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## PhD exit seminar: Investigating the prevalence of an unusual form of alternative splicing

Thursday 19 December 2013 1 – 2pm

Laurence Wilson Fahrer Lab, BSB

Slatyer seminar room R.N. Robertson Building (Bldg. 46), Linnaeus Way, ANU



Alternative splicing is one of the most significant contributors to proteome diversity. Through the production of multiple mRNA transcripts, a single gene can encode multiple and functionally distinct protein isoforms. My project has focused on investigating the prevalence of an unusual form of alternative splicing. The alternate splicing differs from the canonical gene transcript by deletion of a length of sequence not divisible by three, but where translation can be rescued by an alternative start codon. This results in a predicted protein in which the amino terminus differs markedly in sequence from the known protein product(s), as it is translated from an alternative reading frame. My work has used a computational approach to identify instances of this splicing across several different genomes. In addition to identifying conserved instances, experimental evidence for the translation of these protein isoforms was also provided through the use of a variety of publicly available data.

Presented by

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