

Patent Trends in Protein Folding Domain †

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Abstract: Protein folding determines the function of a protein. For the past fifty years, protein structures have been investigated by their amino acid sequences. Since 1994, biennial competition (a global experiment) for protein structure prediction has been CASP (Critical Assessment of protein Structure Prediction). In December 2018, CASP13 won by DeepMind's AlphaFold, which is later on improvised to CASP14 in the year 2020, gained the limelight to predict the protein structure more accurately. To comprehend the patent landscape of protein folding, the present study was conducted on the patents filed in this domain. The data was collected from USPTO, Espacenet, and various patent office databases for the patents filed in the last five years to identify the active technologies used. As a result, various machine learning algorithms, deep learning programming, and neural network approaches were used predominantly in solving protein folding puzzles.

Keywords: protein folding; protein structure; machine learning; neural networks; patent analytics.

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Conflicts of Interest

The authors declare no conflict of interest.