

Supplementary figures

Figure S1. Evaluation of predictive accuracy and residual analysis for pIC₅₀ values of *ADCY8*, *DDC*, and *PPP2R5C* with interacting ligands using a random forest regressor model

Figure S2. Applicability domain analysis of interacting ligands using principal component analysis (PCA).

Figure S3. Interactive Venn diagrams depicting the distribution and overlap of NCs across various food sources

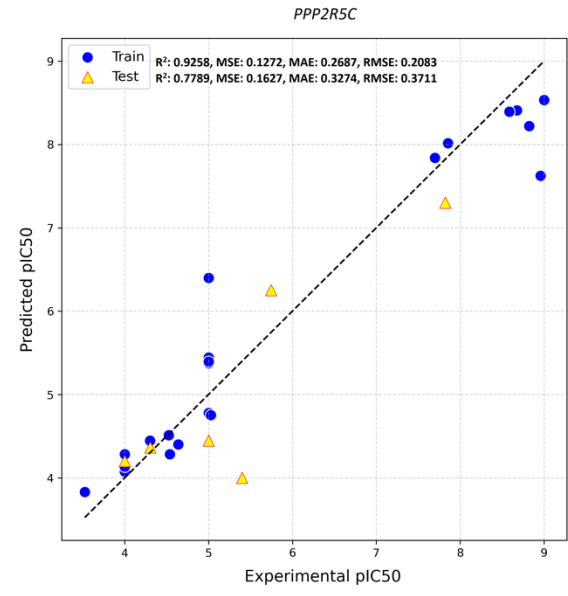
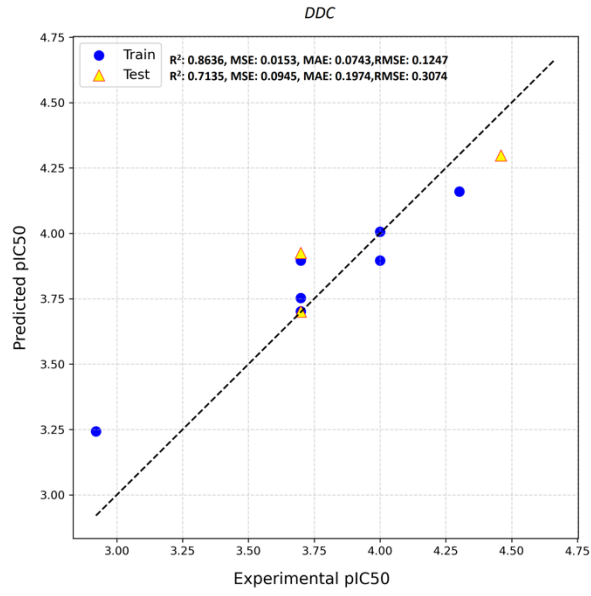
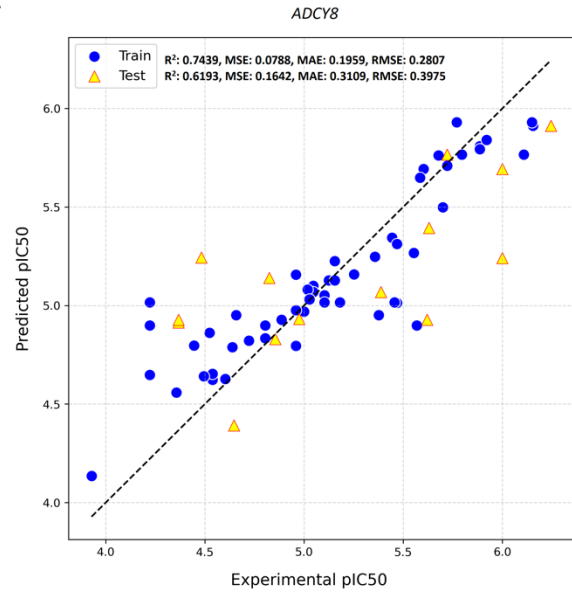
Figure S4. Dotted vertical histogram of average molecular docking scores for nine target proteins and comparison of metabolic characteristics and bioactivity of natural compounds in docking with DDC.

Figure S5. pIC₅₀ distribution across activity levels.

Figure S6. Maximum common substructures (MCS) across activity levels, segregated based on their bioactivity levels.

