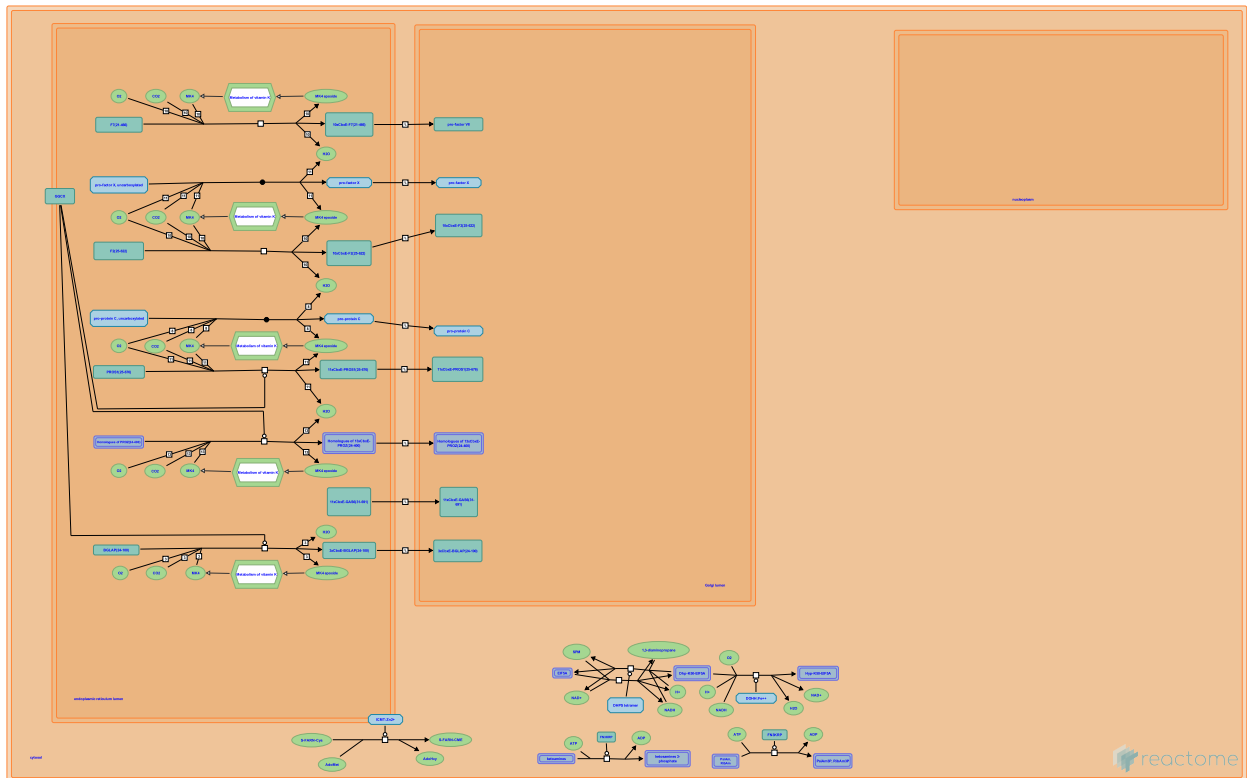


Gamma carboxylation, hypusine formation and arylsulfatase activation



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

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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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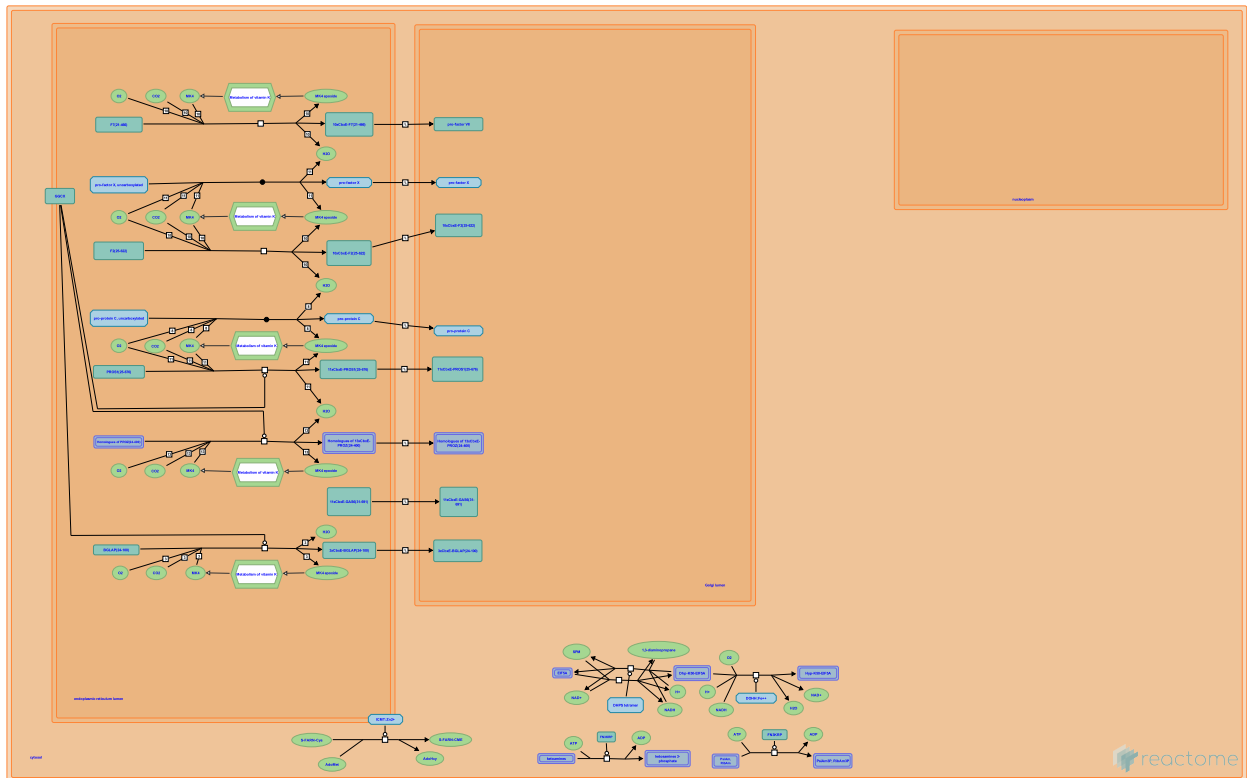
Reactome database release: 69

