

A code within the genetic code: codon usage regulates co-translational protein folding

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Video Byte

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Abstract

Of the 20 standard amino acids, 18 can be coded by two to six synonymous codons. The preference for certain synonymous codons over others is a phenomenon known as “codon usage bias,” and it's been found in all genomes examined to date. Growing evidence suggests that codon usage regulates protein structure and gene expression through translation-dependent and translation-independent mechanisms. In fact, codon usage has been discovered to play an important role in controlling the speed of translation elongation during mRNA translation, as well as in regulating protein folding and function in both prokaryotes and eukaryotes. Additionally, studies show that intrinsically disordered domain structures are sensitive to codon usage. These disordered structures play a critical role in many biological processes and are sites for important post-translational modifications. More work is needed to confirm the broad significance of codon usage in protein folding and to determine whether silent mutations are broad contributors to human disease due to the role of codon usage in protein structure and function.