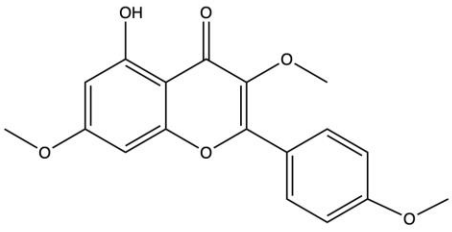
International Journal of
*Molecular Sciences*

MDPI

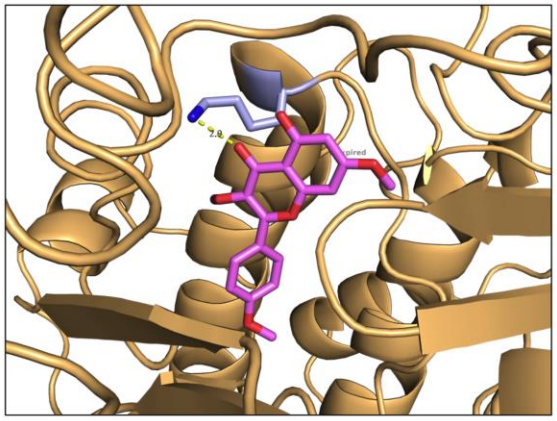
*Supplementary Data*

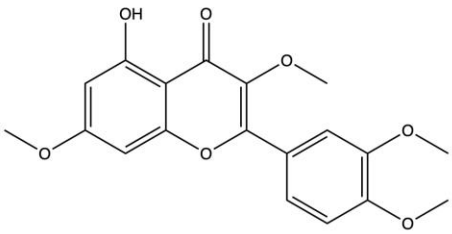
# Network pharmacology and molecular docking-based approach to explore potential bioactive compounds from *Kaempferia parviflora* on chemokine signaling pathways in the treatment of psoriasis disease

