



## 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. [↗](#)
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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. [↗](#)

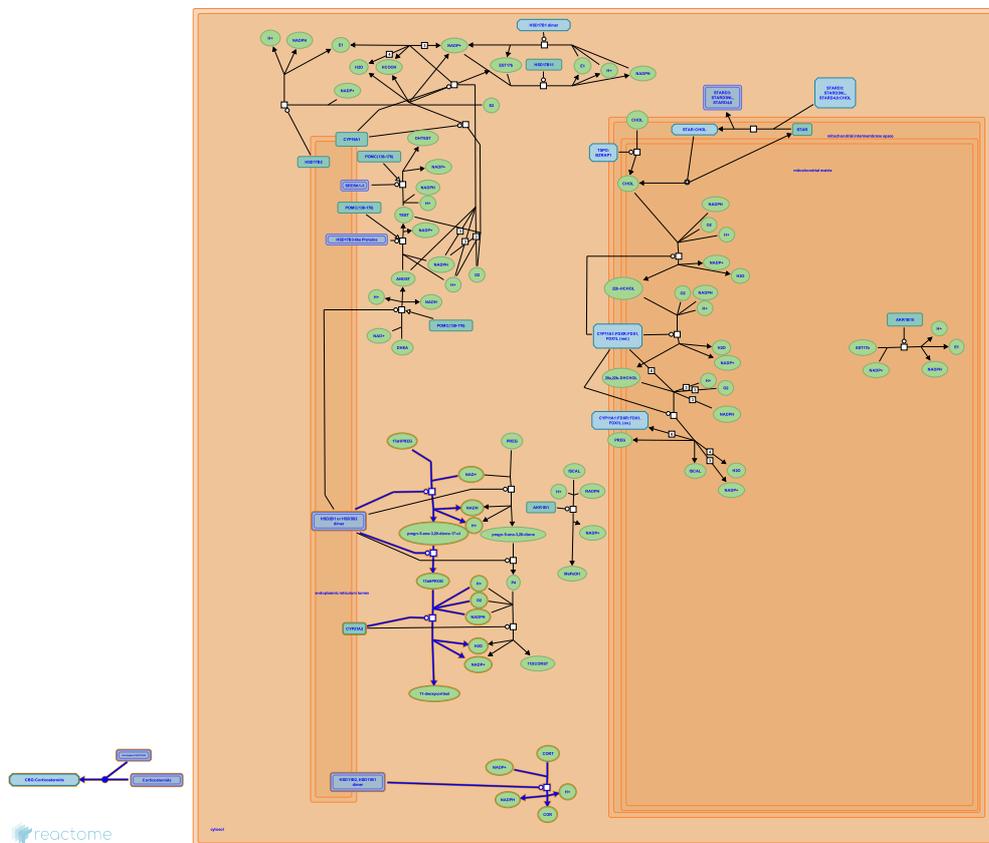
Reactome database release: 70

This document contains 1 pathway and 5 reactions ([see Table of Contents](#))

## Glucocorticoid biosynthesis ↗

**Stable identifier:** R-GGA-194002

**Inferred from:** [Glucocorticoid biosynthesis \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## 17-Hydroxypregnenolone is dehydrogenated to form pregn-5-ene-3,20-dione-17-ol [↗](#)