This document contains 3 pathways and 3 reactions ([see Table of Contents](#))

Gamma carboxylation, hypusine formation and arylsulfatase activation ↗

Stable identifier: R-DRE-163841

Inferred from: Gamma carboxylation, hypusine formation and arylsulfatase activation (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.

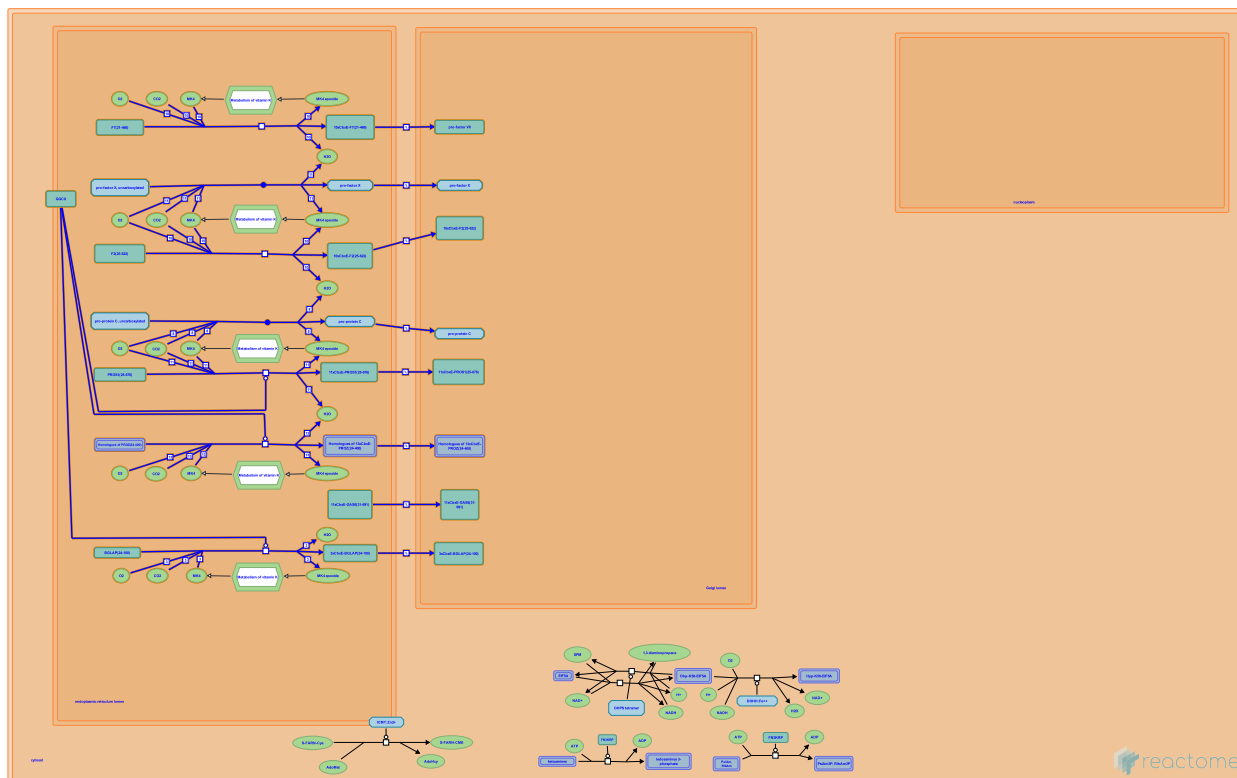
[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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

