

Dipeptidyl peptidase IV inhibition of phytochemicals from *Artocarpus champeden* (Lour.) Stokes: *In silico* molecular docking study and ADME-Tox prediction approach

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ABSTRACT

The present study examines the potential activity prediction based on free binding energy (ΔG) and interaction confirmation of phytochemicals from *Artocarpus champeden* (Lour.) Stokes with macromolecule protein receptor of dipeptidyl peptidase IV (DPP-IV) using *in silico* molecular docking studies and physicochemical and pharmacokinetic properties (ADME-Tox) prediction approaches. The active subsites of the DPP-IV receptor macromolecule protein Protein Data Bank (ID: 1 × 70) were docked using Autodock v4.2.6 (100 docking runs). A grid box of 52 × 28 × 26 Å points spaced by 0.37 Å was centered on the active site of x = 40.926 Å; y = 50.522 Å; z = 35.031 Å. For ADME-Tox prediction, Swiss ADME online-based application programs were used. The results show that 12 phytochemicals from *A. champeden* have the potential as DPP-IV inhibitors based on ΔG value and interaction conformation. There are five phytochemicals with lower ΔG values and inhibition constants than the native ligand and seven phytochemicals with ΔG values and inhibition constants close to the native ligand. The 12 compounds form an interaction conformation at the active subsites of the DPP-IV receptor. At the same time, the results of the ADME-Tox prediction analysis showed that the 12 compounds had different physicochemical and pharmacokinetic properties.

Key words: ADME-tox, *Artocarpus champeden* (Lour.) stokes, dipeptidyl peptidase IV, free binding energy, *in silico* molecular docking

INTRODUCTION

Artocarpus champeden (Lour.) Stokes belongs to the Moraceae family, locally known as "Chempedak," an annual fruit plant with a tall, strong woody tree. This fruit plant is a native that grows wild in tropical forests, mainly in India,

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Vietnam, Myanmar, Thailand, Malaysia, and Indonesia.^[1] This plant is widespread in Sumatran, Kalimantan, Sulawesi, Maluku, and West Papua in Indonesia. Traditionally, this plant treats diarrhea, fever, malaria, and diabetes mellitus. However, no scientific evidence has been reported of *A. champeden* as a potential antidiabetic agent to the best of our knowledge. Therefore, our team is interested in researching the potential of this plant.

Meanwhile, several studies have isolated and identified phytocompounds found in *A. champeden*.^[2-5] However, data regarding the potential pharmacological activity of phytocompounds from *A. champeden* is still minimal, mainly as antidiabetic, whereas it has traditionally been used for generations. This series of work fills research gaps by examining the potential activity and interactions of phytocompound from *A. champeden* using the *in silico* molecular docking study and ADME-Tox prediction approach.

In silico molecular docking is a modeling method based on computer simulation to search for possible bindings of the test ligand and receptor-interacting under topographical conditions and the match between both molecules with the conformation that has the best interaction.^[6-9] ADME-Tox prediction is performed using an online-based application such as SWISSADME, which aims to study physicochemical and pharmacokinetic properties.^[10,11] Some studies that have been reported successfully related to the use of these application programs include ADMET analysis of three relevant natural components of the medicinal plant,^[12] ADMET prediction of mangosteen derivatives,^[13] ADME-Tox prediction of phytocompounds from *Merremia peltata*,^[14] and drug-likeness prediction of bioactive compounds from *Punica granatum* L.^[15]

The current study predicts the interaction conformation and the potential activity of phytocompounds from *A. champeden* with macromolecules protein of dipeptidyl peptidase IV (DPP-IV) as a receptor target, hoping to fill research gaps on an *in silico* assay scale, thereby accelerating the development of further studies.

MATERIALS AND METHODS

Hardware and software

The analysis of molecular docking was carried out by a computer HP Pavilion, Autodock-v4.2.6, AutodockTools, ChemOffice-Pro-v15.00 PerkinElmer, Phyton Molecular Viewer (PMV-1.5.6), OpenBabel GUI, Accelrys Discovery Studio Visualizer 4.0. Software, and SWISSADME (<http://www.swissadme.ch/>) online tools program.

