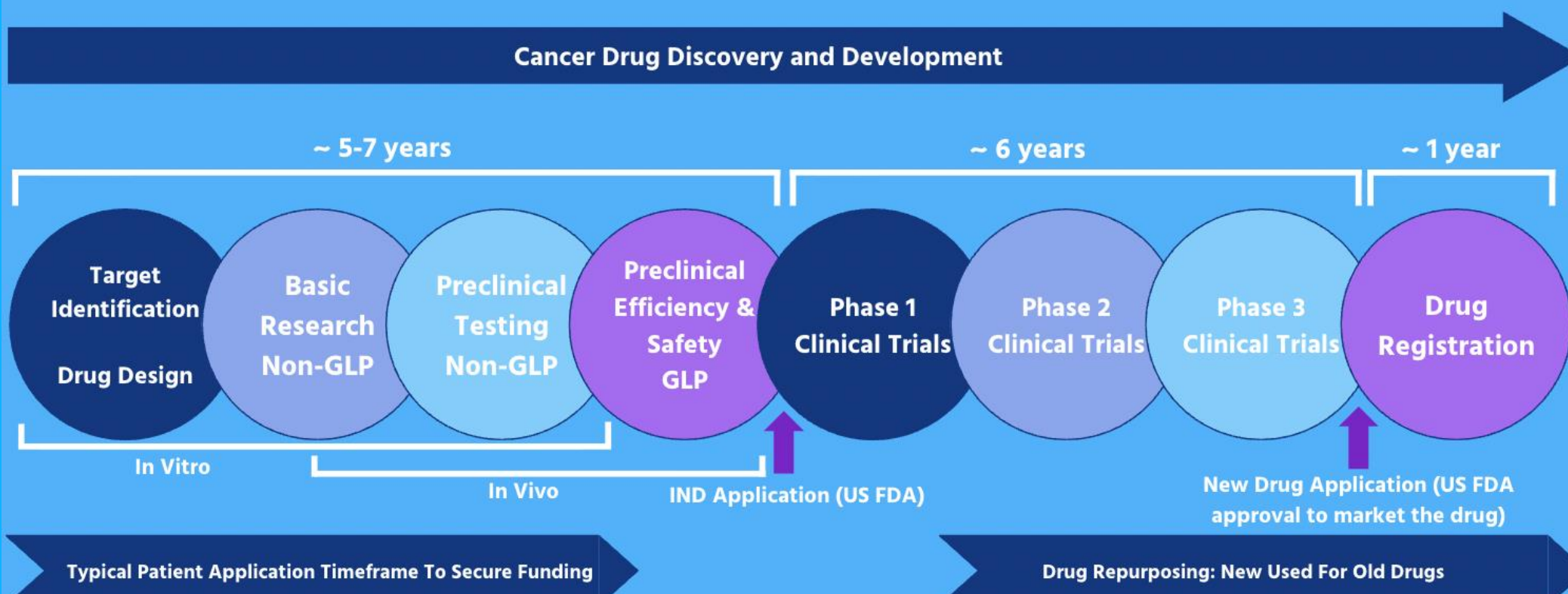


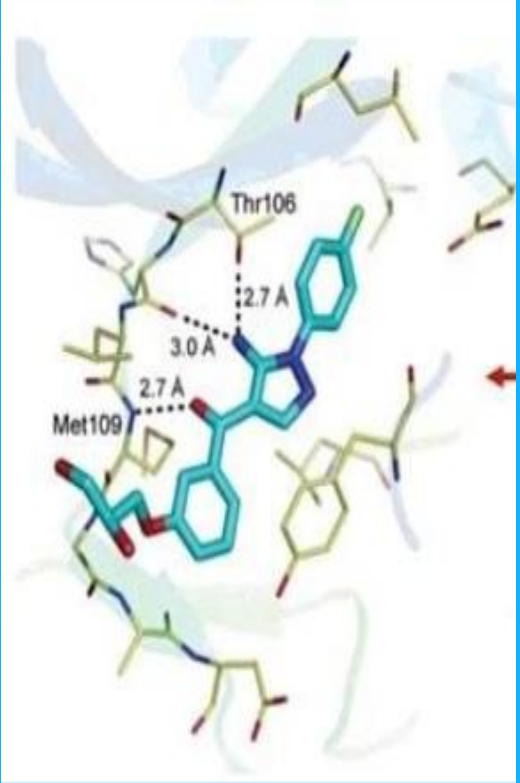
HIGH-THROUGHPUT MOLECULAR PIPELINE

PROJECT INTRO

- Drug development takes **10-15** years, \$1-2 billion, and an **incredibly small** (1/10,000) chance of FDA **approval**