Location: Gamma carboxylation, hypusine formation and arylsulfatase activation

Stable identifier: R-DRE-159854

Inferred from: Gamma-carboxylation, transport, and amino-terminal cleavage of proteins (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>

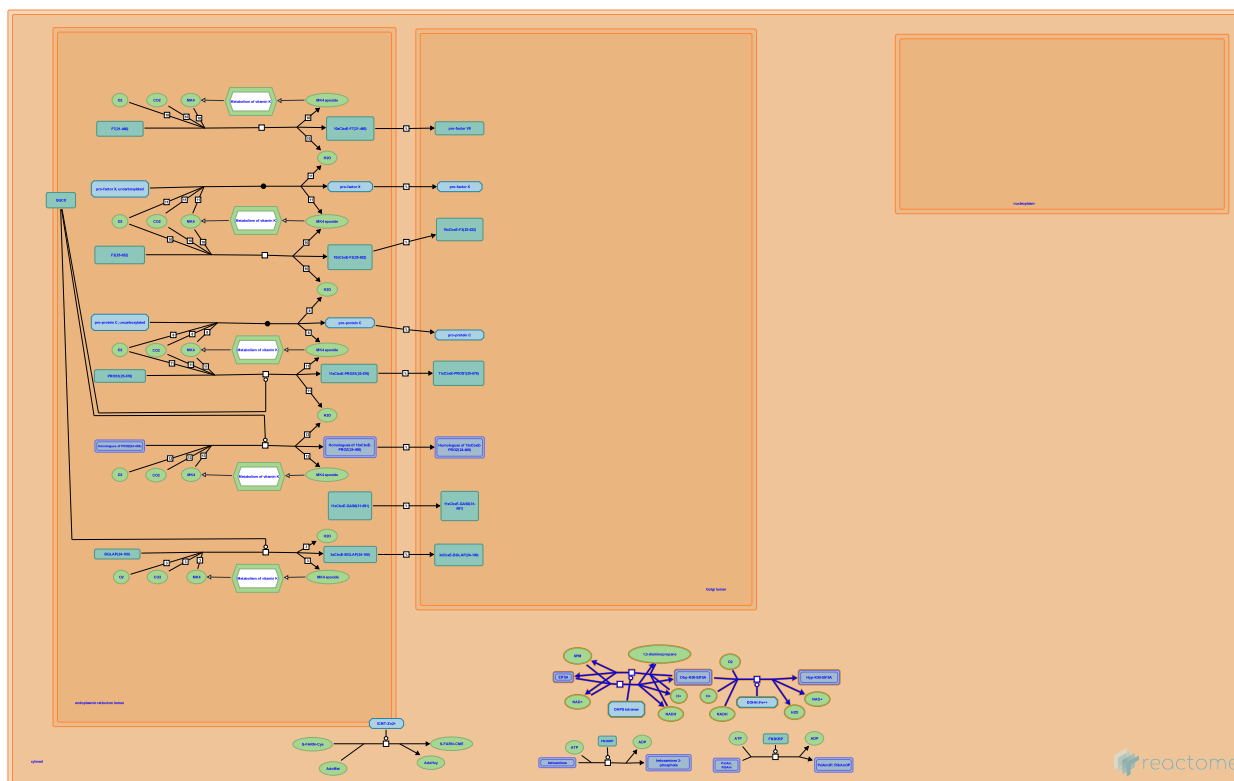
Hypusine synthesis from eIF5A-lysine ↗

Location: Gamma carboxylation, hypusine formation and arylsulfatase activation

Stable identifier: R-DRE-204626

Compartments: cytosol

