Pharmacogn J. 2022; 14(2): 282-288
A Multifaceted Journal in the field of Natural Products and Pharmacognosy
www.phcogj.com

Original Article

Molecular Docking, Physicochemical and Drug-likeness Properties of Isolated Compounds from *Garcinia latissima Miq*. on Elastase Enzyme: *In Silico* Analysis

Neneng Siti Silfi Ambarwati[1], Azminah Azminah[2], Islamudin Ahmad[3,*]

[1]Department of Cosmetology, Faculty of Engineering, Universitas Negeri Jakarta, East Jakarta 13220, INDONESIA.
[2]Faculty of Pharmacy, University of Surabaya, Surabaya, East Java, INDONESIA.
[3]Department of Pharmaceutical Sciences, Faculty of Pharmacy, Universitas Mulawarman, Samarinda 75119, East Kalimantan, INDONESIA.

Correspondence

Islamudin Ahmad

Department of Pharmaceutical Sciences, Faculty of Pharmacy, Universitas Mulawarman, Samarinda 75119, East Kalimantan, INDONESIA.

E-mail: islamudinahmad@farmasi.unmul.ac.id

History

- Submission Date: 12-01-2022;
- Review completed: 28-01-2022;
- Accepted Date: 07-02-2022.

DOI : 10.5530/pj.2022.14.35

Article Available online

http://www.phcogj.com/v14/i2

ABSTRACT

Garcinia latissima Miq. belongs to the *Clusiaceae* family that has been studied with activity as an antibacterial and anti-elastase *in vitro*. The inhibitory ability of the elastase enzyme from the *G. latissima* extract. This needs to be tested further by an *in silico* molecular docking study of the compound. Previous studies have shown that 4-oxo-β-lactam crystals are selective against the human neutrophil elastase (an enzyme protease). It has a structural relationship with its activity to become the basis for inhibiting the elastase enzyme. The purpose of this in silico study was to test whether the isolated compounds from *G. latissima* (including friedelin, 6-deoxyjacareubin, amentoflavone, and Robusta flavone). The *in silico* molecular docking method used was Autodock 4.2.6 molecular docking software. This protocol is used to test friedelin, 6-deoxyjacareubin, amentoflavone, and Robusta flavone as ligands for the elastase enzyme receptor. The protocol's output was analyzed using the Accelrys Discovery Studio Visualizer 4.0 post-docking analysis method. The results showed that isolated compounds, including amentoflavone, friedelin, and 6-deoxyjacareubin, are active ligands against porcine pancreatic elastase with the free binding energy of -10.94, -7.17, and -6.72 kcal/mol, respectively, and form hydrogen bonds, van der Walls, alkyl, electrostatic, and hydrophobic interaction. *In silico* physicochemical, lipophilicity, water-soluble, pharmacokinetics, and drug-likeness properties prediction showed characteristics prediction of isolated compound. This study provides an overview of the molecular interactions of isolates compounds from *G. latissima* against the elastase enzyme.

Key words: Drug likeness, *Garcinia latissima* Miq., Molecular docking study, Elastase enzyme, Physicochemical properties.

INTRODUCTION

Garcinia latissima Miq. is a plant in the *Clusiaceae* family known "Dolomagota (Maluku).[1] Some compounds isolated from this plant include friedelin, 6-deoxyjacareubin, robustaflavone, and amentoflavone.[2,3] An *in vitro* elastase inhibition activity assay of *G. latissima* was also reported, showing that the inhibition activity was more significant than the positive control (quercetin).[4] Elastase is a proteinase enzyme found in the skin layer of the dermis. It prevents elastin by cleaving specific peptide bonds to affect skin elasticity with the aging process.[4,5]

Elastin is an extracellular matrix protein produced by connective tissue cells (fibroblasts) in the skin's dermis layer. The breakdown of elastin fibers causes a decrease in skin elasticity.[5] Exposure to ultraviolet rays can also cause skin elasticity to decrease, resulting in sagging and wrinkled skin. This is due to elastin's degradation, an elastic protein found in connective tissue, including the skin.[6] Elastin is a major component of elastic fibers in connective tissue and tendons. Elastic fibers in the skin, together with collagen fibers, form the underlying tissue of the epidermis. The enzyme elastase activity can attack all major connective tissue matrix proteins, including elastin, collagen, proteoglycans, and keratin. This is what triggers wrinkles on the face.[7]

Elastin and collagen are the main components of the skin's connective tissue. Catechins, including eipgalocatekins, can inhibit the activity of the enzyme elastase. Polyphenols obtained from persimmon leaves also exhibit anti-elastase activity. Rosemary extract (*Rosmarinus officinalis*) has also been shown to have intense anti-elastase activity.[8] Elastin, an insoluble fibrous protein, occupies only 2–4% of the dermis matrix but plays an essential role in maintaining skin elasticity. Elastin is degraded by elastase, which can hydrolyze peripheral and structural proteins in connective tissue. Elastin decomposition by elastase activation can be caused by ultraviolet light or ROS. Inhibition of the elastase enzyme activity can be a therapeutic target for protecting aging skin. ROS itself can induce proteinase, resulting in remodeling of the skin's extracellular matrix.[8]