In silico molecular docking study

Native ligand and receptor preparation

The protein structure of macromolecule DPP-IV complexes with native ligand sitagliptin Protein Data Bank (PDB ID:

1 × 70, with 2.1 Å resolution) was downloaded from the Research Collaboratory for Structural Bioinformatics PDB via the website: <https://www.rcsb.org/>. Macromolecule DPP-IV receptors and native ligand were separated using PMV-1.5.6. Gasteiger charges were added to each ligand atom. Water molecules were eliminated from each protein receptor and protonated. Then, a native ligand and protein receptor was prepared and converted in the PDBQT format (.pdbqt) using AutodockTools and OpenBabel programs.^[17,16]

Preparation of phytocompounds as a test ligand

In this study, the structure of phytocompounds from *A. champeden* was collected from some literature,^[2-5] as shown in Figure 1. Each phytocompounds were prepared as a test ligand using ChemDraw[®] Pro v15 to build a two-dimension structure of each phytocompounds. Chem three-dimensional (3D)[®] Pro v15 was converted to a 3D structure, minimized using the MMFF94 force field, and saved to PDB (.pdb).^[18]

Analysis of *in silico* molecular docking

According to its protocols, the analysis of *in silico* molecular docking of 41 phytocompounds from *A. champeden* was conducted using Autodock 4.2.6.^[7] Using the Lamarckian Genetic Algorithm (LGA) based on the lowest free energy of binding (ΔG), the native ligand was simulated in various conformations for best binding to the protein DPP-IV receptor binding site. The parameters of LGA were: elitism of 1, crossover rate of 0.8, the mutation rate of 0.02, the population size of 150, energy evaluation of 2500,000, and 100 runs. Moreover, the grid box comprised of 52 × 28 × 26 Å points spaced by 0.375 Å was centered on the active site of x = 40.926 Å; y = 50.522 Å; z = 35.031 Å (XYZ-coordinates) according to a previous study.^[17] The grid condition was used for molecular docking analysis of 41 phytocompounds from *A. champeden*. The results of molecular docking data were visualized using Accelrys Discovery Studio Visualizer-4.0.^[18]

Determination of ADME-tox prediction

According to the literature, ADME-Tox prediction of the best docking results was determined using SWISSADME online tools.^[11] Briefly, each phytocompounds (PDB format) structure was converted in SMILES format using OpenBabel GUI. SWISSADME online tools program was used to determine ADME-Tox of 12 phytocompounds.^[18]

RESULTS

In silico molecular docking study

Validation of molecular docking method

In the present study, the docking results of the native ligand (sitagliptin) demonstrated a root mean square deviation (RMSD) value of 0.55 Å (<2 Å) with a binding free energy (ΔG) value of -8.59 kcal/mol (inhibition constant

