

Using computational modeling to design new antivirals

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Influenza is a major public health threat, but here are low efficacy of seasonal flu vaccines and increasing in drug-resistant. To develop new drug to against influenza, scientists found a antibodies to bind to a highly conserved region on viral hemagglutinin, which can prevent from a wide range of diverse influenza. However, current vaccines vary on strain and is low efficiency to against the drifted or shifted strains. Then D.H Fuller etl. optimized one of HA stem binding protein to tight binding using computational modeling. Finally, new designed protein show the ability to disrupts different influenza.