At the age of 40, skin elasticity significantly decreases due to the elastase activity of this enzyme. Biologically, the enzyme elastase activity increases considerably with age, which results in reduced skin elasticity and the appearance of wrinkles or stretchmarks.[9] Materials that can inhibit the elastase enzyme can inhibit the aging process in the skin and can be a cosmetic ingredient in treating skin aging.[4] Therefore, inhibition of elastase activity in the dermis layer can be used to maintain skin elasticity.[1]

The methanol and ethyl acetate extracts of *G. latissima* have been studied *in vitro* to have higher inhibitory activity against the elastase enzyme than quercetin. Meanwhile, the methanol extract of the fruit and leaves of *G. latisima* has lower activity than quercetin.[4]

Cite this article: Ambarwati NSS, Azminah A, Ahmad I. Molecular Docking, Physicochemical and Drug-likeness Properties of Isolated Compounds from *Garcinia latissima Miq.* on Elastase Enzyme: *In Silico* Analysis. Pharmacogn J. 2022;14(2): 282-288.

In this study, an *in silico* test of the elastase enzyme's inhibitory activity from these plant isolates will be carried out. *In silico* is an experiment conducted using a computer. It can determine the interaction between a compound and target molecules such as receptors, with allows visualization of interactions between compounds and receptors using computational methods to assess the pharmacophore groups.[10]

This computational method requires a database of bioinformatics data sets that include data on DNA or protein sequences obtained through laboratory experiments. One example of this bioinformatics data is the Protein Data Bank (PDB), owned by the Research Collaboratory for Structural Bioinformatics Protein Data Bank (RCSB PDB).[11] The computational method can also determine a molecular structure's biological activity and understand the interaction between a ligand or molecule and a receptor according to the receptor's three-dimensional structure. It can also be used to see geometric fit (see which types of bonds are most likely) and energy match (predict bond affinity), thus saving time, energy, and costs.[11,12]

In this research, an *in silico* molecular docking study will be carried out from isolated compounds from the *G. latissima* against the inhibition of the elastase enzyme, namely an experimental approach using a computer to determine the interaction between a compound and the target molecule or receptor. The interaction of the compound with the receptor can determine the pharmacophore of the compound. The purpose of this study was to test the compounds friedelin, 6-deoxyjacareubin, amentoflavone, and Robusta flavone, which are isolates from the *G. latissima* Miq plant. In silico computational method, it compounds act as a ligand at the elastase receptor. *In silico* molecular docking was used in this study to identify the ability of compounds to inhibit the elastase enzyme.

MATERIALS AND METHODS

Preparation of native ligand and receptor

The protein structure of porcine pancreatic elastase (PPE) in the complex with native ligand (novel inhibitor JM102) at PDB ID: 4YM9 (1,8 Å resolution) was downloaded from the protein data bank (www.rcsb.org). The native ligand was separated using PMV 1.5.6. Hydrogen was added and a water molecule was deleted. Then, the native ligand and receptor were saved in PDBQT format (.pdbqt) by the Autodock Tools and the Open Babel GUI program.[13,14]

Ligand sample preparation

The isolated compound structure from *G. latissima* is based on our previous study (Figure 1). The ligand sample preparation was carried out using ChemDraw® Pro v15 to build the chemical structure in two-dimensional form. It was then converted into the three-dimensional form using Chem3D® Pro v15 and minimized using the MMFF94 force field, which was also found in Chem3D® Pro v15. Last, the file was saved in PDB format.[15]

In silico molecular docking analysis

An *in silico* molecular docking analysis was performed using Autodock 4.2.6 on some isolated compounds from *G. latissima* as a PPE inhibitor. The docking simulation was conducted using Lamarckian parameters, including the mutation rate of 0.02, elitism of 1, the population size of 150, the crossover rate of 0.80, and 2500000 energy evaluations. The grid box (28 x 40 x 30 Å) was used on the receptor of 4YM9, which was centered from the active site: X= 11.03Å; Y= 8.605 Å; Z= 1.208Å (XYZ-coordinates). The grid box was used to analyze an*in silico* molecular docking of the isolated compounds from *G. Latissima* with a distance of 0.375Å.The docking result was visualized using Accelrys Discovery Studio Visualizer 4.0.[16]

Physicochemical and drug likeness properties calculation

The physicochemical and drug-likeness properties were calculated using the online free website server of Swiss ADME (via http://swissadme.ch/).[17] Physicochemical and drug-likeness properties were predicted with some parameters, including lipophilicity, absorption, water-solubility, drug-likeness, and physicochemical descriptors for isolated compounds from *G. latissima.*