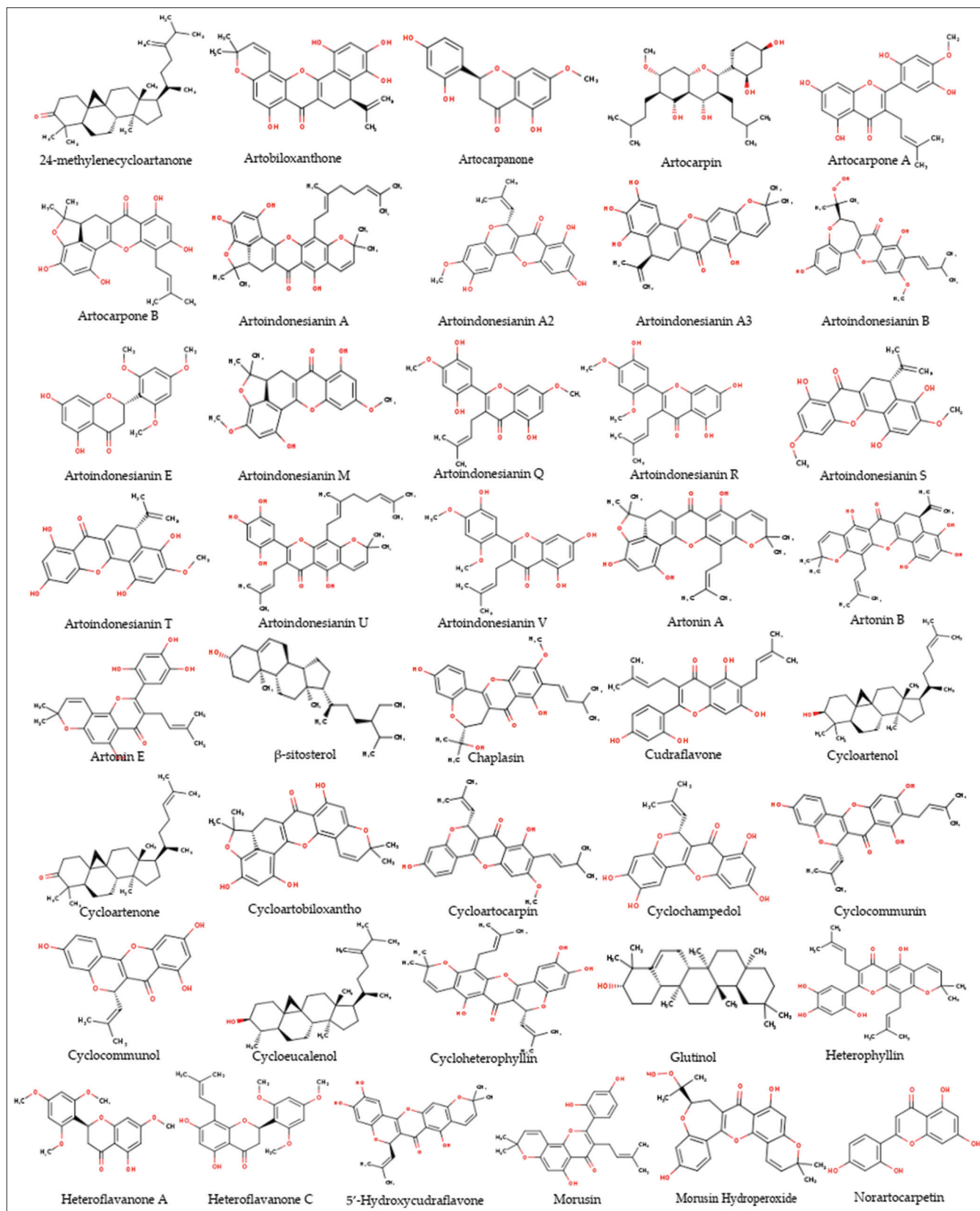


Figure 1: 2D structure of phytochemicals from *Artocarpus champeden*. 2D: Two-dimension

of 508.58 nM) and clusters of 82% for 100 times running. Figure 2 shows that the overlay position between the

docking results and the original native ligand does not significantly different positions according to the RMSD

value $< 2 \text{ \AA}$, indicating that the grid size and grid center of the docking process was different valid.

The docking results of 41 phytochemicals from *A. champeden* in Table 1 show that five compounds had a lower ΔG value and inhibition constant than the native ligand. Seven compounds have ΔG value and inhibition constant close to the native ligand.

Studies on molecular interaction

Figure 3 demonstrates visualization of native ligand interaction with active site residue of DPP-IV macromolecule receptors.

In Figure 4, it was shown that 12 phytochemicals have conformational interactions with subsites of the DPP-IV receptor.

ADME-tox prediction

The ADME-Tox properties prediction of selected 12 phytochemicals from *A. champeden* according to the molecular docking study is presented in Table 2. The physicochemical properties prediction provides an overview of bioavailability levels of phytochemicals, as shown in Figure 5.

