Indian Journal of Chemistry
Vol. 63, May 2024, pp. 506-517
DOI: 10.56042/ijc.v63i5.9396

Molecular docking and dynamic simulation analysis of natural polyphenols for identifying potential PTP1B inhibitors for type 2 diabetes

Pratik Khona & Uma Kabra*

Department of Pharmaceutical Chemistry, Parul Institute of Pharmacy, Parul University, Vadodara, Gujarat, India
E-mail: uma.kabra16205@paruluniversity.ac.in

Received 8 March 2024; accepted(revised) 25 April 2024

Type 2 diabetes (T2D) is a complex illness and a significant source of morbidity and mortality globally. Insulin resistance is characterized by defect in insulin signaling pathway. Development of novel therapeutic agent that can improve insulin resistance could be beneficial for the treatment of T2D. Activation of insulin receptor involves phosphorylation of its tyrosine residues. However, dephosphorylation of these residues by protein tyrosine phosphatases reduces the insulin receptor kinase activity. PTP1B negatively regulate insulin signaling and leptin signaling pathways. Naturally occurring polyphenols can improve insulin resistance by a range of actions, including lowering postprandial blood sugar levels, modulating the signaling of insulin pathways, and sparing insulin-secreting pancreatic β-cells from harm. Therefore, in the present study we screened natural polyphenol from phenol explorer library using molecular docking and molecular dynamics simulation techniques to predict possible PTP1B inhibitors. Our virtual molecular docking data have showed that ten natural polyphenol compounds displayed stronger binding affinity and essential amino acid interaction toward the PTP1B inhibitory site. Further, molecular dynamics simulation findings have indicated that Theaflavin 3,3'-O-digallate (136), Naringin 4'-O-glucoside (216), and Naringin 6'-malonate (217), exhibit a significant number of dynamic features such as stability, flexibility and binding energy. Our *in silico* analysis shows that the above listed natural polyphenols may potentially be used as PTP1B inhibitor for the management of T2D.

Keywords: Protein tyrosine phosphatase 1B, Polyphenols, Type 2 diabetes, Insulin resistance, Molecular docking, Molecular dynamic simulation