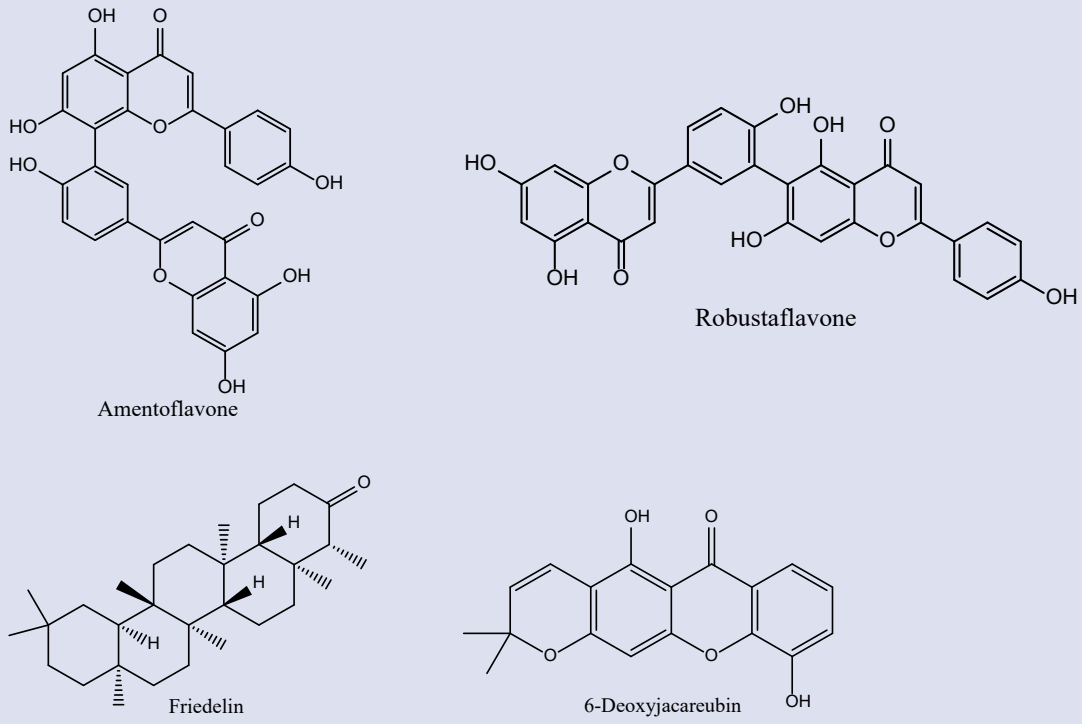


Figure 1: The structure of isolated compounds from *G. latissima* .

RESULT AND DISCUSSION

In silico molecular docking study

An *in silico* molecular docking study needs to be done to predict the strength of the relationship between the isolate molecules and the target protein. This study focuses on the elastase enzyme.[18] Nenengand her colleague has been previously studied that the extract of *G. latissima* has acted as an inhibitor of the enzyme elastase beyond its positive control, namely quercetin.[4] Researchers have obtained four isolates from this plant, and it is necessary further to investigate these isolates' activity against the elastase enzyme.

Regarding the re-docking result of the native ligand, then compared between before and after docking to know and verification of the root square mean deviation (RSMD) with the RSMD value of 1.306 Å (< 2 Å) (Figure 2) with a free binding energy value of -5.20 kcal/mol on 31 of clusters and inhibition constant of 155.19 µM. The lowest energy of the backbone atom and their interaction with the receptor's active site can be seen in Table 1. At the same time, the interaction with the active site of this receptor is the interaction or nucleophilic attack on the Ser195 amino acid residue, which is strengthened by the interaction on His57.[19]

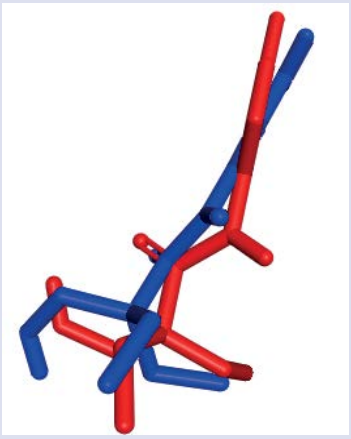


Figure 2: Comparison of native ligand before docking (blue) and the re-docking result (red) with an RMSD value of 1.306 Å (< 2 Å).

Table 1: Free energy binding, inhibition constant, and ligand-receptor interaction.

No	Ligand Compound	Free Energy Binding (kcal/mol)	Inhibition Constant	Interaction
1.	Native ligand	-5.20	155.19 µM	**His57**, Trp94, Thr96, Val99, Cys191, Gln192, Gly193, Asp194, **Ser195**, Thr213, Ser214, Phe215, Val216
2.	Amentoflavone	-10.94	9.61 nM	Thr41, Cys42, **His57**, Cys58, Asp60, Arg61, Trp94, Thr96, Val99, Gly190, Cys191, Gln192, Gly193, Asp194, **Ser195**, Thr213, Ser214, Phe215, Val216, Cys220, Thr226
3.	Friedelin	-7.17	5.57 µM	**Hi57**, Thr96, Val99, Gly190, Cys191, Gln192, Gly193, Asp194, **Ser195**, Thr213, Ser214, Phe215, Val216, Thr226
4.	6-Deoxyjacareubin	-6.72	11.82 µM	**His57**, Asp60, Trp94, Thr96, Val99, Cys191, Gln192, **Ser195**, Thr213, Ser214, Phe215, Val216, Cys220
5	Robustaflavone	+50.33	-	-

As can be seen in Table 1, it was demonstrated that interaction of the native ligand with the receptor formed hydrogen bonding atthe residues of His57, Gly193, and Ser195; Van Der Waals binding at the residues of Thr96, Cys191, Thr213, Ser214, and Phe215; and alkyl binding at Trp94, Val, 99, and Val216. Meanwhile, based on the results of the docking of the ligand test compounds, it shows that the compounds of amentoflavone, friedelin, and 6-deoxyjacareubin have potential with Gibbs free energy values of -10.94 kcal/mol with an inhibition constant(IC) value of 9.61 nM, -7.17 kcal/mol with an IC value of 5.57 µM, and -6.72 kcal/mol with anIC value of 11.82 µM. In comparison, robustaflavone has an enormous free binding energy of +50.33 kcal/mol, respectively.

