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Overexpression of human proto-oncogene DEK induces apoptosis in drosophila by histone modification and caspase activation

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The proto-oncogene protein DEK is an abundant and ubiquitous nuclear protein that is associated with chromatin. DEK was originally identified in a fusion protein with the CAN nucleoporin NUP214 in acute myeloid leukemias (AML). Recent reports have suggested that the DEK protein has vital roles in chromatin remodeling, through the alteration of the chromain topology. Recently, we suggested that DEK is able to bind both to histones and to histone acetyltransferases (HATs), and shows HAT inhibitory activity. The acetylation of nuclear core histones is thought to play important roles in level of transcription. To explore of further functional roles of DEK in vivo, we used human DEK overexpressing transgenic Drorophila that driven by UAS/GAL4 system. Adult fly eyes phenotype diaplayed a severe rough eye and activated caspase-dependent apoptotic induction. In the histone modification patterns, levels of acetylation were decreased in histone H3 and H4 by hDEK overexpression. Induction of apoptosis in HeLa cells was also examined in FACS and caspase-3 activity analysis through DEK overexpression. Furthermore, we profiled other apoptosis related genes in DEK induced cell death in HeLa cells using RT-PCR with specific primers.

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Predicting contact-dependent secondary structure propensity: Relevance to amyloidogenic sequences and protein misfolding diseases

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Chameleon sequences that contain the characteristics of secondary structural conversions have received considerable attention since such a structural change may induce many amyloidogenic proteins to self-assemble into fibrils thus causing fatal diseases. In order to predict protein misfolding in amyloid diseases, we first analyzed the energetics of secondary structural conversions in a collection of chameleon sequences retrieved from the Protein Data Bank. Major energetic contributions to the secondary structural conversion were analyzed by carrying out energy decomposition on a pairwise per-residue basis. The result of the present study was used to develop an advanced predictor for the accurate calculation of Contact-dependant Secondary Structure Propensity (CSSP) in protein sequences.

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Protein kinase CK2 is negatively regulated by hNopp140 in an inositol-6-phosphate dependent manner

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Protein kinase CK2 is a ubiquitous protein kinase that can phosphorylate various proteins that are involved in central cellular processes such as signal transduction, cell division and proliferation. We have shown that the nucleolar phosphoprotein p140, hNopp140, which was previously shown to interact with CK2, is able to regulate the catalytic activity of CK2. Unphosphorylated or phospho-hNopp140 binds to the regulatory or catalytic subunit of CK2, respectively, and inhibits the phosphorylation of α-casein by CK2. Furthermore, it is found that the interaction between hNopp140 and CK2 is abrogated by inositol-6-phosphate, and the activity of CK2 is no longer inhibited by hNopp140 in the presence of inositol-6-phosphate. These observations propose that hNopp140 serves as a negative regulator of CK2, and the increased level of inositol-6-phosphate stimulates the cellular activity of CK2 by preventing its interaction with hNopp140.

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Proteomic analysis of heat, osmotic and oxidative stress response in Thermococcus koradaraensis KOD1

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Thermococcus kodakaraensis KOD1, is an anaerobic and obligated heterotrophic and grows on complex organic compounds in the presence of elemental sulfur near its optimal growth temperature, 85oC. To analyze the response to various stresses (heat, osmotic and oxidative shock) at the protein synthesis level, we performed the two-dimensional electrophoresis (2-DE) and the matrix-assisted laser desorption/ionization-time of flight-mass spectrometry (MALDI-TOF-MS) analysis. We have cloned and expressed one of the stress inducible proteins. This is a thermo-stable protein that has highly conserve domain to OsmC (osmotically inducible proteins C). Also this protein has a hydroperoxide peroxidase activity. To examine the structural organization and change according to variable factors, we performed the size exclusion chromatography and electron microscopy analysis.