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The eukaryotic translation initiation relies not only on the cap-dependent mechanism of mRNA binding to the ribosome, but also on poorly studied cap-independent ways of recruiting mRNAs to ribosomes.

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The corresponding structural elements are called cap-independent translation enhancers (CITEs). By recruiting initiation factors, CITEs promote cap-independent initiation from the 5' end of mRNA. We discuss in this review that this mechanism is also employed in animal cells.

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cap-independent translation of cellular mRNAs is the use of internal ribosome entry sites (IRESs). However, some of the cap-independent mechanisms cannot be explained with the IRES concept. This review proposes an alternative mechanism for cap-independent initiation. It is based on the presence (in the UTRs of mRNAs) structural elements that bind the factors recruiting mRNAs to the ribosome cap.

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Eukaryotic translation initiation relies on the m7G cap present at the 5' end of all mRNAs. Some viral mRNAs employ alternative mechanisms of initiation based on internal ribosome entry. The IRES

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element (CITE or 3'CITE) is an RNA sequence found in the 3'UTR of many RNA plant viruses. Eukaryotic mRNAs contain a 5' cap structure which is required for efficient binding of translation initiation factors.

Cap-dependent and cap-independent translation in ...

1. IntroductionThe purpose of this article is to re-affirm that eukaryotic cells perform both cap-dependent and cap-independent (IRES-mediated) protein synthesis, in spite of several recent articles that would appear to question whether cap-independent translation really occurs in eukaryotic cells Kozak, 2001a, Kozak, 2003.

Cap-Dependent and Cap-Independent Translation: Operational ...

Pause A, Methot N, Svitkin Y, Merrick WC, Sonenberg (1994) Dominant negative mutants of mammalian translation initiation factor eIF-4A define a critical role for eIF-4F in cap-dependent and cap-independent initiation of translation.

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Cap-independent translation by DAP5 controls cell fate ...

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Abstract. Multiple transcriptional and epigenetic changes drive differentiation of embryonic stem cells (ESCs). This study unveils an additional level of gene expression regulation involving noncanonical, cap-independent translation of a select group of mRNAs.

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