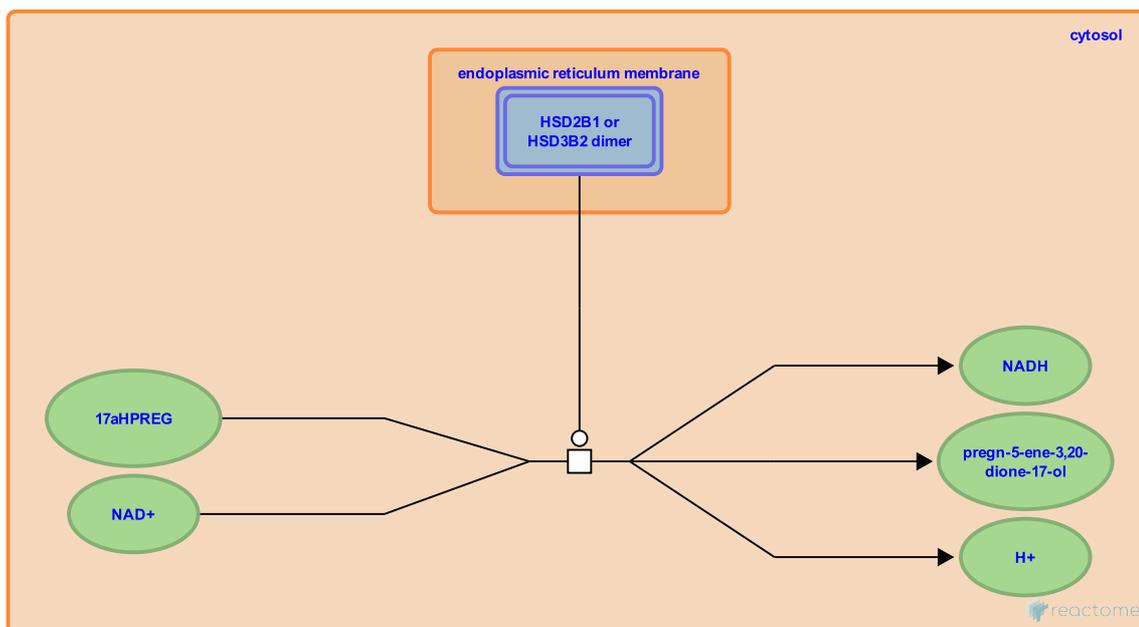
**Location:** [Glucocorticoid biosynthesis](#)

**Stable identifier:** R-GGA-196372

**Type:** transition

**Compartments:** cytosol, endoplasmic reticulum membrane

**Inferred from:** [17-Hydroxypregnenolone is dehydrogenated to form pregn-5-ene-3,20-dione-17-ol \(Homo sapiens\)](#)



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.

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**Followed by:** [Pregn-5-ene-3,20-dione-17-ol isomerizes to 17-hydroxyprogesterone](#)

## Pregn-5-ene-3,20-dione-17-ol isomerizes to 17-hydroxyprogesterone ↗

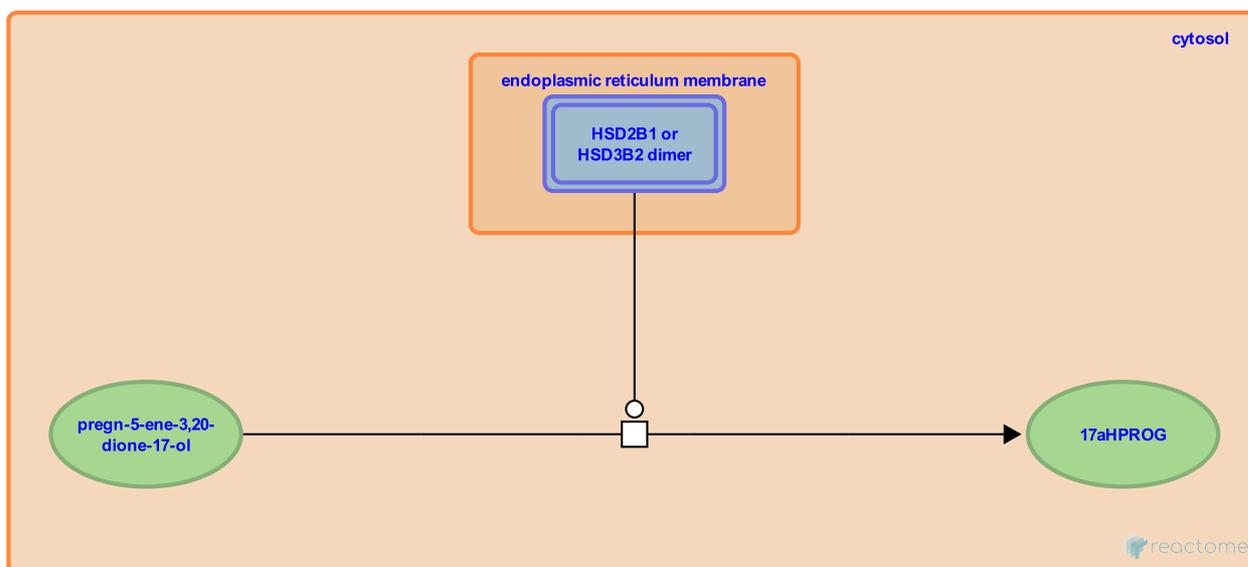
**Location:** [Glucocorticoid biosynthesis](#)

