

Multi-Target Drug Design Using Cheminformatics Approaches



Sudeep Roy, Ph.D.

Assistant Professor-Cheminformatics(SysBio)

Department of Biomedical Engineering

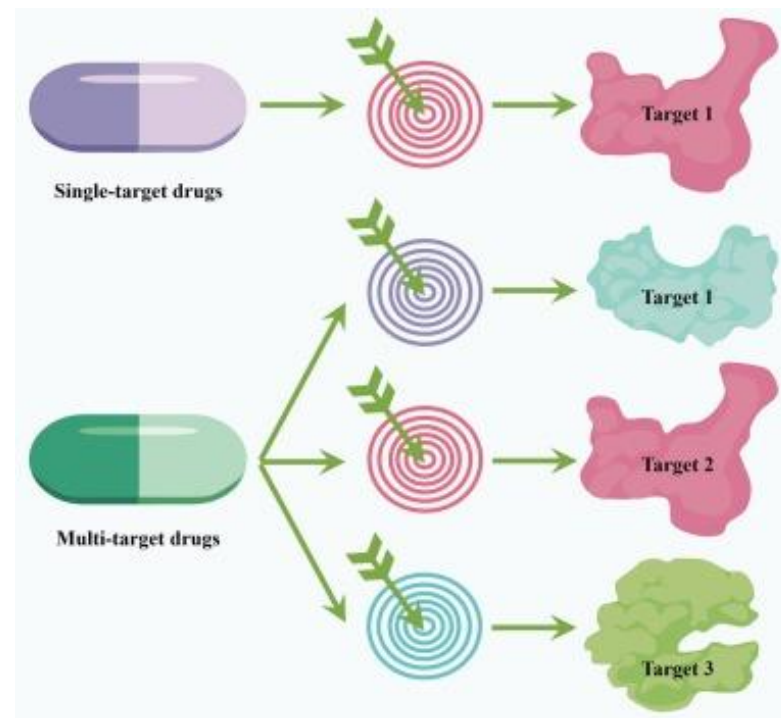
Brno University of Technology-Brno

Introduction

Definition: Multi-target Drug Design (MTDD) aims to develop single molecules acting on multiple biological targets.

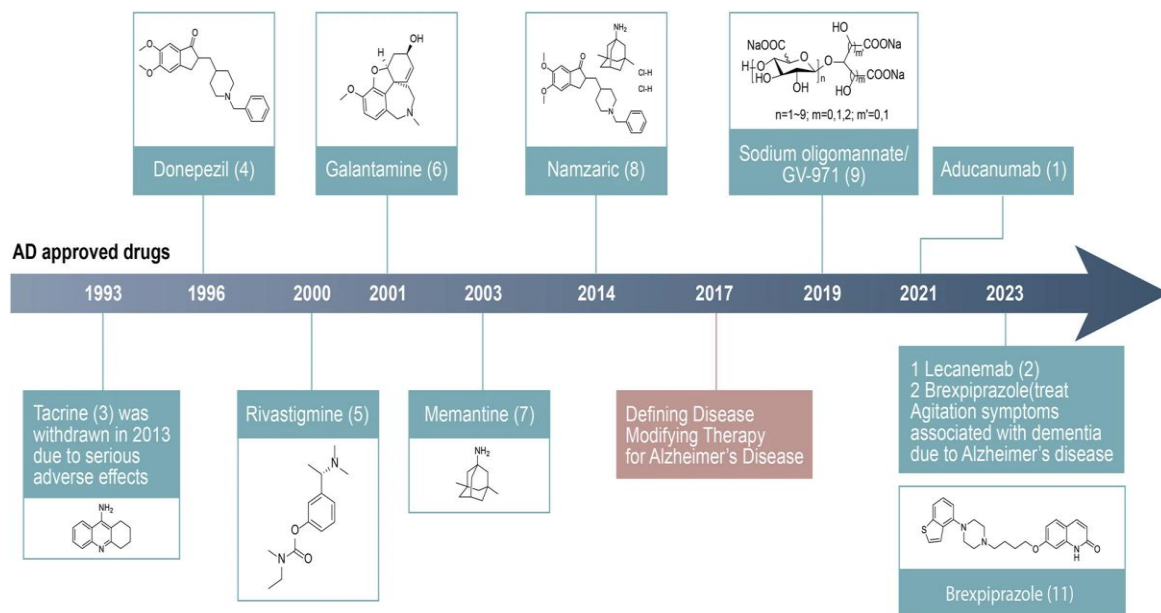
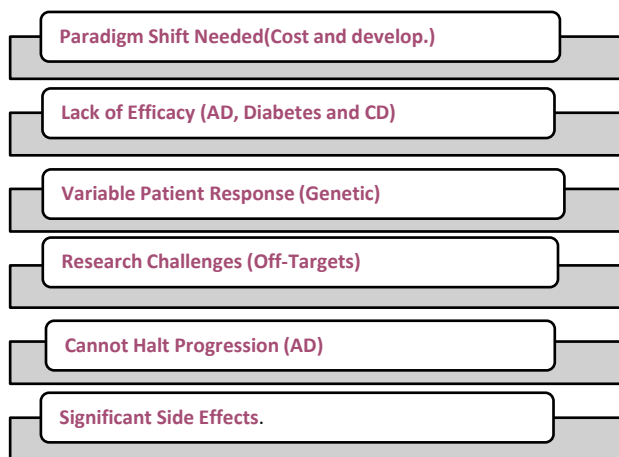
Importance: Suitable for multifactorial diseases like cancer, neurodegeneration.

