

Figure 1. Venn diagrams for influenza target. Based on Drugbank, GeneCard, OMIM, TTD, PharmGkb database, 229 influenza-related targets were found.

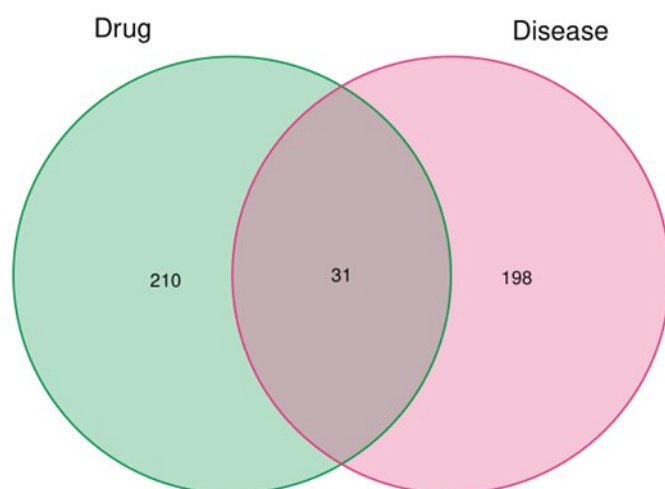


Figure 2. Venn diagrams for the co-target between 242 targets of active ingredients and 229 influenza-related targets. 31 key targets were obtained after the duplicative terms deleted.

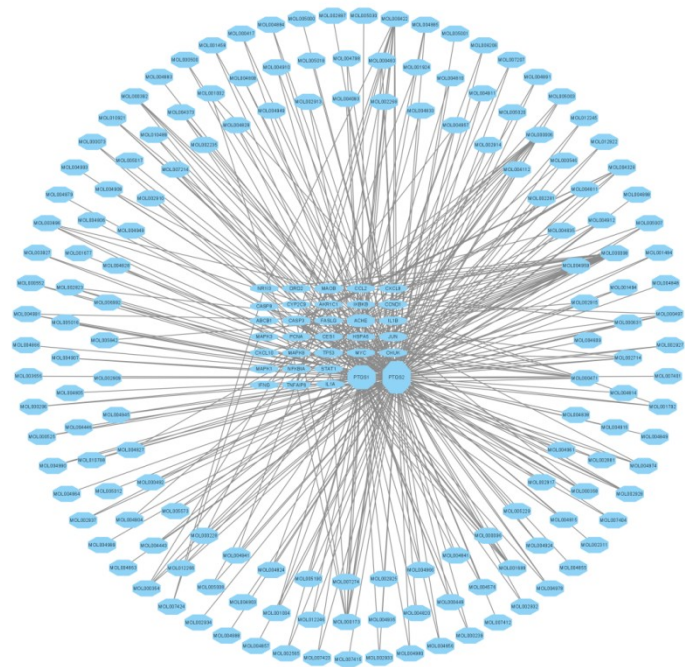


Figure 3. Network diagram between active components and target genes. The circle hexagon nodes represent the active components, the blue hexagon nodes represent the target genes. Nodes size are proportional to their degree.

