NEWS:

Kinases are among the most intensively pursued enzyme superfamilies as targets for anti-cancer drugs. Large data sets on inhibitor potency and selectivity for more than 400 human kinases became available recently, offering the opportunity to design rationally novel kinase-based anti-cancer therapies. However, the expression levels and activities of kinases are highly heterogeneous among different types of cancer and even among different stages of the same cancer. Recent proteomic study (1) showed it is now easy to assess simultaneously the expression of more than 300 kinases in human cells and tissues. This is done by LC-MS/MS, either in shotgun proteomics or MRM method.
We have now invaluable method to determine which kinase is targeted by an inhibitor and to predict the effectiveness of kinase inhibitor drugs and offer the opportunity for individualized cancer chemotherapy.

A targeted quantitative proteomics strategy for global kinome profiling of cancer cells and tissues. Xiao Y, and all.2014 http://www.ncbi.nlm.nih.gov/pubmed/24520089

High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID™ data processing: The efficient tool

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