Supplement figure legend:

Fig 1.lncRNA-mRNA-network analysis in urine sample of LN patients.Purple nodes represent lncRNAs,orange nodes represent mRNAs.Orange frame highlights the

PARK2(Parkin) -lncRNA NONHSAG017222.3 network.

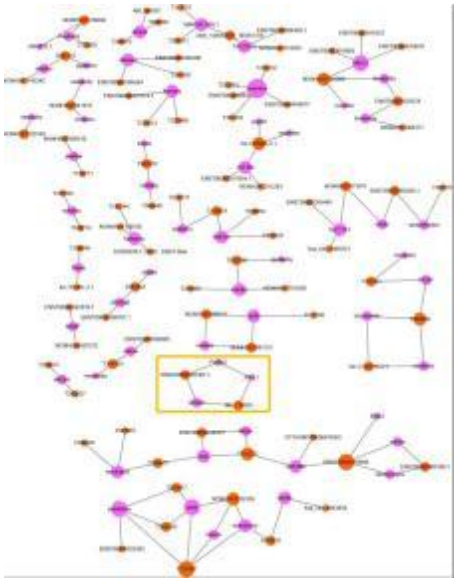


Fig 7. Molecular docking diagram of target protein and drug ingredient

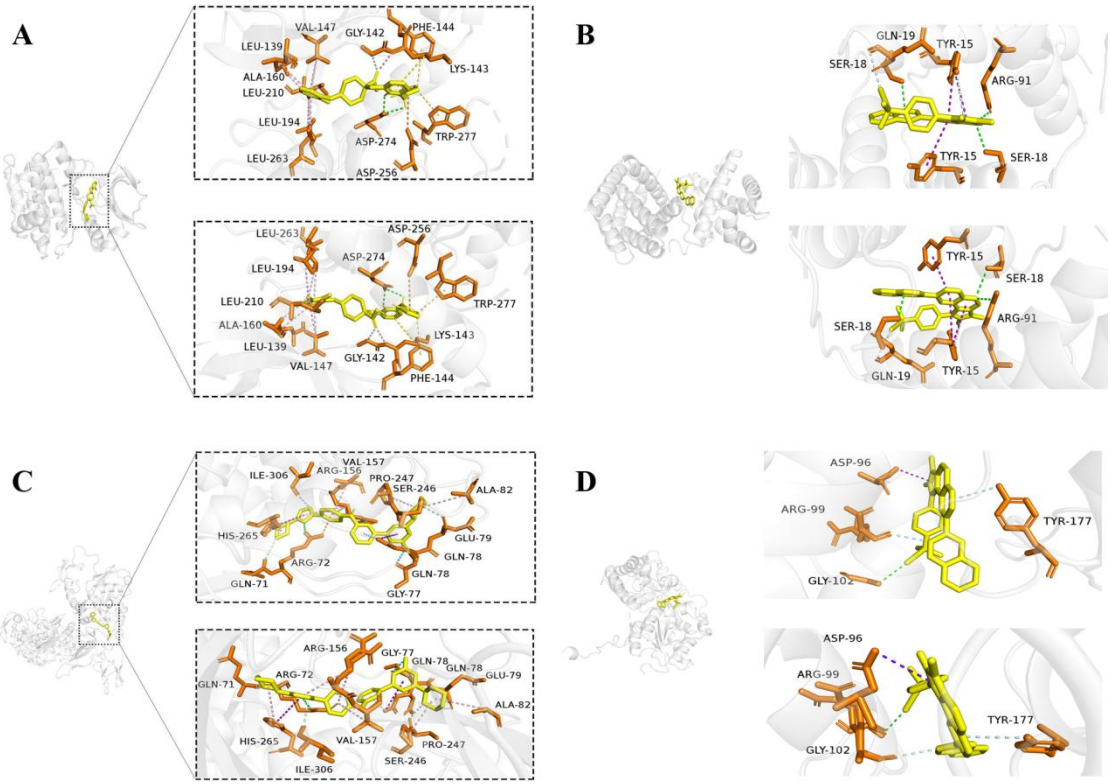
The different active binding modes in the results obtained from molecular docking are indicated as different colored dashed lines:Conventional hydrogen bonds (green), π- cation bonds (Orange), hydrophobic bonds with π- hydrophobic bonds (pink and light pink), π-π bonds (purple), π-σ bonds (dark purple), halogen action (blue). The forces corresponding to each color above were also plotted against each other in 3D plots, and the specific docking of each group of target protein receptors and small molecule ligands of drugs were detailed in 3D plots.

(A)ARUKA vs MK-5108 (binding energies-9.4 kcal / mol-1)

(B) BECN1 vs dactolisib (binding energies-10 kcal / mol-1)

(C)PARK2 vs JNK-L9 (binding energies-11 kcal / mol-1)

(D) SNCA vs dactolisib (binding energies-10.2 kcal / mol-1)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LYS-143
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ASP-256
LEU-263
ASP-256
ASP-274
LEU-194
TRP-277
LEU-210
ALA-160
LYS-143
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