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Genomic Sciences Center

Protein Research Group

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Public Release of Database of the predicted three-dimensional structures of influenza viral neuraminidase

We predicted using homology modeling the three-dimensional structures of neuraminidase protein that is necessary for influenza virus proliferation, and world-widely released their database on January 20th, 2006.

Neuraminidase, a protein that regulates the proliferation of influenza virus, is the most popular target for the development of anti-influenza drugs.

The information can be useful for various research including the drug development against pandemic and seasonal influenza. Employing the full automatic modeling system originally developed by their research group and using already published structures of neuraminidase as templates, we could predict the 1603 three-dimensional models of all subgenomic types of neuraminidase protein based on their amino acid sequences entried in NCBI (National Center for Biotechnology Information) nonredundant protein sequence database.

This database is world-widely published on our web site (http://protein.gsc.riken.jp/Research/index_na.html).

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