mRNA3 is translated to protein 3a

Acencio, ML., D'Eustachio, P., Mazein, A., Stephan, R.

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


Reactome database release: 77

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There is a mixed population of mRNA3 clones having six, seven, eight and nine T stretches located 14 nt downstream of the initiation codon that occur in vivo. The transcribed Us practically act as slippery sequences in heterogenous ORFs. Translation efficiency is reduced in slipping clones, however (Thiel et al, 2003; Tan et al, 2005; Wang et al, 2006).

**Literature references**


**Editions**

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