PTMScan® Control Peptides Succinyl-Lysine

1 vial

Number Peptide Precursor mass (M+H⁺) Recommended m/z to monitor
1 STVAQLVK(succ)[R] 1111.63452 m/z 556.32090 m/z (z = +2)
2 IGFAEK(succ)VAA[K] 1141.63430 m/z 571.32079 m/z (z = +2)
3 FFK(succ)FS[R] 941.47550 m/z 471.24139 m/z (z = +2)

Peptides included in the PTMScan® Control Peptides Succinyl-Lysine mix. All peptides are stable-isotope labeled, designated by bracketed R or K, and contain a succinyl group designated by parentheses.

Description: The PTMScan® Control Peptides Succinyl-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: Lysine is subject to a wide array of regulatory post-translational modifications due to its positively charged ε-amino group side chain. The most prevalent of these are ubiquitination and acetylation, which are highly conserved among prokaryotes and eukaryotes (1,2). Acetyl group transfer from the metabolic intermediates acetyl-, succinyl-, malonyl-, glutaryl-, butyryl-, propionyl-, and crotonyl-CoA all neutralize lysine’s positive charge and confer structural alterations affecting substrate protein function. Lysine acetylation is catalyzed by histone acetyltransferases, HATs, using acetyl-CoA as a cofactor (3,4). Deacetylation is mediated by histone deacetylases, HDACs 1-11, and NAD-dependent Sirtuins 1-7. Lysine acetylation is subject to a wide array of regulatory post-translational modifications due to its positively charged ε-amino group side chain. The most prevalent of these are ubiquitination and acetylation, which are highly conserved among prokaryotes and eukaryotes (1,2). Acetyl group transfer from the metabolic intermediates acetyl-, succinyl-, malonyl-, glutaryl-, butyryl-, propionyl-, and crotonyl-CoA all neutralize lysine’s positive charge and confer structural alterations affecting substrate protein function. Lysine acetylation is catalyzed by histone acetyltransferases, HATs, using acetyl-CoA as a cofactor (3,4). Deacetylation is mediated by histone deacetylases, HDACs 1-11, and NAD-dependent Sirtuins 1-7. Some sirtuins have little to no deacetylase activity, suggesting that they are better suited for other acyl lysine substrates (5). Sirt5 is a predominantly mitochondrial deacetylase and deamylase (5,6). In the absence of a known succinyltransfase, succinylation is likely driven by the concentration of succinyl-CoA and intracellular pH and is subject to metabolic fluctuations (7,8). Protein succinylation is especially prevalent among mitochondrial metabolic proteins and bacteria, further solidifying the evolutionary link between mitochondria and prokaryotes. It often occurs at lysine residues that are alternatively acetylated or ubiquitinated. More than a thousand lysine succinylations sites were identified on hundreds of proteins, including glutamate dehydrogenase (15 sites), malate dehydrogenase, citrate synthase, carbamoyl phosphate synthase 1, and histone proteins (9).

Directions for Use:
5. Add 10 µL of PTMScan® Control Peptides Succinyl-Lysine to IAP beads and sample peptides and mix well.
6. Continue with PTMScan® or PTMScan® HS workflows at the 2-hour incubation step.

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

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

Background References:

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