Based on the molecular docking analysis as presented in Figure 2, it shows that all of the ligand tested are three compounds, namely amentoflavone, friedelin, and 6-deoxyjacareubin, which have better potential than native ligand, while the robustaflavone is the opposite. Amentoflavone has interaction with the active site, andit formsvan der Waals interaction with His57 and Ser195 residues. Moreover, interaction with other residues includesThr41, Cys42, Cys58, Asp60, Arg61, Trp94, Thr96, Val99, Gly190, Cys191, Gln192, Gly193, Asp194, Thr213, Ser214, Phe215, Val216, Cys220 and Thr226. Friedelin formed a Pi-sigma bond interaction with His57 anda van der Waals bond interaction with Ser195.It also interacts with Thr96, Val99, Gly190, Cys191, Gln192, Gly193, Asp194, Thr213, Ser214, Phe215, Val216, andThr226. 6-Deoxyjacareubin interacts with Pi-alkyl binding type at His57 residue and hydrogen binding at Ser195 residue and also forms interactions with other residues like Asp60, Trp94, Thr96, Val99, Cys191, Gln192, Thr213, Ser214, Phe215, Val216, and Cys220.

Physicochemical and drug-likeness properties calculation

The physicochemical and drug-likeness properties of isolated compounds from *G. latissima* were predicted using the free web server SwissADME.[17] Swiss ADME is a validated free web tool for analyzing and predicting the physicochemical properties, lipophilicity, water-solubility, pharmacokinetics, and drug-likeness based on Lipinski's rule-of-five and other models in computer-aided drug design.[20,21]

Table 2 and Figure 3 show the *in silico* physicochemical properties, lipophilicity, water-solubility, pharmacokinetics, and drug-likeness of isolated compounds from *G. latissima* and native ligand as a comparison.

The molecular weight (MW) of all compounds showed a range of 250 to 1000 g/mol. In this case, all isolated compounds have a MW of less than 1000 g/mol, which makes them easily absorbed, diffused, and transported throughout the human body.[22] Amentoflavone, 6-deoxyjacareubin, has robustaflavone with many hydrogen bonds (donor or acceptor), except friedelin (there is only one number of hydrogen bonds). Molar refractivity affects the degree of flexibility of the molecule to rotate, the more flexible the molecule, the stronger the bias potential. Friedelin and 6-deoxyjacareubinhave a value of topological polar surface area (TPSA) of 17.07 and 79.90 $Å^2$, respectively (where the ideal value of < 140 $Å^2$).[23]

The predicted octanol/water partition coefficient (Log P) value of all isolated compounds showed that only friedelin has a Log P value of more than 5, which means friedelin has high lipophilicity and can cause low absorption and rapid metabolic turnover.[24]

In general, Figure 3 exhibited the ideal of physicochemical indices for oral bioavailabilty, where INSOLU is insolubilty: 0 < Log S < 6; INSATU is insaturation: 0.25 < Fraction Csp3 < 1; FLEX is Flexibilty: 0 < Number of rotatable bonds < 9: LIPO is lipophilicity: -7 < XLOGP3 < +5; SIZE is molecular size: 150 g/mol < molecular weight < 500 g/mol; and POLAR is polarity: 20 $Å^2$< TPSA < 130 $Å^2$.[25,26]According to the biavailability radar result (Figure 3), 6-deoxyjacareubin has the potential to be a recommended compound for further research.

Table 2: Physicochemicals and drug-likeness properties calculation of isolated compounds from *G. latissima* .

Compounds	Native ligand	Amentoflavone	Friedelin	6-deoxyjacareubin	Robustaflavone
Molecular weight (g/mol)	236.31	538.46	426.72	310.30	538.46
Number of hydrogen bond acceptor	3	10	1	5	10
Number of hydrogen bond donor	2	6	0	2	6
Number of rotatable bonds	6	3	0	0	3
Molar Refractivity	68.45	146.97	134.39	88.16	146.97
Topological polar surface area (Å^2)	62.22	181.80	17.07	79.90	181.80
Lipophilicity	1.54	3.62	7.45	2.99	3.62
Water solubility	Soluble	Poorly soluble	Poorly soluble	Moderate soluble	Poorly Soluble
Gastrointestinal absorption	High	Low	Low	Low	Low
Blood-brain barrier permeation	Yes	No	No	No	No
P-glycoprotein substrate	No	No	No	No	No
CYP1A2 inhibitor	No	No	No	Yes	No
CYP2C19 inhibitor	No	No	No	No	No
CYP2C9 inhibitor	No	No	No	Yes	No
CYP2D6 inhibitor	No	No	No	Yes	No
CYP3A4 inhibitor	No	No	No	Yes	No
Skin permeation (cm/s)	-6.41	-6.01	-1.94	-5.54	-6.01
Number of Lipinski role violation	0	2	1	0	2
Bioavailability score	0.55	0.17	0.55	0.55	0.17