- Project goal:** Develop a high-throughput molecular dynamics (MD) pipeline to accelerate early-stage drug discovery



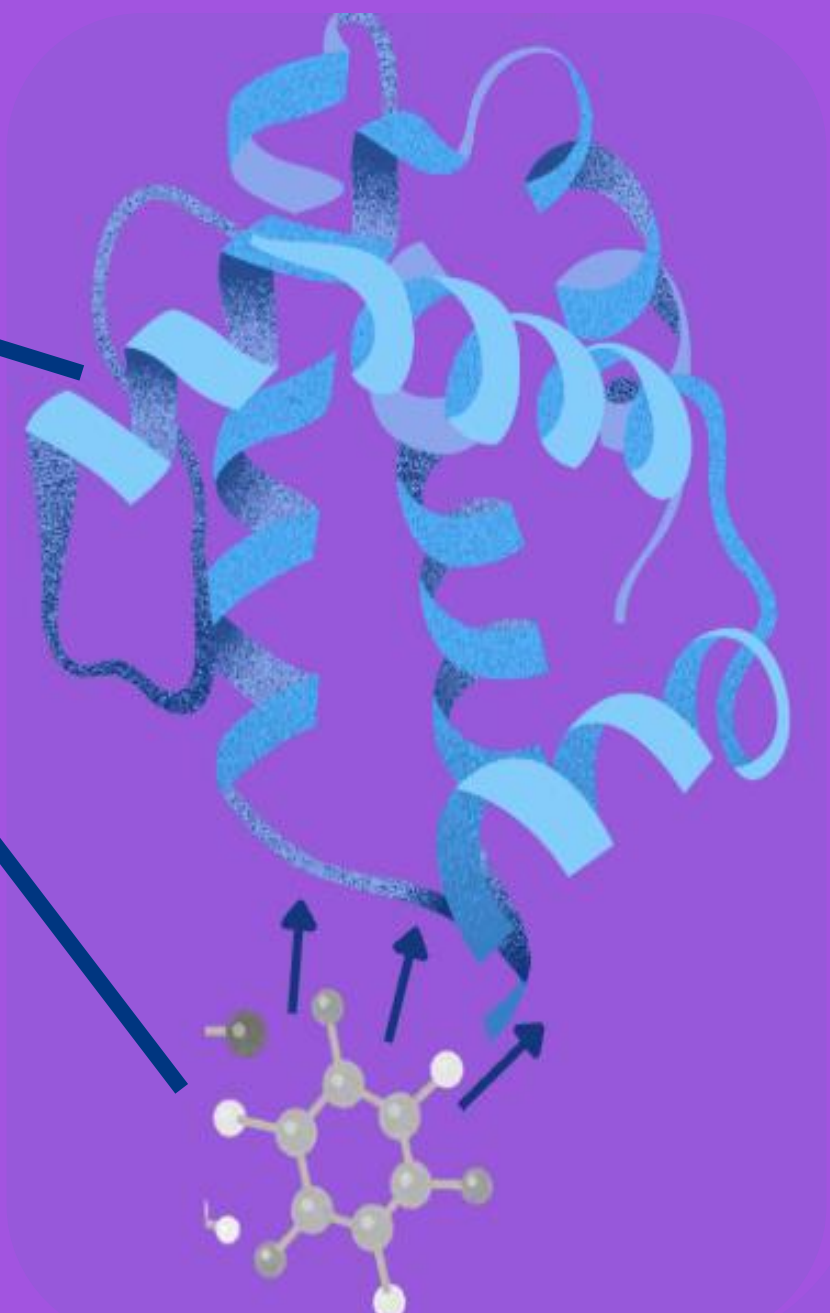
We prioritize compounds with selective binding to disease-relevant targets to reduce toxicity

