

Two-hybrid screen of human Nek6 reveals a large spectrum of protein interactions

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The NIMA-related kinases (Neks) represent an evolutionarily conserved family of serine/threonine kinases (designated Nek1 to Nek11), containing 40-45% identity to the *Aspergillus nidulans* mitotic regulator NIMA within their N-terminal catalytic domain. Among the mammalian Nek proteins, Nek6 was recently found to be linked to carcinogenesis. It is over-expressed in gastric cancer and up-regulation of Nek6 mRNA correlates with Pin1 up-regulation in 70% of hepatic cell carcinomas. The over-expression of a catalytically-inactive Nek6 on the other hand reduces the growth rate of human breast cancer cells. Considering the relevance of hNek6 as a putative chemotherapeutic target and aiming at a better understanding of its cellular function, we screened for hNek6 interacting proteins, using the yeast two-hybrid system. In this work, we present a preliminary interaction network of hNek6, composed of proteins classified into 15 functional categories, based on the Gene Ontology database. The screens were performed with three different human cDNA libraries (fetal brain, bone marrow and leucocytes). We have also performed a pepchip analysis for both recombinant wildtype Nek6 and its mutated version Nek6(S206A), both expressed and purified from *E. coli*, in order to search for novel possible substrates and compare the differences between them.

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