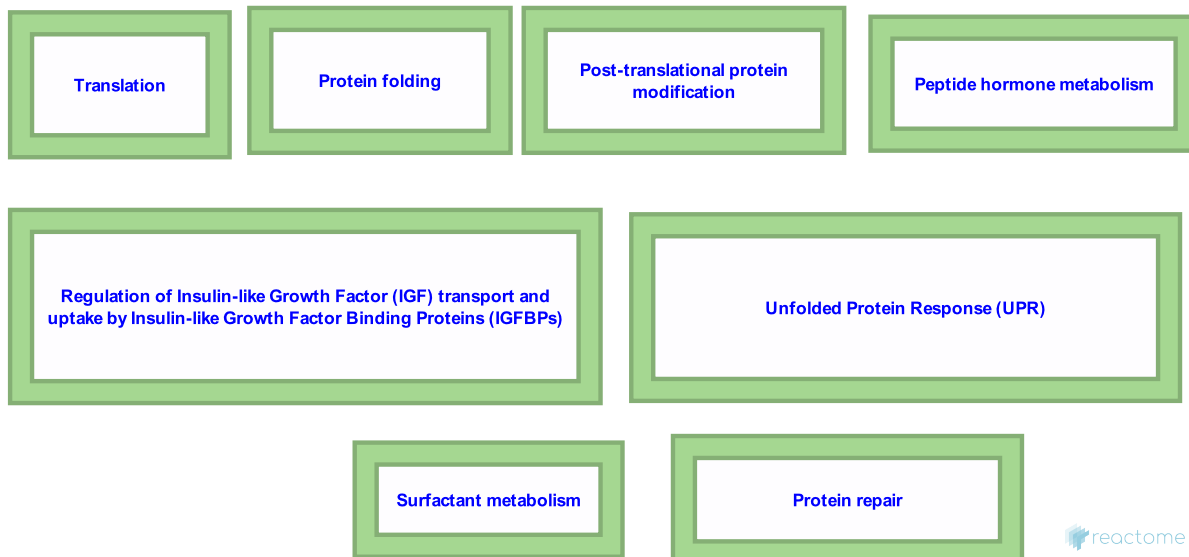


Metabolism of proteins



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.

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. [↗](#)
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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. [↗](#)

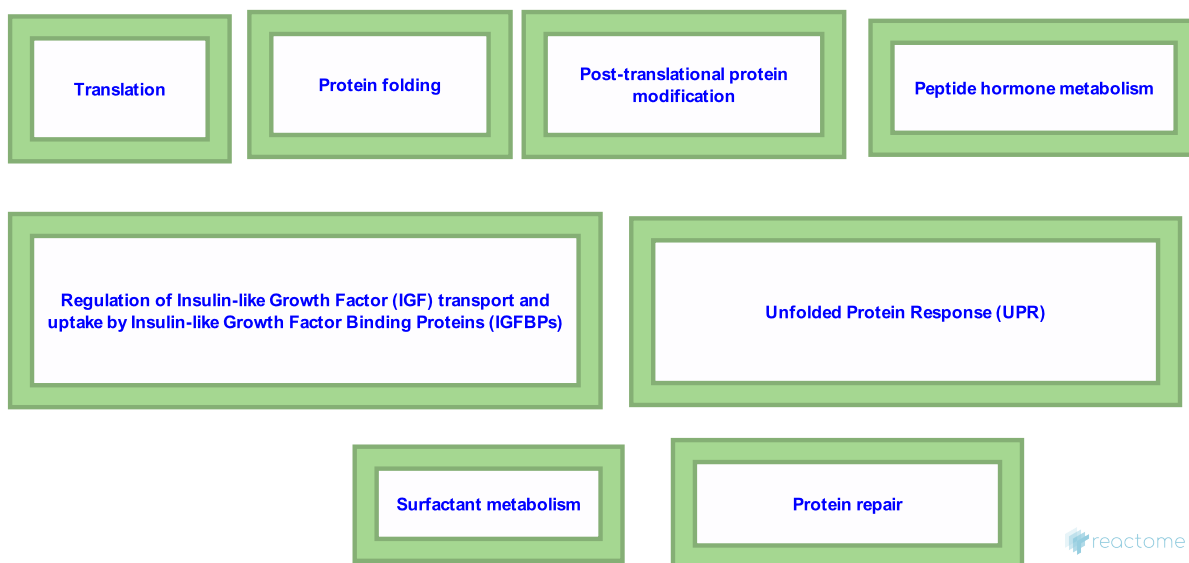
Reactome database release: 74

This document contains 9 pathways ([see Table of Contents](#))