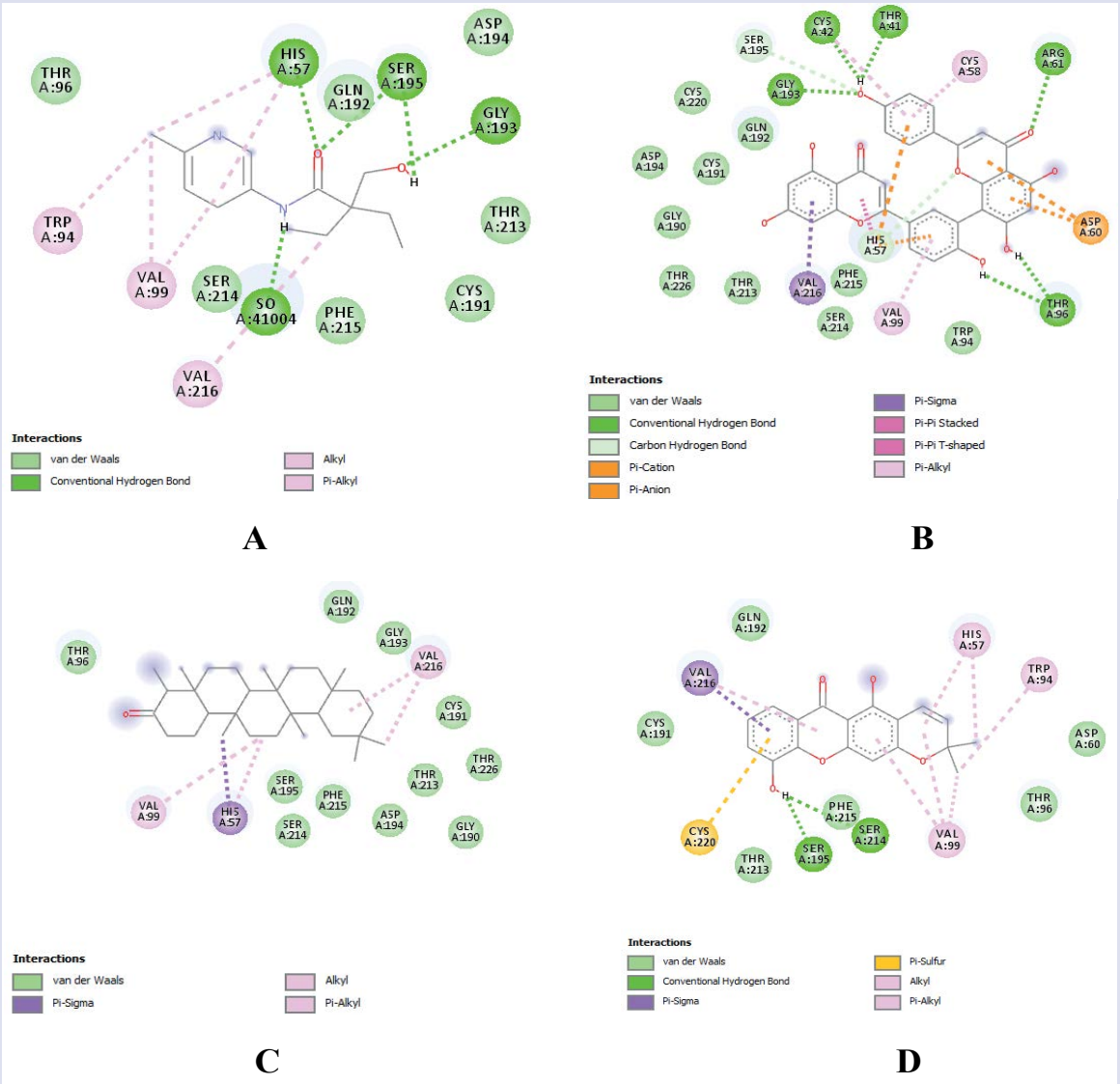


Figure 3: Ligand-Receptor Interaction. Where **A** is a native ligand, **B** is Amentoflavone, **C** is Friedelin and **D** is 6-Deoxyjacareubin.

