

Abstract

Prediction of the Potential of Food Proteins as Sources of Biopeptides Using BIOPEP-UWM Database [†]

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Abstract: Peptides derived from food proteins exhibit a variety of bioactivities, such as the inhibition of angiotensin converting enzyme (ACE; EC 3.4.15.1), dipeptidyl peptidase IV (DPP4; EC 3.4.14.5), α -glucosidase (EC 3.2.1.20), α -amylase (EC 3.2.1.1), etc., as well as antioxidative, immunomodulating, and antithrombotic functions, etc. The above-mentioned inhibitory functions of peptides are related to the regulation of blood pressure level (ACE inhibitors) and blood glucose concentration (DPP IV, α -glucosidase, α -amylase inhibitors). Thus, bioactive peptides are considered as food components that play an important role in the prevention of, e.g., hypertension, type 2 diabetes, and/or metabolic syndrome. Progress in the development of computer technologies has contributed to the elaboration of tools that are useful in the theoretical prediction of the properties of food components. Such methodologies are called *in silico* analyses and have become one of the three approaches applied in the study of proteins and peptides. *In silico* analyses are less costly and time-consuming when compared to classical approaches relying on the involvement of laboratory procedures to produce peptides from food. Thus, the aim of this study is to present the options available in the BIOPEP-UWM[®] database of proteins and bioactive peptide sequences that can be useful in the evaluation of proteins as sources of bioactive peptides. Such options can be exemplified on any protein sequence available in the BIOPEP-UWM database. They include the elaboration of the profile of the potential biological activity of a protein, the frequency of the occurrence of peptides with a given activity within a protein, and the prediction of the enzymatic release of biopeptides from a protein using qualitative and quantitative criteria. Moreover, the search options of this database, as well as new updates, will be presented.



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