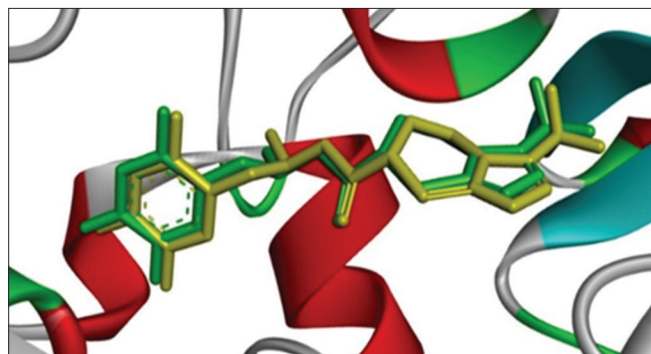


Figure 2: Visualization of original (yellow) and re-docked (green) native ligand overlay position

DISCUSSION

The result of re-docking of native ligand indicates the level of validity of grid box and box size used with an RMSD value of 0.55 \AA ($< 2 \text{ \AA}$), which refers to the previous study,^[17,19] indicating that the grid size and grid center of the docking process was different valid. The docking result demonstrated native ligand and test ligand interaction with the active site of DPP-IV receptor macromolecules. The DPP-IV receptor has some active site areas at subsites area of amino acid residues known as S_1 , S_1' , S_2' , S_2 , and S_2 extensive.^[20-22] The test ligand activity can generally be predicted based on interactions at subsites (S_1 , S_2 , and S_2 ext.) of the DPP-IV receptor.^[21,22]

In this study, it was found that five phytochemicals had lower ΔG values than the native ligand, including 24-methylencycloartanon, cycloartenon, cycloartenol, β -sitosterol, and cycloeucaenol, and seven phytochemicals that had an ΔG value close to the native ligand include cudraflavon C, artoindonesianin A, 5'-hydroxycudraflavon A, artoindonesianin B, artoindonesianin R, artoindonesianin A3, and cyclocommunim. In addition, the 12 phytochemicals showed conformational interactions that were specific to the active subsite of the DPP-IV receptor. Each amino acid residue of the active subsites of the DPP-IV receptor can form seven different interaction conformations with the test ligand.^[23]

The ADME-Tox properties play a crucial role in the drug industry. They are generally used in drug development, mainly using the computer-aided drug design approach to reduce unwanted effects. 24-Methylencycloartanon has an MW value that is in the unacceptable range, while the others are in the acceptable range. Artoindonesianin A, artoindonesianin A3, artoindonesianin B, artoindonesianin R, cudraflavon C, cyclocommunim, and 5'-hydroxycudraflavon A obey the Lipinski rule, except six other compounds (RO5 value > 0).^[24]

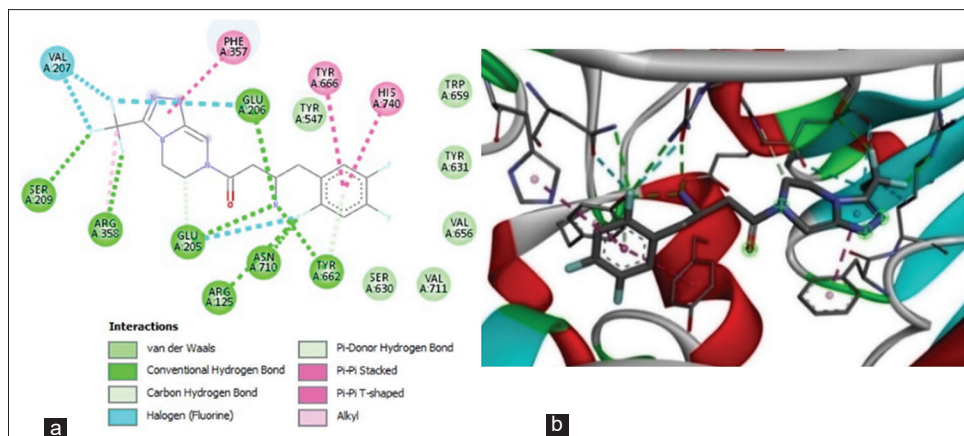


Figure 3: Visualization of (a) two-dimension and (b) three-dimension of molecular interaction between native ligand against macromolecule of DPP-IV receptor (PDB ID: 1X70). PDB: Protein Data Bank, DPP-IV: Dipeptidyl peptidase IV