Cheminformatics role: Integrates chemical, biological, and pharmacological data.



Source: <https://doi.org/10.1016/j.pharmthera.2023.108550>

Limitations of Single-Target Drugs and Recent Therapies



Source: <https://www.nature.com/articles/s41392-024-01911-3>

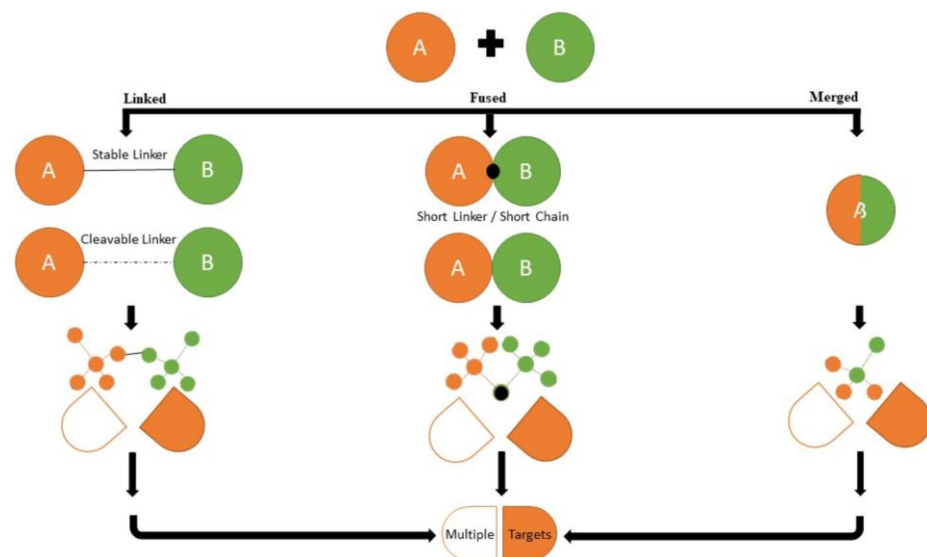
Advantages of MTDD

Synergistic effects-(Lower Doses)

Lower likelihood of resistance-single point mutation (Cancer and Infectious Diseases)

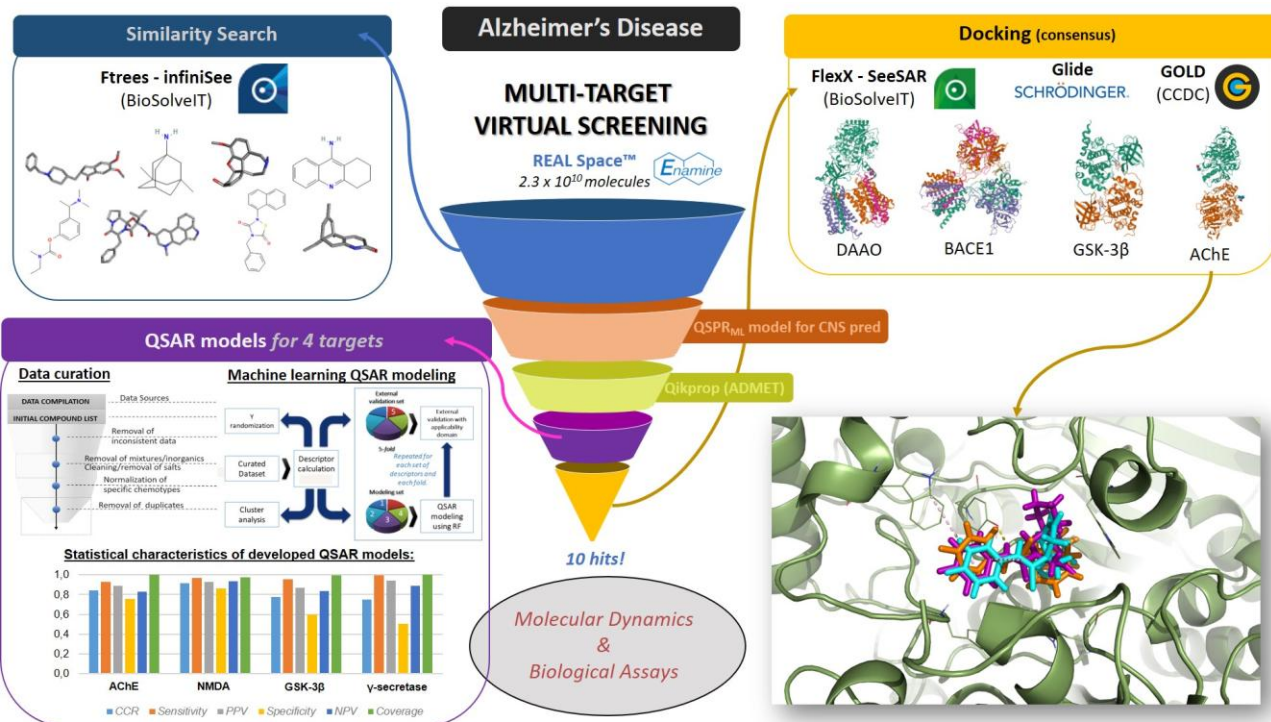
Reduced pill burden (Drug-Drug Interaction)