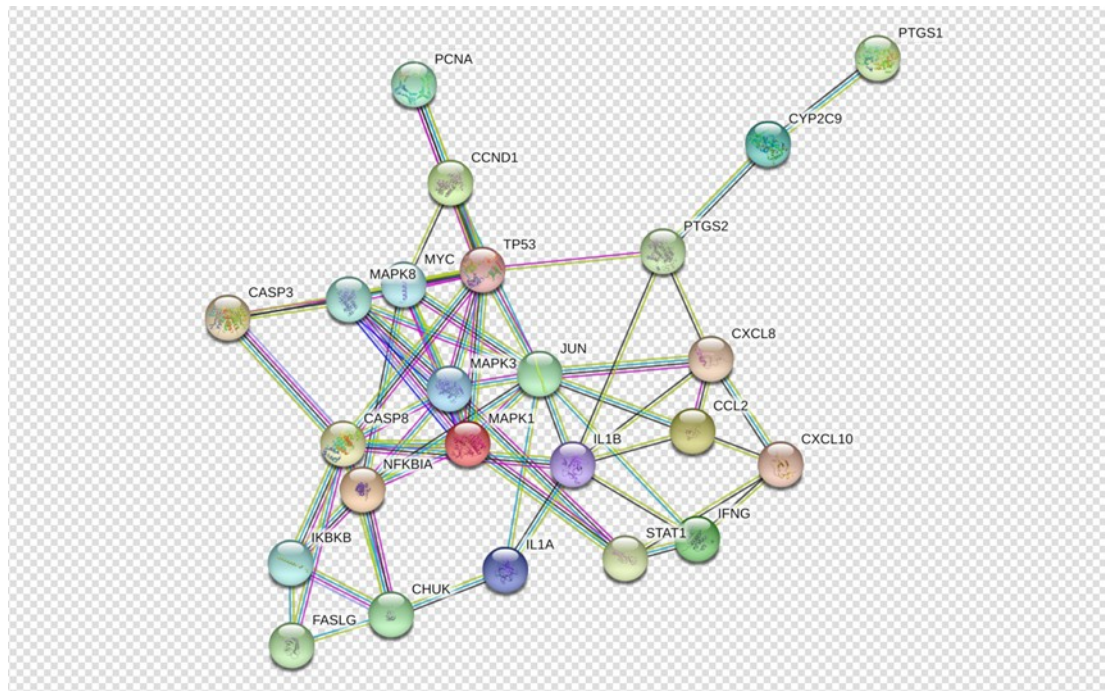


Figure 4. PPI network construction and analysis. PPI network of the co-expressed genes. The PPI network was constructed via the Search Tool for the Retrieval of Interacting Genes online, degree values of 11 target proteins are higher than the average for further analysis.

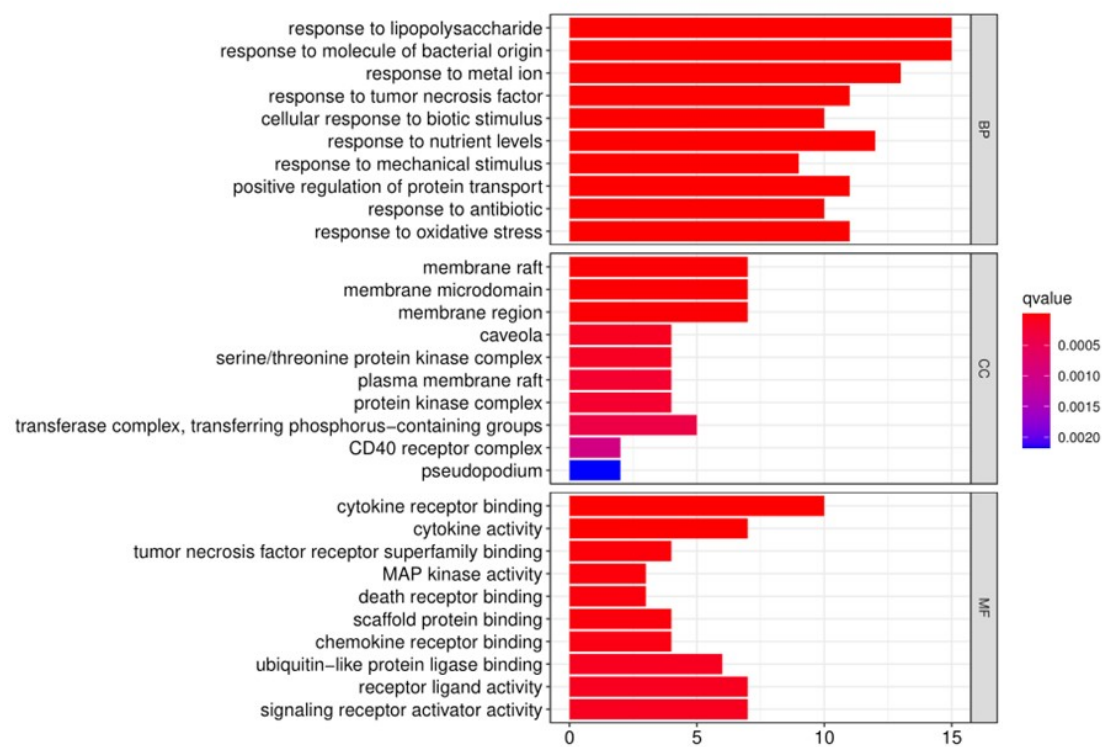


Figure 5. Top 10 GO enrichments in BP, CC, MF (fig 5) GO enrichment. X-axis is

enrichment gene ratio, Y-axis is biological process, molecular function and cellular component analysis. Color represents the adjusted p-value, the bluer the color, the smaller the adjusted p-value.

