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Drug target protein-protein interaction networks: A systematic perspective

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The identification and validation of drug targets are crucial in biomedical research and many studies have been conducted on analyzing drug target features for getting a better understanding on principles of their mechanisms. But most of them are based on either strong biological hypotheses or the chemical and physical properties of those targets separately. In this paper, we investigated three main ways to understand the functional biomolecules based on the topological features of drug targets. There are no significant differences between targets and common proteins in the protein-protein interactions network, indicating the drug targets are neither hub proteins which are dominant nor the bridge proteins. According to some special topological structures of the drug targets, there are significant

differences between known targets and other proteins. Furthermore, the drug targets mainly belong to three typical communities based on their modularity. These topological features are helpful to understand how the drug targets work in the PPI network. Particularly, it is an alternative way to predict potential targets or extract nontargets to test a new drug target efficiently and economically. By this way, a drug target's homologue set containing 102 potential target proteins is predicted in the paper.

Speaker Biography

Ragae Shokralla has completed his Pharm D degree at the age of 26 years from Alexandria University, Egypt. He is a clinical pharmacist at Ministry of Health - Kuwait.

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