Gamma-carboxylation, transport, and amino-terminal cleavage of proteins

D'Eustachio, P., Stafford, DW.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of Creative Commons Attribution 4.0 International (CC BY 4.0) License. For more information see our license.

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.

14/11/2022
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: 82

This document contains 4 pathways (see Table of Contents)

https://reactome.org
A number of proteins, including eight required for normal blood clot formation and its regulation (Prothrombin (factor II), factor VII, factor IX, factor X, protein C, protein S, protein Z, and Gas6) share a sequence motif rich in glutamate residues near their amino termini. Carboxylation of the glutamate residues within this motif followed by removal of an aminoterminal propeptide is required for each of these proteins to function. These modifications occur as the proteins move through the endoplasmic reticulum and Golgi apparatus.
Gamma-carboxylation of a cluster of glutamate residues near the amino termini of thrombin, factor VII, factor IX, factor X, protein C, protein S, protein Z, and Gas 6 is required for these proteins to bind Ca++ and function efficiently in blood clotting. A single enzyme, vitamin K-dependent gamma-carboxylase, catalyzes the gamma-carboxylation of all eight proteins involved in clotting (Morris et al. 1995; Brenner et al. 1998; Spronk et al. 2000). In the carboxylation reaction, the enzyme binds its substrate protein via a sequence motif on the amino terminal side of the glutamate residues to be carboxylated (Furie et al. 1999), then processively carboxylates all glutamates in the cluster before releasing the substrate (Morris et al. 1995; Berkner 2000; Stenina et al. 2001). The reaction occurs in the endoplasmic reticulum (Bristol et al. 1996).

Literature references


https://reactome.org

**Editions**

<table>
<thead>
<tr>
<th>Date</th>
<th>Action</th>
<th>Author</th>
</tr>
</thead>
<tbody>
<tr>
<td>2005-03-17</td>
<td>Authored</td>
<td>D'Eustachio, P.</td>
</tr>
<tr>
<td>2022-08-23</td>
<td>Edited</td>
<td>D'Eustachio, P.</td>
</tr>
</tbody>
</table>
Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus

**Location:** Gamma-carboxylation, transport, and amino-terminal cleavage of proteins

**Stable identifier:** R-HSA-159763

**Compartments:** COPII-coated ER to Golgi transport vesicle

Gamma-carboxylated proteins are moved by anterograde transport from the endoplasmic reticulum to the Golgi apparatus (Kirchhausen 2000).

**Literature references**


**Editions**

<table>
<thead>
<tr>
<th>Date</th>
<th>Event</th>
<th>Author</th>
</tr>
</thead>
<tbody>
<tr>
<td>2005-03-17</td>
<td>Authored</td>
<td>D'Eustachio, P.</td>
</tr>
<tr>
<td>2022-08-23</td>
<td>Edited</td>
<td>D'Eustachio, P.</td>
</tr>
</tbody>
</table>
Removal of aminoterminal propeptides from gamma-carboxylated proteins

Location: Gamma-carboxylation, transport, and amino-terminal cleavage of proteins

Stable identifier: R-HSA-159782

Compartments: Golgi lumen

Furin is an endopeptidase localized to the Golgi membrane that cleaves many proteins on the carboxyterminal side of the sequence motif Arg-[any residue]-(Lys or Arg)-Arg (Jones et al. 1995; Leduc et al. 1992). In the case of gamma-carboxylated proteins, if this cleavage does not occur, the proteins are still secreted but do not function properly (Bristol et al. 1993; Lind et al. 1997; Wasley et al. 1993). The aminoterminal fragments, "propeptides", generated in this reaction have no known function; the carboxylated, cleaved proteins are delivered to the cell membrane or secreted from the cell.

Literature references


Thulin, CD., Fry, MD., Molloy, S S., Jones, BG., Walsh, KA., Thomas, L. et al. (1995). Intracellular trafficking of furin is modulated by the phosphorylation state of a casein kinase II site in its cytoplasmic tail. EMBO J, 14, 5869-83.

Editions

2005-03-17 Authored
2022-08-23 Edited

https://reactome.org