



Article

Exploring Probenecid Derived 1,3,4-Oxadiazole-Phthalimide Hybrid as α -Amylase Inhibitor: Synthesis, Structural Investigation, and Molecular Modeling

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Abstract: 1,3,4-Oxadiazole moiety is a crucial pharmacophore in many biologically active compounds. In a typical synthesis, probenecid was subjected to a sequence of reactions to obtain a 1,3,4-oxadiazole-phthalimide hybrid (**PESMP**) in high yields. The NMR (¹H and ¹³C) spectroscopic analysis initially confirmed the structure of **PESMP**. Further spectral aspects were validated based on a single-crystal XRD analysis. Experimental findings were confirmed afterwards by executing a Hirshfeld surface (HS) analysis and quantum mechanical computations. The HS analysis showed the role of the $\pi \cdots \pi$ stacking interactions in **PESMP**. **PESMP** was found to have a high stability and lower reactivity in terms of global reactivity parameters. α -Amylase inhibition studies revealed that the **PESMP** was a good inhibitor of α -amylase with an s value of 10.60 ± 0.16 $\mu\text{g}/\text{mL}$ compared with that of standard acarbose ($\text{IC}_{50} = 8.80 \pm 0.21$ $\mu\text{g}/\text{mL}$). Molecular docking was also utilized to reveal the binding pose and features of **PESMP** against the α -amylase enzyme. Via docking computations, the high potency of **PESMP** and acarbose towards the α -amylase enzyme was unveiled and confirmed by docking scores of -7.4 and -9.4 kcal/mol, respectively. These findings shine a new light on the potential of **PESMP** compounds as α -amylase inhibitors.

Keywords: oxadiazole; α -amylase inhibition; X-ray diffraction; molecular docking; DFT calculations

within SZYBKI software [69,70]. The Gasteiger method was utilized to assign the atomic charges of PESMP and acarbose compound [71]. In this work, docking computation was conducted utilizing AutoDock4.2.6 software [72]. The genetic algorithm number (GA) was adjusted to 250. The maximum number of energy evaluations (*eval*) was set to 25,000,000. Other docking parameters were set to default values. The grid box was tailored to involve the binding pocket of the α -amylase enzyme, with a grid size of 60 Å × 60 Å × 60 Å. The coordinates of the grid center were $x = 32.644$, $y = 38.464$, and $z = -3.166$. The AutoGrid program was employed to extract the grid maps with a spacing of 0.375 Å. All molecular interactions were represented using BIOVIA Materials Studio [73].

4. Conclusions

An efficient, multistep synthetic approach was followed to synthesize good yields of 4-(5-((1,3-dioxoisindolin-2-yl)methylthio)-1,3,4-oxadiazol-2-yl)-N,N-dipropylbenzenesulfonamide (PESMP). Its synthesis was confirmed via structural validation using NMR (^1H , ^{13}C), FT-IR, and single-crystal X-ray diffraction analyses. The purity of PESMP was established on the basis of thin-layer chromatography. To obtain further insight into the features of the entitled compound, various DFT calculations were executed accordingly. The band gap value of the PESMP compound (0.1732 a.u.) for the HOMO-LUMO orbital was smaller than the band gap values of HOMO-LUMO ± 1 and HOMO-LUMO ± 2 . The testing of PESMP against α -amylase revealed an $\text{IC}_{50} = 10.60 \pm 0.16 \mu\text{g/mL}$ using acarbose ($\text{IC}_{50} = 8.80 \pm 0.21 \mu\text{g/mL}$) as a standard drug. Molecular docking revealed the binding mode of the PESMP compound against the active site of α -amylase. PESMP and acarbose showed docking scores of -7.4 and -9.4 kcal/mol against the α -amylase enzyme, respectively. These findings shine new light on the potential of the PESMP compound as an α -amylase inhibitor.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/ph16030424/s1>, Figure S1: ^1H NMR spectrum of PESMP; Figure S2: ^{13}C NMR spectrum of PESMP; Figure S3: 2D fingerprint plots of the remaining contacts; Figure S4: Graphical representation of voids, (a) 1st view, and (b) 2nd view along the a-axis; Figure S5: 3D superimposition of the resolved experimental structure (in gray) and the portended binding mode (in cyan) of acarbose complexed with α -amylase enzyme; Table S1: Selected bond lengths and bond angles in the PESMP compound; Table S2: Interaction energies (kJ/mol); Table S3: Cartesian coordinates of the selected atoms that are involved in interaction energy calculations.

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