Metabolism of proteins ↗

Stable identifier: R-CFA-392499

Inferred from: [Metabolism 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.

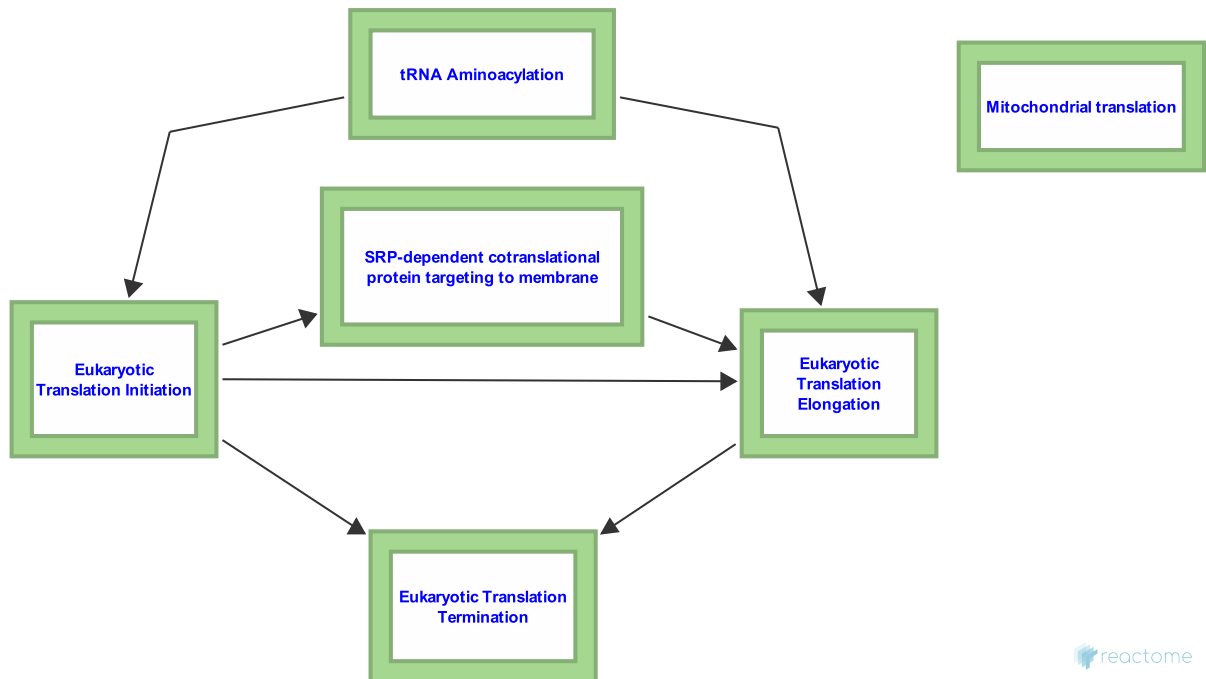
[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Translation ↗

Location: Metabolism of proteins

Stable identifier: R-CFA-72766

Inferred from: Translation (Homo sapiens)



