

## RESEARCH ARTICLE

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# The Antifungal Activities of *Syzygium aromaticum* and *Alpinia purpurata* Extracts Against *Candida krusei*: Bioactivity Tests, Molecular Modeling, and Toxicity Tests

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## Abstract

**Background:** *Candida krusei* is the cause of the fungal infection candidiasis, which has a high mortality rate. Intrinsic resistance to fluconazole can cause the failure of *Krusei* candidiasis treatment. Therefore, it is necessary to find alternative drugs to eliminate the fungus. Extracts of *Syzygium aromaticum* and *Alpinia purpurata* have been proven to be alternative solutions for treating *Candida krusei* resistance. **Objective:** This study aims to explore the active compounds *Syzygium aromaticum* and *Alpinia purpurata* as treatments against *Candida krusei* through bioactivity tests, molecular modeling, and toxicity tests. **Methods:** Determination of antifungal activity with the agar well diffusion and microbroth dilution method. Molecular modeling was conducted using the following software: Marvin Sketch, LigandScout 4.4.5, AutoDock ver 4.2.6, PyMOL, LigPlus, MOE ver 2008. **Result:** Bioactivity test results of the two natural extracts against *C. krusei* ATCC 6258, it was found that the *S. aromaticum* and *A. purpurata* extracts have MIC<sub>50</sub> values of 0.031 µg/mL and 1.435x10<sup>5</sup> µg/mL. The molecular modeling found that the compounds Benzotriazole, 1-(4-methyl-3-nitrobenzoyl)-, 1,3,4-Eugenol Acetate, Stigmasta-5,22-dien-3-ol, acetate (3 beta)- and Farnesyl acetate from the two natural extracts, interacts with the active site of the enzyme lanosterol-14- $\alpha$ -demethylase with a binding energy of -8.91, -6.04, -13.53, and -7.15 kcal/mol. The oral acute toxicity test of *S. aromaticum* and *A. purpurata* extracts proved that the LD<sub>50</sub> was >6000 mg/kg BW and >8000 mg/kg BW. The acute dermal toxicity test of the two extracts showed that the LD<sub>50</sub> was >6000 mg/kg BW. **Conclusion:** *S. aromaticum* and *A. purpurata* extracts have been proven to be alternative solutions for treating *Candida krusei* resistance.

**Keywords:** *Candida krusei*- *Syzygium aromaticum*- *Alpinia purpurata*- lanosterol-14- $\alpha$  demethylase

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## Introduction

The rise in the number of immunocompromised patients, such as premature babies, HIV (Human Immunodeficiency Virus) patients, cancer patients, and recipients of immunosuppressive drug therapy, has led to an increase in the number of fungal infections in recent years (Denning & Bromley, 2015). More than 300 million people worldwide suffer from serious fungal infections, causing more than 1.5 million deaths each year, with the highest cause of death being *Candida* spp (Schmiedel & Zimmerli, 2016). As many as 35% -65% of *Candida* spp infections are caused by non-*Candida albicans* (Tan et al., 2010). *Candida glabrata* and *Candida krusei* are common

causes of candidiasis in the bloodstream. Treatment failure due to *Candida krusei*'s intrinsic resistance to fluconazole is one of the causes of the high mortality rate from *Candida krusei* infection, with a prevalence of 20-40% (Krcmery & Barnes, 2002)(Quindós et al., 2008)Whaley et al., 2017).

*Candida krusei*'s resistance mechanism to fluconazole is attributed to several factors: the drug's lower affinity towards lanosterol-14 $\alpha$ -demethylase, the overexpression of lanosterol-14 $\alpha$ -demethylase, the decreased effective concentration of antifungal drugs by efflux pump activity, and the formation of biofilms that hinder the antifungal diffusion process (Berkow & Lockhart, 2017; Jamiu et al., 2021; Cuéllar-Cruz et al., 2012). An alternative solution to handling *Candida krusei* resistance is the development

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of natural products, provided that they have low toxicity to humans (Cuéllar-Cruz et al., 2012; Khoddami et al., 2013). Phenolic compounds in many vegetable sources can be an alternative to antifungal drugs (Khoddami et al., 2013). This is because the hydrophobic properties of phenolic compounds allow them to enter the lipid membrane of the fungus, thereby affecting the function of the cell membrane and causing homeostasis disturbances, resulting in the disruption of the integrity of the fungal cell (Rao et al., 2010).

