Electronic-Structure Informatics for Natural Product Drug Discovery: Discovery of α-glucosidase Inhibitors

Y. Tateishi, Kumamoto University

Molecular descriptors proposed in the electronic structure information (ESI) method were used to predict the activity of α-glucosidase inhibitor candidates. ESI was proposed by the authors' laboratory, focuses on the electronic features of molecules, and includes energy-related parameters that describe intermolecular interactions without directly referring to the molecular structural features of ligands. In this study, we applied the ESI method to the construction of a regression model in order to predict the pIC50 values of known inhibitors reported in the literature. The inhibitory activity values were collected from the ChEMBL database. The obtained regression model reasonably reproduced the experimental values. Using this model, we searched for highly active diabetes drugs in the Japanese traditional medicine database called KampoDB. As a result, we found promising compounds as α-glucosidase inhibitors. The discovered compounds had different scaffolds from the molecules in the training data. This suggests that ESI can be used as a new approach for compound screening.