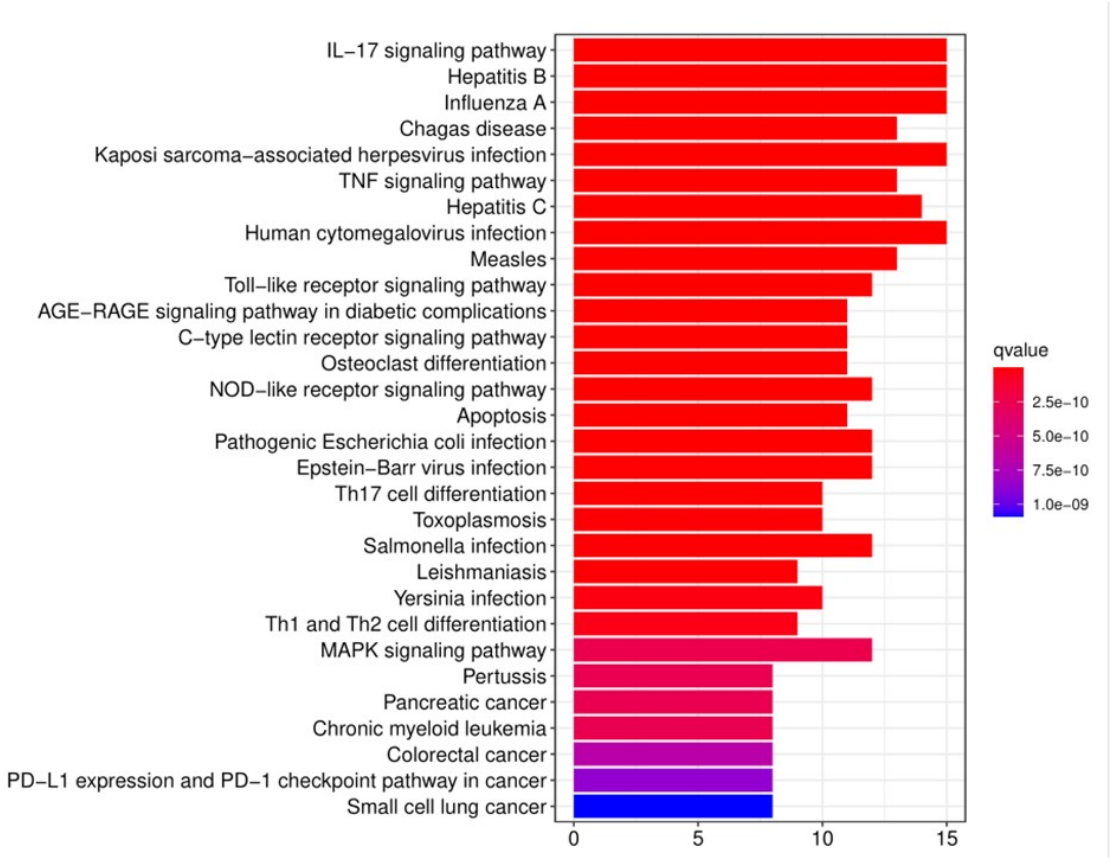
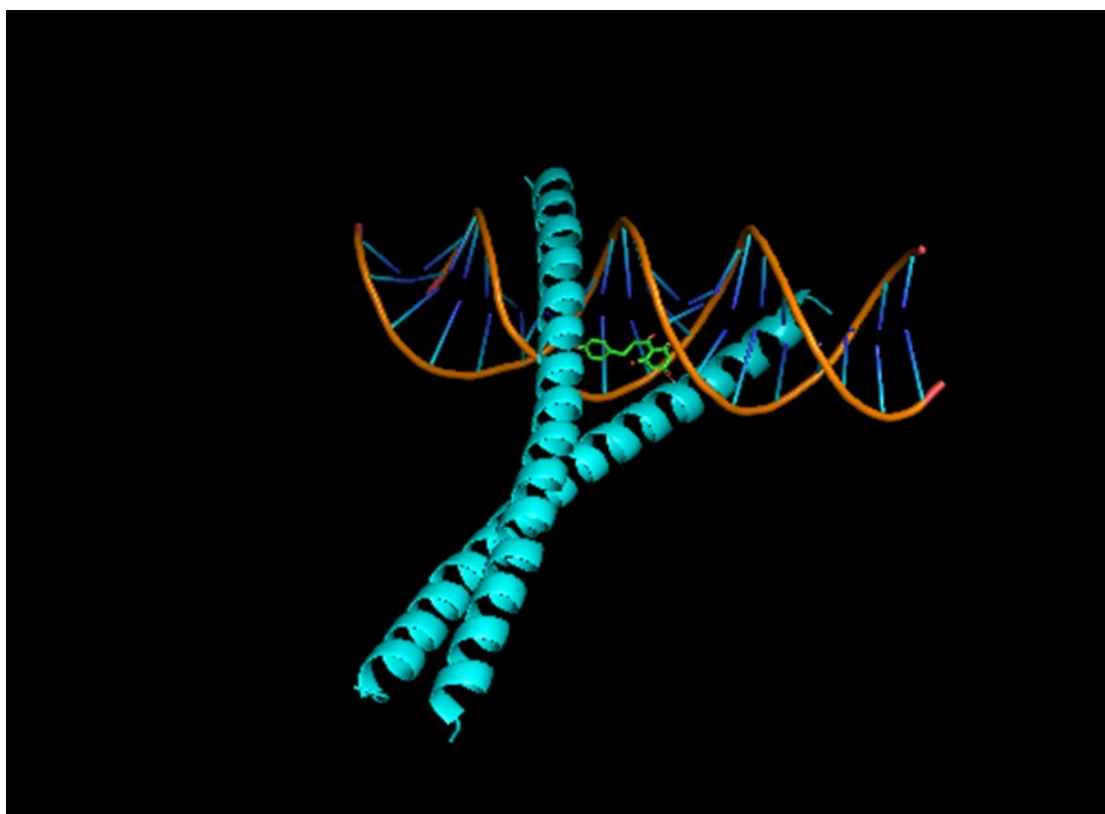
