

**P013** Expansion of the proteome by use of alternative initiation codons

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The “optimal” sequence context surrounding the eukaryotic translation initiation codon was established a number of years ago as GCC(A/G)CCAUGG, but has since been found to occur in only a small number of mRNAs, with many mRNAs being found that can initiate translation at a non-canonical, i.e. non AUG, initiation codon. Furthermore, the use of differing in-frame initiation codons may be able to direct the translation of several variants of a protein.

Recent large scale bioinformatic studies indicate that the use of non-canonical initiation codons may be far more widespread than previously thought and we have previously identified a CUG initiation codon that extends the ORF of the eukaryotic initiation factor eIF4GII by over 140 amino acids.

This work describes a set of data-mining tools written in the Perl programming language to identify other human mRNAs that may have extended ORFs, which are conserved in other mammalian species. While this screening of mRNAs from the human genome is still very much a work in progress, preliminary work to confirm the presence of N-terminal extensions in interesting candidates will be presented, alongside data examining the possible cell type specificity of the selection of alternative initiation codons.