

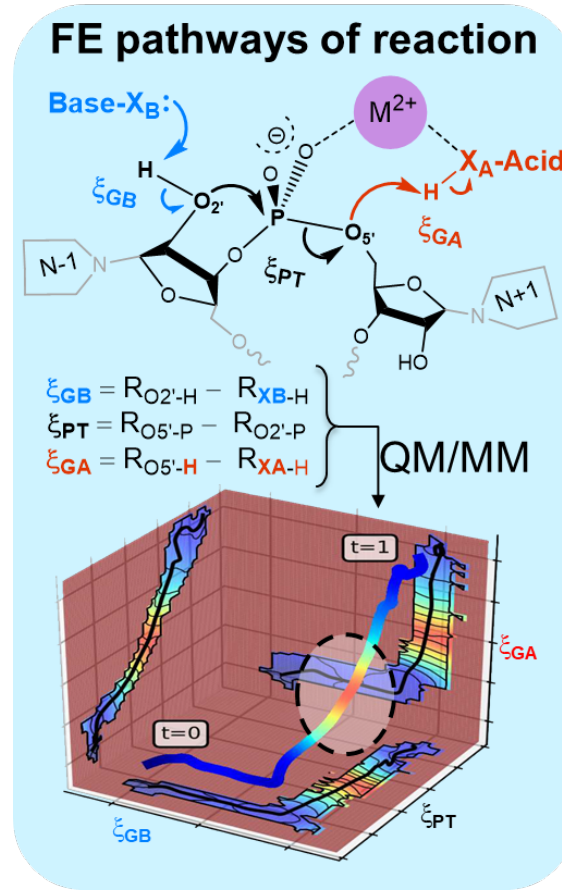
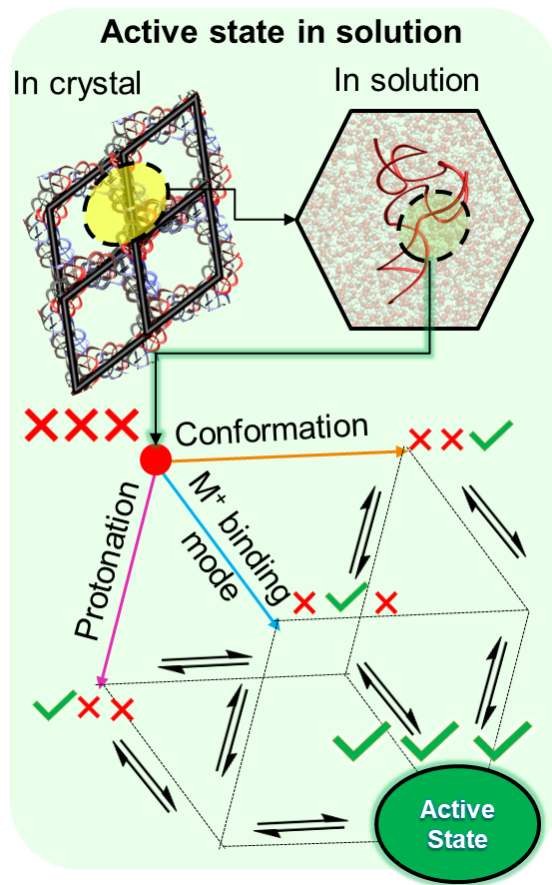
# Advancing AI tools for drug discovery and enzyme design

