Store at -20°C

PTMScan® Control Peptides Acetyl-Lysine

#23068

1 vial

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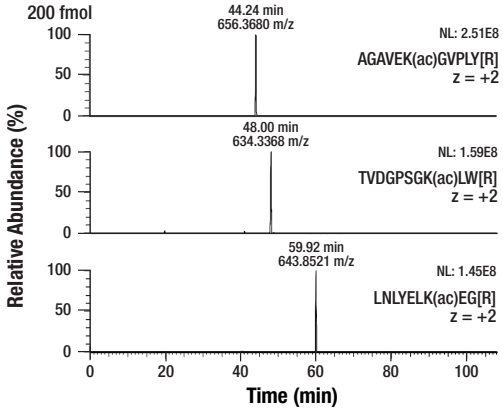
For Research Use Only. Not For Use In Diagnostic Procedures.

Number	Peptide	Precursor mass (M+H⁺)	Recommended m/z to monitor
1	AGAVEK(ac)GVPLY[R]	1311.72948 m/z	656.36838 m/z (z = +2)
2	TVDGPSGK(ac)LW[R]	1267.66688 m/z	634.33708 m/z (z = +2)
3	LNLYELK(ac)EG[R]	1286.69785 m/z	643.85256 m/z (z = +2)

Peptides included in the PTMScan® Control Peptides Acetyl-Lysine mix. All peptides are stable-isotope labeled, designated by bracketed R, and contain an acetyl group designated by parentheses.

Description: The PTMScan® Control Peptides Acetyl-Lysine enable quality control of immunoaffinity enrichment performance using PTMScan® or PTMScan® HS workflows. These synthetic peptides contain a specific post-translational modification (PTM) that can be enriched by the associated PTMScan® or PTMScan® HS immunoaffinity purification (IAP) beads, as well as a stable heavy isotope that can be distinguished from endogenous peptides by the mass spectrometer.

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).



Extracted ion chromatograms of PTMScan® Control Peptides Acetyl-Lysine added at supplied concentration (1X at 200 fmol) to mouse liver peptides prior to immunoaffinity enrichment using PTMScan® Acetyl-Lysine Motif [Ac-K] Kit #13416. Desalted peptides were analyzed on Q Exactive™ mass spectrometer and resolved using a 90 min reversed phase gradient from 7.5% to 32% acetonitrile on a C18 column. The peak corresponding to the specific Control Peptide is marked with retention time and observed precursor mass, with peak height reported as the normalized level (NL) for each row per panel.

Storage: This product is stable for 12 months when stored at -20°C. *Aliquot to avoid multiple freeze/thaw cycles.*

Please visit www.cellsignal.com for a complete listing of recommended complementary products.

Directions for Use:

Use with Cell Signaling Technology's PTMScan® kit protocol from the Immunoaffinity Purification (IAP) step. Because the optimal amount of PTMScan® Control Peptides Acetyl-Lysine for each user's experiments will depend on unique factors such as mass spectrometer sensitivity, users may dilute these control peptides as needed.

1. Aliquot PTMScan® Control Peptides Acetyl-Lysine for storage as single-use units at -20°C or proceed to immediate usage.
2. Resuspend sample peptides in the appropriate buffer and volume, e.g., 1.4 mL of PTMScan® IAP Buffer (1X).
3. Clear sample peptides by centrifugation.
4. Transfer clarified sample peptides to tubes containing IAP beads.
5. Add 10 µL of PTMScan® Control Peptides Acetyl-Lysine to IAP beads and sample peptides and mix well.
6. Continue with PTMScan® or PTMScan® HS workflows at the 2-hour incubation step.
7. Detect PTMScan® Control Peptides Acetyl-Lysine in the LCMS data file.

Background References:

(1) Hassig, C.A. and Schreiber, S.L. (1997) *Curr Opin Chem Biol* 1, 300-8.
(2) Allfrey, V.G. et al. (1964) *Proc Natl Acad Sci U S A* 51, 786-94.
(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.

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Applications: **W**—Western **IP**—Immunoprecipitation **IHC**—Immunohistochemistry **ChIP**—Chromatin Immunoprecipitation **IF**—Immunofluorescence **F**—Flow cytometry **E-P**—ELISA-Peptide **Species Cross-Reactivity:** **H**—human **M**—mouse **R**—rat **Hm**—hamster **Mk**—monkey **Mi**—mink **C**—chicken **Dm**—D. melanogaster **X**—Xenopus **Z**—zebrafish **B**—bovine **Dg**—dog **Pg**—pig **Sc**—S. cerevisiae **Ce**—C. elegans **Hr**—Horse **All**—all species expected Species enclosed in parentheses are predicted to react based on 100% homology.