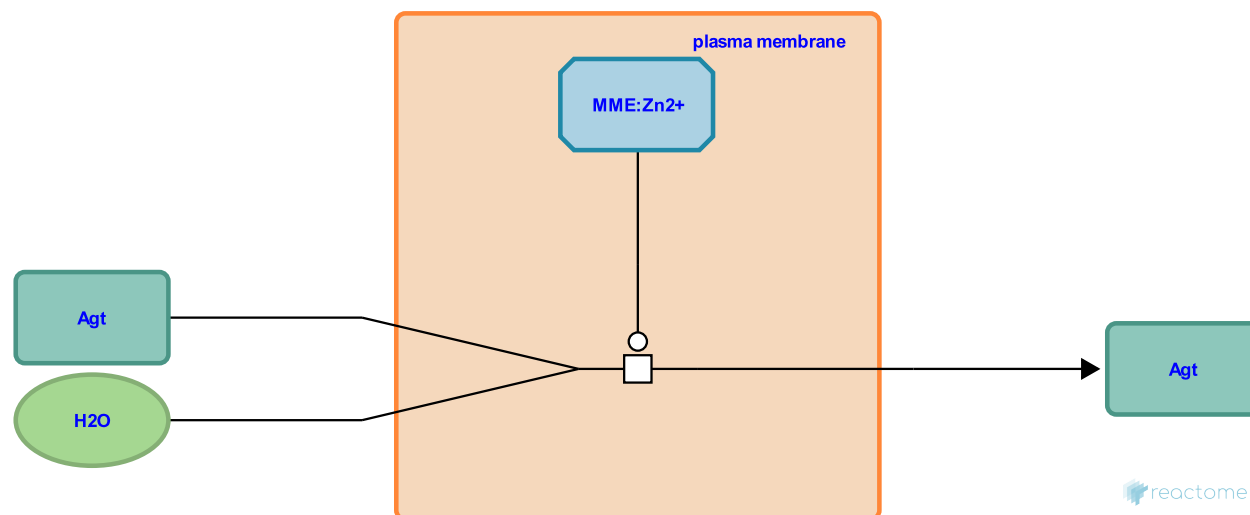
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022396

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [MME:Zn<sup>2+</sup> \(Neprilysin\) hydrolyses AGT\(34-43\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Prorenin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#)

## ENPEP:Zn<sup>2+</sup> hydrolyzes Angiotensin-(1-8) to Angiotensin-(2-8) ↗

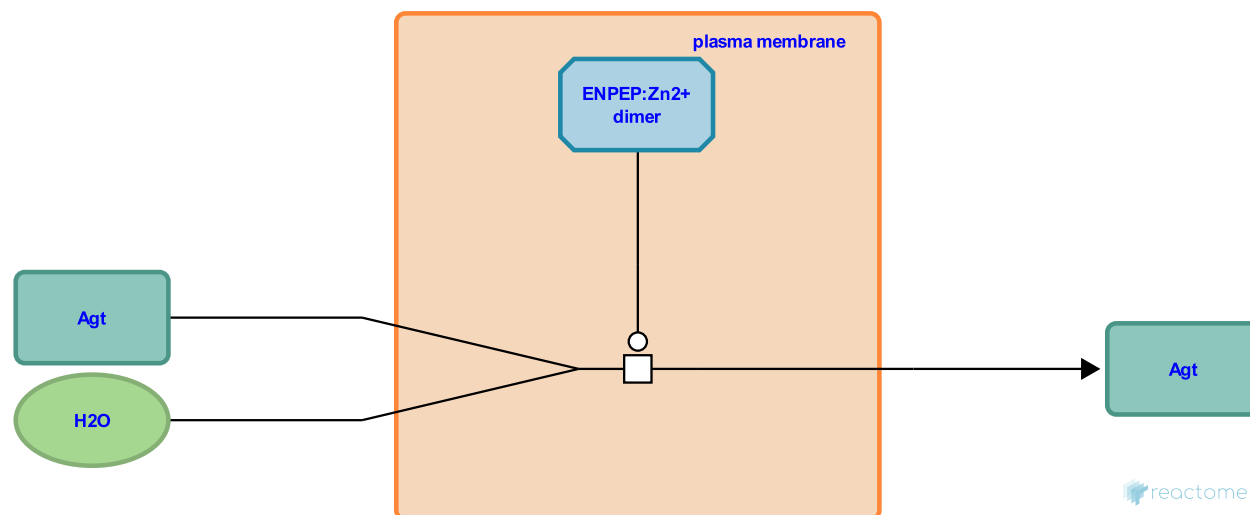
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022399