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## Enzyme Design



MM FF



se-QM 10<sup>3</sup>X

MLP

10-10<sup>3</sup>X



ai-QM 10<sup>6</sup>X

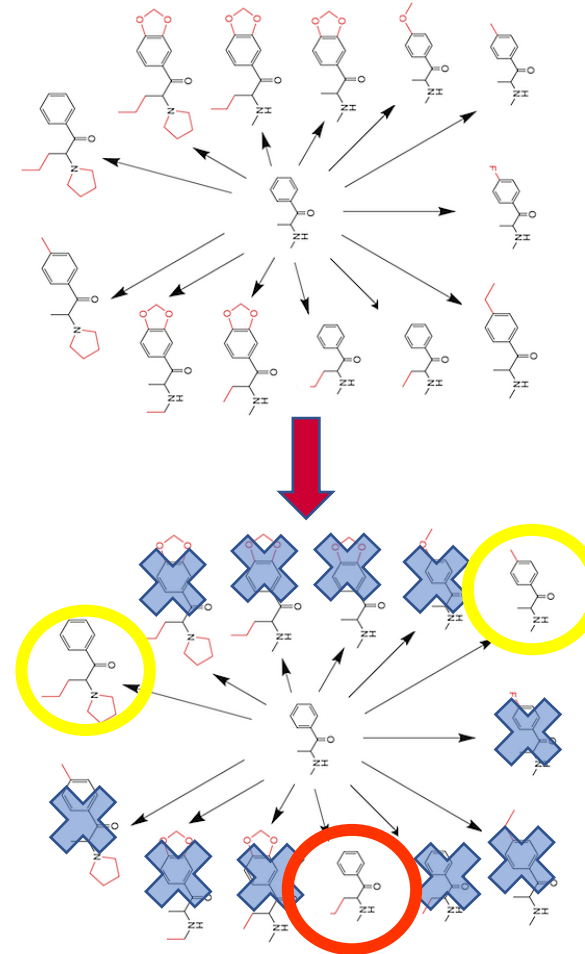
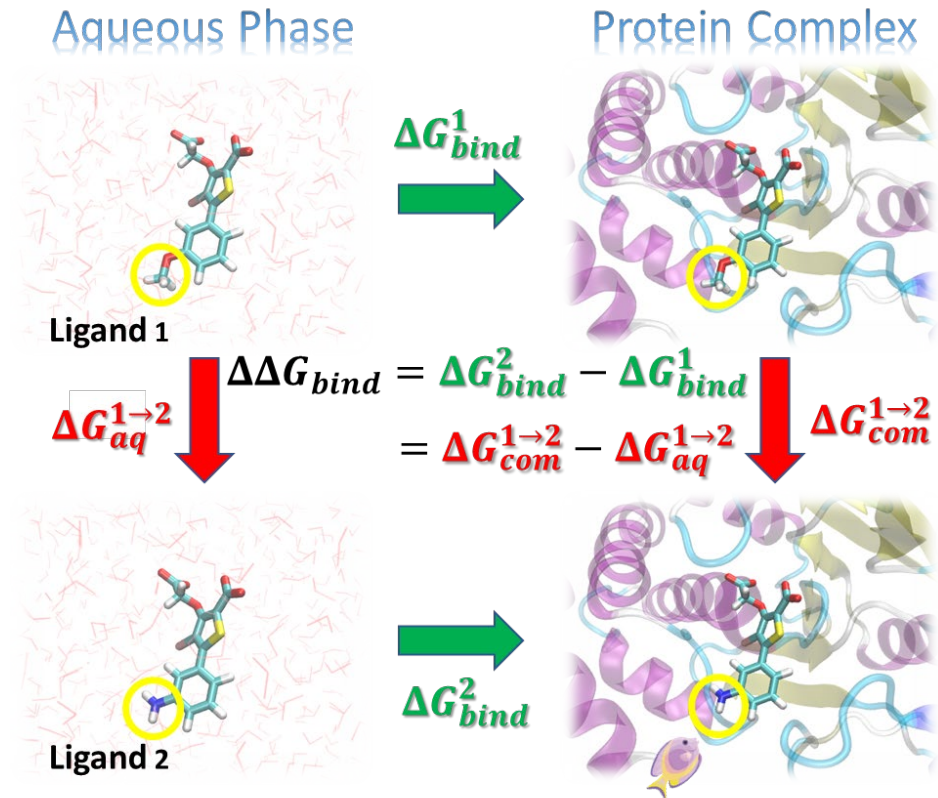


hc-QM

## AI/DS Opportunities

- Prediction of the “active state”
- QM/ML-potential for catalysis
- ML prediction of minimum free energy paths in collective variables