CHEMISTRY OVERVIEW

Protein: large molecules produced by cells in the body

Ligand: smaller molecules that can attach to proteins and change what they do

Goal: Identify ligands with highest binding affinity to certain proteins



METHODOLOGIES

1. INPUT PREPARATION

Protein sequences and ligand structures → Clean sequences, Validate chemical structures → Validated, protein and ligand files

2. COMPLEX PREDICTIONS

3-D models of predicted complex structures ← Use AI (Boltz-1) to predict how they bind together

3. SYSTEM PREPERATION

Add water and ions to mimic physiological conditions → Equilibrate system at physiological conditions → Solvated, simulation-ready system

4. MOLECULAR DYNAMICS

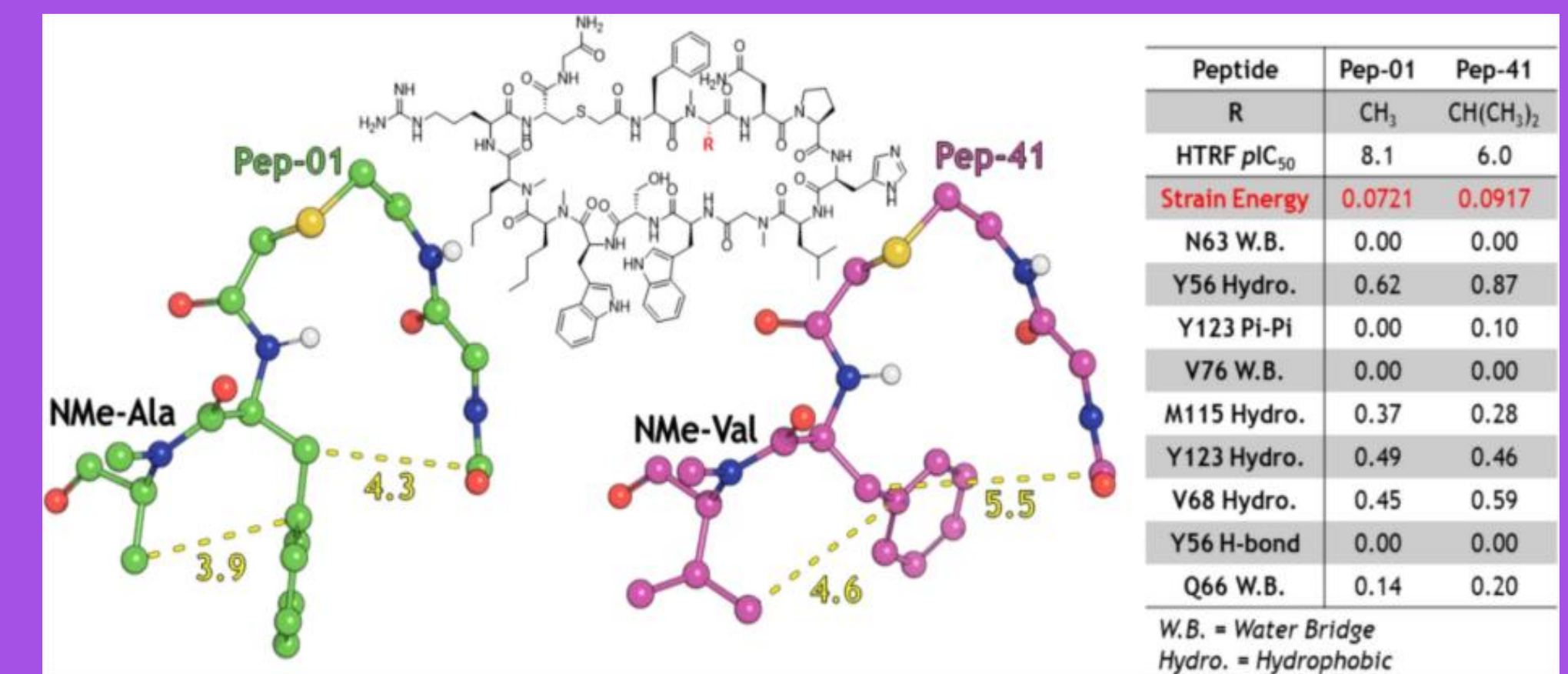
Time-resolved trajectory data ← Cleans structure, stabilize system, run 50-100 ns simulations

5. ML INSIGHTS & ANALYSIS

Analyze RMSD, RMSF, stability, Extract molecular descriptors for ML → Features and predictive insights