Better efficacy in complex diseases (Heterogenous Diseases or Diverse patient population)



Source: <https://doi.org/10.1002/prp2.70131>

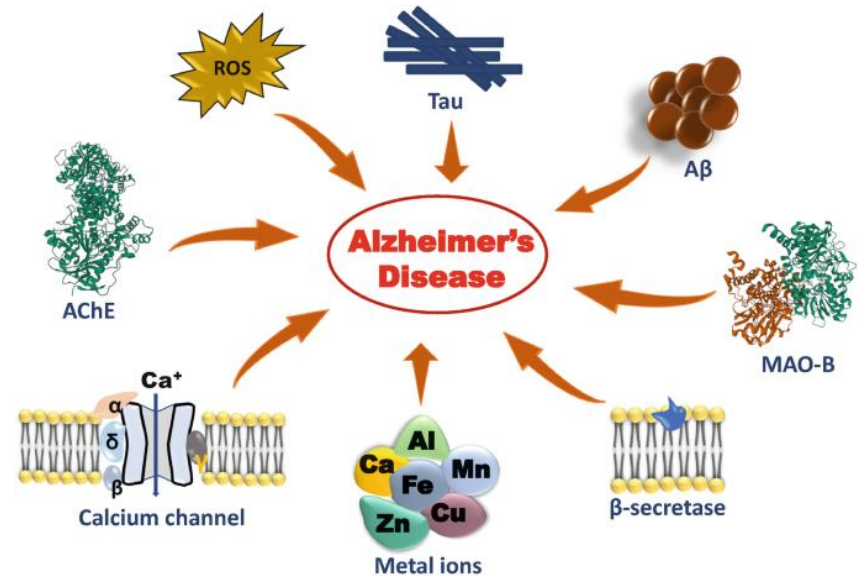
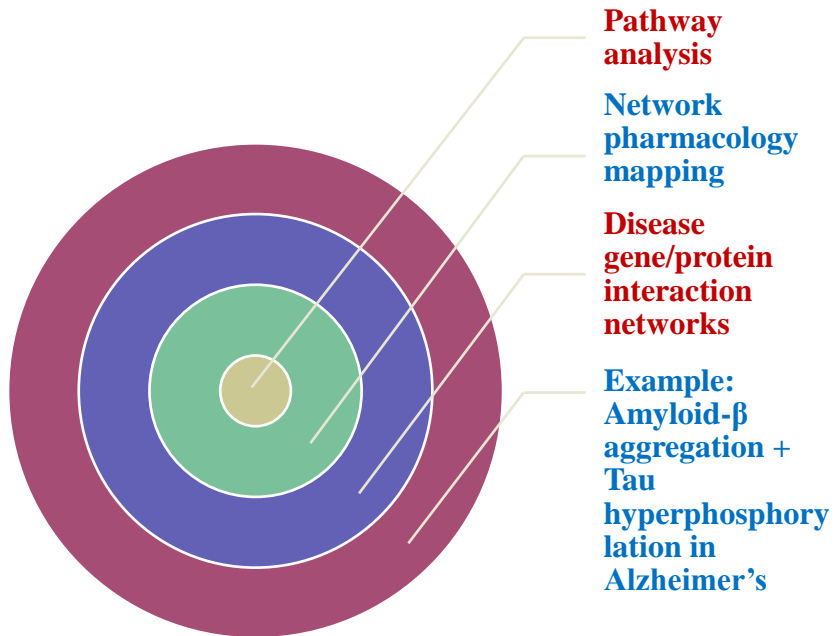
MTDD Workflow