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

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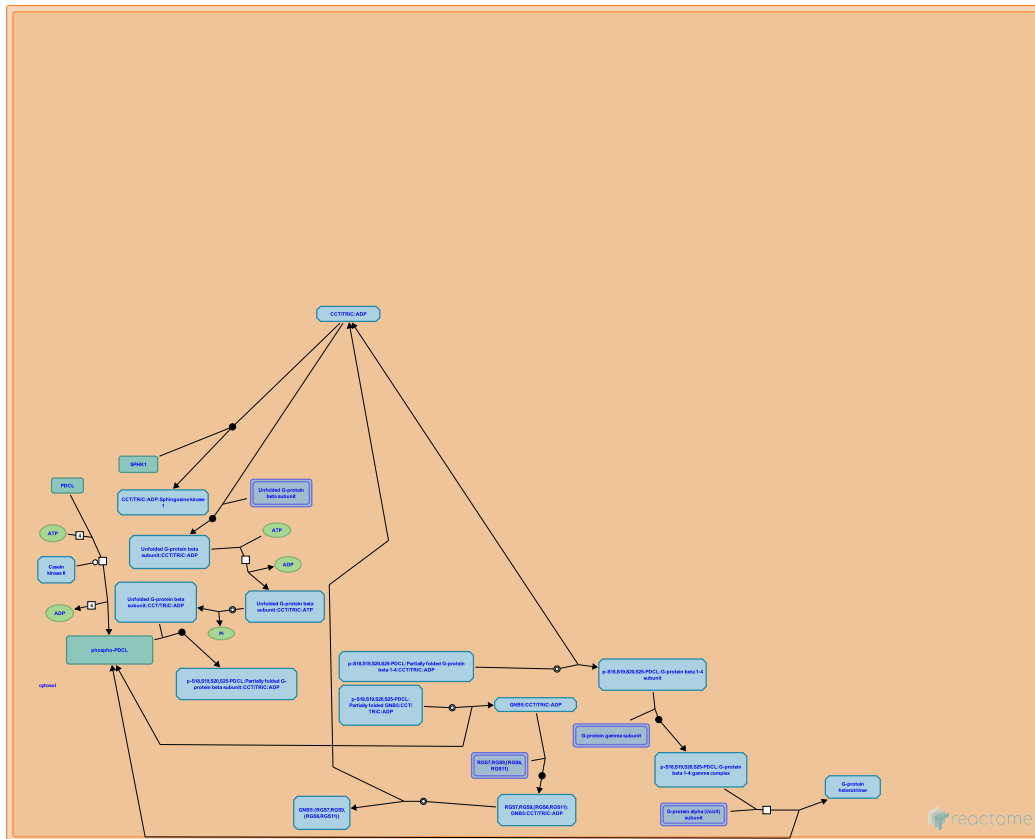
Protein folding ↗

Location: Metabolism of proteins

Stable identifier: R-CFA-391251

Compartments: cytosol

Inferred from: Protein folding (Homo sapiens)



