

New analysis path of protein
Case: Calcium-binding proteins

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Calcium-binding proteins biomarker pro and anti-stress, are characterized by a conserved calcium binding motif known as an EF hand, but the difference of sequences is the peculiarity of each protein type causes so a variety of physicochemical characteristics. This is clearly visible in the mobility at migration in native gels (PAGE) observed in similar polypeptides (in length) with and without Calcium (J. Viviano et al, 2016).

Our in-silico analysis of protein sequences combined at the mobility in native gels or other technique as TOF in MALDI/LCMS, based on the principle of proximity.We have considered the protein sequences as a biological language similar to that of natural language. By matrix calculations, we obtained values of AA according the words formed in this sequence. This allows us to analyze the protein sequences via graphical presentations in 2D/3D, as EF hand.

The first results we indicate a new pathway for quality analysis of protein sequences plus the apparent molecular weight by native gels and by TOF in MALDI/ LCMS, for the best prediction the profile both structure and function of proteins.

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