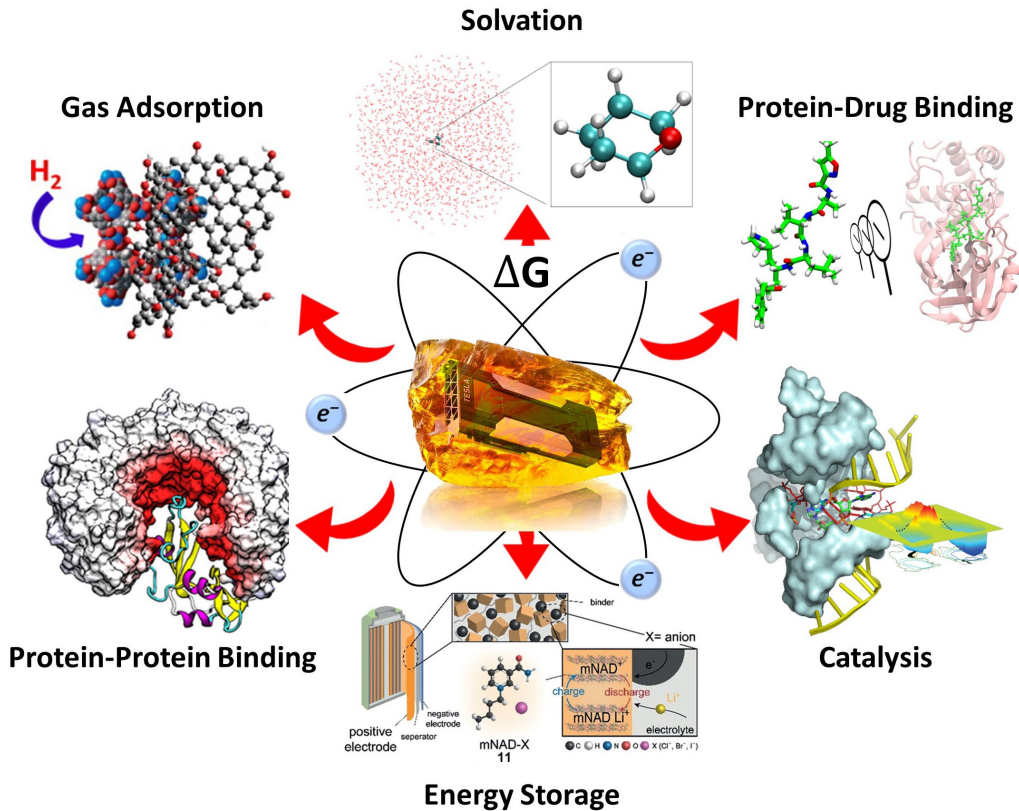
## Drug Discovery



## AI/DS Opportunities

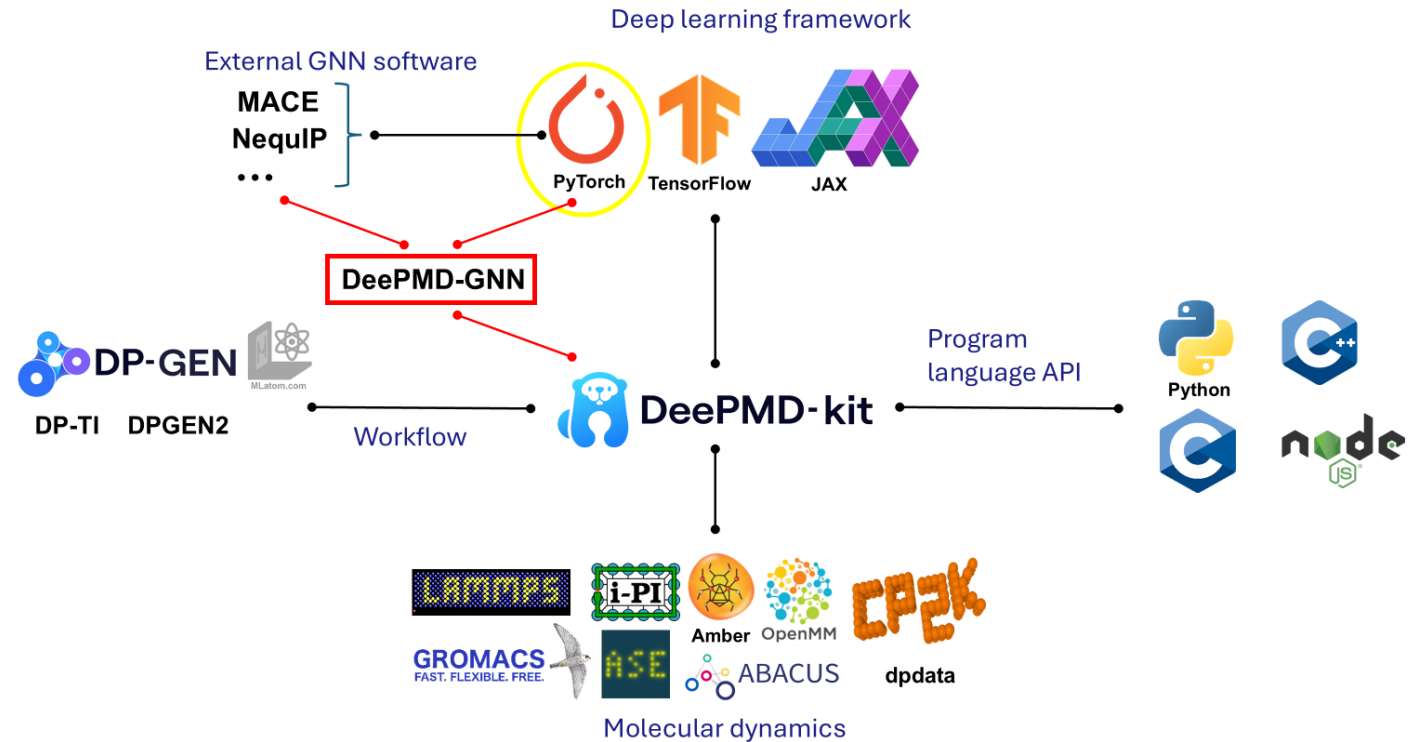
- Protein variant structure prediction
- Ligand docking prediction
- ML-potential for drug-like molecules (tautomers/protonation states)
- AI-FEP for large-scale target-specific screening
- Fast new models for  $\Delta G_{bind}$  prediction

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**AMBER Molecular Simulation  
Software Suite**

[Darrin.York@rutgers.edu](mailto:Darrin.York@rutgers.edu)



**DeePMD-kit software for deep learning-based  
interatomic potential energy models**

[Theory.Rutgers.edu](http://Theory.Rutgers.edu)