

Exploration of binding mechanism of a potential Streptococcus pneumoniae neuraminidase inhibitor from herbaceous plants by molecular simulation

Shanshan Guan ^{1,2*}, Ketong Zhu ^{1,2}, Yanjiao Dong ^{1,2}, Hao Li ^{1,2}, Shuang Yang ^{1,2}, Song Wang ³, Yaming Shan ^{4*}

1 College of Food Engineering, Jilin Engineering Normal University, Changchun, Jilin 130052, China

2 Key Laboratory of Molecular Nutrition at Universities of Jilin Province, Changchun, Jilin 130052, China

3 Laboratory of Theoretical and Computational Chemistry, Institute of Theoretical Chemistry, Jilin University, Changchun 130023, China

4 National Engineering Laboratory for AIDS Vaccine, School of Life Sciences, Jilin University, Changchun, Jilin 130012, China

* Corresponding authors at:

College of Food Engineering, Jilin Engineering Normal University; Key Laboratory of Molecular Nutrition at Universities of Jilin Province, Changchun, Jilin, China.

(Guan Shanshan) (email: guanshanshan@jlenu.edu.cn);

National Engineering Laboratory for AIDS Vaccine, School of Life Sciences, Jilin University, Changchun, Jilin 130012, China.(Shan Yaming).

(email: shanyam@jlu.edu.cn)

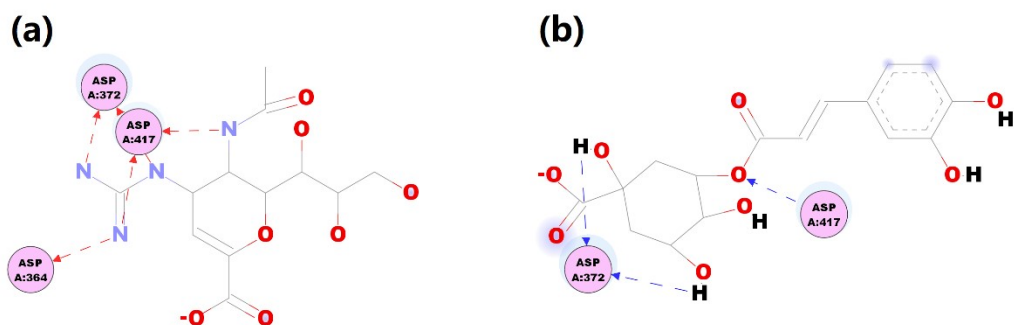


Fig. S1 The detail difference of binding mode between (a) zanamivir and (b) chlorogenic acid

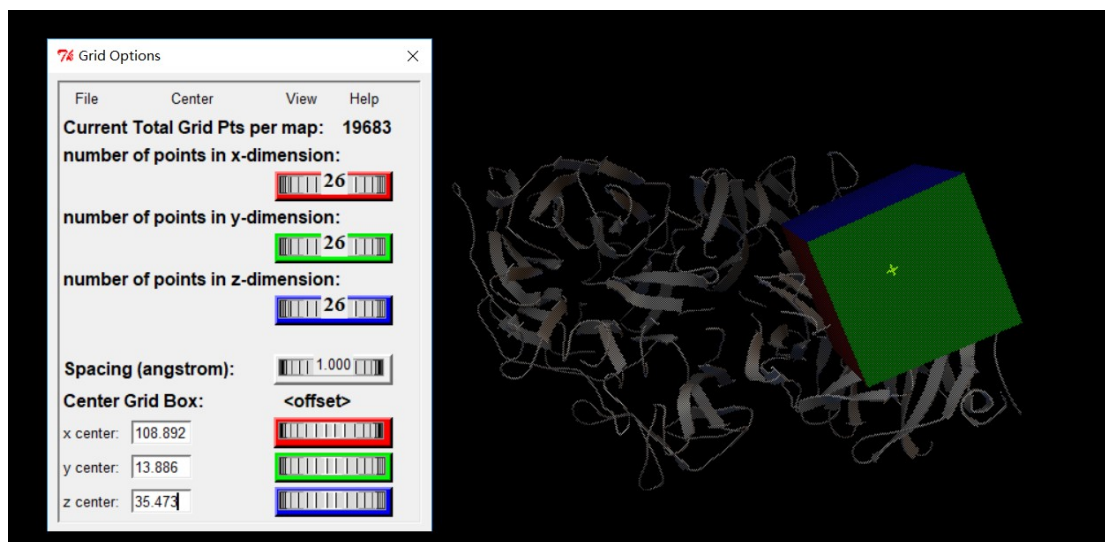


Fig. S4 The grid detail used in the docking simulation

Tab. S1 Protonation states for titratable residues of NanA

Protonated residues in complex	
ChainA	ChainB
all Arg, all Lys; Asp417, Asp434, Glu620, His612, His 634	all Arg, all Lys; Asp364 Asp417, Asp434, His612, His634