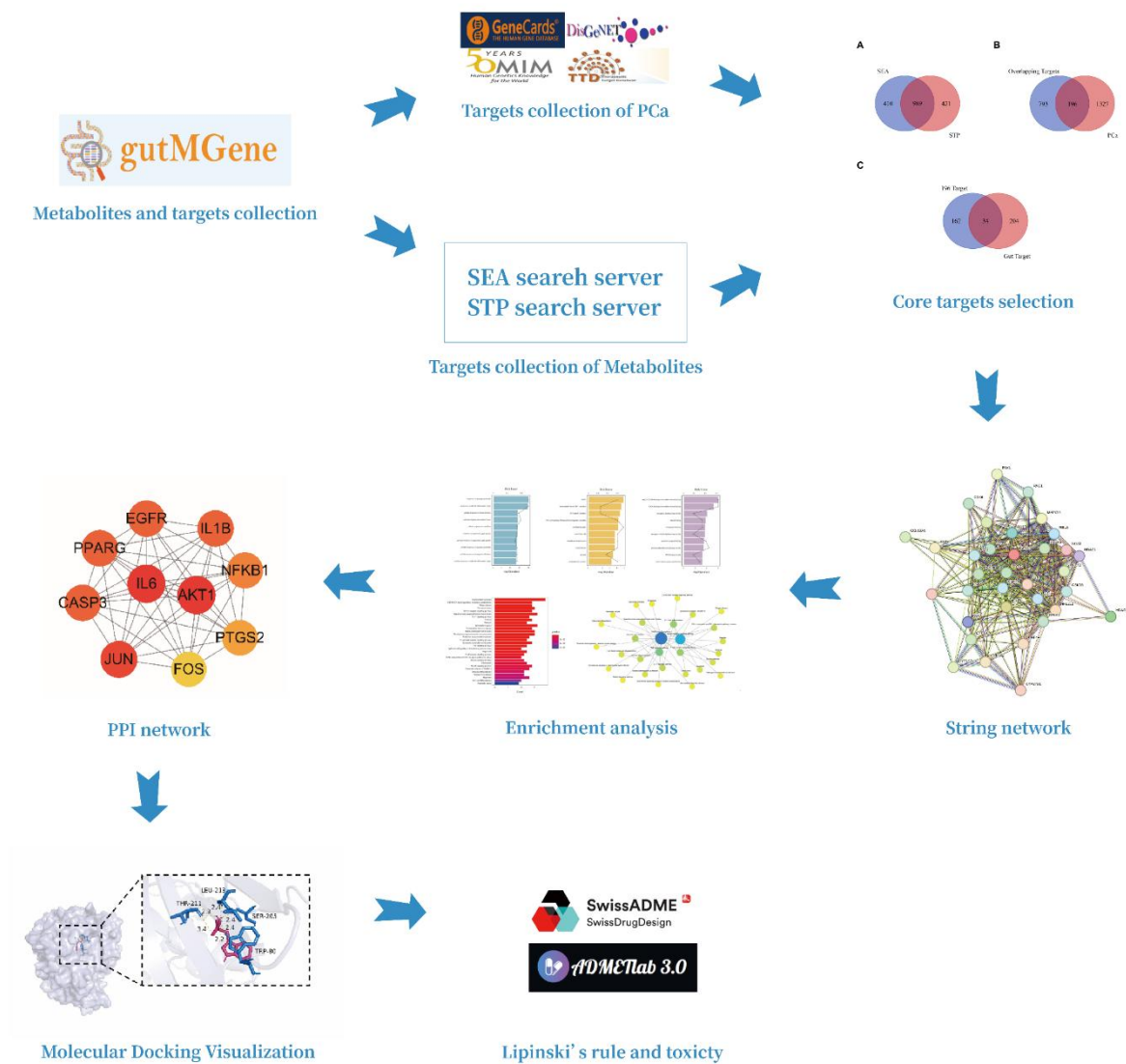
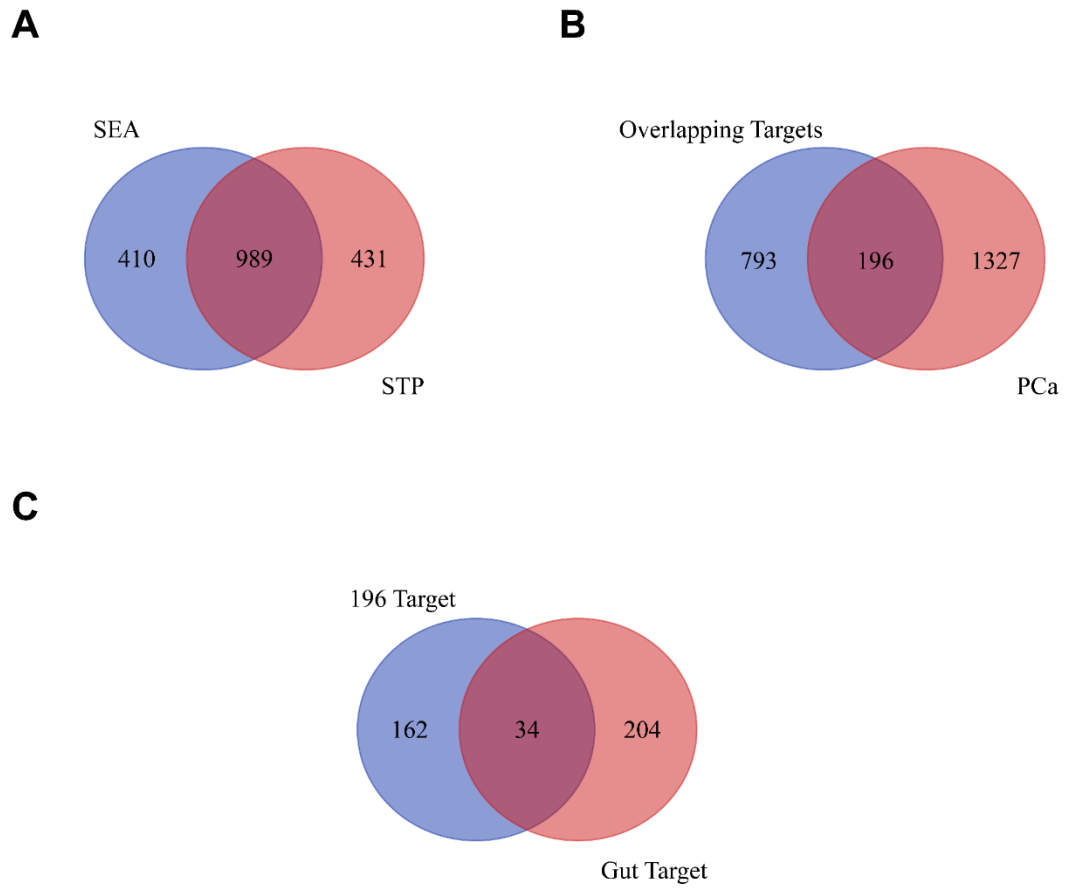
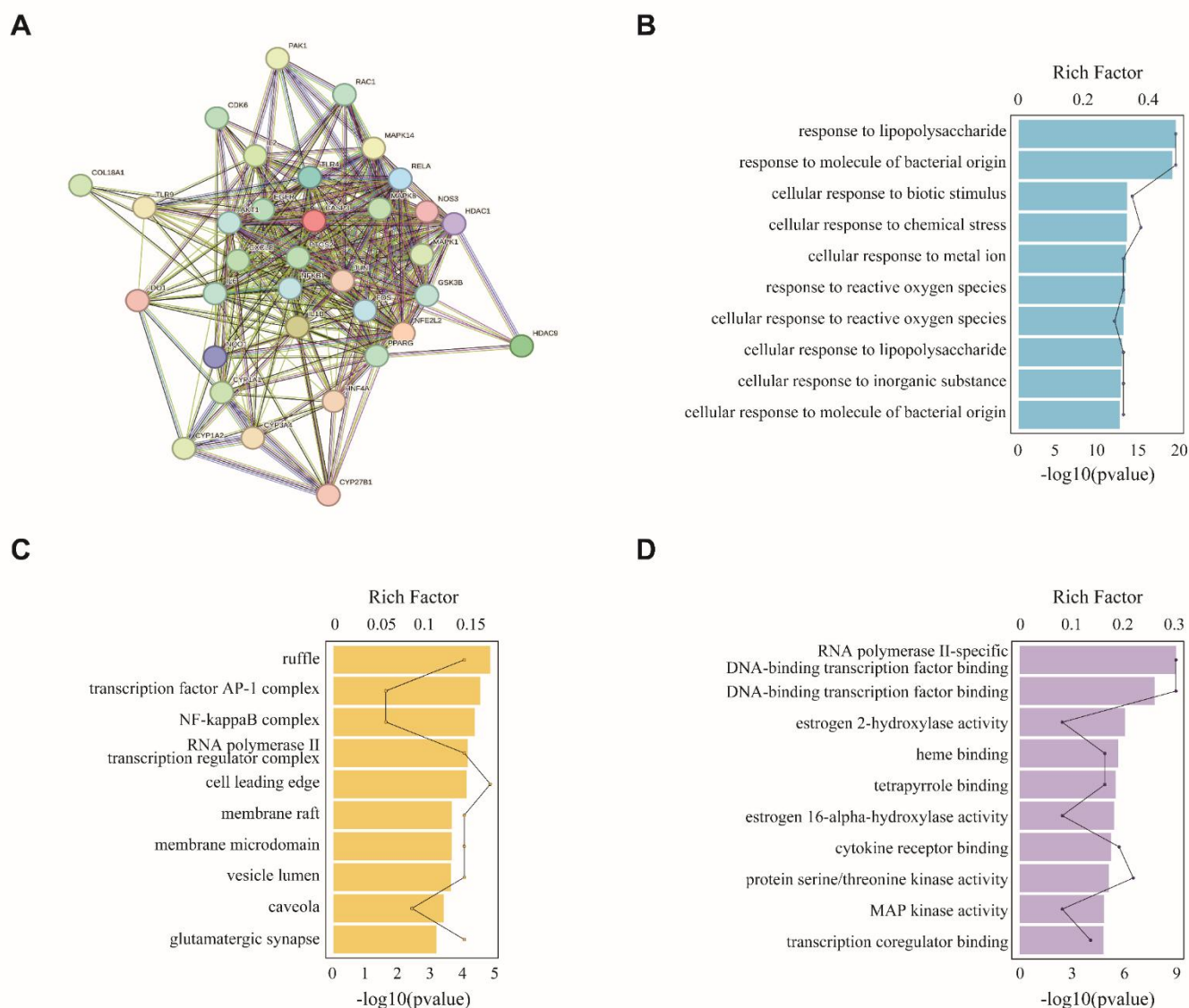




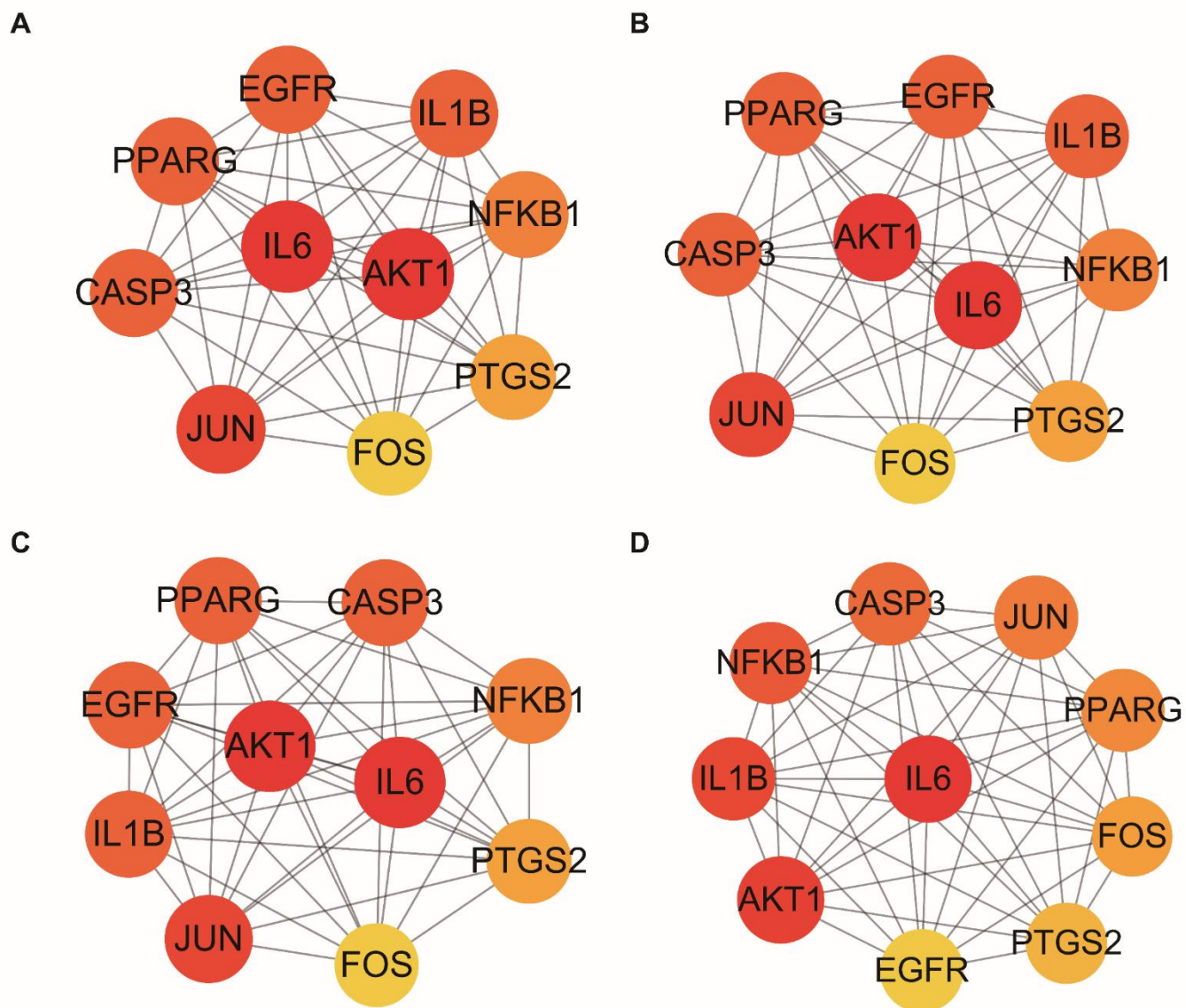
**Figure S1.**The workflow of this study.



**Figure S2.** (A) The number of overlapping microbial metabolite targets identified from the SEA and STP databases was 989.(B) The overlap between predicted targets of microbial metabolites and PCa targets comprised 196 targets.(C) The intersection between PCa-related microbial metabolite targets and targets from the gutMGene database yielded 34 core targets.



**Figure S3.** (A) Construction of a PPI network for the 34 core targets based on the STRING database. (B) GO Biological Process analysis of the 34 core targets by GO enrichment. The line chart shows the Rich Factor on the x-axis, and the bar chart shows  $-\log_{10}(p\text{-value})$  on the x-axis. (C) GO Cellular Component analysis of the 34 core targets. The line chart shows the Rich Factor on the x-axis, and the bar chart shows  $-\log_{10}(p\text{-value})$  on the x-axis. (D) GO Molecular Function analysis of the 34 core targets. The line chart shows the Rich Factor on the x-axis, and the bar chart shows  $-\log_{10}(p\text{-value})$  on the x-axis.



**Figure S4.** (A) Degree algorithm. (B) Closeness Score. (C) MNC algorithm. (D) MCC algorithm.