Table 1: Docking results characteristic and ligand-receptor interaction

Ligand	ΔG value (kcal/mol)	Inhibition constant (nM)	Interaction
Sitagliptin (native)	-8.59	508.58	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Phe ²⁰⁸ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
24-methylcycloartanon	-10.77	12.16	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artobioxanton	-6.92	8520	Tyr ⁶⁷⁰ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³⁰ ; Ser ⁵⁵² ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Phe ²⁰⁸ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵
Artocarpanon	-6.13	32070	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Artocarpin	-6.95	7990	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Artocarpon A	-7.76	2040	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Ser ⁵⁵² ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artocarpon B	-6.82	9990	Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artoindonesianin A	-8.50	592	Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁸⁵ ; Ser ⁵⁵² ; Cys ⁵⁵¹ ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Arg ³⁵⁶ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artoindonesianin A2	-6.20	28340	Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Asp ⁶⁶³ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Artoindonesianin A3	-8.06	1240	His ⁷⁴⁰ ; Val ⁷¹¹ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artoindonesianin B	-8.14	1080	His ⁷⁴⁰ ; Val ⁷¹¹ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Phe ²⁰⁸ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artoindonesianin E	-6.26	25580	Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Ser ⁵⁵² ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵
Artoindonesianin M	-7.39	3850	Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Phe ²⁰⁸ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artoindonesianin Q	-7.19	5370	His ⁷⁴⁰ ; Val ⁷¹¹ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Asp ⁶⁶³ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Artoindonesianin R	-8.10	1160	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Ser ⁵⁵² ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Artoindonesianin S	-6.60	14410	His ⁷⁴⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Artoindonesianin T	-6.22	27750	His ⁷⁴⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Artoindonesianin U	-6.08	34950	His ⁷⁴¹ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Ser ⁵⁵² ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artoindonesianin V	-7.73	2140	His ⁷⁴¹ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Ser ⁵⁵² ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artonin A	-7.95	1490	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artonin B	-7.60	2700	Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Tyr ⁵⁸⁵ ; Ser ⁵⁵² ; Cys ⁵⁵¹ ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Arg ³⁵⁶ ; Ser ²⁰⁹ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Artonin E	-7.70	2250	His ⁷⁴⁰ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Ser ⁶³⁰ ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Phe ²⁰⁸ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
β -sitosterol	-9.97	49.17	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Phe ²⁰⁸ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Chaplasin	-7.21	5160	His ⁷⁴⁰ ; Val ⁷¹¹ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Cudraflavon C	-8.53	558.13	Val ⁷¹¹ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁸⁵ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Cycloartenol	-10.06	42	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Cycloartenon	-10.48	21	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵

Contd..

Table 1: Contd...

Ligand	ΔG value (kcal/mol)	Inhibition constant (nM)	Interaction
Cycloartobiloxanton	-7.26	4780	Val ⁷¹¹ ; Asn ⁷¹⁰ ; Tyr ⁶⁷⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Cycloartocarpin	-7.04	6870	His ⁷⁴⁰ ; Val ⁷¹¹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Phe ²⁰⁸ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Cyclochampedol	-5.97	42060	Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Cyclocommunin	-8.06	1240	Val ⁷¹¹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Phe ³⁵⁷ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Cyclocommunol	-7.06	6720	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Ser ⁵⁵² ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Cycloeucaleanol	-9.96	50	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Cycloheterofilin	-7.54	2990	Asn ⁷¹⁰ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁵⁸⁵ ; Cys ⁵⁵¹ ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Arg ³⁵⁶ ; Ser ²⁰⁹ ; Phe ²⁰⁸ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Glutinol	-6.62	14130	Asn ⁷¹⁰ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Heterofilin	-7.15	5760	Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁵⁸⁵ ; Ser ⁵⁵² ; Pro ⁵⁵⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Heteroflavin A	-6.33	22800	Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Heteroflavin C	-5.74	61750	Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
5'- Hydroxycudraflavin A	-8.33	788	His ⁷⁴⁰ ; Val ⁷¹¹ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Arg ³⁵⁸ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Morusin	-7.82	1850	His ⁷⁴⁰ ; Val ⁷¹¹ ; Tyr ⁶⁷⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵
Morusin Hydroperoxide	-7.94	1510	His ⁷⁴⁰ ; Val ⁷¹¹ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Trp ⁶⁵⁹ ; Val ⁶⁵⁶ ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Val ²⁰⁷ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; His ¹²⁶ ; Arg ¹²⁵
Norartocarpin	-6.74	11550	His ⁷⁴⁰ ; Val ⁷¹¹ ; Asn ⁷¹⁰ ; Arg ⁶⁶⁹ ; Tyr ⁶⁶⁶ ; Tyr ⁶⁶² ; Tyr ⁶³¹ ; Ser ⁶³⁰ ; Gly ⁵⁴⁹ ; Tyr ⁵⁴⁷ ; Phe ³⁵⁷ ; Ser ²⁰⁹ ; Glu ²⁰⁶ ; Glu ²⁰⁵ ; Arg ¹²⁵