Indonesia has diverse flora and medicinal plants that could potentially work against *Candida* (Karo et al., 2017). Phenolic compounds of *Syzygium aromaticum* and *Alpinia purpurata*, such as eugenol, flavonoids, hydroxybenzoic acid, hydroxycinnamic acid, hydroxyphenyl propane, saponins, and tannins, are known to have the potential to be used against *Candida* (Kochuthressia et al., 2010; Yassin et al., 2020; C et al., 2012). Flavonoids work by inhibiting the fungal nucleic acid synthesis process and destabilizing cell membranes by changing the properties of fungal cell membranes. In comparison, saponins work as antifungals by interfering with the permeability of the fungal cell wall (Fakhrurrazi et al., 2012).

The potency of *Syzygium aromaticum* and *Alpinia purpurata* as anti-*Candida krusei* agents was discovered through bioactivity tests, molecular modeling, and toxicity tests. The agar well diffusion and microbroth dilution bioactivity methods were conducted to determine the antifungal activity of *Syzygium aromaticum* and *Alpinia purpurata* based on their fungal growth patterns (Balouiri et al., 2016). For the development of antifungal drugs, molecular modeling using the in-silico method through molecular docking and dynamic simulations was performed to determine the affinity of new compounds toward target enzymes (Bitencourt-Ferreira & de Azevedo, 2019). Overall, it is necessary to study the antifungal activity of extracts of *Syzygium aromaticum* and *Alpinia purpurata* in inhibiting the growth of *Candida krusei* as potential agents that can overcome antifungal drug resistance in *Candida krusei* infections. The antifungal activities of the above-mentioned extracts can be investigated through bioactivity testing, molecular modeling, and toxicity testing.

## Materials and Methods

### Preparation of *Candida krusei* ATCC 6258 Fungus Test Samples

The test fungus were grown on Sabouraud Dextrose Agar at room temperature for 24 hours. The fungal suspensions were formed with sterile NaCl 0.9% with a concentration of 0.5 McFarland.

### Preparation of Test Solutions

Five concentrations of fluconazole controls (4, 8, 16, 32, and 64 µg/mL) along with five concentrations of ethanol extracts of *Syzygium aromaticum* and *Alpinia purpurata* were made (1600, 800, 400, 200, 100 mg/mL with 10% DMSO solution) (Omar, 2017; Kamoda et al., 2020).

### Determination of Antifungal Activity with the Agar Well Diffusion Method

The *Candida krusei* suspension was smeared on Müller Hilton's media, and holes of 6 mm diameter were made aseptically. 50 µL of fluconazole and the ethanol extracts of *Syzygium aromaticum* and *Alpinia purpurata* were added to the wells. They were then incubated at 37 °C for 24 hours. Antifungal activity was observed based on the diameter of the inhibition area (Sahal et al., 2019; Cordeiro et al., 2014). Guidelines for the disk diffusion susceptibility test of *Candida* species were adapted from the M44 document from the Clinical and Laboratory Standards Institute (CLSI) (Sheehan et al., 2004).

### Determination of Antifungal Activity with the Microbroth dilution method

Guidelines for the in vitro susceptibility of *Candida* species were adapted from the M27-A3 document from the Clinical and Laboratory Standards Institute (CLSI) (Song et al., 2015). RPMI 1640 media was placed into a 96-well round-bottom microplate. Then, the fungal suspensions were tested. The fluconazole and ethanol extracts of *Syzygium aromaticum* and *Alpinia purpurata* were added to the positive control and test columns. Negative controls and growth controls were included in each run. Each test was conducted three times and incubated at 35°C. Antifungal activity was read using an ELISA reader based on optical density (OD) values at a wavelength of 405 nm before and after 24 hours of incubation. The value of antifungal inhibition was calculated by the following formula:

$$\% \text{ of inhibition} = \left( \frac{1 - ((\text{OD}_{t24} - \text{OD}_{t0}) / (\text{OD}_{k24} - \text{OD}_{k0}))}{1} \right) \times 100$$

Key:

$\text{OD}_{t24}$  = The test sample's optical density value after 24 hours of incubation.

$\text{OD}_{t0}$  = The test sample's optical density value before 24 hours of incubation.

$\text{OD}_{k24}$  = The optical density value of the control after 24 hours of incubation.