**Figure S1:** Molecular docking of complex structure between AKT1-L8, AKT1-L11, and PIK3R1-L12

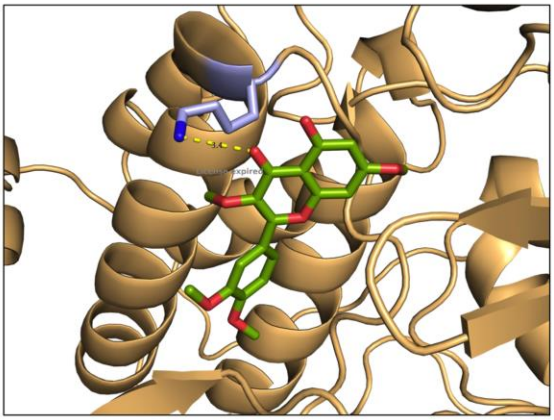


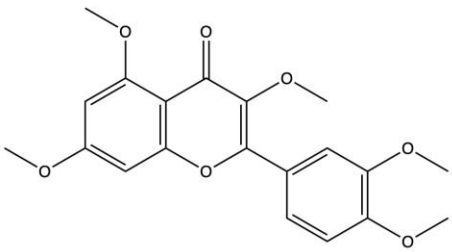

5-hydroxy-3,7,4'-trimethoxyflavone



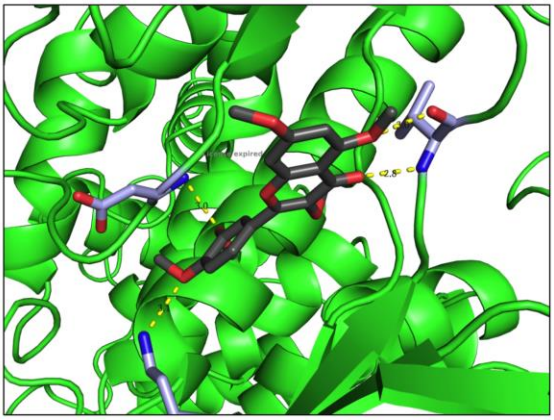



5-hydroxy-3,7,3',4'-tetramethoxyflavone






3,5,7,3',4'-pentamethoxyflavone




https://doi.org/10.3390/ijms26115243

**Figure S2:** 2D Molecular Docking Analysis of Selected Compounds with SRC, AKT1, and PIK3R1.

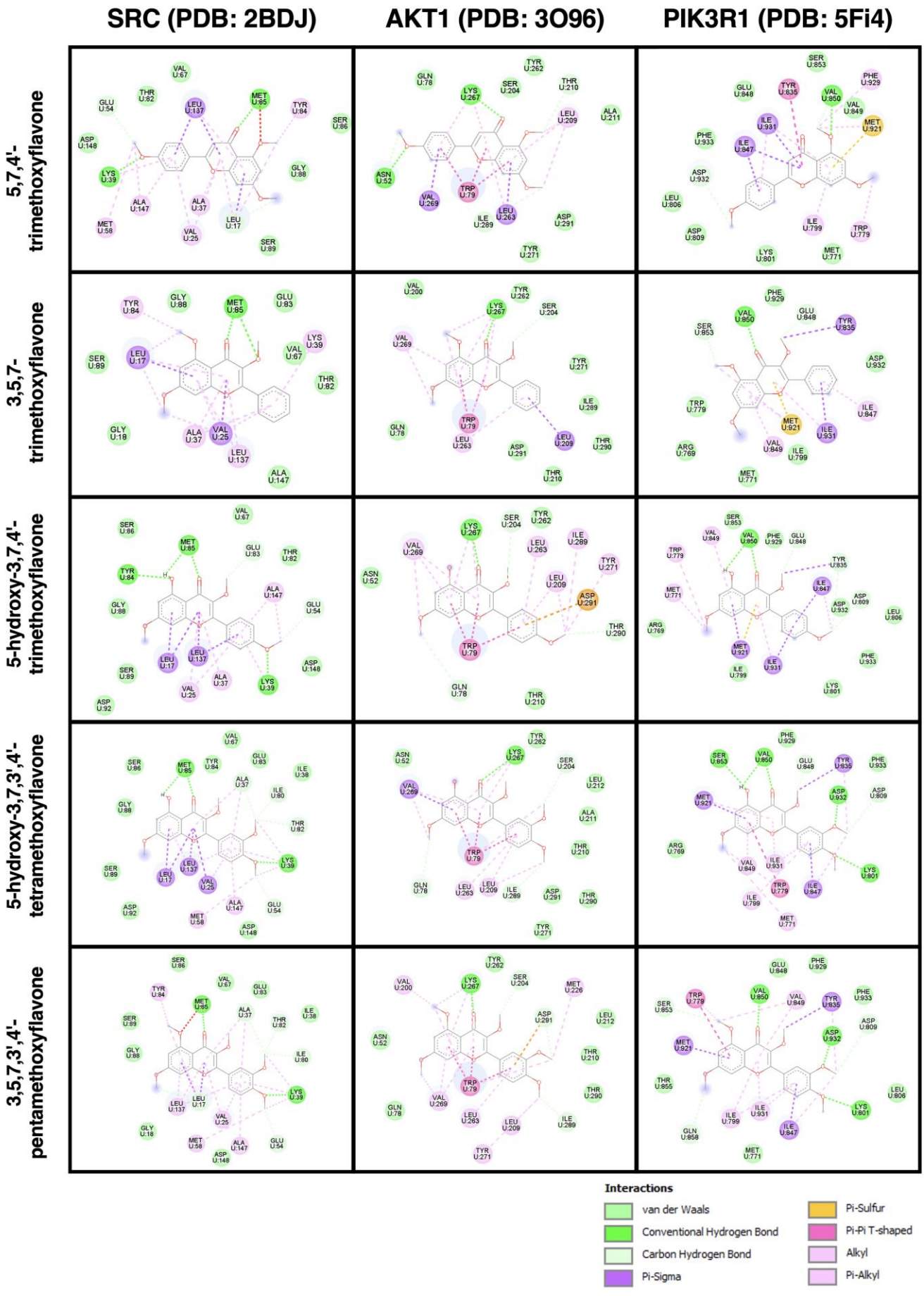


