

HARVARD UNIVERSITY
Office of Technology Development



Extract-based Functional Assay (EFA) for the Detection of Post-Translational Modifications

Principal Investigator

Marc Kirschner, PhD, Carl W. Walter Professor of Systems Biology, Harvard Medical School

Technology

The Kirschner lab developed a powerful technology enabling mapping of all post-translational modifications (PTM) in whole cells in a manner that simulates a living cell environment. This high throughput profiling method currently measures PTMs from thousands of proteins and could be applied to the whole genome.

Although post-translational modifications are suspected in playing a role in a number of diseases, including cancer and neurodegeneration, analytical methods for looking at large-scale post-translational modifications are limited. Genome-wide biochemical assays are not currently available and proteomic studies have mainly focused on phosphorylation/kinase activity. The extract-based functional assay (EFA) seeks to provide a platform to analyze physiological conditions based on biomarker activity, not abundance.

Detection of biomarkers via EFA is not based solely on protein abundance, but on activity downstream to the genome and expression. EFA provides the ability to perform complex biochemical reactions for thousands of proteins in parallel.

Market and Applications

This platform technology is highly relevant for biomarker discovery, target identification and validation, and drug discovery, via secondary screens for inhibitors. Short term commercial applications include diagnostics and prognostics of cancer, autoimmune and neurodegenerative diseases, as well as personalized medicine applications such as optimization of therapy choice, dose, and regime for individual patients.

Specifically within target identification and validation, this technology can identify targets that are either pathway or modification specific and can compare genome-wide response to drugs between animal models and humans. Also, the effect of drug combinations on the enzymatic activity specificity of the targets can be analyzed.

Research applications include the study of substrate specificities for different E3 classes, F-box proteins, etc. and comparing KD/KO cells with wild-type to study effects on pathway activation.

Product Advantages

This technology has the ability to perform complex biochemical reactions for thousands of proteins in parallel and may be applied to the whole genome. It can be used to process various rare samples, including patient samples, and provides a PTM signature rather than the activity of a single biomarker. In addition, because the technology assays activity downstream of the genome and protein expression, detection is not limited by the abundance of a protein.

Licensing Opportunity:

This technology is available for worldwide, exclusive licensing.

Contact:

Michal Preminger, PhD, MBA
Sr. Director of Business Development
Harvard Medical School
Gordon Hall, Suite 414
Boston, MA 02115
(617) 432-3896
Michal_preminger@harvard.edu