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Ke ord : Proteins; Protein structure; Protein function; X-ray crystallography; Nuclear magnetic resonance; Cryo-electron microscopy

of a protein's active site can be pinpointed, providing a roadmap for understanding its catalytic function [5].

S b ra e binding and peci ci : By observing how substrates or ligands interact with a protein's structure, researchers can uncover the molecular basis of binding speci city and a nity.

Mechani m el cida ion: Structural snapshots of proteins in action allow researchers to propose detailed mechanisms for biochemical processes. For instance, the structure of the ribosome, the cellular machinery that synthesizes proteins, has provided critical insights into translation.

Dr g de ign: Knowledge of a protein's structure can guide the design of small molecules that target speci c sites, inhibiting or enhancing protein function. is underpins the eld of structure-based drug design [6].

Challenge and f re direc ion

While signi cant progress has been made in protein structure/function analysis, challenges remain. Some proteins are notoriously di cult to crystallize, and certain protein complexes are dynamic and transient, making their structural determination complex. Furthermore, computational methods for predicting protein structures are still improving [7, 8]. e future of this eld is exciting. As cryo-EM technology advances, we can expect even more high-resolution structures of intricate protein complexes. Integrating structural data with functional assays and computational simulations will provide a comprehensive understanding of protein behavior in complex cellular environments.

Di c ion

Unveiling the three-dimensional structure of proteins has been