KANPHOS (Kinase-Associated Phospho-Signaling) Platform - A comprehensive database for kinase-associated neural phosphorylation signaling

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Protein phosphorylation is a major and essential post-translational modification in eukaryotic cells that plays a critical role in various cellular processes. While recent advances in mass spectrometry based proteomics allowed us to identify approximately 200,000 phosphorylation sites, it is not fully understood which sites are phosphorylated by a specific kinase and which extracellular stimuli regulate the protein phosphorylation via intracellular signaling cascades. Recently, we have developed an in vitro approach termed the kinase-interacting substrate screening (KISS) method and an in vivo approach termed kinase-oriented substrate screening (KIOSS) method. Using KIOSS method, we analyzed the phosphorylation signals downstream of dopamine in mouse striatal slices, and found that about 100 proteins including ion channels and transcription factors were phosphorylated probably by PKA or MAPK. Here, we present an on-line database system which provides the phosphorylation signals identified by our KISS and KIOSS methods as well as those previously reported in the literature. The database system and its web portal, named KANPHOS (Kinase-Associated PHOspho-Signaling), were built based on the Next Generation XooNIps. We also demonstrate how to retrieve proteins and pathways in striatal medium-sized spiny neurons modulated by extracellular dopaminergic stimulation.