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Identifying Non-Traditional Slippery Sequences Associated with Translational Frameshifts

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Genetic frameshifts are a mutation in which a nucleotide skip leads to a shift in the reading frame. In viruses, these frameshifts can be programmed using a slippery sequence to bypass the stop codon associated with the initial protein. This allows for variable control of protein expression. In bacteriophages, translational frameshifts have been identified, but only a few slippery sequences have been proven experimentally. Using experimental data and comparative genomics, slippery sequences that differ from the experimentally found procedure can be identified in controlling the protein coding throughout viruses. Identifying more slippery sequences can build the groundwork for automating the search for frameshifts using computer programs. Novel slippery sequences can aid in the understanding of protein expression in biological environments and further the understanding of how viruses utilize the frameshift to their advantage. This advantage can potentially lead the way in controlling the expression of select proteins in pharmaceutical industry.