

The Discovery of Novel Targets for Anti-infective Agents by Protein Network Modeling

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In post-genomic view, the protein's role can be expanded to an element in the protein network constructed by protein interaction analysis. It's been suggested that highly connected proteins in the network are more likely to be essential than those with only a small number of links to other proteins. Here we demonstrate that the essential genes can be predicted through computational modeling of protein interaction network in the yeast *Saccharomyces cerevisiae*. We applied PreDIN system to yeast genome and constructed a virtual protein interaction map. The predicted network we constructed has 2,944 yeast proteins and connected by 72,880 interactions covering 44% of known interactions. We found that about 80% of proteins in the network have nine or fewer links and only about 4% of them are essential. By contrast, 20% of yeast protein in the network has more than 10 links and 22% of them are essential. This suggests that proteins with high connectivity in the network are 5 times more likely to be essential than proteins with low connectivity. Based on this finding, we are now applying PreDIN system on microbial genomes to identify essential genes for anti-microbial drug targets.