**MATERIALS AND METHODS:**

**1.Identification of Target and Validation:**

the biological target was identified by using pubmed database (<https://pubmed.ncbi.nlm.nih.gov/>) . the protein and gene sequence of target were retrived from uniprot ( <https://www.uniprot.org/> ) and genbank (<https://www.ncbi.nlm.nih.gov/genbank/>) respectiverly .

The physical and chemical properties of selected proteins were then accesed using protparam tool of ExPASy website (<https://web.expasy.org/protparam/>). the 3-Dimensional structure of CAPN10 protein was retrived from AlfaFold database of EMBL\_EBI server .(<https://alphafold.ebi.ac.uk/>). the secondary structure analysis of caplain protein was done by using PredictProtein tool (<https://predictprotein.org/>). the 3D model pf protein were validated by using PDBsum databse (<http://www.ebi.ac.uk/thornton-srv/databases/pdbsum/).The> biological targets Alpha glucosidase and Alpha amylase 3Dimentional structures were retrieved from PDB Database.

**2. Binding site Prediction:**

**3. Compound Library construction and Structure Elucidation :**

**4.Drug Likeliness :**

**5.Molecular Docking and Simulation :**