

# Abstract

## Background

Guanonine-protein (G-protein) is known as molecular switches inside cells, and is very important in signals transmission from outside to inside cell. Especially in transport protein, most of G-proteins play an important role in membrane trafficking; necessary for transferring proteins and other molecules to a variety of destinations outside and inside of the cell. The function of membrane trafficking is controlled by G-proteins via Guanosine triphosphate (GTP) binding sites. The GTP binding sites active G-proteins initiated to membrane vesicles by interacting with specific effector proteins. Without the interaction from GTP binding sites, G-proteins could not be active in membrane trafficking and consequently cause many diseases, i.e. cancer, Parkinson... Thus it is very important to identify GTP binding sites in membrane trafficking, in particular, and in transport protein, in general.

## Results

We used an independent data set to evaluate the performance of the proposed method, which had an accuracy of 98.7%. We compared the performance of the proposed method in analysing two newly discovered transport protein sequences with that of the GTPBinder, NsitePred, TargetSOS and determined that the performance result of the proposed method improved remarkably. Furthermore, the proposed method enabled reducing the number of false positives significantly and can provide useful information for biologists.

## Conclusions

We developed a method that is based on PSSM profiles and SAAPs for identifying GTP binding sites in newly discovered transport protein sequences. This approach achieved a significant

improvement after we added SAAPs to PSSM features to analyse GTP binding proteins in the transport proteins. The proposed method can serve as an effective tool for predicting GTP binding sites in transport proteins and can help biologists to understand the functions of the transport proteins, particularly those of GTP binding sites. We also developed a web server which identifies GTP binding sites in transporters available for academics.