Arizona State University

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A Method to Identify Synthetic and Natural RNA Elements that Enhance Protein Translation

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Inventors

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Invention Description

Non-classical translation initiation sites are believed to play an important role in the human genome. Studies of these, however, have been limited by the absence of effective tools for identifying their sequences at the DNA level. There is a pressing need then for new functional tools that can be used to identify and map these sequences in known genomes.

Researchers at Arizona State University have applied a novel *in vitro* selection scheme to survey the entire human genome for RNA elements that are capable of initiating protein translation. This technique may solve many interesting questions about the role of RNA and may reveal many unknown coding regions.

This powerful new technology may be useful in identifying RNA elements that function by a variety of other translation initiation mechanisms. The pursuit of such sequences could lead to a more complete view of the translational landscape of the human genome.

Potential Applications

- Research into identification of RNA elements that function in a variety of unconventional translation mechanisms
- Discovering translation initiation elements in human and other higher order genomes

Benefits and Advantages

- Able to locate sequences of translation initiation elements at the DNA level
- Fewer limitations than computational methods

Intellectual Property Status:

Pending

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