**Stable identifier:** R-GGA-193961

**Type:** transition

**Compartments:** cytosol, endoplasmic reticulum membrane

**Inferred from:** [Pregn-5-ene-3,20-dione-17-ol isomerizes to 17-hydroxyprogesterone \(Homo sapiens\)](#)



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.

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**Preceded by:** [17-Hydroxypregnenolone is dehydrogenated to form pregn-5-ene-3,20-dione-17-ol](#)

**Followed by:** [CYP21A2 oxidises 17HPROG](#)

## CYP21A2 oxidises 17HPROG ↗

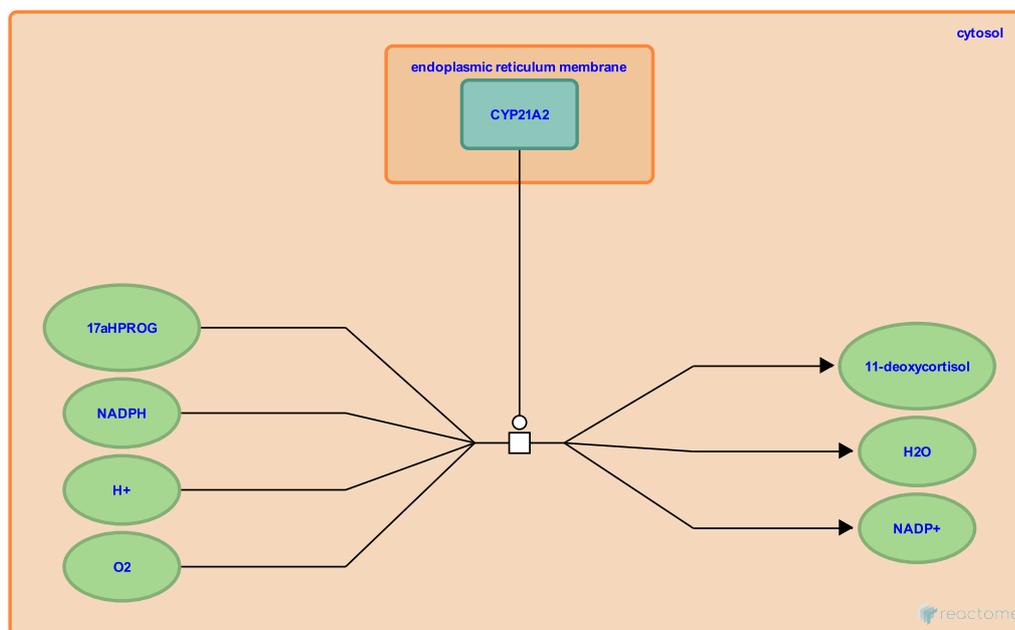
**Location:** [Glucocorticoid biosynthesis](#)

**Stable identifier:** R-GGA-193981

**Type:** transition

**Compartments:** cytosol, endoplasmic reticulum membrane

**Inferred from:** [CYP21A2 oxidises 17HPROG \(Homo sapiens\)](#)



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.