**Figure S3:** Chemical Structures of Methoxyflavones Isolated from KP

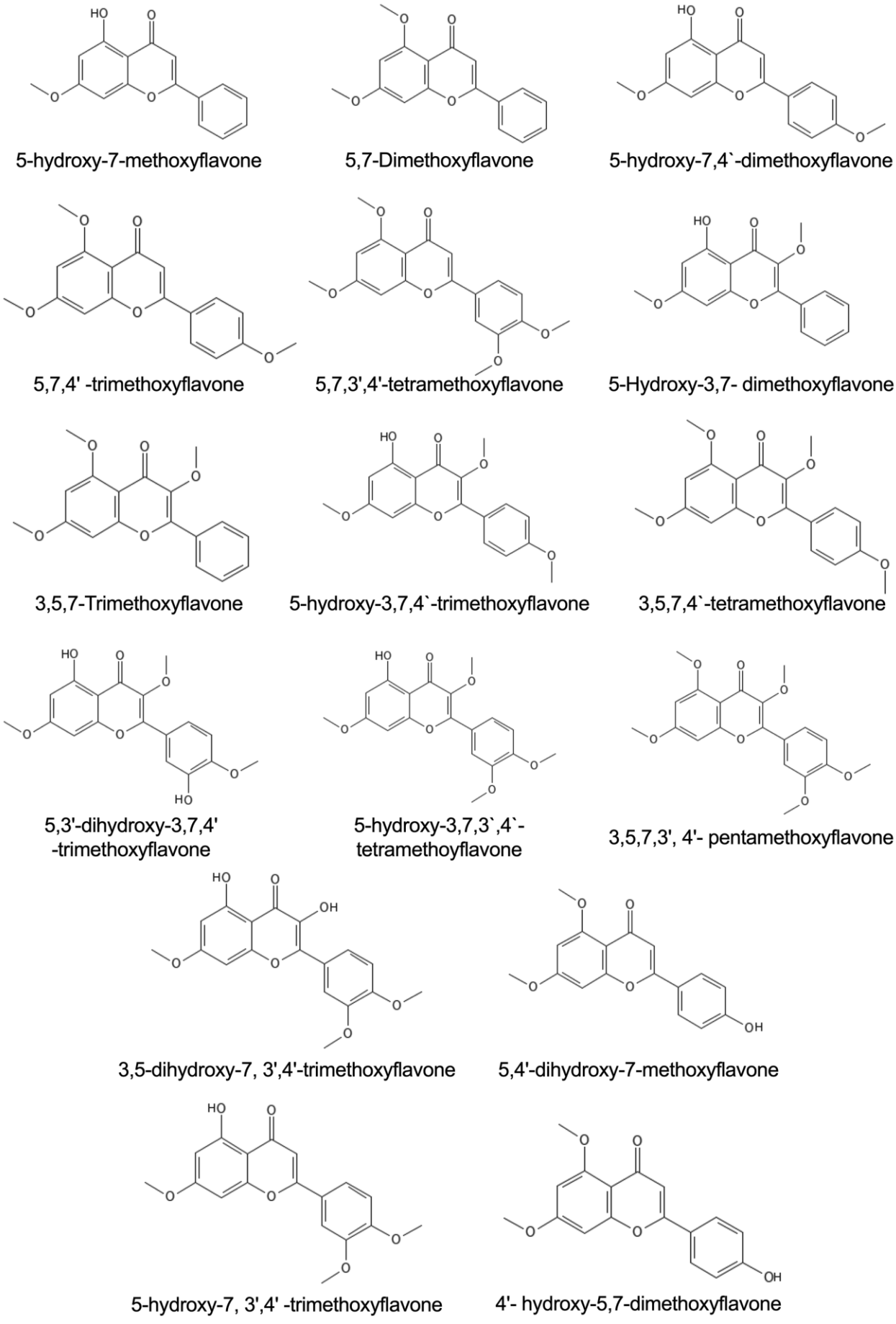
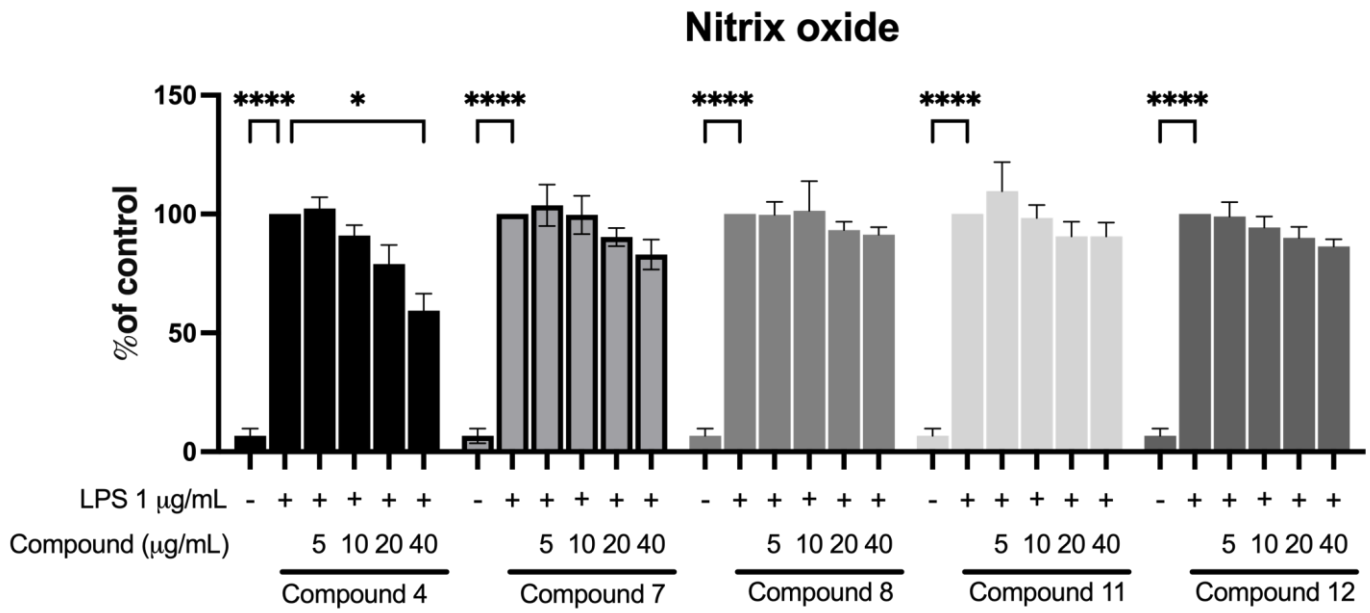


**Figure S4:** Effects of Bioactive Compounds in KP on Nitric Oxide Production in LPS-Induced RAW264.7 Cells.




RAW264.7 macrophages were treated with LPS (1 μg/mL) to induce an inflammatory response, followed by exposure to different concentrations (0, 5, 10, 20, and 40 μg/mL) of each compound for 48 hours. Data are presented as mean ± S.D. from at least three independent experiments. Statistical significance was determined using one-way ANOVA followed by post hoc analysis (*$p < 0.05$ and ****$p < 0.01$). compound 4; 5,7,4'-trimethoxyflavone, compound 7; 3,5,7-trimethoxyflavone, compound 8; 5-hydroxy-3,7,4'-trimethoxyflavone, compound 11; 5-hydroxy-3,3',4',7-tetramethoxyflavone, and compound 12; 3,5,7,3',4'-pentamethoxyflavone.