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Original article

Repurposing benzimidazole and benzothiazole derivatives as potential inhibitors of SARS-CoV-2: DFT, QSAR, molecular docking, molecular dynamics simulation, and *in-silico* pharmacokinetic and toxicity studies



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ABSTRACT

Density Functional Theory (DFT) and Quantitative Structure-Activity Relationship (QSAR) studies were performed on four benzimidazoles (compounds 1–4) and two benzothiazoles (compounds 5 and 6), previously synthesized by our group. The compounds were also investigated for their binding affinity and interactions with the SARS-CoV-2 M^{pro} (PDB ID: 6LU7) and the human angiotensin-converting enzyme 2 (ACE2) receptor (PDB ID: 6M18) using a molecular docking approach. Compounds 1, 2, and 3 were found to bind with equal affinity to both targets. Compound 1 showed the highest predictive docking scores, and was further subjected to molecular dynamics (MD) simulation to explain protein stability, ligand properties, and protein–ligand interactions. All compounds were assessed for their structural, physico-chemical, pharmacokinetic, and toxicological properties. Our results suggest that the investigated compounds are potential new drug leads to target SARS-CoV-2.

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1. Introduction

The current COVID-19 pandemic, caused by the highly contagious newly emerged SARS-CoV-2, is a global health threat that affects millions of people worldwide, and impacts negatively on all sectors of society (Mohapatra et al., 2020a; b; Mohapatra and Rahman, 2021). Although the fatality rate for SARS-CoV-2 (~4%) is lower compared to that of SARS-CoV (~10%) and MERS-CoV (~35%), its transmission rate is much higher than that of previously reported coronaviruses (CoVs) (Guo et al., 2020). In many countries, this led to lockdown measures being put into place to minimize human-to-human transmission (Mohapatra et al., 2021b). COVID-19 related deaths have now surpassed those from