Journal of Applied Pharmaceutical Science

Available online at http://www.japsonline.com

Network pharmacology and molecular dynamics studies unveil the therapeutic mechanisms of *Zingiber officinale* against dyspepsia

Stefeny Theresia Simatupang[1], Doni Dermawan[1], Nadia[1], Santi Tan[1], Raymond Rubianto Tjandrawinata[1,2]

[1]Department of Dexa Omic Sciences (Dexomics), Dexa Medica, South Tangerang, Indonesia.
[2]Center for Pharmaceutical and Nutraceutical Research and Policy (CPNRP), Atma Jaya Catholic University of Indonesia, South Jakarta, Indonesia.

Doi: http://doi.org/10.7324/JAPS.2025.240961

SUPPLEMENTARY MATERIALS

The following supplementary materials can be downloaded from this link: https://japsonline.com/supplementary-materials/19-1738640443-ADDL-250707041053.xlsx

1. Supplementary Table S1. Compounds of *Zingiber officinale*.
2. Supplementary Table S2. Bioactive compounds of *Zingiber officinale*.
3. Supplementary Table S3. Target proteins associated with *Zingiber officinale*.
4. Supplementary Table S4. Unique *Zingiber officinale* target proteins.
5. Supplementary Table S5. Dyspepsia target proteins (*Homo sapiens*).
6. Supplementary Table S6. Common target proteins of *Z. officinale* and dyspepsia.
7. Supplementary Table S7. Network topology analysis of all common target proteins between *Z. officinale* and dyspepsia.
8. Supplementary Table S8. Network topology analysis of potential target proteins from *Z. officinale*.
9. Supplementary Table S9. GO enrichment analysis of biological processes (BPs), molecular functions (MFs), and cellular components (CCs).
10. Supplementary Table S10. KEGG signaling pathways linked to dyspepsia in *Z. officinale*.
11. Supplementary Table S11. Molecular docking results.
12. Supplementary Table S12. Molecular docking atom-type interaction results.