Figure S1

A



B

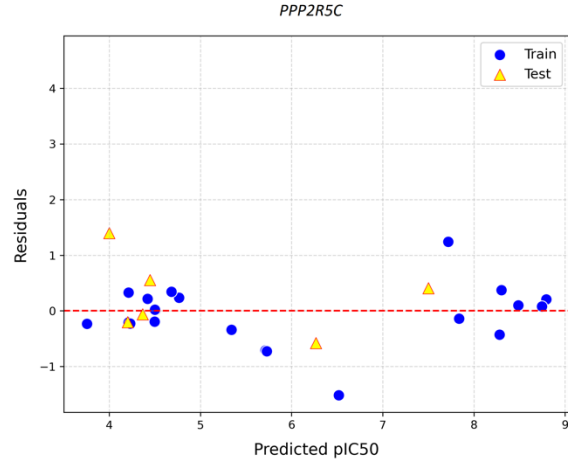
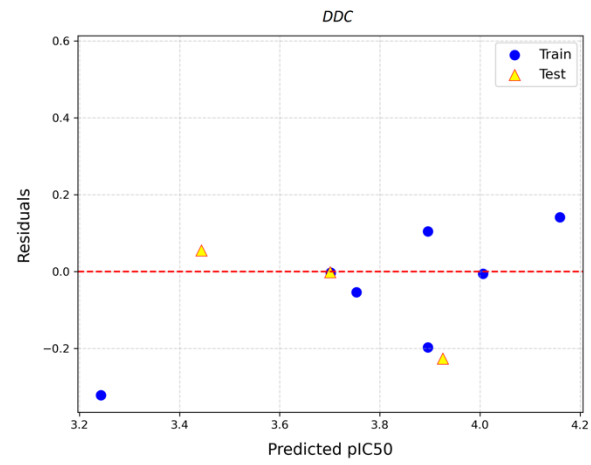
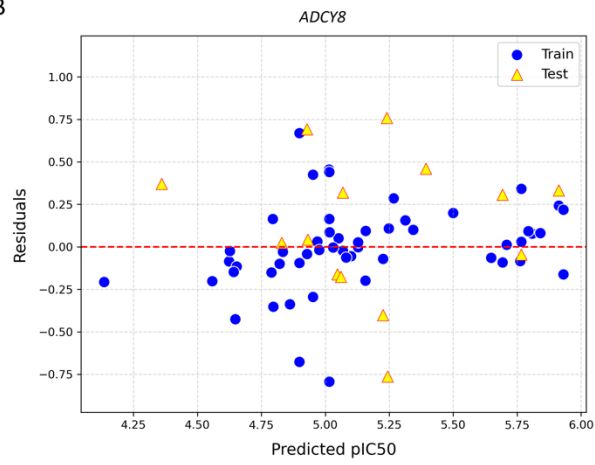