Source: <https://www.biosolveit.de/scientific-challenge/project/?projectId=16376243929290>

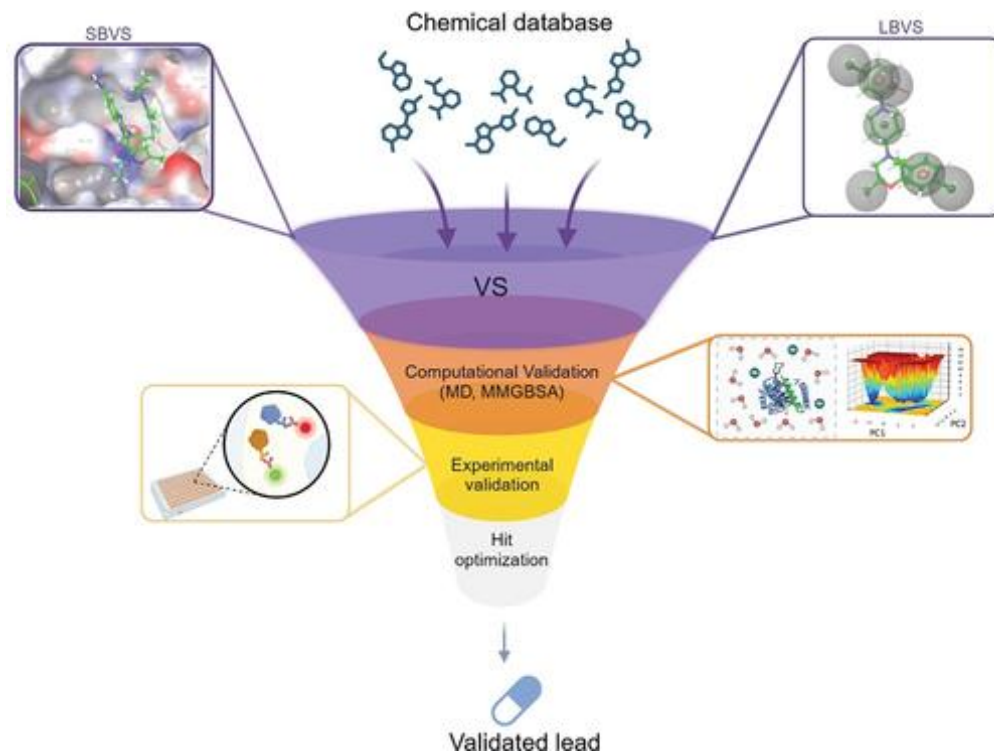
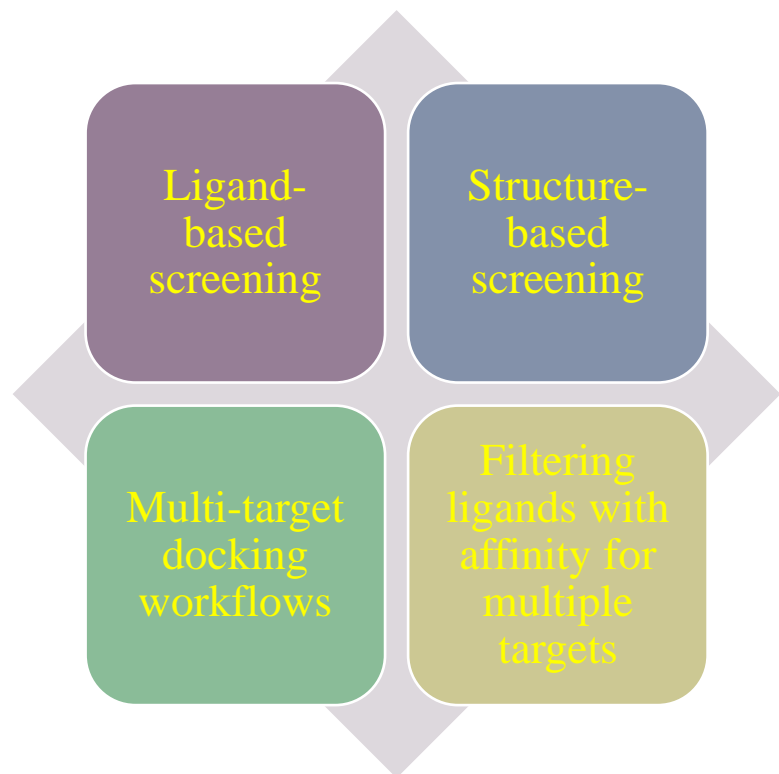
1. Target Identification (System Biology, Network Pharmacology, Disease mapping).
2. Ligand Design / Selection (SBDD, Scaffold Hopping, Fragment based Methods)
3. Virtual Screening (SBVS, LBVS, Optimal Pharmacological Profiles)
4. ADMET Prediction (Exclude Unfavourable pharmacokinetics or high toxicity risk compounds)
5. Molecular Dynamics Simulation (Assess Binding stability and potential off-target effects)
6. In vitro / In vivo Validation (Synthesis, Animal Models)