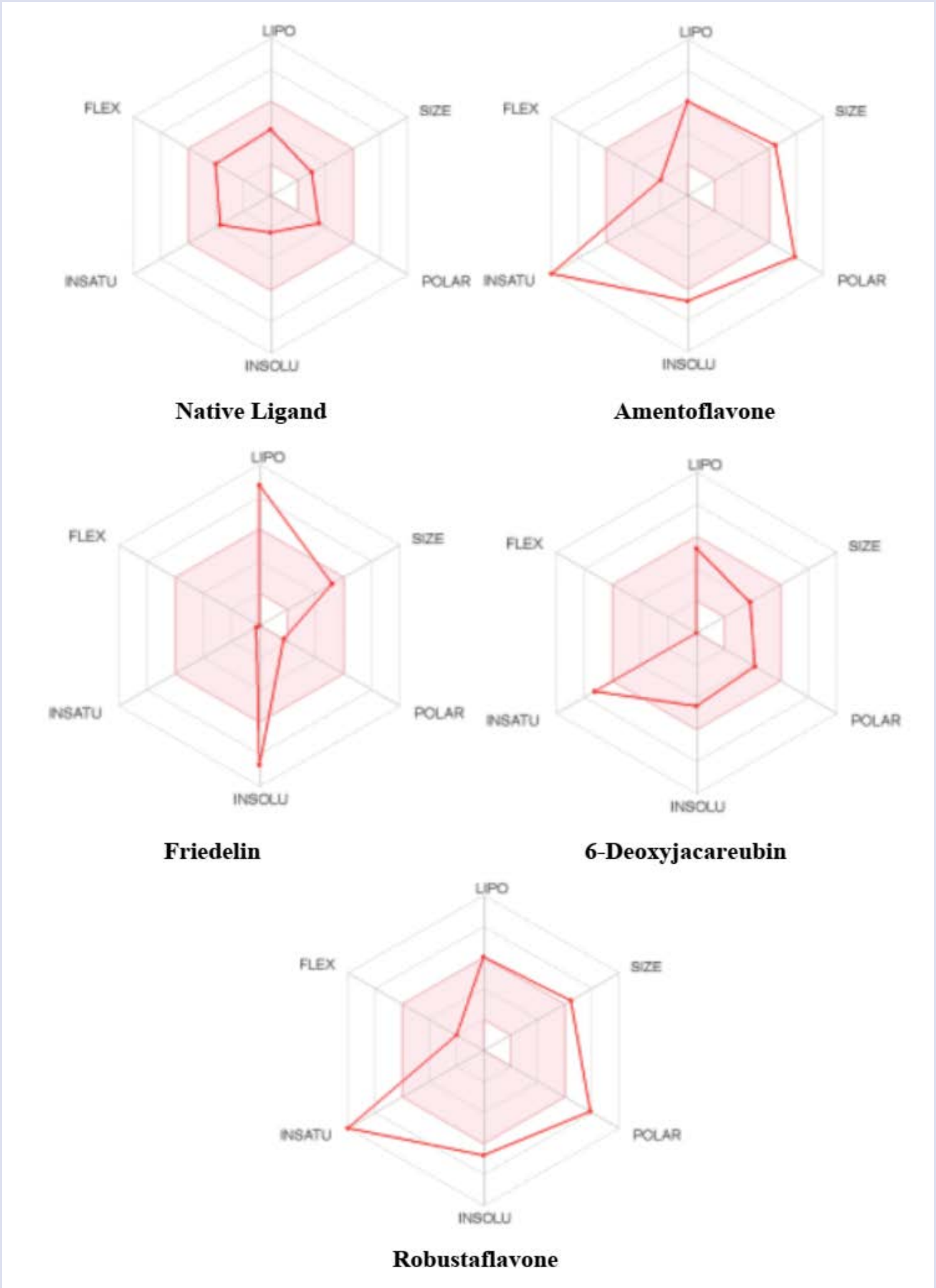


Figure 4: Bioavailability radar of isolated compound from *G. latissima* based on physicochemical indicates for oral bioavailability.

According to the pharmacokinetic properties viewpoint, all isolated compounds indicated better pharmacokinetics properties than other compounds that zero violate Lipinski's rule-of-five. However, 6-deoxyjacareubin is significantly involved in cytochrome P450 (CYP) interactions, especially in CYP1A2, CYP2C9, CYP2D6, and CYP3A4, as it is known that the role of the cytochrome P450 enzyme family is vital, which can form interactions in the form of induction (causing rapid metabolism) or inhibition (bioaccumulation) drugs with any of the CYP isoenzymes. Both roles should be avoided because of overdose or toxicity may occur.[27] Meanwhile, other compounds did not interact with members of the cytochrome P450 enzyme family, which may have a metabolic profile similar to that of the native ligand.

These results show that three of the four compounds have the potential as inhibitors of the elastase enzyme. Amentoflavone compounds have the best potential, as shown based on the calculation of the value of free binding energy and inhibition constant (IC). Amentoflavone is a compound found in other plants such as *Chamaecyparis obtuse, Ginkgo biloba, Hypericum perforatum, Xerophyta plicata.*[28] Amentoflavone molecularly has a mechanism for muscle strength, inhibits the phosphodiesterase and acetylcholinesterase enzymes, has a vasodilating effect, and inhibits fatty acid synthesis.[28]

