

Summary

A method for optimizing a nucleotide sequence for expression of a predefined amino acid sequence in at least one target organism is disclosed. The nucleotide sequence comprises a plurality of base triplets, wherein in at least one modification position of the nucleotide sequence, a base triplet encoding an amino acid of the predefined amino acid sequence is substituted with a synonymous base triplet encoding the same amino acid of the predefined amino acid sequence to optimize the nucleotide sequence for expression in the at least one target organism. The modification position comprises a direct succession of n base triplets that constitutes a first codon n-tuple and encodes a sequence portion of n amino acids of the predefined amino acid sequence that constitutes an amino acid n-tuple that is encoded with a predetermined number of amino acid n-tuple events in the genome or part thereof of the at least one target organism and/or in genomes or parts thereof of viruses capable of infecting the at least one target organism. At least one of said n base triplets of said direct succession is substituted with a synonymous base triplet being selected such that a second codon n-tuple results that, in relation to said number of amino acid n-tuple events, has a higher relative codon n-tuple frequency in the genome or part thereof of the at least one target organism and/or in the genomes or parts thereof of the viruses capable of infecting the at least one target organism than the first codon n-tuple.

Significant figure: 1