**Discussion**

We set up the exocytosis network from the Gene ontology and BioGRID database, and then we analyze the database by our methods. We rank our proteins in the network with FPC score. The top 5 proteins are all belong to SNARE complex, which are responsible for the vesicle fusion to the cell membrane. The SNARE complex is very important to the exocytosis, which makes our analysis meaningful.

We notice that for the endocytosis network, the top five FPC score proteins are all involved in the signal receptors, such as EGFR. These results are outside of our original expectation, because these signal pathways don’t take part in endocytosis? other than in regulation. However, looking closely at the structure of the network as well as what is known about endocytosis resolves this issue. It is well-known that endocytosis has four different subtypes: clathrin-mediated endocytosis, non-clathrin-mediated endocytosis, macropinocytosis and phagocytosis. Clathrin-mediated endocytosis has been well studied for many years, so most of the proteins in the endocytosis network come from this pathway. Similarly, signaling cascades have been highly implicated in clathrin-mediated endocytosis pathway. Therefore, clathrin-mediated endocytosis accounts for the most important part in our endocytosis network, as well as the difference in the results from the expection

We have only 20 proteins both in exocytosis network and endocytosis network, which is far less than our expectation. This is clearly due to the limitations of existing pathway databases. For example, the roles of dynamin and synapin in both endocytosis and exocytosis are well-studied. However, neither protein is in the exocytosis pathway in the dataset that comes from Gene Ontology. There does not seem to be any method to resolving this, as there is no exocytosis pathway in the KEGG database (<http://www.genome.jp/kegg/>). One possible method of attempting to resolve this issue is to combine the networks of endocytosis and exocytosis.

Utilizing this combined network gives some interesting results. Interestingly, we find the COPS5 in the top 5 score from the FPC method. COPS5 is a regulator of E3 ligase, which can regulate many proteins expression. COPS5 FPC score ranks very low in exocytosis network and didn’t appear in endocytosis network. However, when combine these two network, COPS5 becomes to be the most core proteins in the network. In another word, COPS5 have potential to be a very important proteins in the regulation of exocytosis and endocytosis. Here we can see the efficacy of the methods used to find this easily omitted protein.

Finally, we set up the vesicle network, trying to find the most complete database. Even though we couldn’t distinguish the exocytosis and endocytosis in the vesicle network, we can prove the limitation of the network we set up before. We also have the top 5 rank proteins, which are ALB (binding to water, Ca(2+), Na(+), K(+)), CLTC (Clathrin heavy chain 1), ARRB1 (Arrestin beta 1), YWHAQ (mediate signal transduction), UBC (ubiquitin). These five proteins are most widely used in the cell. For example UBC is the necessary for all the proteins degradation in the cell, which is the most essential protein in the cell activity.