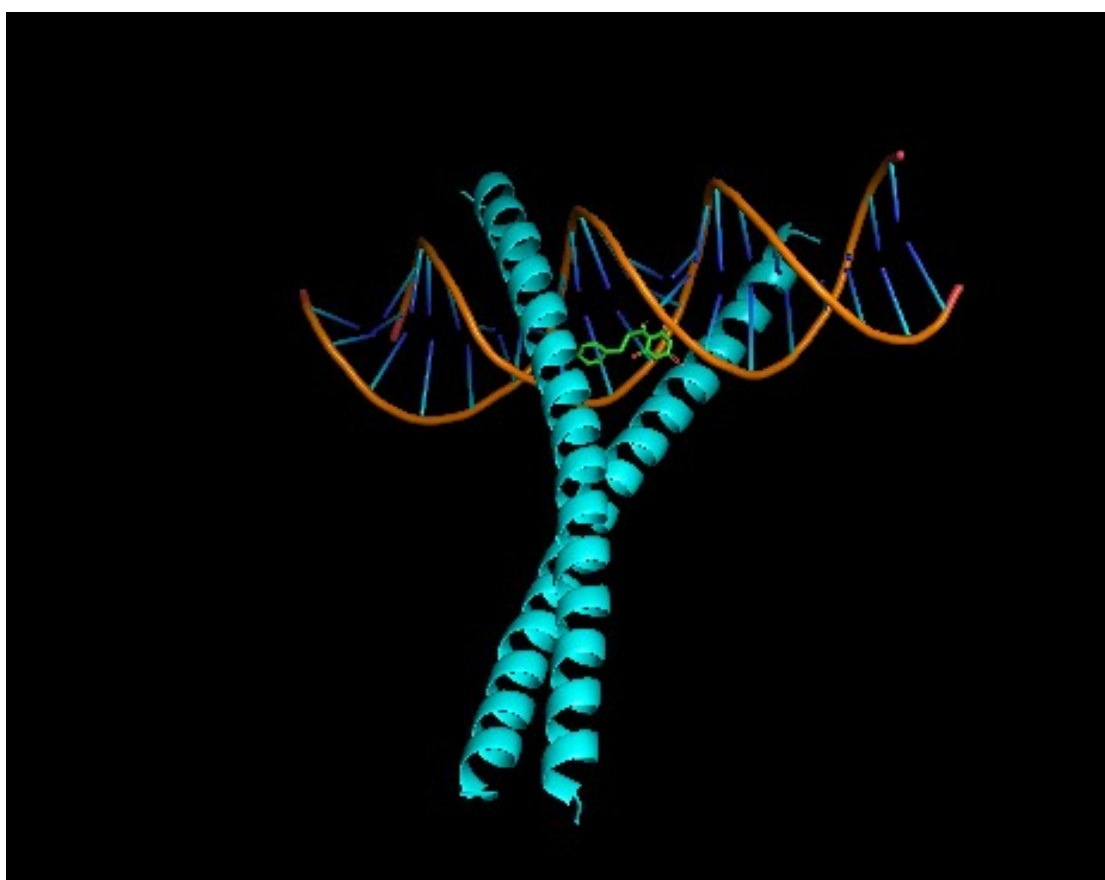