RESULTS

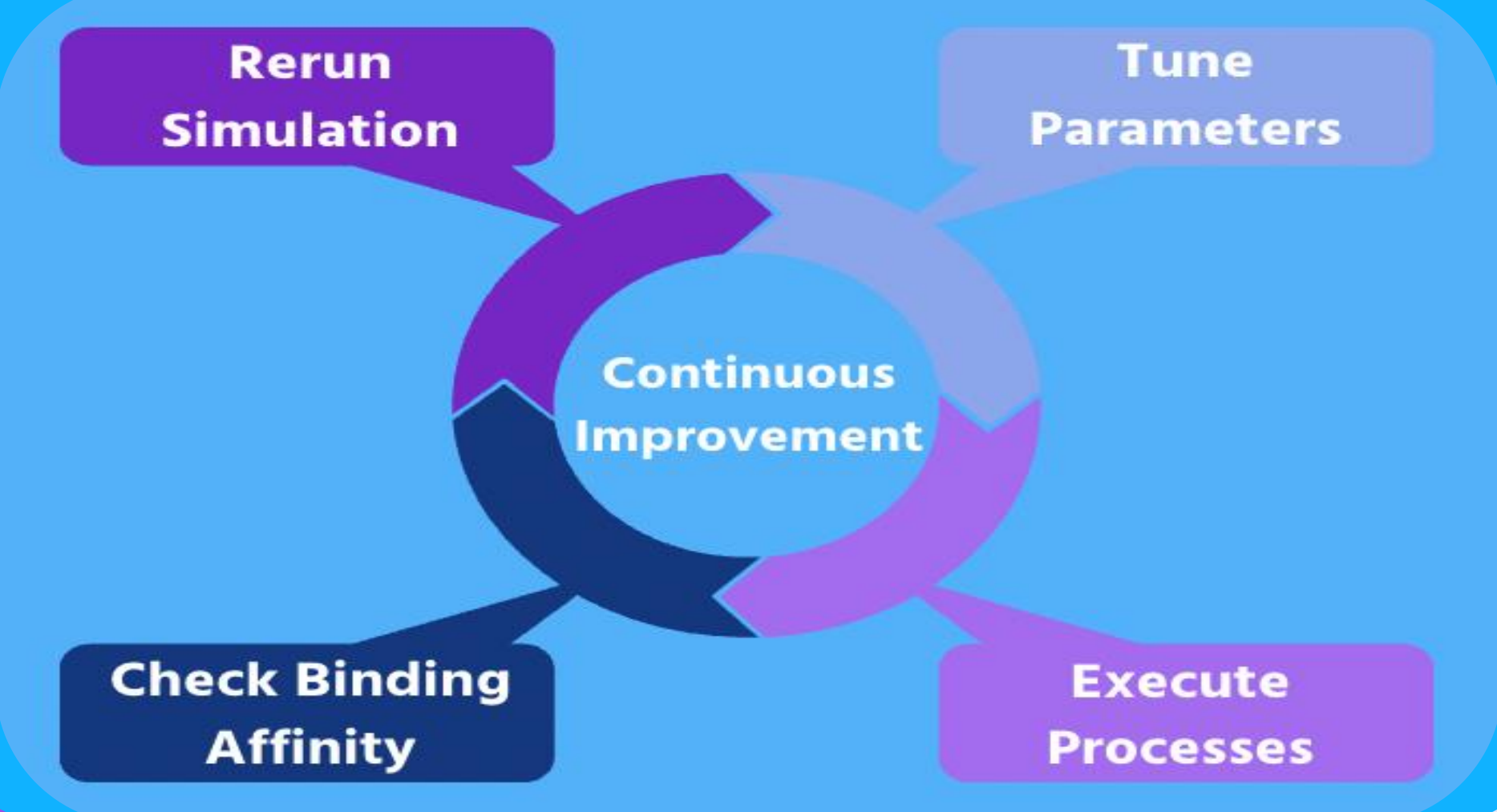
- Automated pipeline producing dynamic simulations of protein-ligand interaction
- Improved viability of therapeutic compounds



Mock results sourced from MDFit paper

FUTURE SCOPE

Future development of framework focused on improving predictive accuracy, expansion, and scalability



REFERENCES/ACKNOWLEDGEMENTS

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