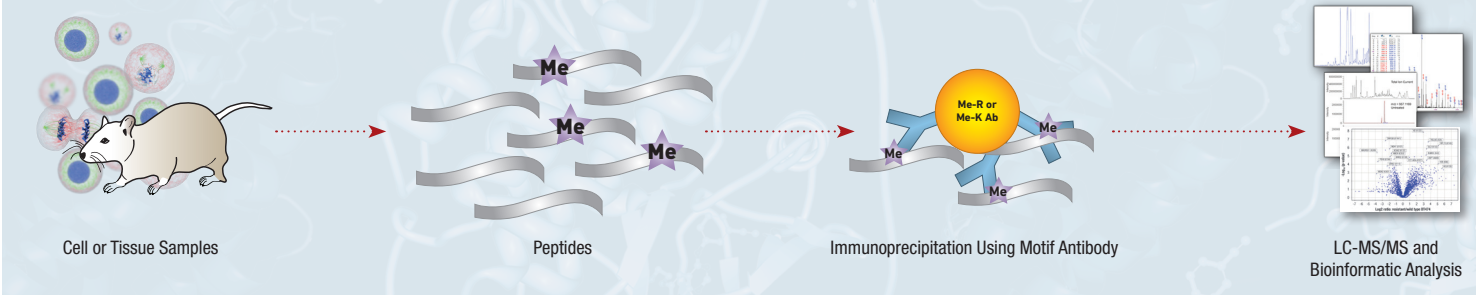
MethylScan®

Methylation Proteomics

FROM CELL SIGNALING TECHNOLOGY



Protein methylation is a common post-translational modification (PTM) that occurs mostly on arginine and lysine residues. Arginine methylation regulates processes such as RNA processing, gene transcription, DNA damage repair, protein translocation, and signal transduction. Lysine methylation is best known to regulate histone function and is involved in epigenetic regulation of gene transcription.

MethylScan®, PTMScan® technology for methylation proteomics, uses proprietary methyl arginine (Me-R) or methyl lysine (Me-K) antibodies to enrich methyl-containing peptides from trypsin digested samples prior to LC-MS/MS analysis.

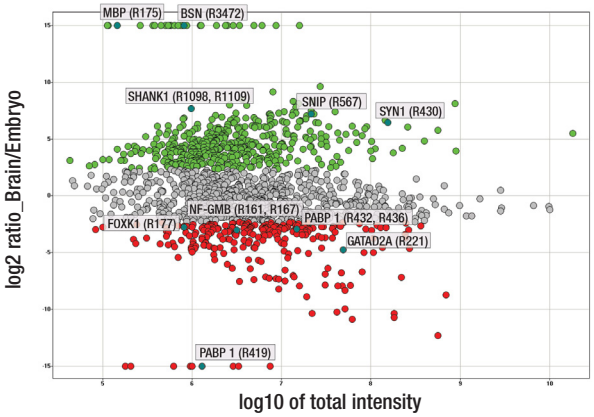
Features and Benefits

- Antibodies used for MethylScan are exceptionally specific, as demonstrated by peptide blocking experiments, to help ensure the most accurate results.
- PTMScan technology can be applied to many biological systems and species to encompass diverse research interests.
- Experienced CST scientists provide technical support throughout the PTMScan workflow to facilitate research progress.

Available Products and Services

- **PTMScan® Pan-Methyl Lysine Kit #14809**
- **PTMScan® Mono-Methyl Arginine Motif (mme-RG) Kit #12235**
- **PTMScan® Asymmetric Di-Methyl Arginine Motif [adme-R] Kit #13474**
- **PTMScan® Symmetric Di-Methyl Arginine Motif [sdme-RG] Kit #13563**
- **MethylScan® Arginine Proteomics Services**
- **MethylScan® Lysine Proteomics Services**

Quantitative analysis of arginine monomethylation in mouse brain and embryo: Each dot in the scatter plot represents a unique arginine monomethylated peptide identified using PTMScan® Mono-Methyl Arginine Motif [mme-RG] Kit #12235. The x-axis is the log10 value of the total intensity of the representative peptide for a methylation site in mouse brain and embryo, and the y-axis shows the log2 ratio of intensity of the peptide in mouse brain vs. embryo. A cutoff of 5-fold was set to indicate increased arginine monomethylation peptide abundance in either brain (green dots) or embryo (red dots). For the methyl peptides that uniquely existed in a specific tissue, arbitrary log2 ratios of 15 (brain specific) and -15 (embryo specific) were assigned.*



*This research was originally published in Molecular and Cellular Proteomics. Guo, A., et al. Immunoaffinity enrichment and mass spectrometry analysis of protein methylation. *Mol. Cell. Biol.* 2014; 13(1):372–387.

For additional information on PTMScan methylation proteomics visit: **www.cellsignal.com/methylscan**

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Cell Signaling TECHNOLOGY®

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