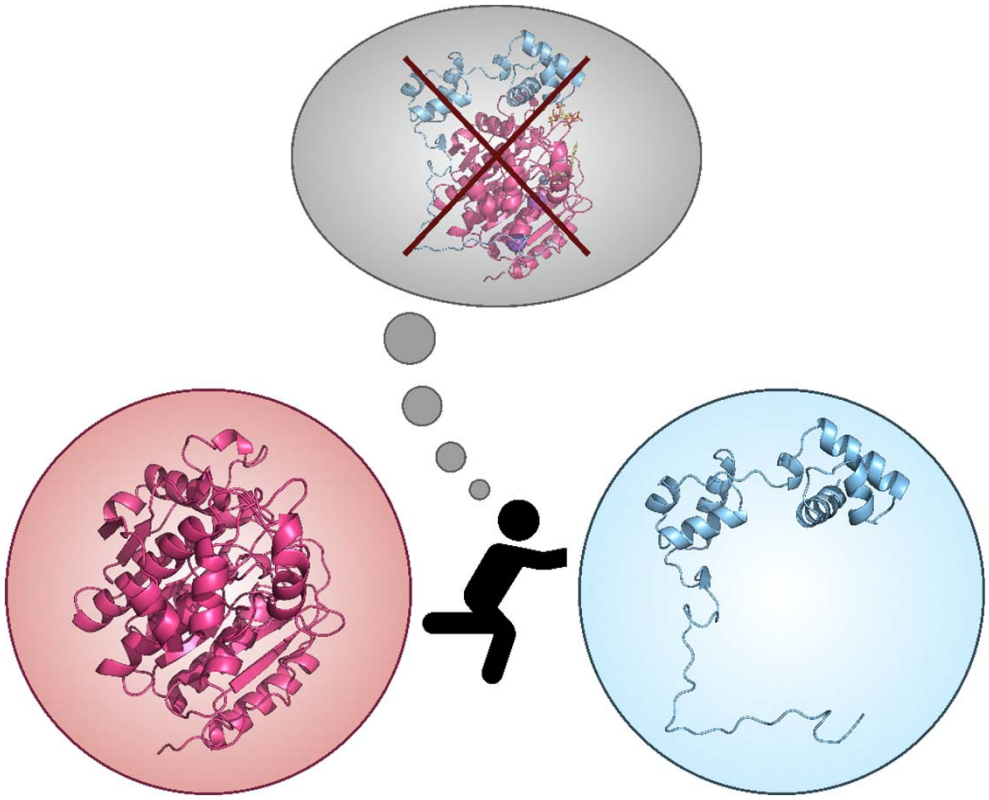
# Yu-Lin Ho

## Modulating protein-protein interactions to inhibit HDAC function selectively



HDAC inhibitors have been approved for certain cancer types and are being tested for other diseases. However, reaching selectivity for different HDAC isoforms is challenging due to the similarity of their binding sites. This project aims to find new HDAC inhibitors that modulate protein-protein interactions involving HDACs, using computational and experimental methods focusing on the CoREST HDAC complex. Computational methods will include homology modeling for generating desired protein complex models and molecular dynamics simulations, which will subsequently be used for identifying hotspot residues via MM-PBSA (Molecular Mechanics Poisson-Boltzmann Surface Area) calculations. Potential modulators of HDAC activity will then be determined with virtual screening methods. The identified potential modulators will be validated using HDAC1/2 activity assay and cytotoxicity assay to confirm their activity and specificity. Other multi-protein complexes involving HDACs, including NuRD and SIN3, will be studied as well to find targets to modulate different HDACs selectively. This research will contribute to the development of new HDAC inhibitors with improved selectivity and potency, which can lead to the discovery of new treatments for various diseases.

**Yu-Lin Ho is working in the Institute of Pharmaceutical Medicinal Chemistry (Group of H. Gohlke).**

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