Figure 6. KEGG pathway enrichment and top 30 KEGG pathways annotation. (fig 6). X-axis is enrichment gene count, Y-axis is KEGG pathway, and the color of bar chart represents the adjusted p-value.



7A Quercetin docking with JUN



7B Luteolin docking with JUN

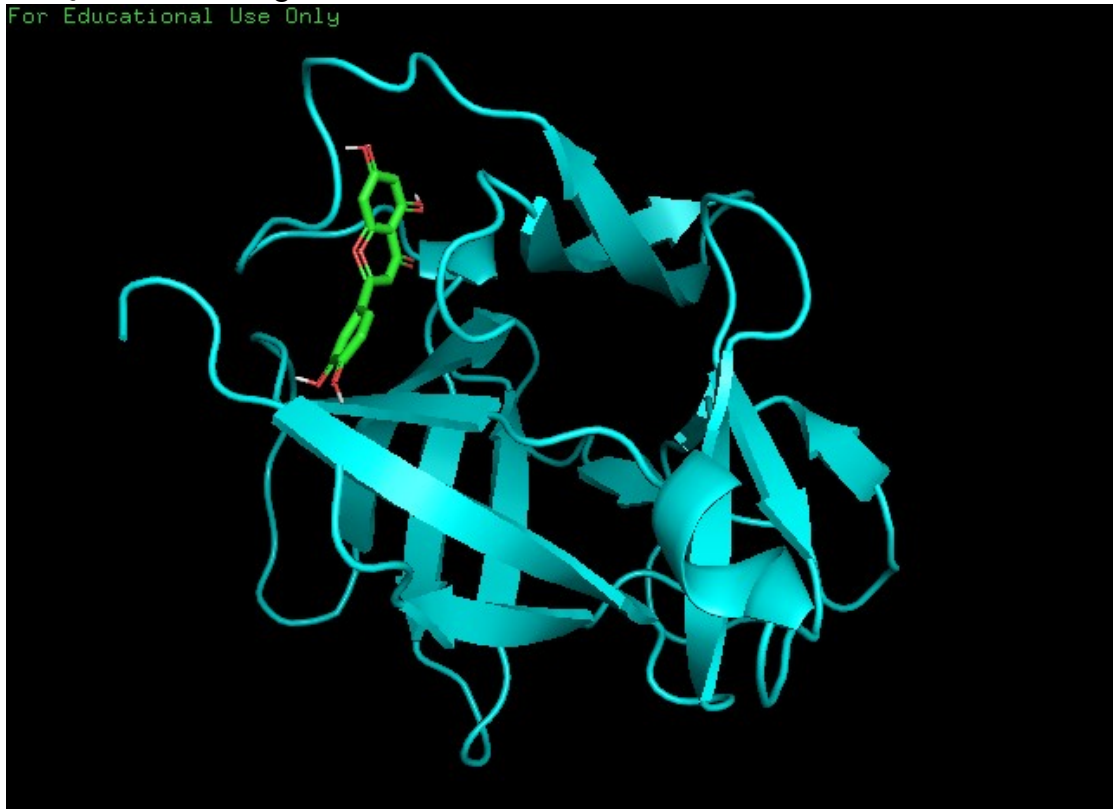


7C Naringenin docking with JUN



7D Quercetin docking with IL1B

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7E Luteolin docking with IL1B

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7F Naringenin docking with IL1B

Figure 7. The docking complex of four targets and their strongest binding

components. the active site residues are shown. JUN (7A-7C) ILIB(7D-7F).