# Affinity Gel-conjugated Pan Succinyl-Lysine Rabbit mAb

**ABclonal** Technology®
www.abclonal.com

**Catalog No.: A26021**  <mark>Recombinant</mark>

## Basic Information

**Observed MW**

**Calculated MW**

**Category**
Primary antibody

**Applications**
IP-MS

**Cross-Reactivity**
Species independent

**CloneNo number**
ARC55837-AG

**Conjugate**
Affinity Gel

## Background

The lysine residue in proteins can undergo to many types of PTMs, such as methylation, acetylation, biotinylation, ubiquitination, ubiquitin-like modifications, propionylation and butyrylation, then leading to the remarkable complexity of PTM networks. Succinylation is a posttranslational modification (PTM) where a succinyl group is added to a Lys (K) residue of a protein molecule .it has been shown that the lysine succinylation responses to different physiological conditions and is evolutional conserved. It has been identified 2,565 succinylation sites from 779 proteins and revealed that lysine succinylation have potential impacts on enzymes involved in mitochondrial metabolism including the amino acid degradation, tricarboxylic acid (TCA) cycle and fatty acid metabolism Thelysine succinylation also occurs in histones, suggesting that it may play an important role in regulating chromatin structures and functions as well

## Recommended Dilutions

**IP-MS**        40 μL antibody (bead slurry) for 200μg-400μg extracts of whole cell

## Immunogen Information

**Gene ID**                    **Swiss Prot**

**Immunogen**
Synthetic peptide. This information is considered to be commercially sensitive.

**Synonyms**

## Contact

## Product Information

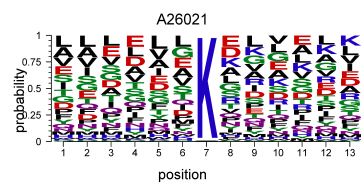| Source | Isotype | Purification |
|---|---|---|
| Rabbit | | Affinity purification |

**Storage**
Store at -20℃. Avoid freeze / thaw cycles.
Buffer: PBS with 50% glycerol,0.09% Sodium azide,pH7.3.

# Validation Data



The Motif Logo was generated from IP-MS experiment using 5000+ nonredundant tryptic peptides derved from mouse liver tissue immunoprecipitated with A26021. The logo represents the relative frequency of amino acids in each position surrounding the central Succinyllysine residue within this data set.