Title: Protein-ATP Binding Residue Prediction Using Multi-View Learning & Co-Attention Networks

1. Introduction ATP-binding proteins play essential roles in cellular metabolism, signaling, and energy transfer. Identifying ATP-binding residues is crucial for protein function annotation, drug discovery, and enzyme engineering. Traditional sequence-based and structural prediction methods often fail to capture the complex contextual dependencies between residues. To address this, we propose a novel **multi-view feature learning** approach utilizing a **contextual-based co-attention network** to enhance ATP-binding residue prediction accuracy.

2. Research Objectives

1. Develop a **deep learning model** integrating sequence, structural, and evolutionary features.
2. Develop a **multi-view feature learning** model that integrates sequence, structural, and evolutionary features.
3. Implement a **contextual-based co-attention network** for improved residue representation.
4. Utilize deep learning techniques to capture residue-level interactions.
5. Benchmark the model against existing state-of-the-art ATP-binding residue prediction methods.