Revision 7

Store at +4C and -20C

#50071

PTMScan® HS Pilot Acetyl-Lysine Motif (Ac-K) Kit

1 Kit (3 assays)

Cell Signaling TECHNOLOGY®

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For Research Use Only. Not for Use in Diagnostic Procedures.

Product Includes	Product #	Quantity	Storage Temp
PTMScan® HS Acetyl-Lysine (Ac-K) Magnetic Immunoaffinity Beads	99064	1 x 60 µl	+4C
PTMScan® HS Immunoaffinity Purification (IAP) Bind Buffer #1 (1X)	25144	1 x 10 ml	-20C
PTMScan® HS Immunoaffinity Purification (IAP) Wash Buffer (1X)	42424	1 x 20 ml	-20C

Description

PTMScan® HS is an enhanced PTMScan® methodology with improved identification of post-translationally modified peptides. PTMScan® technology employs a proprietary methodology from Cell Signaling Technology (CST) for peptide enrichment by immunoprecipitation using a specific bead-conjugated antibody in conjunction with liquid chromatography tandem mass spectrometry (LC-MS/MS) for quantitative profiling of post-translational modification (PTM) sites in cellular proteins. PTMs that can be analyzed by PTMScan® technology include phosphorylation, ubiquitination, acetylation, and methylation, among others. The technology enables researchers to isolate, identify, and quantitate large numbers of post-translationally modified cellular peptides with a high degree of specificity and sensitivity (HS), providing a global overview of PTMs in cell and tissue samples without bias about where the modified sites occur. For more information on PTMScan® products and services, please visit www.cellsignal.com/proteomics.

Storage

All components in this kit are stable for at least 12 months when stored at the recommended temperature. Upon receipt, 99064P should be stored at 4°C. 25144P and 42424P should be stored at -20°C. *Do not aliquot the antibody.*

Background

Acetylation of lysine, like phosphorylation of serine, threonine or tyrosine, is an important reversible modification controlling protein activity. The conserved amino-terminal domains of the four core histones (H2A, H2B, H3, and H4) contain lysines that are acetylated by histone acetyltransferases (HATs) and deacetylated by histone deacetylases (HDACs) (1). Signaling resulting in acetylation/deacetylation of histones, transcription factors, and other proteins affects a diverse array of cellular processes including chromatin structure and gene activity, cell growth, differentiation, and apoptosis (2-6). Recent proteomic surveys suggest that acetylation of lysine residues may be a widespread and important form of post-translational protein modification that affects thousands of proteins involved in control of cell cycle and metabolism, longevity, actin polymerization, and nuclear transport (7,8). The regulation of protein acetylation status is impaired in cancer and polyglutamine diseases (9), and HDACs have become promising targets for anti-cancer drugs currently in development (10).

Background References

1. Hassig, C.A. and Schreiber, S.L. (1997) *Curr Opin Chem Biol* 1, 300-8.
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3. Liu, L. et al. (1999) *Mol Cell Biol* 19, 1202-9.
4. Boyes, J. et al. (1998) *Nature* 396, 594-8.
5. Polevoda, B. and Sherman, F. (2002) *Genome Biol* 3, reviews 0006.
6. Yoshida, M. et al. (2003) *Prog Cell Cycle Res* 5, 269-78.
7. Kim, S.C. et al. (2006) *Mol Cell* 23, 607-18.
8. Choudhary, C. et al. (2009) *Science* 325, 834-40.
9. Hughes, R.E. (2002) *Curr Biol* 12, R141-3.
10. Vigushin, D.M. and Coombes, R.C. (2004) *Curr Cancer Drug Targets* 4, 205-18.

Trademarks and Patents

Limited Uses

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