Target Selection Strategies



Source: https://link.springer.com/chapter/10.1007/978-981-99-6038-5_13

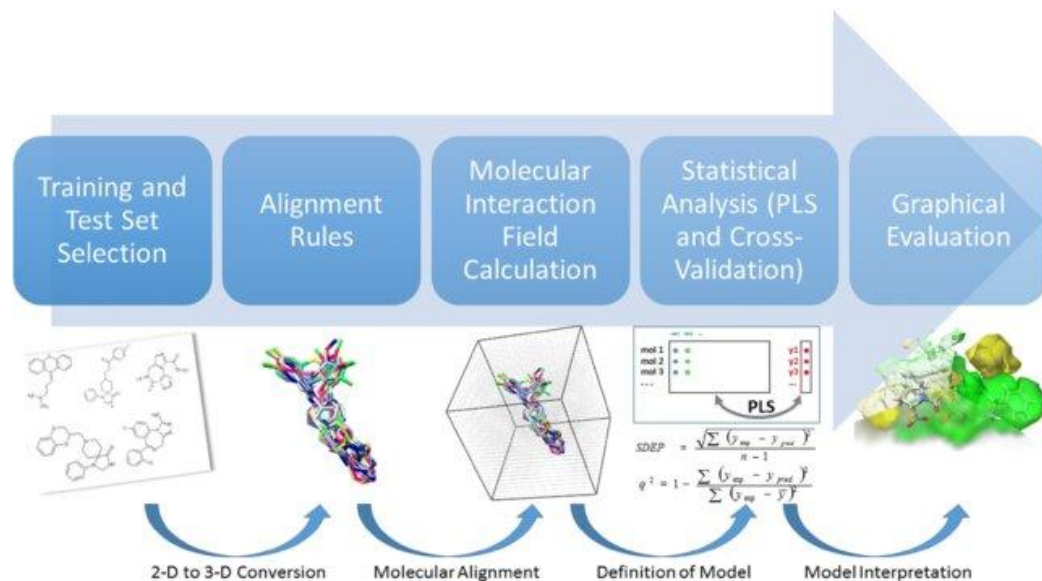
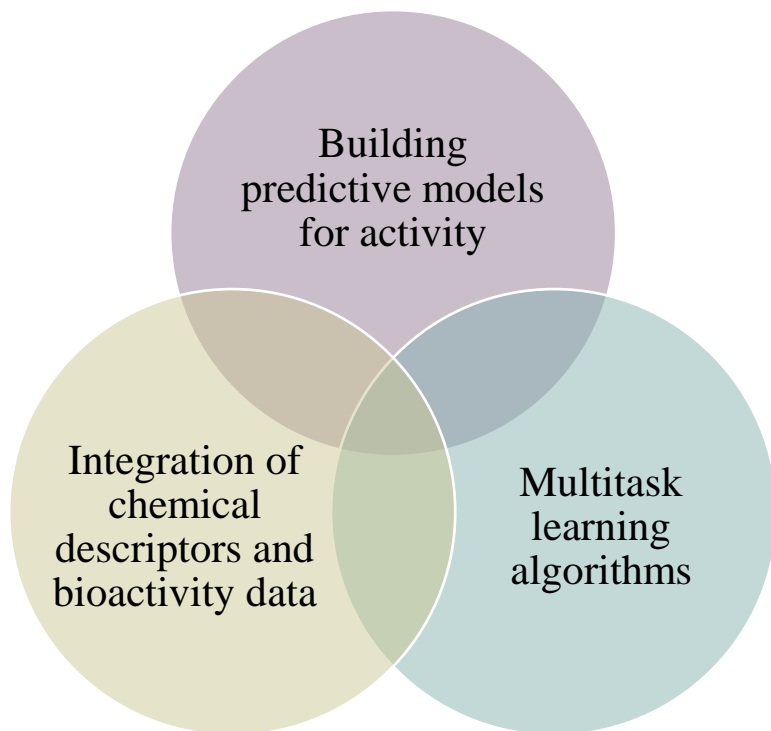
Virtual Screening in MTDD



Source:

<https://www.tandfonline.com/doi/full/10.1080/17460441.2025.2458666?scroll=top&needAccess=true>

