Formation of xylulose-5-phosphate

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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.

28/12/2022
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


Reactome database release: 83

This document contains 1 pathway and 6 reactions (see Table of Contents)

https://reactome.org
The conversion of D-glucuronate to D-xylulose-5-phosphate, an intermediate in the pentose phosphate pathway, proceeds via L-gulonate, 3-dehydro-L-gulonate, L-xylulose, xylitol, and D-xylulose (Wamelink et al. 2008). D-glucuronate can be generated via the degradation of glucuronidated proteins. This pathway would have the effect of returning it to the pentose phosphate pathway or glycolysis.

**Literature references**


**Editions**

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AKR1A1 reduces D-glucuronate to L-gulonate

Location: Formation of xylulose-5-phosphate

Stable identifier: R-HSA-5661256

Type: transition

Compartments: cytosol

Cytosolic AKR1A1 (Aldo-keto reductase family 1 member A1) catalyzes the reduction by NADPH of D-glucuronate to L-gulonate (Barski et al. 1995).

Followed by: CRYL1 dimer dehydrogenates L-gulonate to 3-dehydro-L-gulonate

Literature references


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CRYL1 dimer dehydrogenates L-gulonate to 3-dehydro-L-gulonate

**Location:** Formation of xylulose-5-phosphate

**Stable identifier:** R-HSA-5661290

**Type:** transition

**Compartments:** cytosol

Cytosolic CRYL1 (lambda-crystallin homolog, also known as L-gulonate 3-dehydrogenase) dimer catalyzes the NAD-dependent dehydrogenation of L-gulonate to form 3-dehydro-L-gulonate. The CRYL1 protein also functions as a lens crystallin, hence its name (Ishikura et al. 2005).

**Preceded by:** AKR1A1 reduces D-glucuronate to L-gulonate

**Followed by:** KGPDC decarboxylates 3-dehydro-L-gulonate to L-xylulose

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KGPDC decarboxylates 3-dehydro-L-gulonate to L-xylulose

**Location:** Formation of xylulose-5-phosphate

**Stable identifier:** R-HSA-5662473

**Type:** transition

**Compartments:** cytosol

Cytosolic dehydro-L-gulonate decarboxylase (KGPDC) catalyzes the conversion of 3-dehydro-L-gulonate to L-xylulose and CO2. Studies in vivo provide indirect but strong evidence that this reaction occurs in humans and guinea pigs and dehydro-L-gulonate decarboxylase enzyme has been partially purified from guinea pigs (Winkelman & Ashwell 1961). Its amino acid sequence is unknown, however.

**Preceded by:** CRYL1 dimer dehydrogenates L-gulonate to 3-dehydro-L-gulonate

**Followed by:** DCXR tetramer reduces L-xylulose to xylitol

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DCXR tetramer reduces L-xylulose to xylitol

**Location:** Formation of xylulose-5-phosphate

**Stable identifier:** R-HSA-5661240

**Type:** transition

**Compartments:** plasma membrane, cytosol

L-xylulose reductase (DCXR, also known as dicarbonyl/L-xylulose reductase) catalyzes the reversible NADPH dependent reduction of cytosolic L-xylulose to xylitol (Nakagawa et al. 2002). The enzyme is a tetramer (El Kabbani et al. 2004) and may be associated with the plasma membrane (Boué et al. 1996). Mutations that inactivate DCXR are associated with essential pentosuria (Pierce et al. 2011; Wang & van Eys 1970).

**Preceded by:** KGPDC decarboxylates 3-dehydro-L-gulonate to L-xylulose

**Followed by:** SORD tetramer oxidizes xylitol to D-xylulose

**Literature references**


**SORD tetramer oxidizes xylitol to D-xylulose**

**Location:** Formation of xylulose-5-phosphate

**Stable identifier:** R-HSA-5662471

**Type:** transition

**Compartments:** cytosol


**Preceded by:** DCXR tetramer reduces L-xylulose to xylitol

**Followed by:** XYLB phosphorylates D-xylulose

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XYLB phosphorylates D-xylulose

**Location:** Formation of xylulose-5-phosphate

**Stable identifier:** R-HSA-5662466

**Type:** transition

**Compartments:** cytosol

Cytosolic xylulose kinase (XYLB) catalyzes the phosphorylation of D-xylulose to form D-xylulose-5-phosphate (XY5P) (Bunker et al. 2013).

**Preceded by:** SORD tetramer oxidizes xylitol to D-xylulose

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</tbody>
</table>
# Table of Contents

Introduction 1

- Formation of xylulose-5-phosphate 2
  - AKR1A1 reduces D-glucuronate to L-gulonate 3
  - CRYL1 dimer dehydrogenates L-gulonate to 3-dehydro-L-gulonate 4
  - KGPDC decarboxylates 3-dehydro-L-gulonate to L-xylulose 5
  - DCXR tetramer reduces L-xylulose to xylitol 6
  - SORD tetramer oxidizes xylitol to D-xylulose 8
  - XYLB phosphorylates D-xylulose 9

Table of Contents 10