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(54) Title: METHOD FOR IDENTIFYING PROTEINS WITH N-TERMINAL N-MYRISTOYLATION

(57) Abstract: Two-step procedure for determining possible N-terminal N-myristoylation of proteins from their amino acid sequence. In the first step, a novel computerized algorithm deriving a decision calculated from the N-terminal segment off the amino acid sequence is applied to determine probable substrate proteins. The reduced list of targets may be subjected to experimental verification in a second step. The score function used in the decision does not only evaluate amino acid type preferences on single positions, but penalizes also deviations from the physico-chemical requirements for several positions that either show a general trend of deviation from the average properties of known myristoylated proteins or have been tested for compensatory effects. For risk evaluation, the scores are translated into probabilities of false positive prediction.