Eukaryotic Translation Elongation

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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.

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Introduction

Reactome is an 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 2 pathways and 4 reactions (see Table of Contents)
Eukaryotic Translation Elongation

Stable identifier: R-HSA-156842

Compartments: cytosol

The translation elongation cycle adds one amino acid at a time to a growing polypeptide according to the sequence of codons found in the mRNA. The next available codon on the mRNA is exposed in the aminoacyl-tRNA (aa-tRNA) binding site (A site) on the 30S subunit.

A: Ternary complexes of aa-tRNA:eEF1A:GTP enter the ribosome and enable the anticodon of the tRNA to make a codon/anticodon interaction with the A-site codon of the mRNA. B: Upon cognate recognition, the eEF1A:GTP is brought into the GTPase activating center of the ribosome, GTP is hydrolyzed and eEF1A:GDP leaves the ribosome. C: The peptidyl transferase center of ribosome catalyses the formation of a peptide bond between the incoming amino acid and the peptide found in the peptidyl-tRNA binding site (P site). D: In the pre-translocation state of the ribosome, the eEF2:GTP enters the ribosome, physically translocating the peptidyl-tRNA out of the A site to P site and leaves the ribosome eEF2:GDP. This action of eEF2:GTP accounts for the precise movement of the mRNA by 3 nucleotides. Consequently, deacylated tRNA is shifted to the E site. A ribosome associated ATPase activity is proposed to stimulate the release of deacylated tRNA from the E site subsequent to translocation (Elskaya et al., 1991). In this post-translocation state, the ribosome is now ready to receive a new ternary complex.

This process is illustrated below with: an amino acyl-tRNA with an amino acid, a peptidyl-tRNA with a growing peptide, a deacylated tRNA with an -OH, and a ribosome with A,P and E sites to accommodate these three forms of tRNA.

Literature references
eEF1A complexes with GTP

**Location:** Eukaryotic Translation Elongation

**Stable identifier:** R-HSA-156909

**Type:** transition

**Compartments:** cytosol

**Inferred from:** reEF1A complexes with GTP (Oryctolagus cuniculus)

The cycle of elongation starts with an empty ribosomal A-site and the peptidyl-tRNA in the P-site. eEF1A is activated by GTP binding and allows for the subsequent binding of aminoacyl-tRNA (aa-tRNA). This process is illustrated below with a GTP molecule in white and eEF1A protein in yellow.

**Followed by:** eEF1A:GTP:aminoacyl tRNA ternary complex formation.

**Editions**

2005-03-12 Authored Gopinathrao, G.
The binding of eEF1A:GTP to aminoacyl tRNA (aa-tRNA) results in the formation of a ternary complex (eEF1A:GTP:aa-tRNA). Human eEF1A and rabbit eEF1A are 100% identical, and prokaryotic homologue of eEF1A (EF-Tu) shows 59% identity in the GTP-binding domain. This process is illustrated below with: a GTP molecule in white and eEF1A protein in yellow.

**Preceded by:** eEF1A complexes with GTP, Regeneration of eEF1A:GTP by eEF1B activity

**Editions**

2005-03-12  Authored  Gopinathrao, G.
The mechanism of a peptide bond requires the movement of three protons. First the deprotonation of the ammonium ion generates a reactive amine, allowing a nucleophilic attack on the carbonyl group. This is followed by the loss of a proton from the reaction intermediate, only to be taken up by the oxygen on the leaving group (from the end of the amino acid chain bound to the tRNA in the P-site). The peptide bond formation results in the net loss of one water molecule, leaving a deacylated-tRNA in the P-site, and a nascent polypeptide chain one amino acid larger in the A-site.

For the purpose of illustration, the figures used in the section show one amino acid being added to a peptidyl-tRNA with a growing peptide chain.

**Literature references**


**Editions**

2005-03-13

Authorized

Gopinathrao, G.
The eEF1B complex binds to eEF1A and regulates its activity by catalyzing the release of GDP. Subsequently, GTP is able to bind eEF1A allowing the formation of the ternary complex (eEF1A-GTP-aa-tRNA). In metazoans eEF1 protein family is composed of four subunits: eEF1A and eEF1B alpha, beta, and gamma (formerly EF-1alpha, EF-1beta, EF-1delta, and EF-1gamma, respectively). Both eEF1B alpha and eEF1B beta function as nucleotide exchange proteins. eEF1B gamma associates with eEF1B alpha and stimulates its exchange activity.

This process is illustrated below with a GTP molecule in white and eEF1A protein in yellow. The three subunits of eEF1B are also shown.

**Preceded by:** Formation of eEF1B complex

**Followed by:** eEF1A:GTP:aminoacyl tRNA ternary complex formation.

**Literature references**

Formation of eEF1B complex

Location: Eukaryotic Translation Elongation

Stable identifier: R-HSA-156910

Type: binding

Compartments: cytosol

At the beginning of this reaction, 1 molecule of 'eEF1B alpha', 1 molecule of 'eEF1B gamma', and 1 molecule of 'eEF1B beta' are present. At the end of this reaction, 1 molecule of 'eEF1B complex' is present.

This reaction takes place in the 'cytosol' (Veremieva et al. 2011).

Followed by: Regeneration of eEF1A:GTP by eEF1B activity

Literature references

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