Figure S2

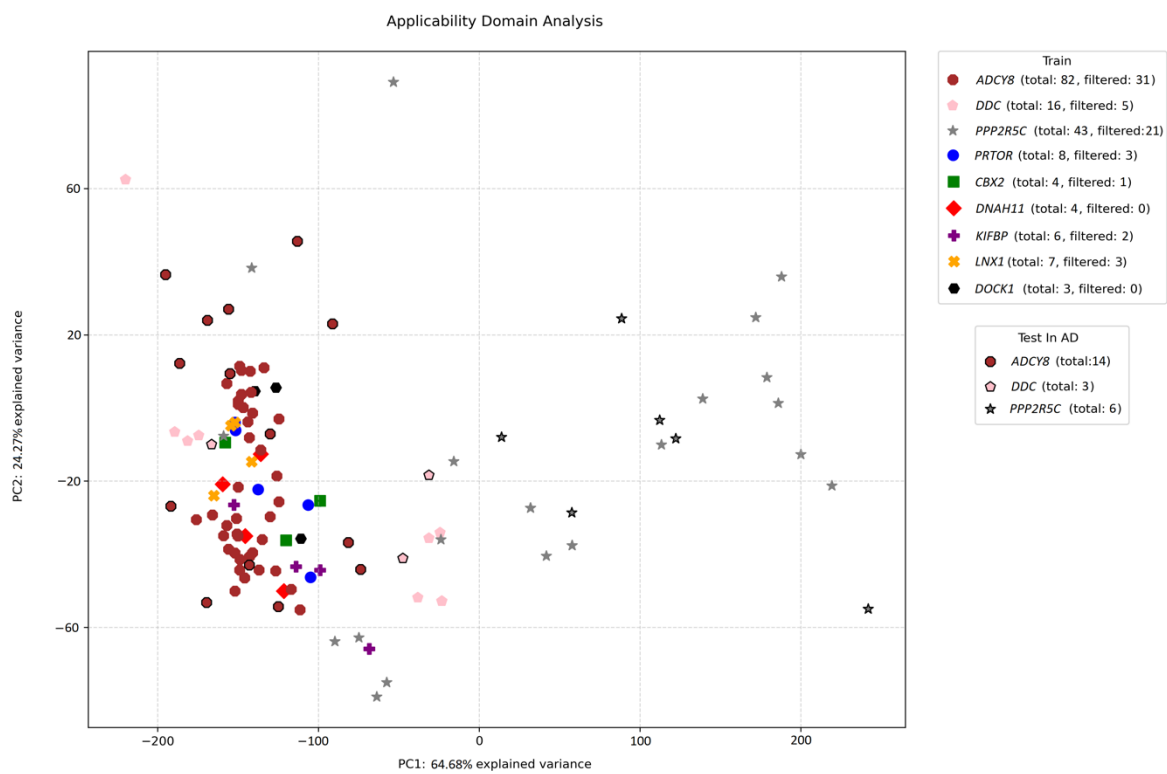
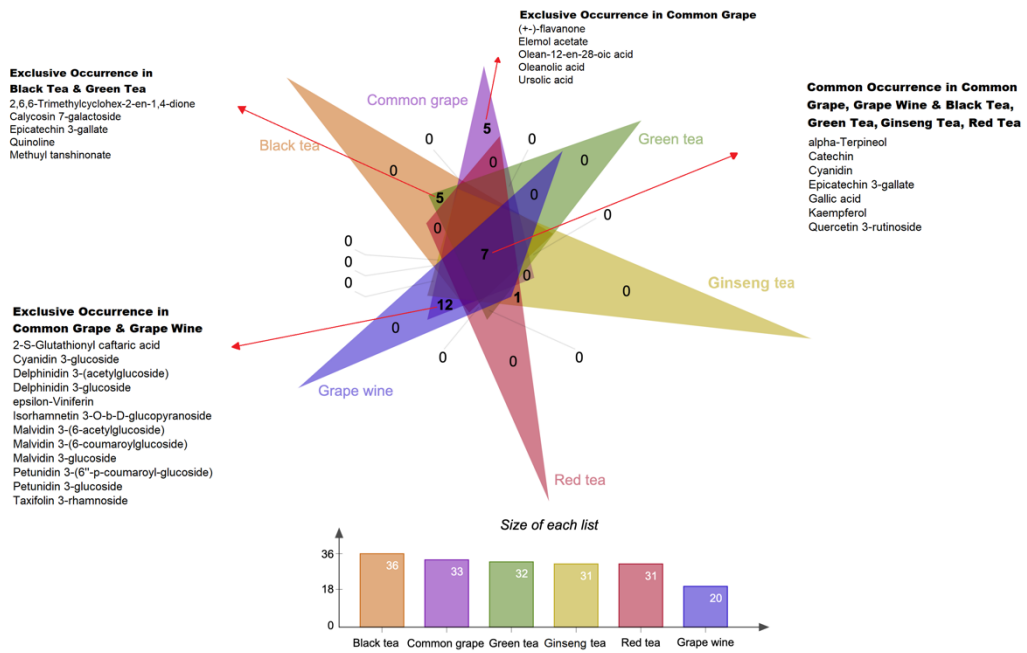
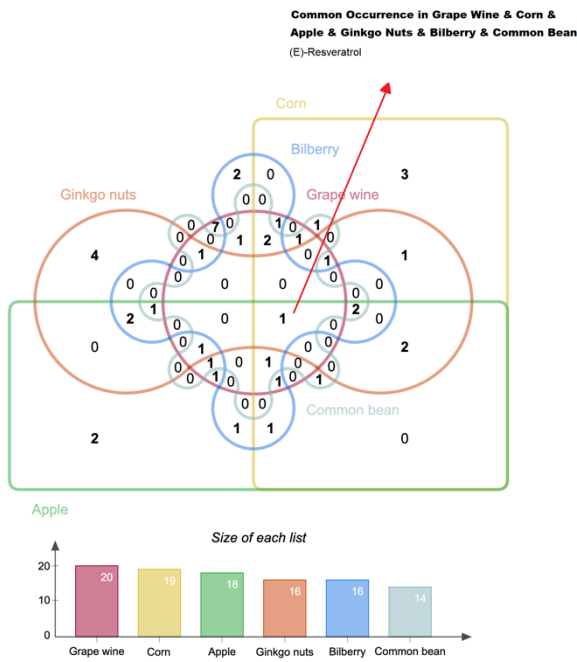