Table 2: ADME-Tox properties prediction of twelve best docking results using SWISSADME online tools software

Sample	MW	HBA	HBD	TPSA	XLOGP3	ESOL	Log Kp	MR	Csp3	NRB	RO5
24-Methylcycloartanon	875.44	1	0	17.07	9.99	2.99e-09	-1.88	138.99	0.90	5	1
Artoindonesianin A	570.67	7	3	109.36	7.83	5.46e-09	-4.22	167.24	0.40	5	1
Artoindonesianin A3	434.44	7	4	120.36	4.76	1.46e-06	-5.57	121.90	0.24	1	0
Artoindonesianin B	468.50	8	3	118.59	4.82	1.59e-06	-5.74	129.43	0.35	8	0
Artoindonesianin R	398.41	7	3	109.36	4.54	5.64e-06	-5.51	110.69	0.23	5	0
β -sitosterol	414.71	1	1	20.23	9.34	1.26e-08	-2.20	133.23	0.93	6	1
Cudraflavin C	422.47	6	4	101.13	5.55	9.82e-07	-4.94	123.45	0.24	5	0
Cycloartenol	426.72	1	1	20.23	9.78	4.14e-09	-1.96	135.14	0.93	4	1
Cycloartenon	424.70	1	0	17.07	9.46	6.78e-09	-2.17	134.18	0.90	4	1
Cyclocommunin	420.45	6	3	100.13	5.85	4.83e-07	-4.71	121.00	0.24	3	0
Cycloeucaleanol	426.72	1	1	20.23	9.91	3.99e-09	-1.87	135.40	0.93	5	1
5'-Hydroxycudraflavin A	434.44	7	3	109.36	4.84	1.30e-06	-5.51	121.40	0.24	1	0

MW: Molecular weight, HBA: Acceptable H-bonds, HBD: Donatable H-bonds, TPSA: Topological polar surface area (TPSA < 140 Å² good intestinal absorptions and TPSA < 70 Å² good brain penetration), XLOGP3: Lipophilicity descriptor, ESOL: Estimated solubility in water, Log Kp: Skin permeant, MR: Molar refractivity, Csp3: The fraction of carbon in the sp³ hybridization, NRB: The number of rotatable bonds, RO5: The rule of five Lipinski rules

All phytochemicals showed the H-bond (acceptor and donor) and skin permeant value in the acceptable range. Based on the topological polar surface area (TPSA) value, which reveals that 24-methylcycloartanon, β -sitosterol, cycloartenol, cycloartenon, and cycloeucaleanol have an excellent brain penetration (TPSA < 70 Å²), and seven other

compounds have good gastrointestinal penetration (with TPSA < 140 Å²).^[25] XLOGP3 shows the lipophilicity and polarity value prediction of phytochemicals. The higher the value, the lower the polarity.^[26,27] ESOL indicates the solubility levels of phytochemicals. The lower the values,^[28] the lower solubility.^[29] Figure 5 demonstrated that