$\text{OD}_{k0}$  = The optical density value of the control before 24 hours of incubation.

(Kaya & Ozbilge, 2012; Pratiwi et al., 2015)

### Molecular modeling

Molecular modeling was conducted using the following software: Marvin Sketch, LigandScout 4.4.5, AutoDock ver 4.2.6, PyMOL, LigPlus, MOE (Molecular Operating Environment) ver 2008, and Notepad++ applications, as well as the NCBI website (<https://www.ncbi.nlm.nih.gov/>), Protein Data Bank, (<https://www.rcsb.org/>), SWISS-MODEL (<https://swissmodel.expasy.org/>), PubChem (<https://pubchem.ncbi.nlm.nih.gov/>), ChemSpider (<http://www.chemspider.com/>).

### Protein and Ligand Preparation

The target protein *Candida krusei* lanosterol-14- $\alpha$ -demethylase was obtained by creating a 3-dimensional structural model on the SWISS-MODEL website (<https://swissmodel.expasy.org/>) based on target FASTA sequences from the NCBI database (<https://www.ncbi.nlm.nih.gov/>).

nlm.nih.gov(Jamiu et al., 2021). The proteins were then optimized into PDBQT files by using AutoDock. The active compounds in the *Syzygium aromaticum* and *Alpinia purpurata* extracts were selected from secondary data from a gas chromatography–mass spectrometry (GC-MS) analysis at the DKI Jakarta Provincial Health Laboratory. The 3D structures of the active compounds were downloaded via PubChem and ChemSpider and optimized using Marvin Sketch and AutoDock.

#### Molecular Docking Analysis and Visualization

The target protein and ligand were entered into AutoDock ver 4.2.6. Gridbox was added at the protein receptor site with the coordinates X:18,701 Y:8,328 Z:23,177 and dimensions X:40 Y:40 Z:40. The Lamarckian Genetic Algorithm method was used to calculate the protein and ligand interactions. The affinity value of the protein bond with the ligand compound determines the strength of the conformation. The lower the binding energy value ( $\Delta G$ ) is the stronger the interaction between the ligand and the protein. The visualization and analysis of the interactions between the target protein and ligands were done using the PyMOL and LigPlus software.

#### Dynamic Simulation Analysis

The molecular dynamic simulation analysis was simulated using MOE (Molecular Operating Environment) version 2008. The simulation consisted of three main steps: initialization, equilibration, and production. The simulation was performed using the ensemble isobaric-isothermal (NPT) and ensemble canonical algorithm (NVT). In the initialization and equilibration stages, the simulation was conducted at 100 ps at 300 K, whereas the production stage was performed at 1000 ps (1 ns) at 300 K. The simulation results were then analyzed to determine the stability of the lanosterol-14- $\alpha$ -demethylase-ligand complex.

#### Acute Oral Toxicity

The acute oral toxicity test was performed per the OECD-423 guidelines (Acute toxic class method) and used male Wistar strain white rats aged 3-4 weeks.

#### Acute Dermal Toxicity

The acute oral toxicity test was performed per the OECD-402 guidelines (Acute dermal toxicity) and used male Wistar strain white rats aged 3-4 weeks.

## Results

#### Antifungal activity test

The antifungal activity test with the agar well diffusion method found that *Syzygium aromaticum* and *Alpinia purpurata* extracts could inhibit the growth of *Candida krusei* ATCC 6258 with an inhibition zone diameter of 19.67-34.33 mm and 7.33-11.0 mm (Figure 1). The antifungal activity test with the microbroth dilution method found that the MIC50 and MIC90 value were defined as the lowest concentration of the antibiotic at which 90 and 50% of *Candida krusei* were inhibited, respectively. The MIC50 and MIC90 of *Syzygium aromaticum* extract (MIC50 : 0,031  $\mu\text{g}/\text{mL}$ , MIC90: 2,15 x103  $\mu\text{g}/\text{mL}$ ) was higher than the *Alpinia purpurata* extract (MIC50 : 1,435x105  $\mu\text{g}/\text{mL}$ , MIC90: 12,03 x105  $\mu\text{g}/\text{mL}$ ) (Figure 2).

