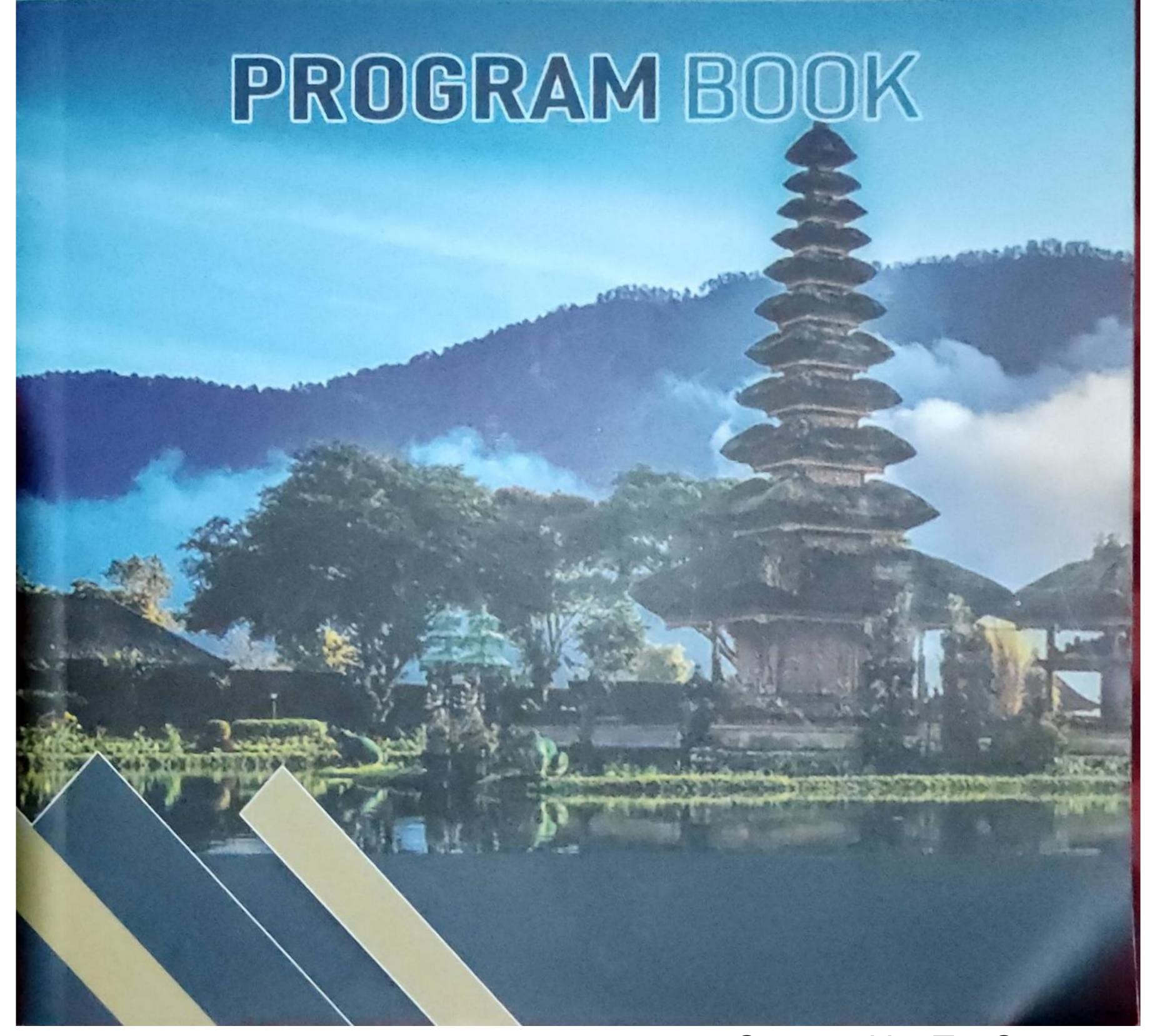




THE ROLE OF PHARMACEUTICAL SCIENCES IN THE EMERGING ERA OF **INDUSTRIAL REVOLUTION 4.0**

PATRA JASA RESORT & VILLAS BALI, INDONESIA

OCTOBER 23RD - 27TH, 2019



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AFPS 2019 ICAPPS

Docking Studies and Molecular Dynamics Simulation of Compounds Contained in *Kaempferia Galanga L.* to Lipoxygenase (LOX) for Anti-Inflammatory Drugs

