Identification of the substrates and interaction proteins of aurora kinases from a protein-protein interaction model

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Abstract

The increasing use of high-throughput and large-scale bioinformatics-based studies has generated a massive amount of data stored in a number of different databases. The major need now is to explore this disparate data to find biologically relevant interactions and pathways. Thus, in the post-genomic era, there is clearly a need for the development of algorithms that can accurately predict novel protein-protein interaction networks in silico. The evolutionarily conserved Aurora family kinases have been chosen as a model for the development of a method to identify novel biological networks by a comparison of human and various model organisms. Our search methodology was designed to predict and prioritize molecular targets for Aurora family kinases, so that only the most promising are subjected to empirical testing. Four potential Aurora substrates and/or interacting proteins, TACC3, survivin, Hec1, and hsNuf2, were identified and empirically validated. Together, these results justify the timely implementation of in silico biology in routine wet-lab studies and have also allowed the application of a new approach to the elucidation of protein function in the post-genomic era.