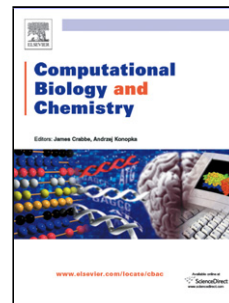


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***In silico* structure prediction and inhibition mechanism studies of AtHDA14 as revealed by homology modeling, docking, molecular dynamics simulation**

Ming-Lang Zhao¹, Wang Wang¹, Hu Nie, Sha-Sha Cao, Lin-Fang Du*

*Key Laboratory of Bio-resources and Eco-environment of the Ministry of Education,
College of Life Sciences, Sichuan University, Chengdu 610064, P.R. China*

*Corresponding author: Tel.: +86 028 85415008; fax: +86 028 85415300.

E-mail: dulinfang@scu.edu.cn (L.F. Du)

¹ These authors contributed equally to this work

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