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INTRODUCTION

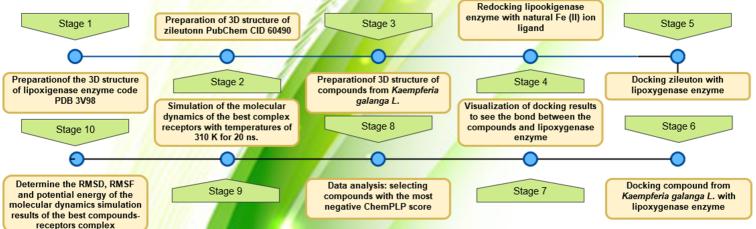


Inflammation is a self-protection response to begin the healing process. The goal is eliminating harmful stimuli, such as damaged cells, irritation and pathogens. However, the appeared symptoms in the form of redness, swelling, heat, pain and loss of function will interfere the body activities. Lipoxygenase (LOX) is an enzyme that plays a role in the oxidation of Arachidonic Acid (AA) to leukotrienes (LTs), the potent pro-inflammatory mediators. *Kaempferia galanga L*. is a natural remedy that suspected of having anti-inflammatory activity potential. Docking studies that dominate computer-aided drug design (CADD) are conducted for virtual screening or optimization of drug screening and design. Docking studies between proteins and ligands can predict ligand orientation when bound to protein receptors or enzymes. Molecular dynamics simulations are used to understand the physical properties of the structure and function of biological macromolecules.

OBJECTIVES

The purposes of this study are predicting the activity of 21 compounds in *Kaempferia galanga L.*, namely ethyl cinnamate, ethyl p-methoxycinamic acid, p-methoxycinamic acid, 3-carene-5-one, camphene, δ -3-carene, p-methoxy styrene, γ -pinene, β -myrcene, p-cymene, 1,8-cineole, iso-myrcene, camphor, α -terpineol, p-cymene- 8-ol, eucarvone, δ -cadinene, kaempferol, quercetin, cyanidin and delphinidin in inhibiting LOX and predicting the stability of ligand-LOX complex which has the greatest binding affinity.



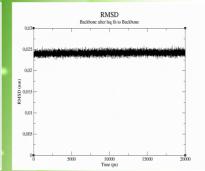


RESULTS AND DISCUSSION

The results of docking compounds from Kaempferia galanga L. and zileuton to 5-lipooksigenase enzyme

ChemPLP Compound Compound ChemPLP Score Score (kcal/mol) (kcal/mol) 12 1,8-cineole 1 Zileuton -18.2282 -20,0000 Ethyl cinnamate -19.9983 13 Iso-myrcene -18 6944 3 Ethyl p-methoxycinamic -19,9923 14 Camphor -20,0000 p-methoxycinamic acid -19,9995 15 α-terpineo -19,9516 5 3-carene-5-one -20,0001 16 p-cymene-8-ol -18,7071 -20.0000 17 -20,0001 Camphene Eucarvone 7 δ-3-carene -20,0002 18 -19,8634 δ-cadinene 8 p-methoxy styrene -19.9990 19 Kaempferol -17.7609-16,9874 γ-pinene -20.0000 20 Quercetin 10 β-myrcene -18,7074 21 Cyanidin -13,3429 11 p-cymene -19,0029 22 Delphinidin -13,3238

Graph of RMSD on molecular dynamics simulations of δ-3-carene with 5-lipoxygenase complex



In the compounds docking result, there is 1 compound that has the greatest affinity, δ -3-carene with the lowest ChemPLP score, -20,0002 kcal/mol. ChemPLP value of δ -3-carene showed its affinity for 5-LOX is greater than zileuton as a comparison drug. It is possible that δ -3-carene has better anti-inflammatory activity compared to zileuton and can be used as a candidate for new anti-inflammatory drug with some further research, in vitro or in vivo research.

The stability of the ligand-receptor complex can be seen from the function of RMSD to the simulation time. The RMSD δ -3-carene with 5-lipoxygenase complex in molecular dynamics simulations for 20 ns is no more than 3 Å. It indicated that the whole system shows good stability.

>>> CONCLUSION

The compound in *Kaempferia galanga L.* which has the greatest affinity in inhibiting the enzyme 5-lipoxygenase (5-LOX) is δ -3-carene with the most negative ChemPLP value, -20,0002 kcal/mol. ChemPLP value of δ -3-carene shows its affinity for 5-LOX is greater than zileuton as a comparison drug. The stability of the δ -3-carene and LOX complex in molecular dynamics simulations showed stable result for 20 ns with RMSD and RMSF of no more than 3 Å and the average potential energy of -1.67392 x 106 kcal/mol.

ACKNOWLEDGMENT

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AFPS-ICAPPS in Bali, Indonesia October 23-27, 2019







Faculty of Pharmacy Universitas Indonesia and The Asian Federation for Pharmaceutical Sciences (AFPS) present this

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in recognition of the valuable contribution as:

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