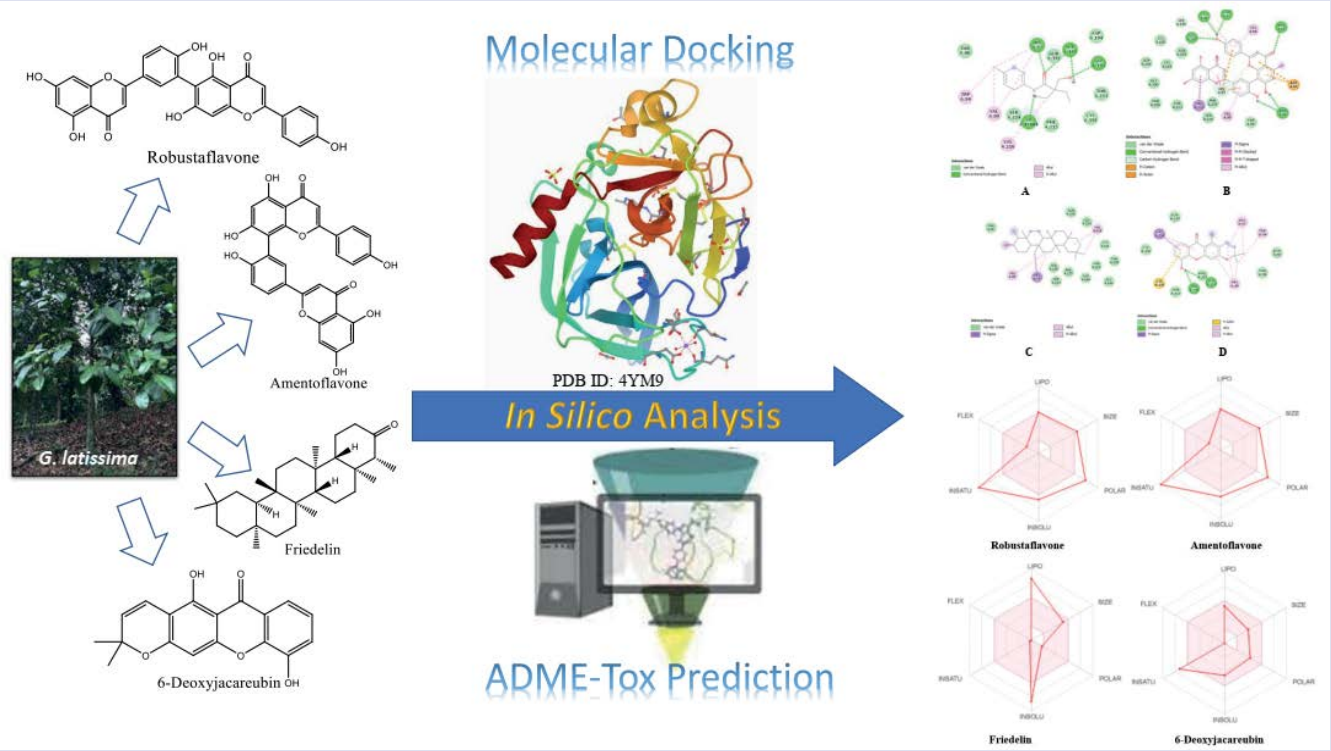
ACKNOWLEDGMENT

This research was founded by Ministry of Riset dan Technologi/Badan RisetInovasi Nasional (RISTEK/BRIN) via grand "Penelitian Dasar Kompetitif Nasional"with contract number of 26/SP2H/DRPM/LPPM/III/2020.