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [ENPEP:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(2-8\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Cathepsin Z \(Cathepsin X\) hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [ACE:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Secreted ACE:Zn<sup>2+</sup> hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Chymase hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Cathepsin G hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#)



## ACE2(18-805):Zn2+ hydrolyzes Angiotensin-(1-8) to Angiotensin-(1-7) ↗

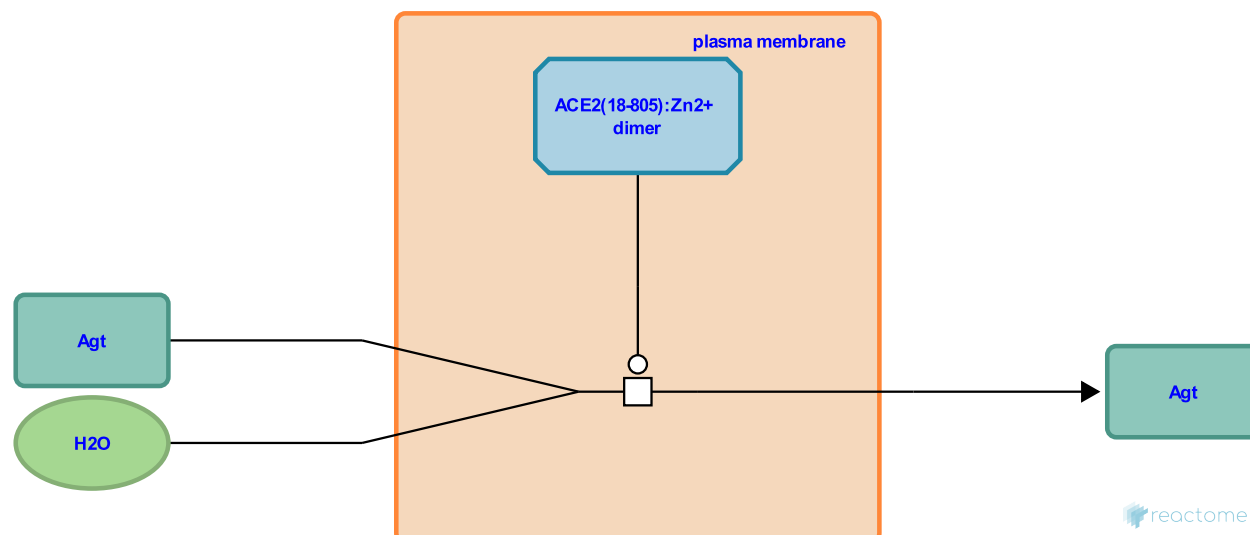
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2022379

**Type:** transition

**Compartments:** plasma membrane, extracellular region

**Inferred from:** [ACE2\(18-805\):Zn2+ hydrolyzes Angiotensin-\(1-8\) to Angiotensin-\(1-7\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Cathepsin Z \(Cathepsin X\) hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [ACE:Zn2+ hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Secreted ACE:Zn2+ hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Chymase hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#), [Cathepsin G hydrolyzes Angiotensin-\(1-10\) to Angiotensin-\(1-8\)](#)

## Mast Cell Carboxypeptidase hydrolyzes Angiotensin-(1-10) to Yield Angiotensin-(1-9)



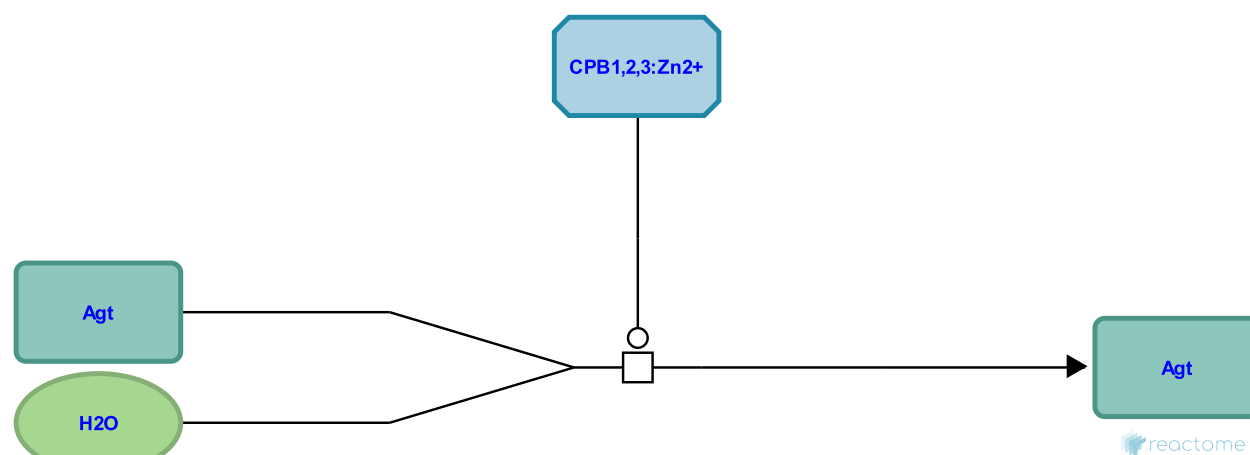
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-2028294

