Kinexus Cracks the Protein Kinase Specificity Code

Prediction of over 4.6 million human-kinase-substrate interactions available in PhosphoNET website

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VANCOUVER, British Columbia – Kinexus Bioinformatics Corporation, a world-leader in molecular communications research, announced major advancements in its PhosphoNET KnowledgeBase (www.phosphonet.ca) for the study of cell signalling systems. This free resource to the scientific community now features data on more than 92,000 human phosphorylation sites, including their occurrence in over 20 other diverse species, and identification of the protein kinases that target these regulatory sites.

The human genome encodes at least 515 protein kinases that regulate each other and another ~22,500 different types of proteins to coordinate all cellular activities. Kinases are networking enzymes that function by tagging proteins at specific sites with phosphates, which act as molecular on/off switches. Scientists at Kinexus and their collaborators in the Mathematics of Information Technology and Complex Systems (MITACS) groups at the University of British Columbia and Simon Fraser University have developed an algorithm that accurately predicts which of nearly 500 different kinases are most likely to target each phosphorylation site. The prediction requires only knowledge of the gene sequence of a kinase. This major breakthrough is allowing Kinexus to identify another 400,000 suspected phosphorylation sites in human proteins. This will permit the company to draft the first high resolution map of the molecular intelligence system of human cells. Through application of its evolutionary analyses of conserved phosphorylation sites in very different organisms, Kinexus is also defining those connections that are the most critical and linked to major diseases.

"Protein kinases are well recognized by the pharmaceutical and biotech industry as highly productive targets for drug development with application to over 400 human diseases," commented Dr. Steven Pelech, President and Chief Scientific Officer of Kinexus and a professor in the Department of Medicine at the University of British Columbia. "Cancer, diabetes, Alzheimer's disease are just a few of many examples of disorders that arise from miscommunication in cell signalling systems. PhosphoNET is a valuable tool to guide biomedical researchers in fruitful directions to define biomarkers for disease diagnosis and kinase drug targets for development of new treatments."

Dr. Pelech added "We are extremely excited by the prospect that our kinase specificity prediction algorithm can be applied to rapidly elucidate the complex structures of protein kinase-based communications systems for any animal, plant or microbes for which their genome has been or will be sequenced. The high definition maps of protein phosphorylation networks that Kinexus can now produce could steer a significant portion of biomedical research over the next decade."

For more than a decade, Kinexus has been a unique provider of proteomics services to academic and industrial laboratories to track protein kinases and their phosphoprotein targets in experimental tissue and cell specimens. The company has developed a diverse panel of protein microarrays that can monitor the presence and activity levels of hundreds of kinases and their targets, their interactions, and the effects of promising drug candidates.

To learn more about the company's proteomics and bioinformatics services, please visit www.kinexus.ca. Kinexus is a private, biotechnology company engaged in the research and development of innovative technologies to map and control signalling proteins in molecular communication networks. The application of this knowledge positions Kinexus and its clients for better disease diagnosis and personalized drug therapies to improve human health.

For further information, please contact Kinexus Bioinformatics Corporation toll free at 1-866-KINEXUS or email csutter@kinexus.ca or visit our website at www.kinexus.ca