

# Dynamic Affinity Prediction: Extending PRODIGY Methods to Molecular Dynamics Simulations

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The PRODIGY suite (PRODIGY, PRODIGY-LIG, PRODIGY-CRYSTAL) provides fast and accurate tools for predicting protein–protein and protein–ligand binding affinities, as well as classifying biological vs. crystallographic interfaces, based solely on structural features such as interfacial contacts and surface properties. These tools have been validated on high-quality experimental structures from the PDB and show strong performance even in the presence of moderate conformational changes.

However, current implementations rely on single static snapshots (e.g., X-ray or modeled structures), which do not capture the dynamic nature of biomolecular interactions. In reality, proteins and ligands sample multiple conformations during binding, and key interactions may only be transiently formed. Molecular Dynamics (MD) simulations offer a way to explore this conformational landscape, revealing time-dependent behavior of interfaces that is invisible in static structures.

This project aims to bridge the gap between static structure-based prediction and dynamic simulation data by adapting the PRODIGY methods to analyze ensembles of frames extracted from MD trajectories. The goal is to assess whether time-averaged or representative-contact-based reimplementations of PRODIGY's scoring functions improve the reliability and biological relevance of affinity and interface classification predictions of *toxin-toxin receptor* complexes.

## Bibliography :

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