**Type:** transition

**Compartments:** extracellular region

**Inferred from:** [Mast Cell Carboxypeptidase hydrolyzes Angiotensin-\(1-10\) to Yield Angiotensin-\(1-9\) \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Prorenin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin:Prorenin Receptor hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#), [Renin hydrolyzes Angiotensinogen to Angiotensin-\(1-10\)](#)

## CES1trimer hydrolyses ACEI pro-drugs to ACEIs ↗

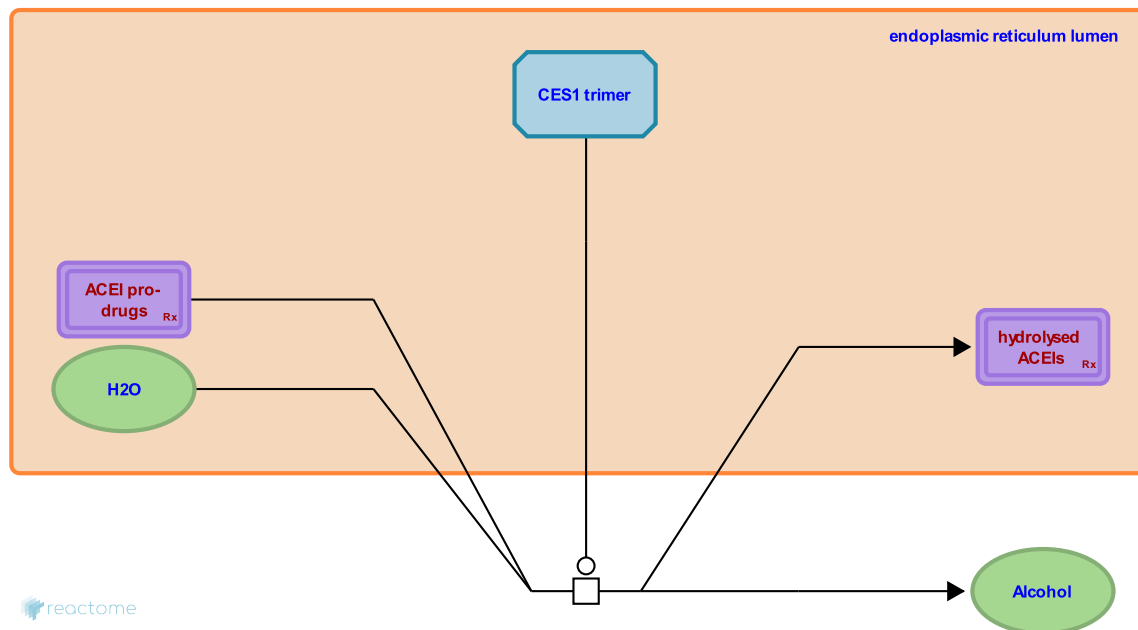
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-9619024

**Type:** transition

**Compartments:** extracellular region

**Inferred from:** [CES1trimer hydrolyses ACEI pro-drugs to ACEIs \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## ACEIs bind ACE ↗

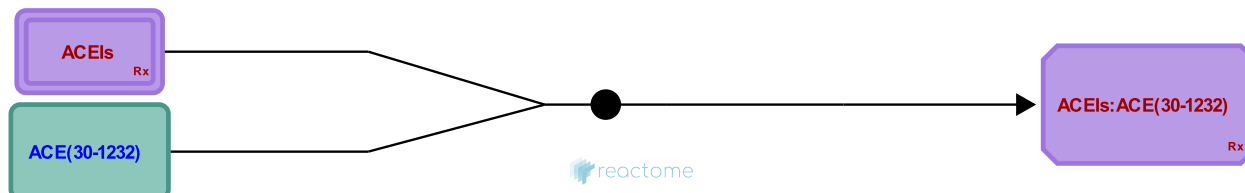
**Location:** [Metabolism of Angiotensinogen to Angiotensins](#)

**Stable identifier:** R-MMU-9614933

**Type:** binding

**Compartments:** extracellular region

**Inferred from:** [ACEIs bind ACE \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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