Inferred from: Hypusine synthesis from eIF5A-lysine (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>

ICMT:Zn²⁺ transfers CH₃ from AdoMet to isoprenylated proteins ↗

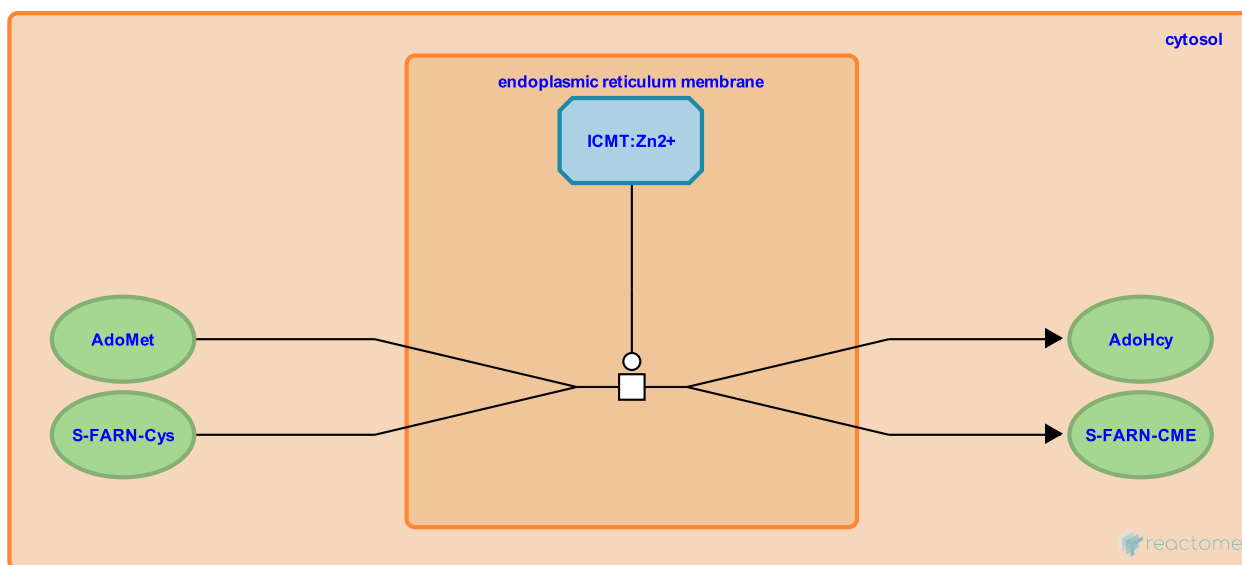
Location: [Gamma carboxylation, hypusine formation and arylsulfatase activation](#)

Stable identifier: R-DRE-6788650

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: [ICMT:Zn²⁺ transfers CH₃ from AdoMet to isoprenylated proteins \(Homo sapiens\)](#)



