Portfolio de Inovação

Computational methodology for protein interaction analysis

Problema

X-ray crystallography and nuclear magnetic resonance are two of the techniques recommended and used to characterize protein structures and complexes in studies. However, a significant portion of the proteins cannot be analyzed by such methods. Currently, there is a limitation of methodologies that allow the analysis of protein-protein interaction on a large scale. Mapping the epitope interaction region, i.e., the area of the antigen molecule that binds to cell receptors and antibodies, is a challenging task, and drug development depends on this mapping.

Solução

The technology proposes a method that, when applied to protein mixtures and subsequent analysis by the mass spectrometry technique, allows the characterization of protein complexes, epitope mapping, and protein-protein interaction on a large scale. Interaction identifications are performed using software developed by our team. In this way, the solution functions as an alternative to conventional methods of structural biology analysis.

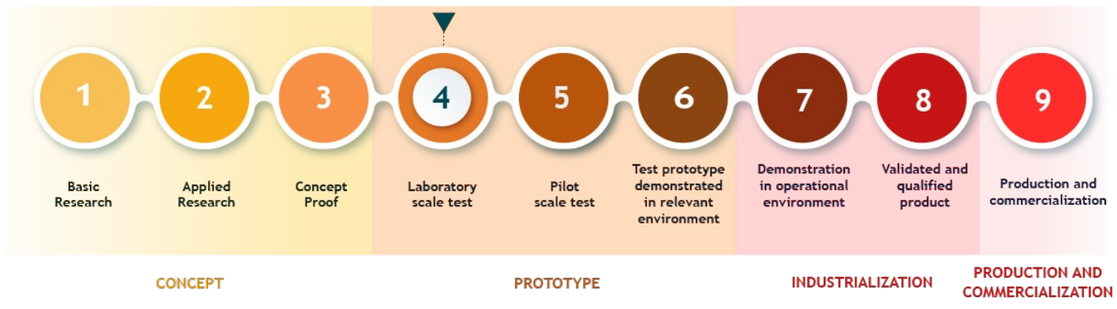
Diferencial

Study of High-Complexity Interaction

Effective and Fast Data Processing

Quantitative Analysis of Interactions

Estágio de Desenvolvimento



O que buscamos?

Commercialization of the methodologies together with the software.

WANT MORE INFORMATION? CONTACT US!

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