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**Preceded by:** [Pregn-5-ene-3,20-dione-17-ol isomerizes to 17-hydroxyprogesterone](#)

## HSD11B2,HSD11B1 dimer oxidise CORT to COR ↗

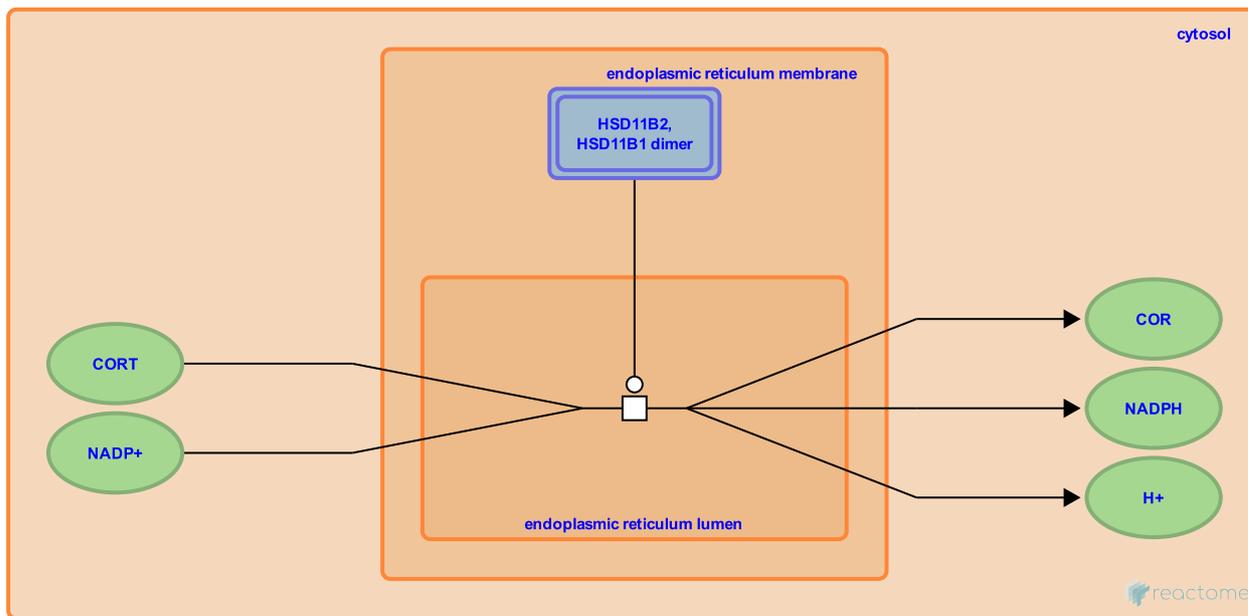
**Location:** [Glucocorticoid biosynthesis](#)

**Stable identifier:** R-GGA-194023

**Type:** transition

**Compartments:** endoplasmic reticulum lumen

**Inferred from:** [HSD11B2,HSD11B1 dimer oxidise CORT to COR \(Homo sapiens\)](#)



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.

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## Corticosteroids bind to CBG in blood ↗

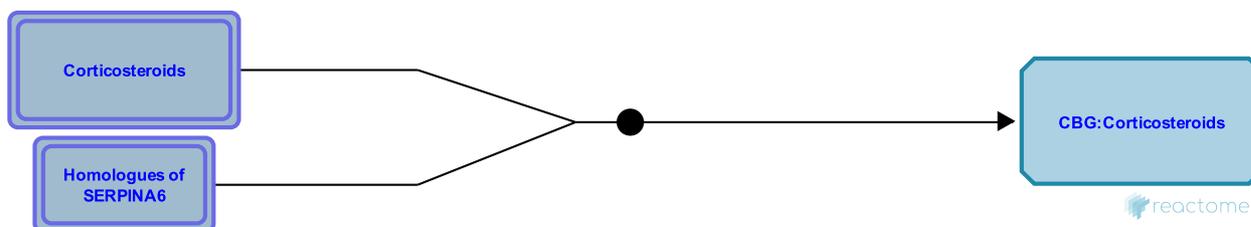
**Location:** [Glucocorticoid biosynthesis](#)

**Stable identifier:** R-GGA-1449687

**Type:** binding

**Compartments:** extracellular region

**Inferred from:** [Corticosteroids bind to CBG in blood \(Homo sapiens\)](#)



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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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