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## PHARMACOPEPTIDOMICS

NEW  
SERVICE

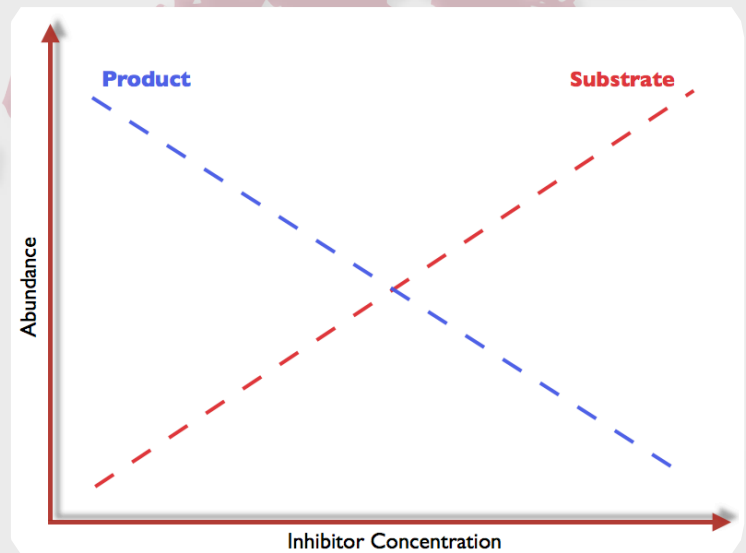
### MONITORING DRUG EFFECTS IN VIVO

The human genome contains more than 550 different proteases and peptidases, and also a considerable number of protease inhibitors. Very successful drugs have been launched based on protease inhibition. However, in many cases proteases do have more than the one substrate that is the target of drug development. Similarly, protease inhibitors may act on more than the target protease and can therefore induce undesired effects in the patient.

*In vivo* characterization of protease inhibitors by analyzing native peptides offers the possibility to determine the specificity of the inhibitor under physiological conditions. Analysis of peptides by Peptidomics allows to monitor protease activity *in vivo* and to describe the influence of protease inhibition.

No other technology can provide you more comprehensive information on your protease inhibitor. Whether you're in a rat model or in humans, isn't it worth knowing how your protease inhibitor is acting? Our bottom-up peptide profiling of the global peptidome delivers fast and affordable results so you can evaluate performance and make decisions.

The proteome is the set of all proteins encoded by the genome and present in a



specific time frame in an organism. While the genome remains stable to a large extent, the proteome is remarkably dynamic and different mechanisms of post-translational control exist. An important irreversible control level is proteolytic processing of proteins. Proteases can initiate, modulate and terminate many important biological functions by specific substrate cleavage. These cleavage events can lead to the generation of native peptides. Consequently the analysis of the full complement of small proteins and peptides is capable to provide insights on the protease activity in a given sample since peptides contain information on the preceding proteolytic processing.

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