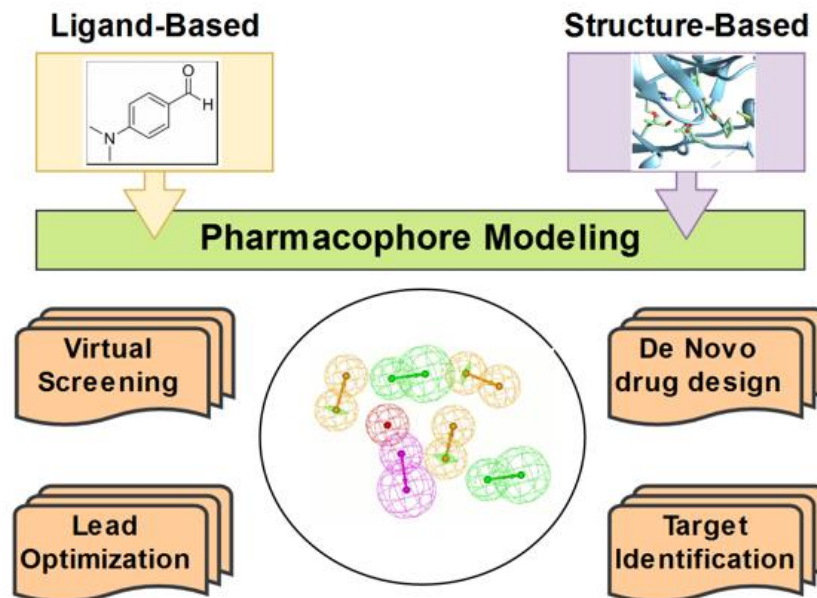
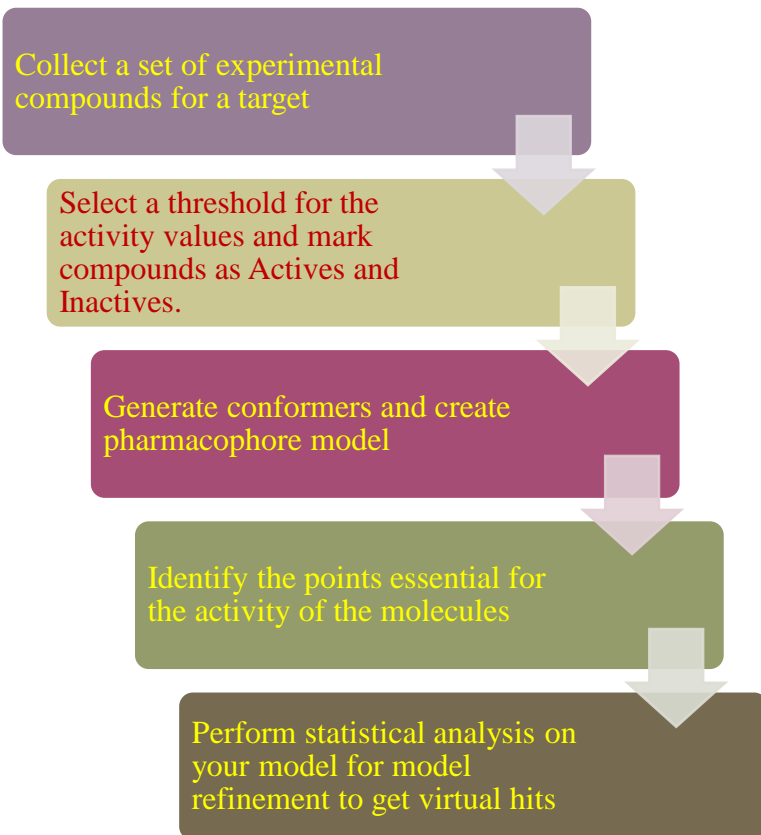
QSAR & Machine Learning



Source:

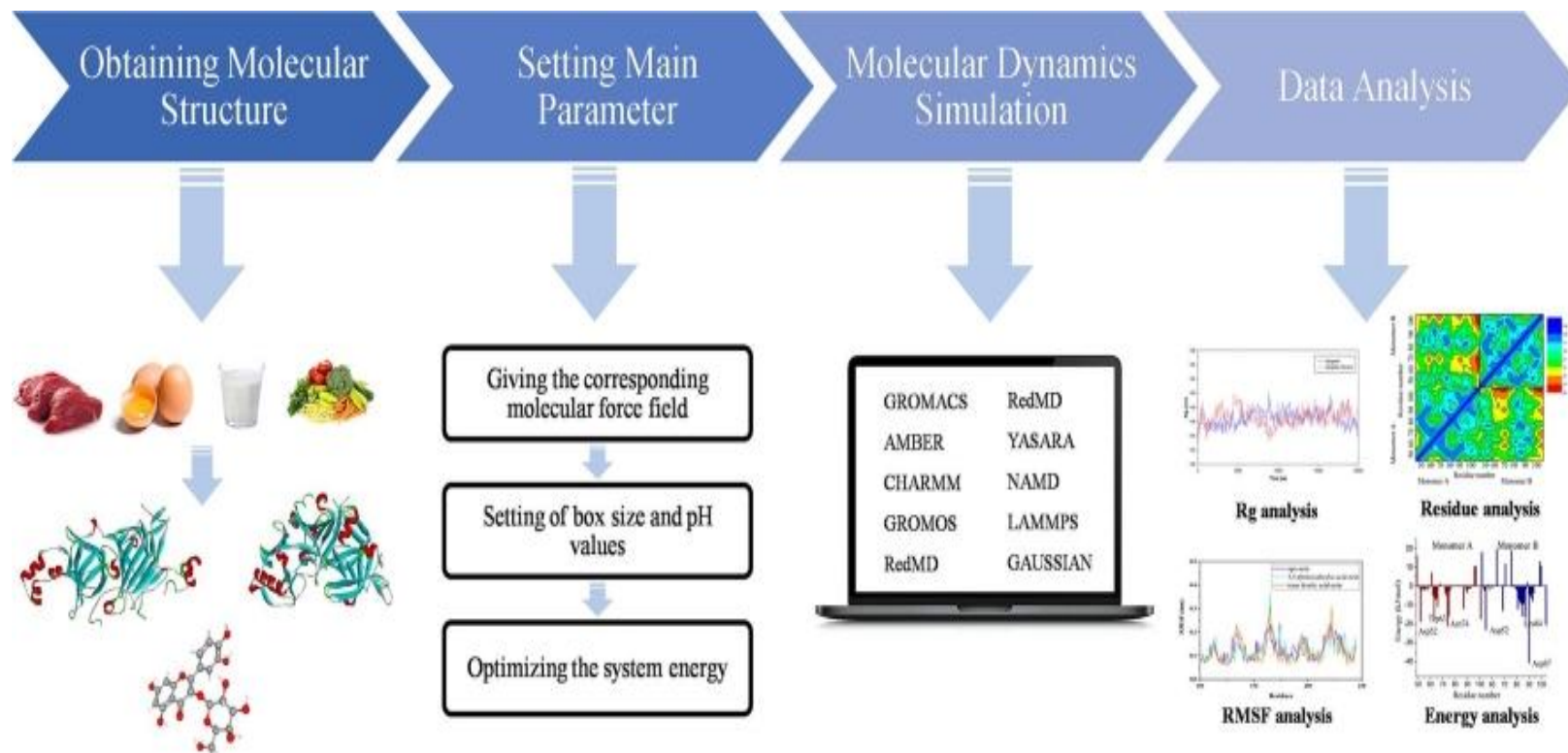
<https://link.springer.com/article/10.1007/s10822-019-00231-x>