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

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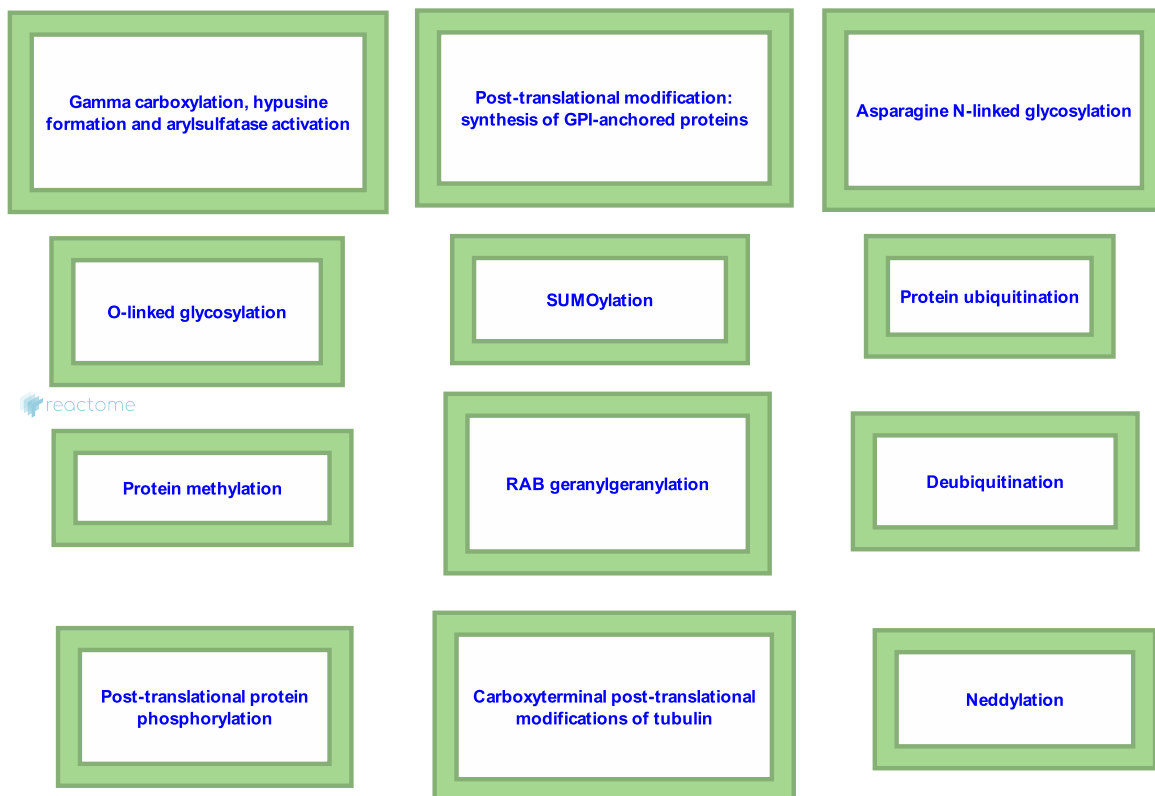
[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Post-translational protein modification ↗

Location: [Metabolism of proteins](#)

Stable identifier: R-CFA-597592

Inferred from: [Post-translational protein modification \(Homo sapiens\)](#)



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

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Peptide hormone metabolism ↗

Location: [Metabolism of proteins](#)

Stable identifier: R-CFA-2980736

Compartments: COPII-coated ER to Golgi transport vesicle, Golgi lumen, cytosol, endoplasmic reticulum lumen, endoplasmic reticulum membrane, extracellular region, nucleoplasm, plasma membrane, secretory granule lumen, secretory granule membrane

Inferred from: [Peptide hormone metabolism \(Homo sapiens\)](#)



 reactome

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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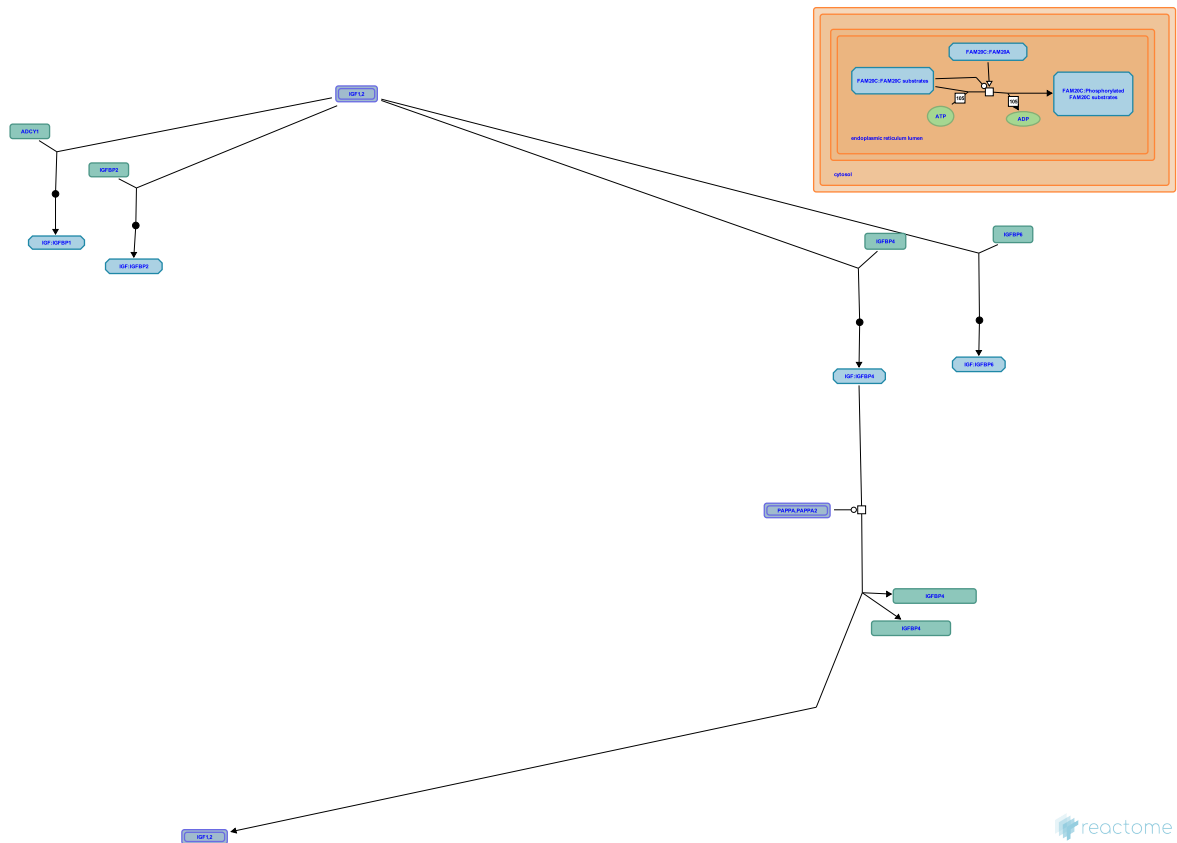
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) ↗

