A template for the arxiv style

A Preprint

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Proteins are involved in several biological reactions by means of interactions with other proteins or with other molecules such as nucleic acids, carbohydrates, and ligands. Among these interaction types, protein–protein interactions (PPIs) are considered to be one of the key factors as they are involved in most of the cellular processes.
In this work we aim to compile a novel benchmark of PPIs with known binding affinity values from refined data and benchmark the resulting deep learning geometry method against existing state-of-the-art approaches.