Figure S3

A



B



C

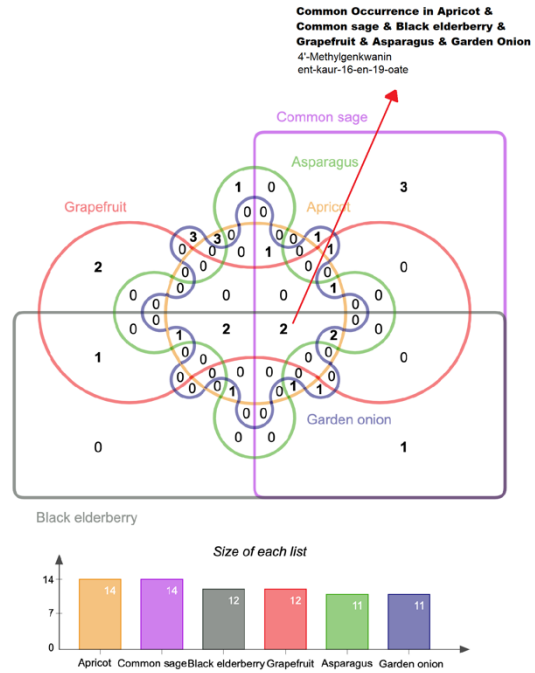


Figure S4

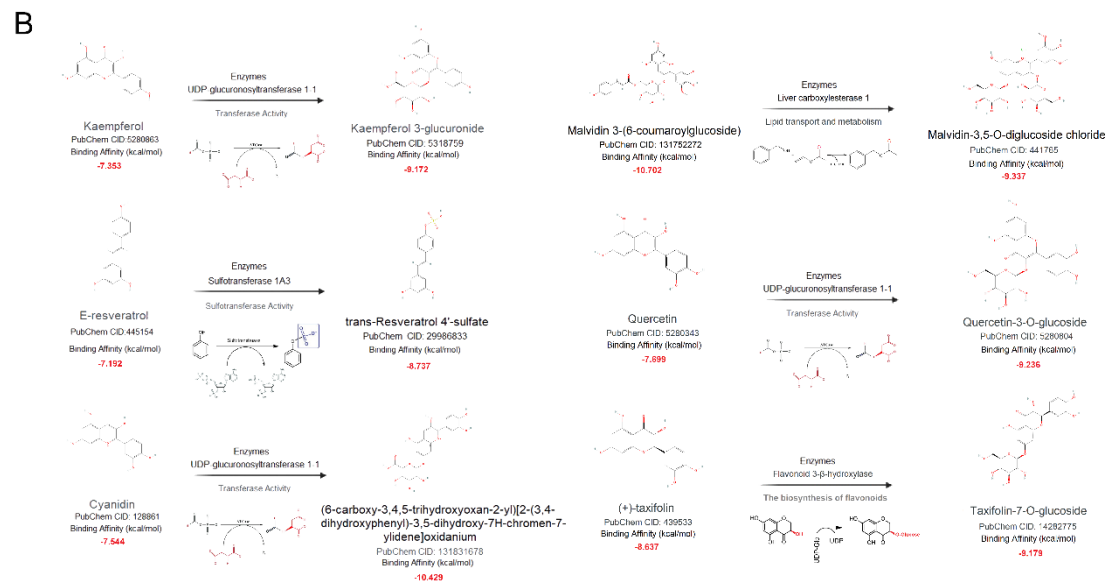
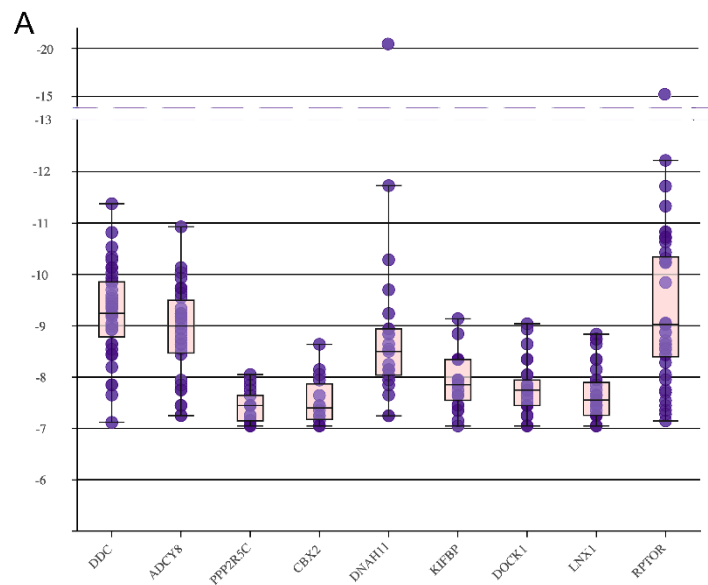