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>

FN3K phosphorylates ketosamines ↗

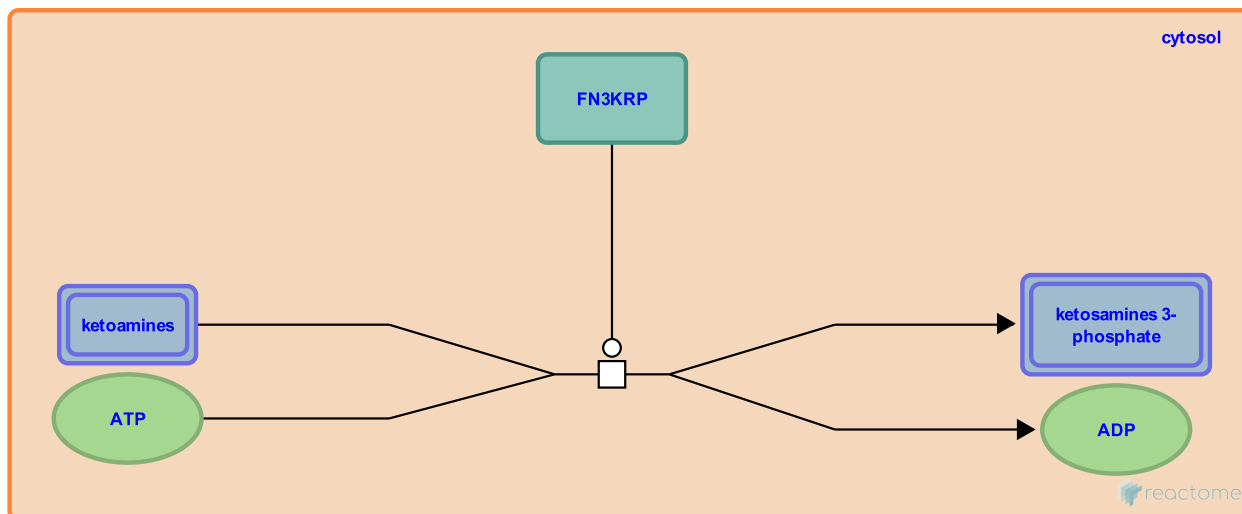
Location: [Gamma carboxylation, hypusine formation and arylsulfatase activation](#)

Stable identifier: R-DRE-6788867

Type: transition

Compartments: cytosol

Inferred from: [FN3K phosphorylates ketosamines \(Homo sapiens\)](#)



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>

FN3KRP phosphorylates PsiAm, RibAm ↗

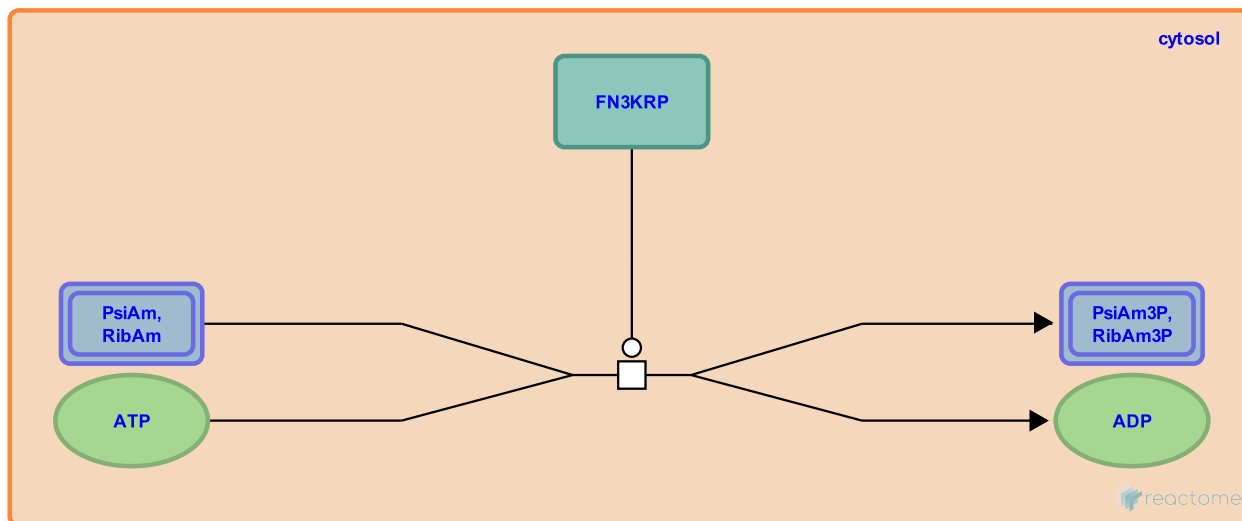
Location: [Gamma carboxylation, hypusine formation and arylsulfatase activation](#)

Stable identifier: R-DRE-6788855

Type: transition

Compartments: cytosol

Inferred from: [FN3KRP phosphorylates PsiAm, RibAm \(Homo sapiens\)](#)



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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