#### Molecular modeling test

The modeling results from the AutoDock program found two compounds with the lowest binding energy from the extract of *Syzygium aromaticum*, namely, Benzotriazole,1-(4-methyl-3-nitrobenzoyl)- and 1,3,4-Eugenol acetate. The benzotriazole compound, 1-(4-methyl-3-nitrobenzoyl), with a binding value of -8.91 kcal/mol, binds to amino acid residues at the active heme binding site at the amino acid position Val306 and Cys475 (Figure 3). Whereas 1,3,4-Eugenol Acetate, with a binding value of -6.04 kcal/mol, binds to amino acid residues on

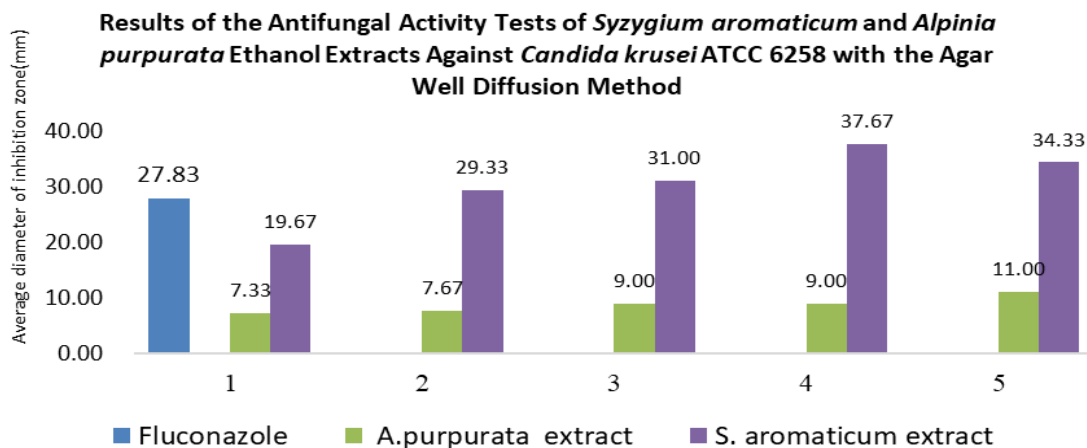


Figure 1. Results of the Antifungal Activity Tests of *Syzygium aromaticum* and *Alpinia purpurata* Ethanol Extracts Against *Candida krusei* ATCC 6258 with the Agar Well Diffusion Method, (1) *Syzygium aromaticum* and *Alpinia purpurata* Ethanol Extracts 100 mg/mL, (2) *Syzygium aromaticum* and *Alpinia purpurata* Ethanol Extracts 200 mg/mL, (3) *Syzygium aromaticum* and *Alpinia purpurata* Ethanol Extracts 400 mg/mL, (4) *Syzygium aromaticum* and *Alpinia purpurata* Ethanol Extracts 800 mg/mL, (5) *Syzygium aromaticum* and *Alpinia purpurata* Ethanol Extracts 1600 mg/mL