Pharmacophore Modeling



Source: <https://www.profacgen.com/pharmacophore-modeling.htm>

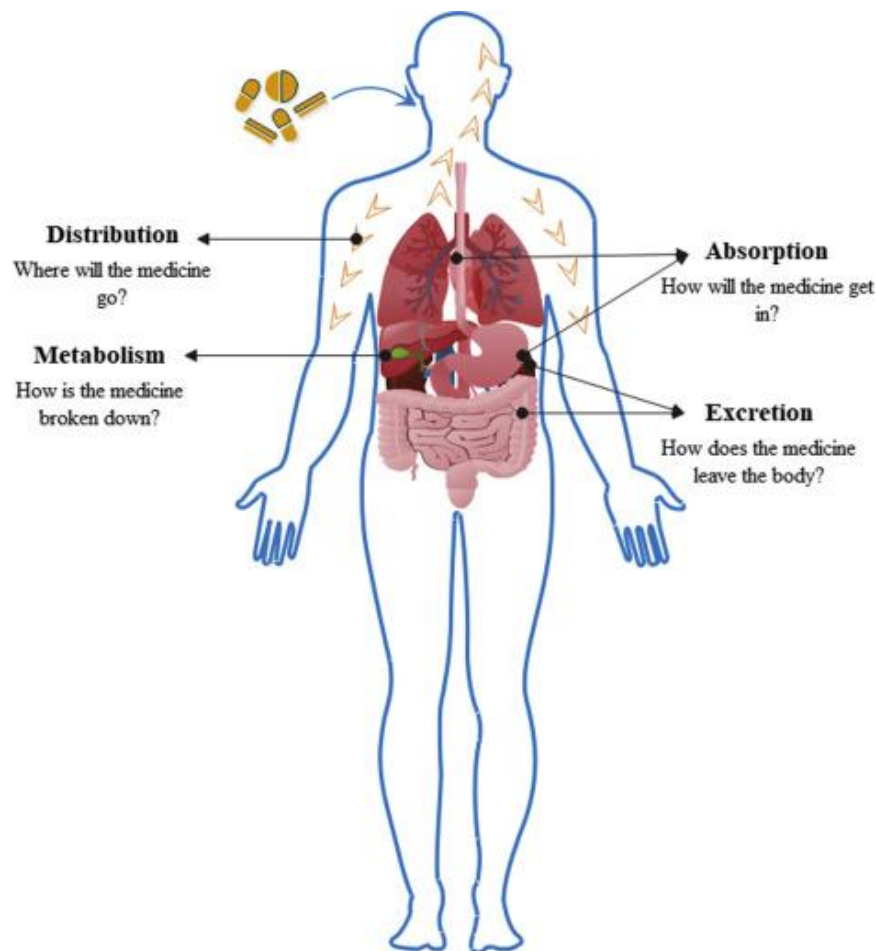
Molecular Dynamics in MTDD



Source: https://www.creative-biostructure.com/molecular-dynamics-simulations.html?srsId=AfmBOopF4wPKdEYd8c0oh_KQmUK2x2-PABIXthn7ZDTEbpcMD0PNd6wU

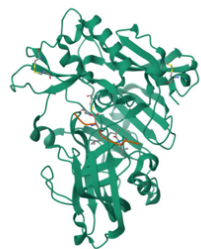
ADMET & Toxicity Prediction

- In silico evaluation of:
 - **A**bsorption
 - **D**istribution
 - **M**etabolism
 - **E**xcretion
 - **T**oxicity
- Filtering out problematic compounds early



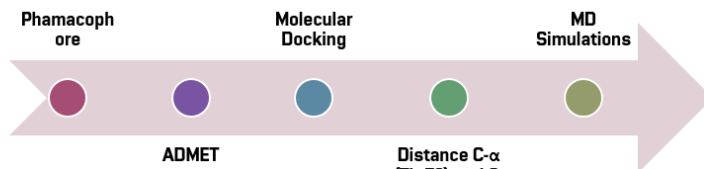
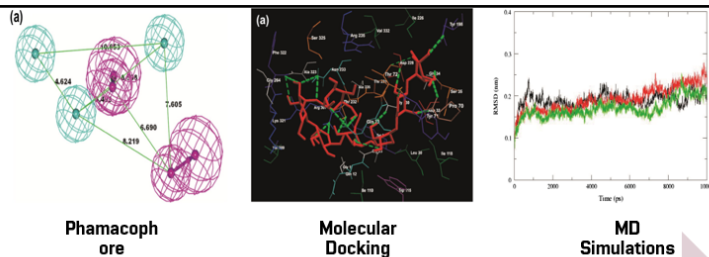
Source:

<https://www.sciencedirect.com/science/article/abs/pii/B978012814421300021X>



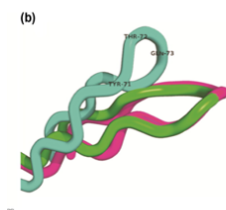
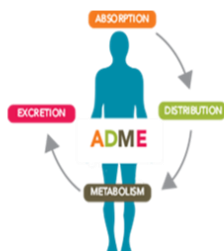
BACE PDB IDs:
1M4H, 2G94, 2P4J,
2Q15, 2ZHR, 3CIC,
3I25, 3LPI,
3LPK, and 2VKM

Ligands
50,536
natural
compounds
from IBS



ADMET

Distance C- α
(Thr72) and C- β
(Asp32)



Ligand 2

Case Study 1: Molecular docking based virtual screening of natural compounds as potential BACE1 inhibitors: 3D – QSAR pharmacophore mapping and molecular dynamics analysis

Source:

<https://www.tandfonline.com/doi/full/10.1080/07391102.2015.1022603>

- **Large flexible binding sites like BACE1.**
- **Catalytic ASPDyad (D32 and D228) and Flexible Flap(V67-E77). Imp Residue: T72.**
- **10ns Run.**
- **BBB, Hepatotoxicity, PPB, solubility and mutagenicity. Scaffolds safe for CNS delivery.**
- **3 Oligosaccharides Hits.**
- **Reduction of amyloid levels in AD**

Purpose

- **Identify natural compounds as potential BACE1 inhibitors using *in-silico* approaches.**

Target Proteins / Pathways

- **BACE1 (β -secretase 1)**
- **Amyloid- β formation pathway in AD.**

Goals Achieved

- **Virtual screening of natural compounds**
- **3D–QSAR pharmacophore model developed**
- **Molecular dynamics confirmed stability**
- **Promising BACE1 inhibitor leads identified**



Contact



BioSys_BUT

Email:

roy@vut.cz