Title : Molecular Dynamics Simulation of Inhibitors Targeting Binding Between ACE2 Receptor and Spike Protein of SARS-CoV-2

Author(s) : Supakit Neerapongthep **Student ID :** 640510182

Major : Biochemistry and Biochemical Innovation

Advisor(s) : Associate Professor Dr. Nuttee Suree

Type of presentation* *(choose 1)* **:**

- ☐ **Oral Presentation** (เฉพาะ ตัวแทนนศ.ที่สาขาเลือกให้นำเสนอแบบบรรยาย)
- ☑ **Poster** (กรณี นำเสนอผลงานปัญหาพิเศษ/การค้นคว้าอิสระ)
- ☐ **Cooperative Education** (กรณี นำเสนอผลงานสหกิจศึกษา)

ABSTRACT

In 2022, the mutation of the SARS-CoV-2 virus into the Omicron variant exacerbated the COVID-19 pandemic in Thailand, significantly impacting the economy and daily life. The mechanism of SARS-CoV-2 entry into host cells uses a protein on the viral surface called Spike (S) protein. This protein binds to the ACE2 (Angiotensin Converting Enzyme 2), a receptor on the host cell surface, and then undergoes the viral replication process. This research aimed to screen compounds capable of blocking the binding between the SARS-CoV-2 S protein and ACE2 receptor of host cells by using a computational approach, which would inhibit viral entry. Two sets of compounds from the digital databases, marine-derived compounds (n=128) and sesamin-derived compounds were analyzed using molecular docking, virtual screening, molecular dynamics (MD) simulations, and energy analysis through Molecular Mechanics Poisson-Boltzmann Surface Area (MM/PBSA). The virtual screening and molecular docking experiments identified the top four ligands predicted to confer the best binding to the target S protein with binding scores of -7.6, -7.5, -8.3, and -7.4 kcal/mol. These four ligands interact with Lys31 of the ACE2, which is a key residue critical for the binding of the Spike protein. Subsequently, the ligands were analyzed using MD Simulation and MM/PBSA methods. It was found that after 100 ns, the ligand SC1 did not interact with the Lys31 position of the ACE2 protein, results in a free binding energy value of -4.36 ± 5.24 kcal/mol. In contrast, other ligands that interacted with Lys31—MC1, MC2, and SC2—exhibit ΔG_{bind} values of -25.17 ± 1.57, -14.20 ± 3.29, and -29.69 ± 2.58 kcal/mol, respectively. These three ligands thus potential for the development of an effective antiviral drug against SARS-CoV-2.

**Type of presentation must be matched with an option you choosing on student upload system.*

***The abstract can be more than one page and must be approved by project advisor before upload.*