Figure S5

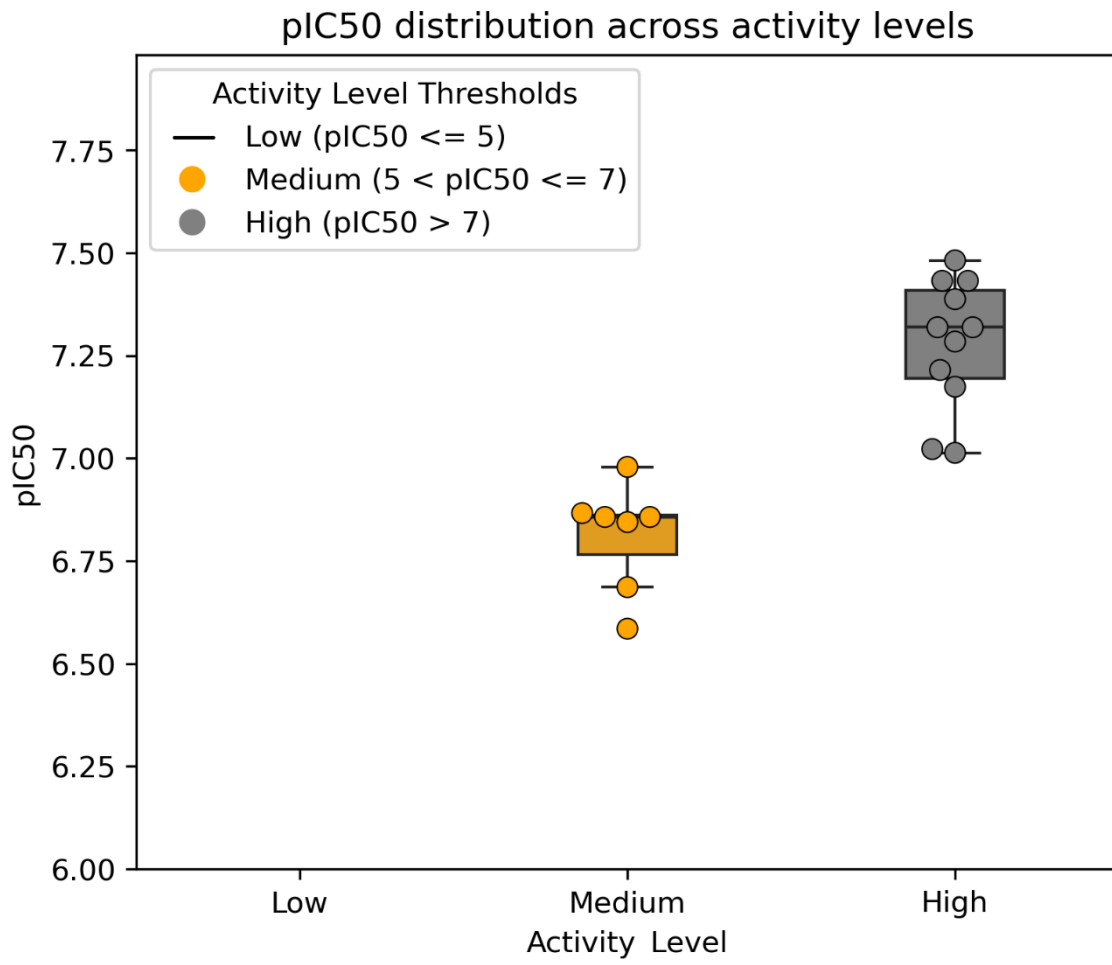


Figure S6