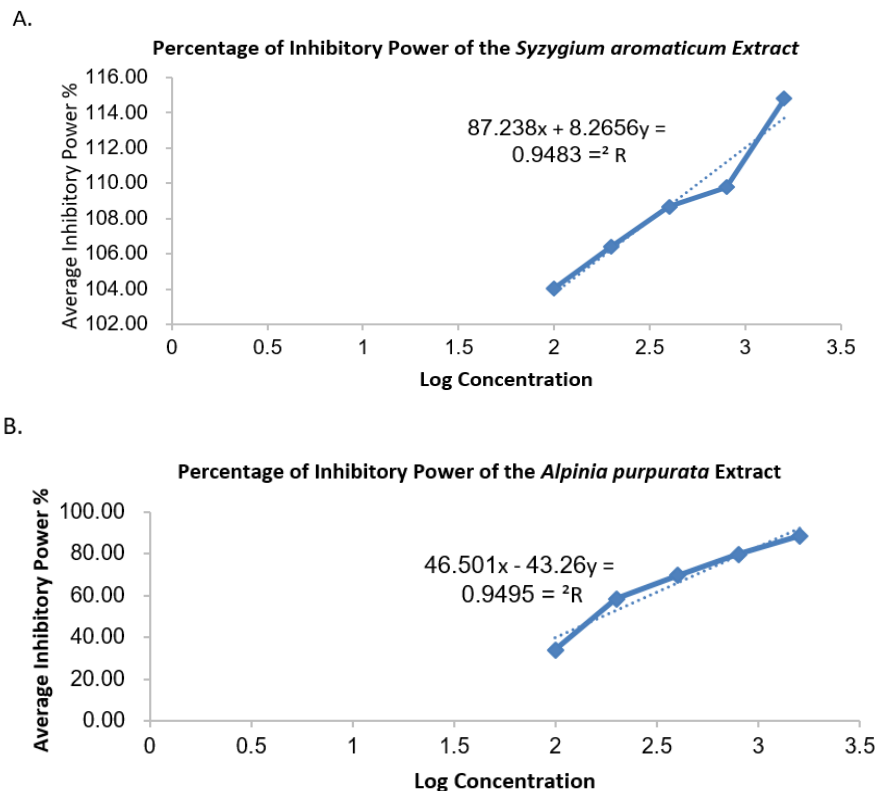


Figure 2. Curve of Percentage Inhibition of Fluconazole Ethanol Extracts of *Syzygium aromaticum* and *Alpinia purpurata* against *Candida krusei* ATCC 6258. The value of antifungal inhibition was calculated by the following formula : % of inhibition =  $(1 - ((OD_{t24} - OD_{t0}) / (OD_{k24} - OD_{k0}))) \times 100$ . (A) Concentrations of *Syzygium aromaticum* to *Candida krusei* ATCC 6258 shows a line equation  $y = 8.2656x + 87.238$ , so that the concentration that can produce an inhibitory power of 50% is  $0.031 \mu\text{g/mL}$ , (B) Concentrations of *Alpinia purpurata* to *Candida krusei* ATCC 6258 shows the line equation  $y = 43.26x - 46.501$ , so the concentration that can produce an inhibitory power of 50% is  $1.435 \times 10^5 \mu\text{g/mL}$ .

the active site of the chemical substrate binding pocket at the amino acid position His377 (Figure 4).

The results of *Alpinia purpurata* extract modeling showed two compounds with the lowest binding energy being Stigmasta-5,22-dien-3-ol, acetate (3 beta)- and Farnesol, acetate. The Stigmasta-5,22-dien-3-ol, acetate (3 beta) compound, with a binding energy value of -13.53 kcal/mol, binds to amino acid residues on the active site of the chemical substrate binding pocket at the amino acid position His377 and Phe380 (Figure 5). The Farnesol compound, acetate, with a binding energy value of 7.15

kcal/mol, binds to amino acid residues in the active site of the chemical substrate binding pocket at the amino acid positions His377 and Phe380 (Figure 6).

The results of the oral and dermal acute toxicity tests of *Syzygium aromaticum* extract found no signs of toxicity and death in the test group with doses of  $> 6000 \text{ mg/kg BW}$  ( $LD_{50} > 6000 \text{ mg/kg BW}$ ). Meanwhile, the *Alpinia purpurata* extract was obtained  $> 8000 \text{ mg/kg BW}$  ( $LD_{50} > 8000 \text{ mg/kg BW}$ ). The results of the acute dermal toxicity test of *Alpinia purpurata* and *Syzygium aromaticum* were  $L > 6000 \text{ mg/kg BW}$  ( $LD_{50} > 6000$

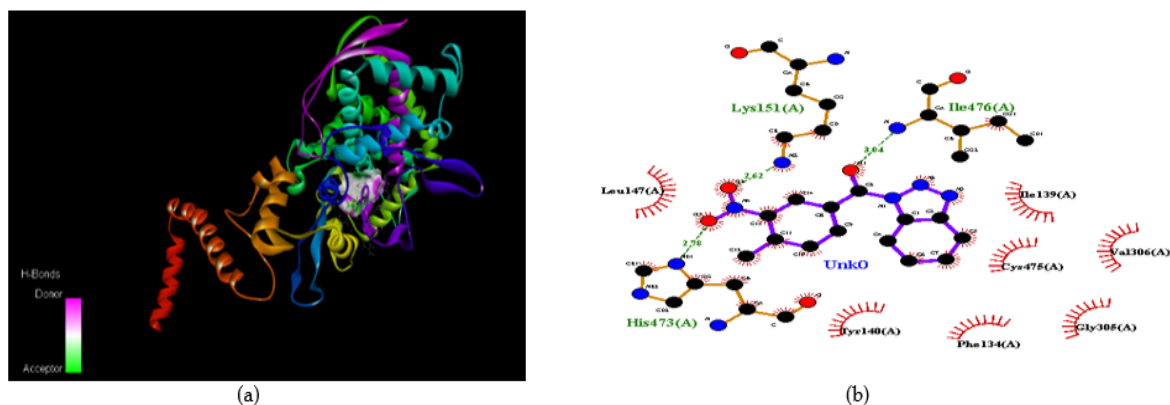


Figure 3. (a) Three-dimensional (b) and two-dimensional visualizations of the interactions between Benzotriazole, 1-(4-methyl-3-nitrobenzoyl)- and lanosterol-14- $\alpha$ -demethylase