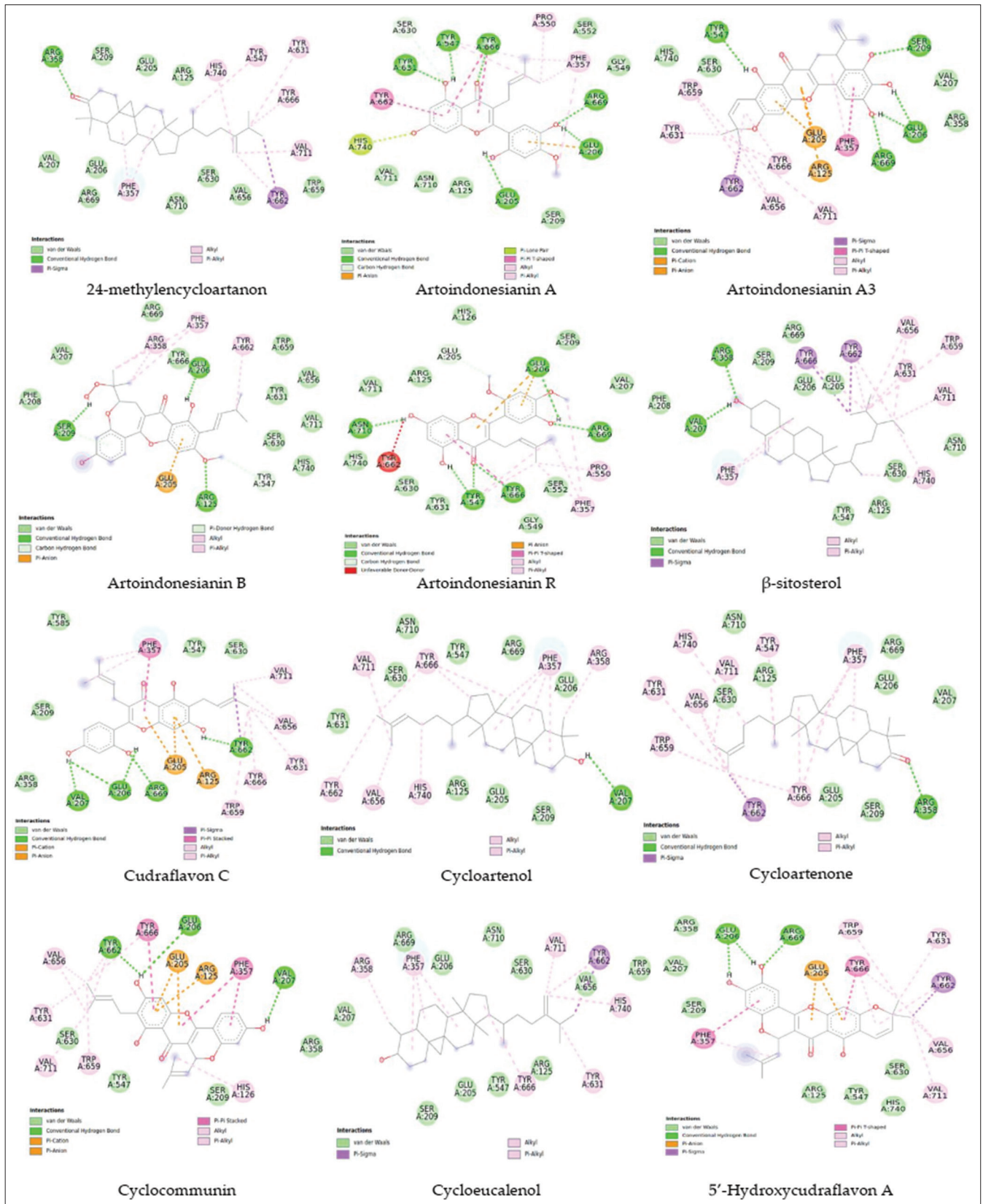


Figure 4: Interaction visualization of twelve best docking results of phytochemicals from *Artocarpus champeden* against macromolecule of DPP-IV receptor. DPP-IV: Dipeptidyl peptidase IV