REFERENCES

1. Ambarwati NSS, Elya B, Malik A, Hanafi M. Evaluation of antimicrobial activities of *Garcinia latissima Miq.* stem bark extract. J Young Pharm. 2017;9(1):118-21.
2. Ambarwati NSS, Elya B, Malik A, Hanafi M, Omar H. Isolation, characterization, and antibacterial assay of friedelin from *Garcinia latissima Miq.* leaves. J Phys Conf Ser. 2019;1402(5):0-12.
3. Ambarwati NSS, Elya B, Malik A, Artha Y, Ahmad I, Azminah A, *et al.* Isolation and antibacterial activity by *in vitro* and *in silico* approach of 6-deoxyjacareubin compound from *Garcinia latissima Miq.* fruit. Indones J Chem. 2020;20(4):773.
4. Ambarwati NSS, Elya B, Desmiaty Y. Anti-elastase activity of methanolic and ethyl acetate extract from *Garcinia latissima Miq.* J Phys Conf Ser. 2019;1402(5).
5. Ko RK, Kim GO, Hyun CG, Jung DS, Lee NH. Compounds with tyrosinase inhibition, elastase inhibition and DPPH radical scavenging activities from the branches of *Distylium racemosum* Sieb. et Zucc. Phyther Res. 2011;25(10):1451-6.
6. Liyanaarachchi GD, Samarasekera JKRR, Mahanama KRR, Hemalal KDP. Tyrosinase, elastase, hyaluronidase, inhibitory and antioxidant activity of Sri Lankan medicinal plants for novel cosmeceuticals. Ind Crops Prod. 2018;111:597-605.
7. Nur S, Rumiyati, Lukitaningsih E. Screening of Antioxidants, Anti-aging and tyrosinase inhibitory activities of ethanolic and ethyl acetate extract of fruit flesh and fruit peel Langsat (*Lansium domesticum* Corr) *in vitro*. Tradit Med J. 2017;22(1):63-72.
8. Hong Y-H, Jung EY, Noh DO, Suh HJ. Physiological effects of formulation containing tannase-converted green tea extract on skin care: physical stability, collagenase, elastase, and tyrosinase activities. Integr Med Res. 2014;3(1):25-33.
9. Mori M, Ikeda N, Kato Y, Minamino M, Watabe K. Inhibition of elastase activity by Essential oils *in vitro*. J Cosmet Dermatol. 2002;1:183-7.
10. Setiawan FF, Istyastono EP. Uji *in silico* senyawa 2,6-dihidroksiantraquinon sebagai ligan pada reseptor estrogen alfa. J Farm Sains dan Komunitas. 2015;12(2):77-80.
11. Yanuar A. Penambatan Molekular: Praktek dan Aplikasi. Vol. 1, Fakultas Farmasi Universitas Indonesia. Depok. 2012.
12. Arunkumar J, Rajarajan S. Study on antiviral activities, drug-likeness and molecular docking of bioactive compounds of *Punica granatum* L. to herpes simplex virus - 2 (HSV-2). Microb Pathog. 2018;118:301-9.
13. Morris GM, Huey R, Lindstrom W, Sanner MF, Belew RK, Goodsell DS, *et al.* AutoDock4 and AutodockTools4: Automated docking with selectivity receptor flexibility. J Comput Chem. 2009;30(16):2785-91.
14. Boyle NMO, Banck M, James CA, Morley C, Vandermeersch T, Hutchison GR. Open Babel : An open chemical toolbox. J Cheminform. 2011;3(33):1-14.
15. Wang L, Wu Y, Deng Y, Kim B, Pierce L, Krilov G, et al. Accurate and reliable prediction of relative ligand binding potency in prospective drug discovery by way of a modern free-energy calculation protocol and force field. J Am Chem Soc. 2015;137(7):2695-703.
16. BIOVA DS. Discovery Studio Visualizer. San Diego, USA. 2020.
17. Daina A, Zoete V. A BOILED-Egg to predict gastrointestinal absorption and brain penetration of small molecules. ChemMedChem. 2016;1117-21.
18. Aguilar-Toalá JE, Hernández-Mendoza A, González-Córdova AF, Vallejo-Cordoba B, Liceaga AM. Potential role of natural bioactive peptides for development of cosmeceutical skin products. Peptides. 2019;122:170170.
19. Ruivo EFP, Gonçalves LM, Carvalho LAR, Guedes RC, Hofbauer S, Brito JA, et al. Clickable 4-Oxo-β-lactam-based selective probing for human neutrophil elastase related proteomes. ChemMedChem. 2016;11:1-7.
20. Martin YC. A bioavailability score. J Med Chem. 2005;48(9):3164-70.
21. Cheng F, Li W, Zhou Y, Shen J, Wu Z, Liu G, *et al.* AdmetSAR: A comprehensive source and free tool for assessment of chemical ADMET properties. J Chem Inf Model. 2012;52(11):3099-105.
22. Ji D, Xu M, Udenigwe CC, Agyei D. Physicochemical characterisation, molecular docking, and drug-likeness evaluation of hypotensive peptides encrypted in flaxseed proteome. Curr Res Food Sci. 2020;3:41-50.
23. Matsson P, Kihlberg J. How big is too big for cell permeability? J Med Chem. 2017;60(5):1662-4.
24. Bahmani A, Saaidpour S, Rostami A. A Simple, Robust and efficient computational method for n-octanol/water partition coefficients of substituted aromatic drugs. Sci Rep. 2017;7(1):1-12.
25. Arnott JA, Planey SL. The influence of lipophilicity in drug discovery and design. Expert Opin Drug Discov. 2012;7(10):863-75.
26. Daina A, Michielin O, Zoete V. SwissADME: A free web tool to evaluate pharmacokinetics, drug-likeness and medicinal chemistry friendliness of small molecules. Sci Rep. 2017;7:1-13.
27. Wang Z, Chen Y, Liang H, Bender A, Glen RC, Yan A. P-glycoprotein substrate models using support vector machines based on a comprehensive data set. J Chem Inf Model. 2011;51(6):1447-56.
28. Bais S, Abrol N. Review on chemistry and pharmacological potential of amentoflavone. Curr Res Neurosci. 2015;6(1):16-22.

GRAPHICAL ABSTRACT



ABOUT AUTHORS

Dr. Neneng Siti Silfi Ambarwati, is a Lecturer at Cosmetology Department, Faculty of Engineering, Universitas Negeri Jakarta, East Jakarta, Indonesia. The research focused on natural products for drug and cosmetic discovery and development, extraction technology, and cosmetic ingredients (cosmeceuticals).

Dr. Azminah, is a Lecturer and Researcher at Department of Chemical Pharmacy, Faculty of Pharmacy, Universitas Surabaya. Indonesia. The research focused on computational-cheminformatic (CADD) and analytical chemistry.

Dr. Islamudin Ahmad, is a lecturer and Researcher at Department of Pharmaceutical Sciences, Faculty of Pharmacy, Universitas Mulawarman, East Kalimantan, Indonesia. He has experience in the area of Pharmacognosy and Natural Product Chemistry, working in drugs discovery of natural products, green extraction engineering, isolation and identification of active compound, screening activity mainly degenerative diseases.

Cite this article: Ambarwati NSS, Azminah A, Ahmad I. Molecular Docking, Physicochemical and Drug-likeness Properties of Isolated Compounds from *Garcinia latissima Miq*. on Elastase Enzyme: *In Silico* Analysis. Pharmacogn J. 2022;14(2): 282-288.