1.4 mm) (Gonelimali et al., 2018) was greater than that of *Alpinia purpurata* (12.4 ± 0.2 mm) (Kochuthressia et al., 2010).

Eugenol from the *Syzygium aromaticum* and *Alpinia purpurata* extracts can inhibit fungal growth by reducing the expression of the *Candida tropicalis* proteinase by 64.92-87.80%. This reduction disrupts fungal cells from obtaining nutrients, enables invasion and dimorphism, and disturbs biofilm formation (Pandey et al., 2018; Khan & Ahmad, 2013). In addition, the binding of eugenol to the cell surface and penetration onto the target site (the lipid bilayer of the cytoplasmic membrane) causes the depolarization of fungal cells, which results in ion leakage and loss of membrane potential. This loss leads to a disruption of cellular function which will eventually cause cell death (Latifah-Munirah et al., 2015).

Based on the MIC50 value in research it was found that the *Syzygium aromaticum* extract was included in the category of good activity, while the *Alpinia purpurata* extract was included in the inactive category in inhibiting the growth of *Candida krusei* ATCC 6258. (Indrayanto et al., 2021) The results of the MIC50 test of the *Syzygium aromaticum* extract are close to the previous MIC50 tests for *C. albicans* at 0.0976 mg/mL. This result is likely due to its high eugenol content (45-90%) (Kamatou et al., 2012). Furthermore, other studies have shown a decrease in the *Candida* virulence factor (Cell Surface Hydrophobicity) after adding *Syzygium aromaticum* extract (R. Goswami et al., 2017; Khan & Ahmad, 2013). According to Afanyibo et al. (2018) and Indrayanto et al. (2021), the *Syzygium aromaticum* L. extract is included in the category of good activity in inhibiting the growth of *Candida krusei* ATCC 6258. Meanwhile, the *Alpinia purpurata* extract results are supported by a previous study where the minimum inhibitory content of *C. albicans* is 200 mg/ml with an inhibition of 60% (Kamoda et al., 2020).

The binding energy value of each ligand can be seen from the molecular modeling of the compounds extracted from *Syzygium aromaticum* and *Alpinia purpurata*. The ligand with the smallest binding energy has the highest possibility to interact well with the target protein. The enzyme lanosterol-14- $\alpha$ -demethylase was chosen in the design of antifungal drugs as a molecular binding target because of its essential role in ergosterol biosynthesis, which is an important component of fungal cell membranes (Rodrigues, 2018). Based on the NCBI database, there are two binding sites for the enzyme lanosterol-14- $\alpha$ -demethylase *Candida krusei*: the heme binding site and the chemical substrate binding pocket. The heme binding site on the enzyme lanosterol-14- $\alpha$ -demethylase plays an important role in the binding of iron, which is a cofactor (Sutak et al., 2008). A decrease in iron causes the down-regulation of ERG11 and failure in ergosterol biosynthesis, thereby increasing membrane fluidity (Prasad et al., 2006).

The in-silico screening test through Admestar (<http://lmm.d.ecust.edu.cn/admetsar2>) based on Lipinski's Rule of Five criteria can be used to evaluate the drug similarity of a chemical compound. These criteria state that the compound should have less than five hydrogen bond donors, less than ten hydrogen bond acceptors, a

molecular mass lower than 500 Daltons, and a log P value of less than five (Turner & Agatonovic-Kustrin, 2006). Overall, the drug candidate compounds from the *Syzygium aromaticum* and *Alpinia purpurata* ethanol extracts showed good compatibility and complied with Lipinski's Rules of Five criteria. Therefore, they showed similar bioavailability orally with the active drug, which allows drug-candidate compounds to bind easily to the receptors and cross cell membranes well (Singh et al., 2013).

## Author Contribution Statement

All authors contributed equally in this study.

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## Conflict of Interest

All authors declared no conflicts of interest

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