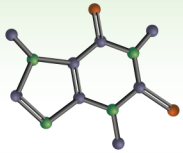
Stage 1 - ***Preparation of ligand library of phytochemicals***

IMPPAT

PubChem

- 14011 phytochemicals from Indian medicinal plants (mainly, from IMPPAT)
- 10510 drug-like phytochemicals based on Lipinski's RO5
- 3D structure from Pubchem and energy-minimization using OpenBabel

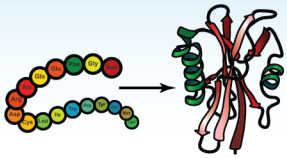


Stage 2 - ***Preparation of structure of target proteins TMPRSS2 & cathepsin L***

SWISS-MODEL

RCSB PDB

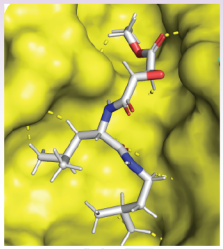
- TMPRSS2 model structure built using SWISS-MODEL
- Cathepsin L crystal structure from PDB (5MQY)



Stage 3 - ***Molecular docking***

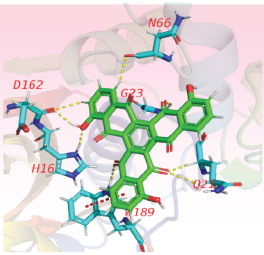
AutoDock Vina

- Stringent docked binding energy cut-off
- Docking using AutoDock Vina



Stage 4 - ***Prediction of binding site & non-covalent protein-ligand interactions***

- Prediction of binding site residues and non-covalent interactions
- Potential top inhibitors of TMPRSS2 and cathepsin L
- Plant sources, physicochemical and ADMET properties



Stage 5 - ***MD simulation of protein-ligand complexes***

- 180 ns MD simulation of protein-ligand complexes
- Binding energy using MM-PBSA method