Location: [Metabolism of proteins](#)

Stable identifier: R-CFA-381426

Compartments: extracellular region

Inferred from: [Regulation of Insulin-like Growth Factor \(IGF\) transport and uptake by Insulin-like Growth Factor Binding Proteins \(IGFBPs\)](#) (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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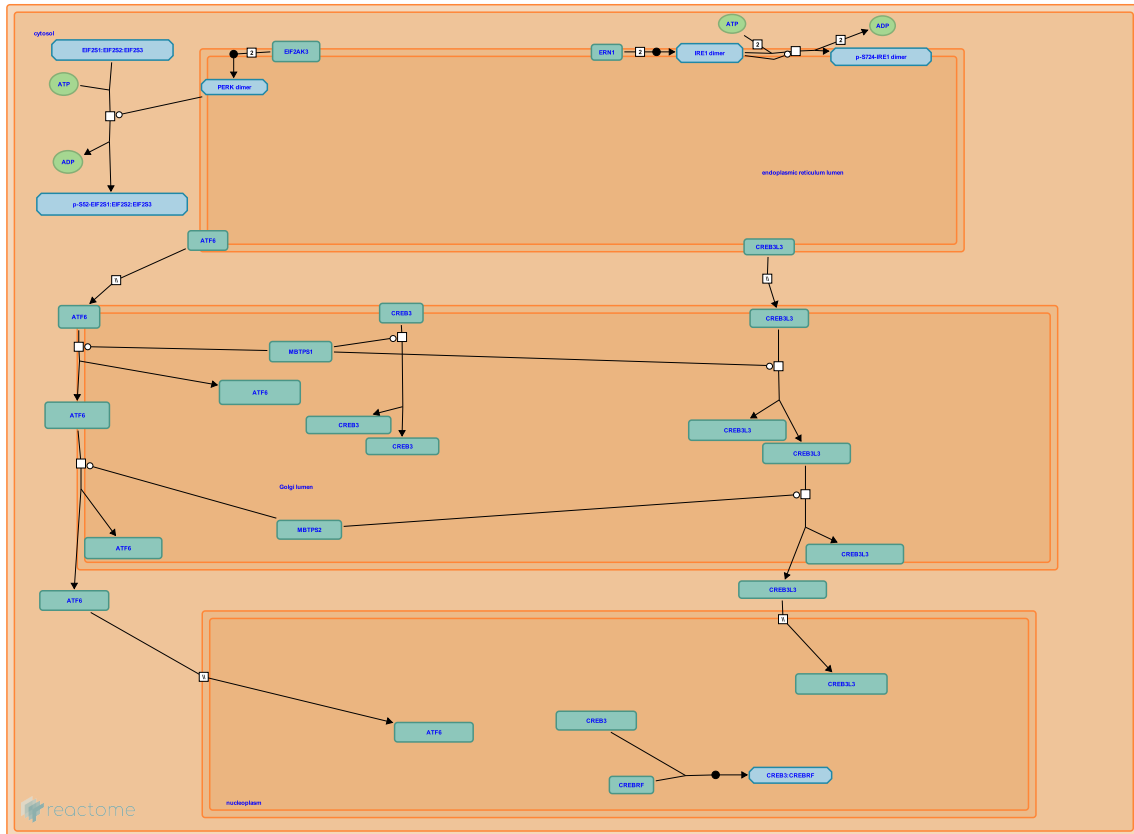
Unfolded Protein Response (UPR) ↗

