Eukaryotic Translation Termination

Bedwell, DM., D'Eustachio, P., Gillespie, ME., Jassal, B.
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


Reactome database release: 82

This document contains 1 pathway and 5 reactions (see Table of Contents)
The arrival of any of the three stop codons (UAA, UAG and UGA) into the ribosomal A-site triggers the binding of a release factor (RF) to the ribosome and subsequent polypeptide chain release. In eukaryotes, the RF is composed of two proteins, eRF1 and eRF3. eRF1 is responsible for the hydrolysis of the peptidyl-tRNA, while eRF3 provides a GTP-dependent function. The ribosome releases the mRNA and dissociates into its two complex subunits, which can reassemble on another molecule to begin a new round of protein synthesis. It should be noted that at present, there is no factor identified in eukaryotes that would be the functional equivalent of the bacterial ribosome release (or recycling) factor, RRF, that catalyzes dissociation of the ribosome from the mRNA following release of the polypeptide.

**Literature references**


**Editions**

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<td>2022-08-23</td>
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N6AMT1:TRMT112 transfers CH3 group from AdoMet to ETF1 dimer

**Location:** Eukaryotic Translation Termination

**Stable identifier:** R-HSA-6800138

**Type:** transition

**Compartments:** cytosol

Class 1 release factors such as eukaryotic peptide chain release factor subunit 1 (ETF1) direct the termination of peptide translation in response to the termination codons UAA, UAG and UGA. ETF1 needs to be complexed with ERF3 in its GTP-bound form to be efficiently post-translationally methylated. HemK methyltransferase family member 2 (N6AMT1) is a heterodimeric methyltransferase that catalyses N5-methylation of ETF1 on glutamine 185 (Q185), using S-adenosyl L-methionine (AdoMet) as the methyl donor (Figaro et al. 2008). N6AMT1 forms a complex with multifunctional methyltransferase subunit TRM112-like protein (TRMT112)

**Followed by:** GTP bound eRF3:eRF1 complex binds the peptidyl tRNA:mRNA:80S Ribosome complex

**Literature references**


**Editions**

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<td>2016-01-11</td>
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https://reactome.org
GTP bound eRF3:eRF1 complex binds the peptidyl tRNA:mRNA:80S Ribosome complex

Location: Eukaryotic Translation Termination

Stable identifier: R-HSA-141691

Type: binding

Compartments: cytosol

Inferred from: GTP bound eRF3:eRF1 complex binds the peptidyl-tRNA:mRNA:Ribosome complex (Saccharomyces cerevisiae)

Please note that this reaction was inferred from experiments performed using Saccharomyces cerevisiae.

Preceded by: N6AMT1:TRMT112 transfers CH3 group from AdoMet to ETF1 dimer

Followed by: GTP Hydrolysis by eRF3 bound to the eRF1:mRNA:polypeptide:80S Ribosome complex

Literature references


Editions

2005-01-27 Authored Gillespie, ME.
GTP Hydrolysis by eRF3 bound to the eRF1:mRNA:polypeptide:80S Ribosome complex

**Location:** Eukaryotic Translation Termination

**Stable identifier:** R-HSA-141673

**Type:** transition

**Compartments:** cytosol

**Inferred from:** GTP Hydrolysis by eRF3 bound to the eRF1:mRNA:polypeptide:80S Ribosome complex (Saccharomyces cerevisiae)

Please note that this reaction was inferred from experiments performed using Saccharomyces cerevisiae.

**Preceded by:** GTP bound eRF3:eRF1 complex binds the peptidyl tRNA:mRNA:80S Ribosome complex

**Followed by:** Polypeptide release from the eRF3-GDP:eRF1:mRNA:80S Ribosome complex

**Literature references**


**Editions**

2005-01-27 Authored Gillespie, ME.
Polypeptide release from the eRF3-GDP:eRF1:mRNA:80S Ribosome complex

**Location:** Eukaryotic Translation Termination

**Stable identifier:** R-HSA-141671

**Type:** dissociation

**Compartments:** cytosol

**Inferred from:** Polypeptide release from the eRF3-GDP:eRF1:mRNA:80S Ribosome complex (Saccharomyces cerevisiae)

Please note that this reaction was inferred from experiments performed using Saccharomyces cerevisiae.

**Preceded by:** GTP Hydrolysis by eRF3 bound to the eRF1:mRNA:polypeptide:80S Ribosome complex

**Followed by:** APEH hydrolyses NAc-Ser-protein

**Literature references**


**Editions**

2005-01-27 Authored Gillespie, ME.
Protein acetylation, which can occur during or after polypeptide chain biosynthesis, helps protect the intracellular proteins from proteolysis. Acylamino-acid-releasing enzyme (APEH) is a cytosolic enzyme able to catalyse the preferential hydrolysis of terminal acetylated amino acids from small acetylated peptides. APEH prefers substrates with acetylated methionine, alanine and serine residues. Hydrolysis produces an acetylated amino acid and a N-terminus protein (Jones et al. 1991). APEH expression is reduced in renal cell carcinoma therefore may represent a tumor suppressor gene, whose loss contributes to the development of renal cell carcinoma (Erlandsson et al. 1991). The hydrolysis of an acetylated serine residue (NAc-Ser-protein) is shown here.

**Preceded by:** Polypeptide release from the eRF3-GDP:eRF1:mRNA:80S Ribosome complex

**Literature references**


**Editions**

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