AI-Driven Virtual Screening and Molecular Docking for Identifying Potential SARS-CoV-2 Inhibitors from Indonesian Marine and Herbal Resources

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Rapid spread of SARS-CoV-2 over the world necessitates for urgent antiviral solutions. Despite the extensive efforts, including vaccine development, effective strategies remain elusive. Indonesia's rich marine and herbal resources hold untapped potential for novel SARS-CoV-2 inhibitors. Leveraging Artificial Intelligence (AI), we established a virtual screening workflow based on Machine Learning (ML) and Deep Learning (DL) techniques for Quantitative-Structure-Activity Relationship (QSAR) modeling. We employed four algorithms (Random Forest, XgBoost, SVR, Deep Learning) for regression QSAR and six (Random Forest, ANN, Naive Bayes, SVM, Xgboost, Deep Learning) for classification QSAR using KNIME software. Random Forest excelled in regression QSAR (R2 = 0.812), while Xgboost led in classification QSAR (accuracy = 92.7%). This workflow facilitates virtual screening of marine invertebrate and Indonesian herbal secondary metabolites from Herbaldb. Subsequent target identification pinpointed 3CLPro for marine invertebrate compounds and Akt1 for Indonesian herbal compounds. Molecular docking revealed potential SARS-CoV-2 inhibitors, including Hydroxycristacarpone from Erythrina orientalis (Dadap Serep plant); and Ingenine D (Acanthostrongylophora ingens) and Variabine B (Luffariealla virabilis) from marine invertebrates. These findings highlight the promise of AI-driven approaches to discover novel antiviral candidates within Indonesia's diverse natural resources