Case Study: Predictive capability of AI-based Hit discovery

In-silico validation
Date: 03.07 2023

Accurate in-silico prediction of the drug-target interactions for AI drug discovery

To validate our AI platform(DeepMatcher-Hit v2.0) by in-silico approaches, we applied a well-established hit finding process using known active compounds, including FDA-approved drugs for seven known targets (TIE2, KDM4D, CLK2, MMP12, EGFR, ABL1, and ACES). Through this process, we identified AI Hits with the best progression properties, which included most of the known FDA-approved drugs for each target, with 7-19 of them ranking in the top 30. Also, our AI program's advanced algorithm facilitated the successful identification of promising novel AI hits that could potentially be developed into drug-like compounds. This demonstrates the potential of our AI platform to identify high-quality compounds with therapeutic potential.

Known active compounds ranked in top 30

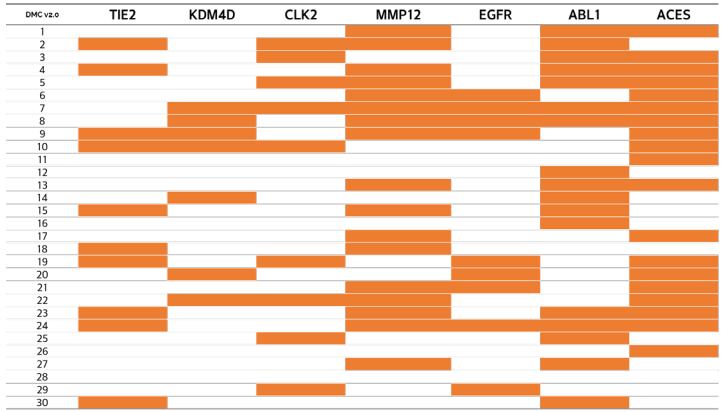


Fig. 1 Known active compounds ranked in the top 30 compounds for 7 targets Orange color represents known compounds within the top 30, and white color shows newly identified compounds.

- DeepMatcher is seen to identify correctly the most known active compounds and places them on the very top of the ranked list for 7 targets.
- Newly identified AI hits targeting 7 test sets are expected to be the best quality compounds in well-categorized disease indications (data not shown).

a) EGFR-Neratinib **b) EGFR-Lapatinib** **c) EGFR-Afatinib**

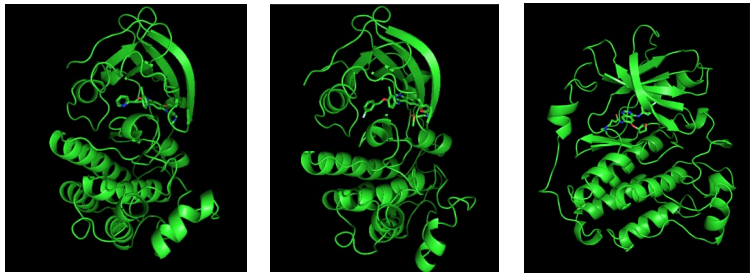
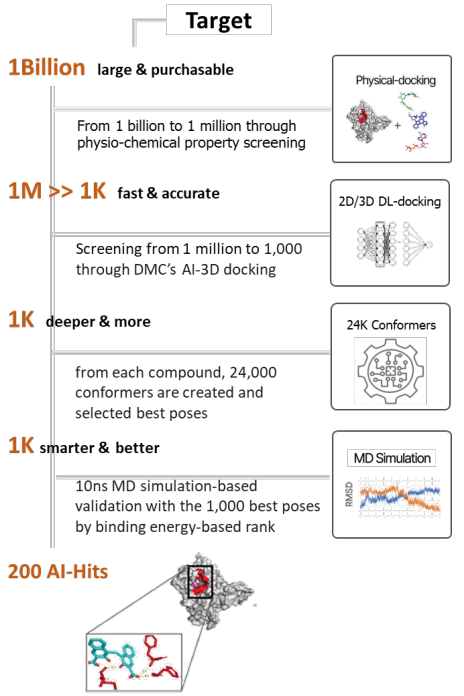


Fig. 2 Predicted 3D structure of targets with known drug a) EGFR-Neratinib, b) EGFR-Lapatinib, c) EGFR-Afatinib, 3D structure with binding conformations of protein–ligand interactions were derived from DeepMatcher-Hit v2.0

- 3D structures of protein–ligand interactions derived from our AI program show highly similar to PDB data.
- Our deep learning-based algorithms enables identification of surface residues as critical residues for protein–ligand binding.

AI program with DeepMatcher-Hit v2.0



- AI-based drug discovery platform "DeepMatcher®-Hit" conducts a comprehensive screening to find appropriate hit compounds using up to 1 billion compound library. The platform is fully automated and modulated into three parts for AI based 2D chemical screening, AI based 3D docking and Molecular docking simulation. Additionally, with our own high-performance computing infrastructure,
- In this study, we selected known active compounds including FDA-approved drugs and mixed them with the 1 billion compound library..