Location: Metabolism of proteins

Stable identifier: R-CFA-381119

Compartments: Golgi membrane, cytosol, endoplasmic reticulum lumen, endoplasmic reticulum membrane, nucleoplasm

Inferred from: Unfolded Protein Response (UPR) (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.

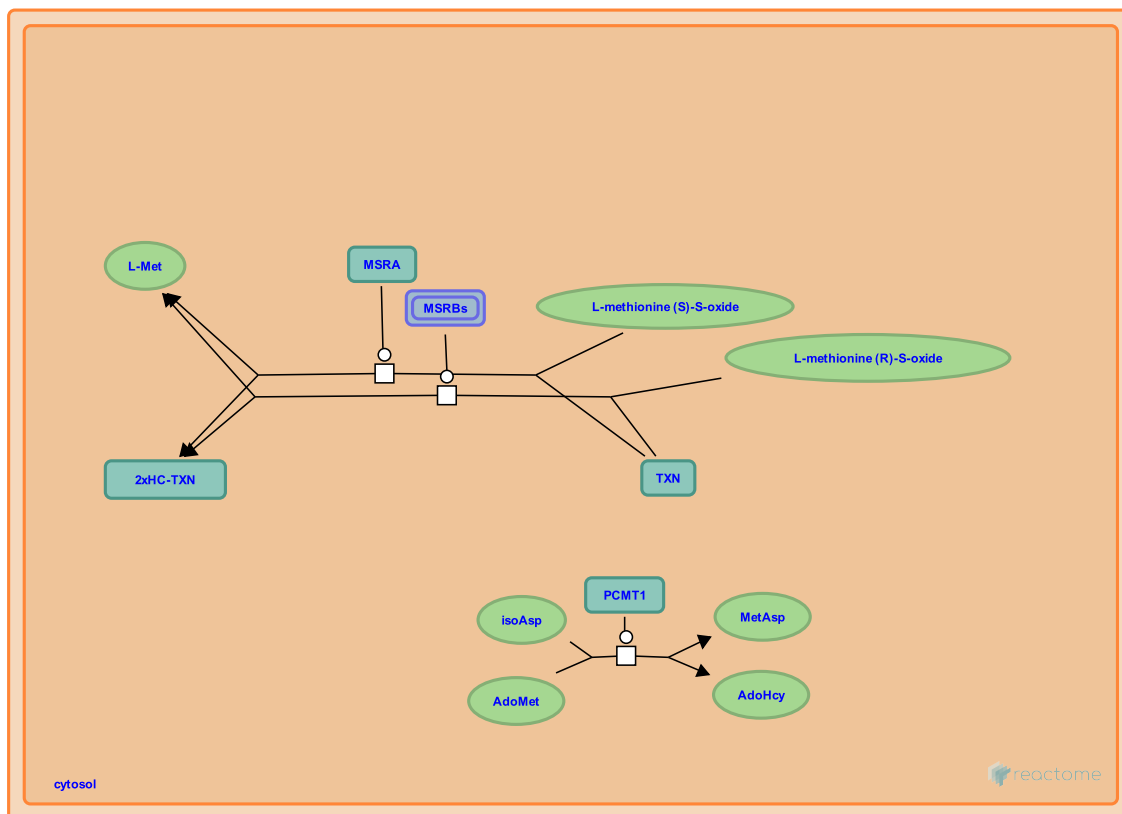
[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Protein repair ↗

Location: Metabolism of proteins

Stable identifier: R-CFA-5676934

Inferred from: Protein repair (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.