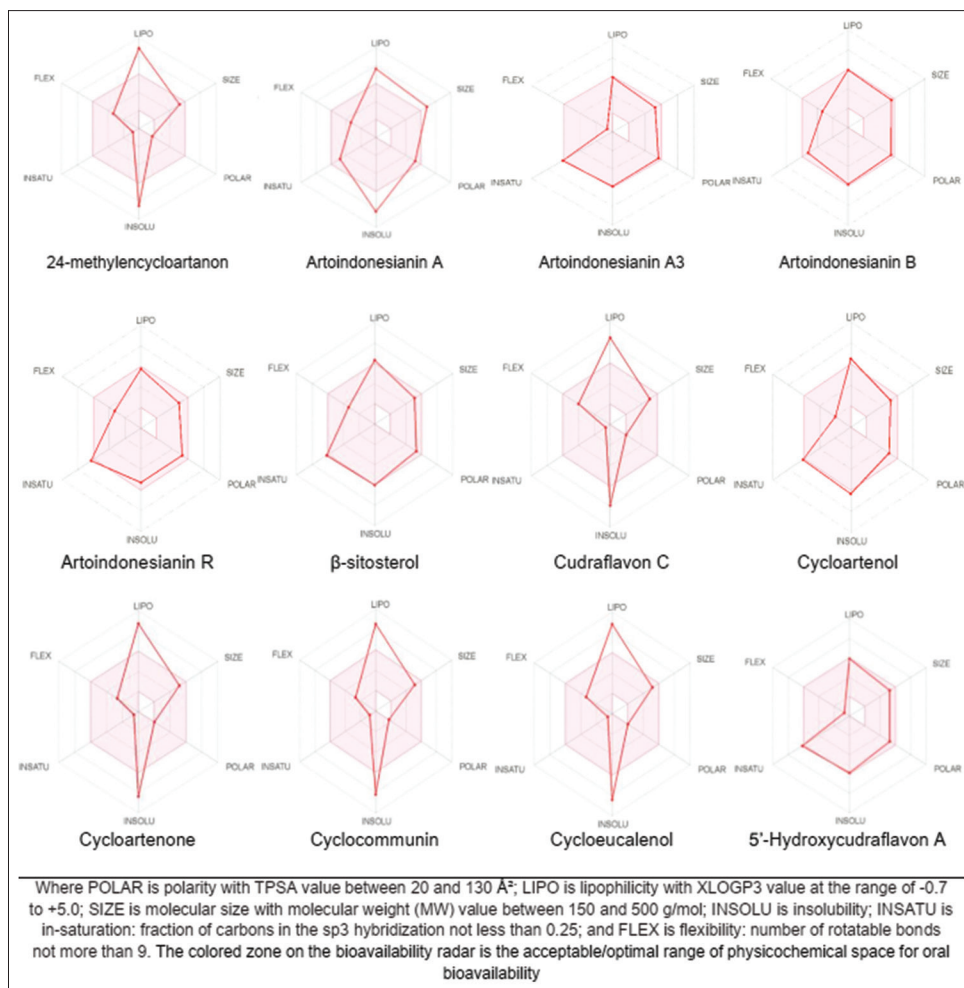


Figure 5: Bioavailability radar representation of the 12 best docking findings of *Artocarpus champeden* phytocompounds

the phytocompounds of artonindonesianin (A3, B, and R), β -sitosterol, cycloartenol, and 5'-hydroxycudraflavon A were the acceptable/optimal range of ADME-Tox/physicochemical space for oral bioavailability.

CONCLUSION

Analysis of *in silico* molecular docking and ADME-Tox prediction were performed to study the potential pharmacological activity of phytocompounds from *A. champeden* as DPP-IV inhibitors. Our findings show that almost all phytocompounds have potential interaction with the receptor at the active subsites. Nevertheless, 12 phytocompounds have the most similar interaction with the DPP-IV receptor and have different physicochemical properties for bioavailability and pharmacokinetics prediction.

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Conflicts of interest

There are no conflicts of interest.

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