

建構亞洲流行性疾病之高效能藥物篩選計算服務

High Throughput Virtual Screening Service against the Epidemic Diseases in Asia

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Abstract

In the modern biomedical drug discovery, molecular docking simulation is a common method for predicting potential interacting complexes of small molecules on protein binding sites. However, searching all optimal conformations of a compound could be a time-consuming process. GAP Virtual Screening Service (GVSS), large scale in-silico protein-ligand virtual screening service, provides a production system to speed-up the searching process. We demonstrated how this high throughput in-silico massive molecular docking service benefits from state-of-the-art Grid technology to the activities for Avian Flu drug refinement and Dengue Fever drug discovery on EUAsiaGrid infrastructure since March 2009. Furthermore, these activities also facilitates more biomedical e-Science applications in Asia, such as other diseases and compounds profiling.

Key Word Drug Discovery 、Molecular simulation 、Grid Computing 、High throughput computing 、e-Science

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