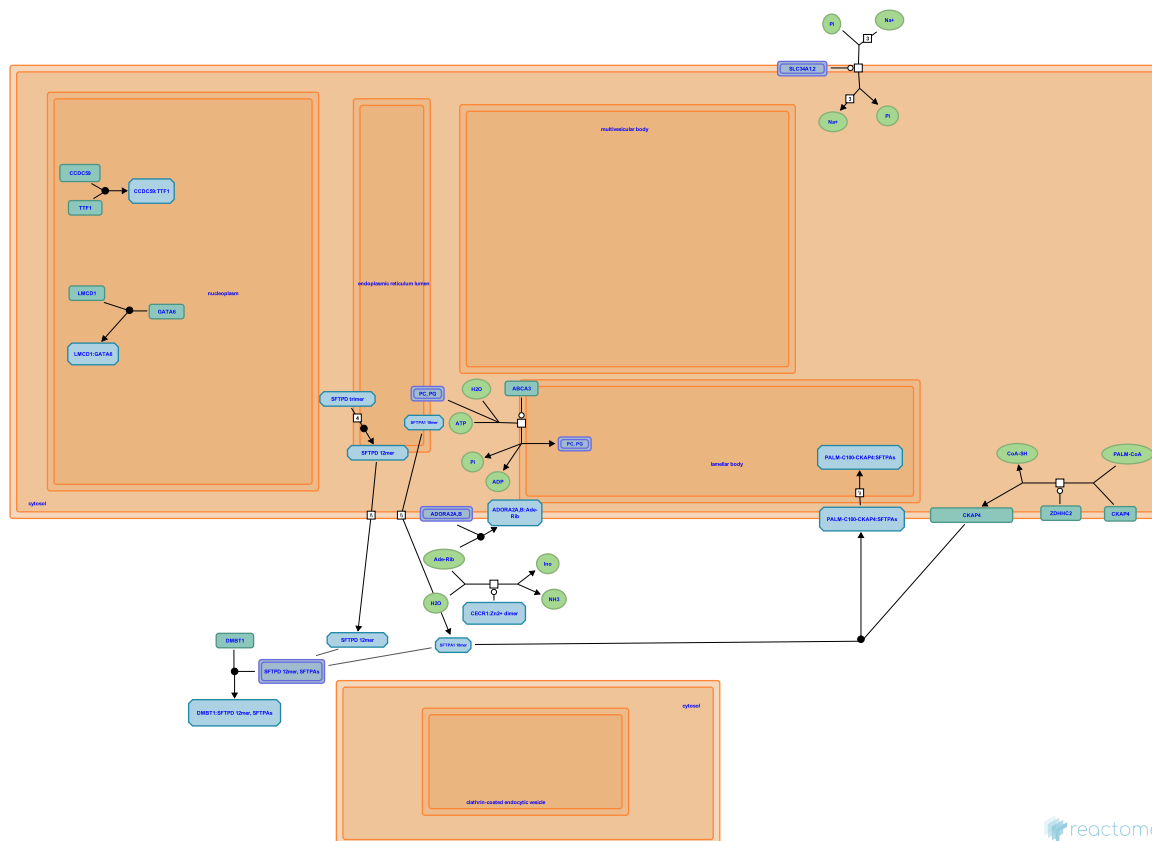
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Surfactant metabolism ↗

Location: Metabolism of proteins

Stable identifier: R-CFA-5683826

Inferred from: Surfactant metabolism (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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