Abstract

Hologram quantitative structure–activity relationships (HQSAR), comparative molecular field analysis (CoMFA) and comparative molecular similarity index analysis (CoMSIA) were implemented on a group of 32 of potent Gram-negative LpxC inhibitors. The most effective HQSAR model was obtained using atoms, bonds and donor and acceptor as fragment distinction, and its q^2 ,r^2, r^2_{Pred} are 0.937, 0.993 and 0.892 respectively. CoMFA model with statistical parameters (r^2=0.967, q^2=0.804, r^2_{Pred}=0.827); and CoMSIA model with (r^2=0.963, q^2=0.752, r^2_{Pred} =0.857) were produced. Molecular docking was employed to validate the results of the HQSAR, CoMFA and CoMSIA models. Moreover, the graphical results of HQSAR, CoMFA, CoMSIA and docking were analyzed. The results of this study provide an insight for designing novel LpxC inhibitors.

Keyword: gram-negative specific LpxC inhibitors, CoMFA, CoMSIA, HQSAR, molecular docking

University of Zabol
Faculty of Science
Department of Chemistry

The Thesis Submitted for the Degree of Master of Science

(In the field of Analytical Chemistry)

An explorative study on potent gram-negative specific LpxC inhibitors: CoMFA,CoMSIA, HQSAR and molecular docking

Supervisors:
Dr. F.Shiri
Dr. M. Nejati yazdi nejad

Advisor:
Dr. M. Salahinejad

By:
Rahmat. A. Dijoor

Winter 2017