# Recombinant Histone Deacetylase 6 (HDAC6)(N-GST-6His)

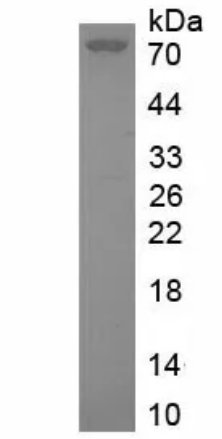
*Catalog#:PEH22447*

## 概述（Summary）

| | |
|---|---|
| **别称（Alternative Names）** | HD6; JM21 |
| **纯度（Purity）** | Greater than 90% as determined by reducing SDS-PAGE. |
| **内毒素（Endotoxin level）** | <1 EU/μg as determined by LAL test. |
| **蛋白构建（Construction）** | 6His-GST-【Ser479-Arg835】 |
| **Accession #** | Q9UBN7 |
| **表达宿主（Host）** | E.coli |
| **种属（Species）** | Homo sapiens (Human) |
| **预测分子量（Predicted MW）** | 69.0 kDa |
| **制剂（Form）** | Lyophilized from a 0.2 μm filtered solution of PBS, pH7.4, containing 0.01% SKL, 1mM DTT, 5% Trehalose and Proclin300. |
| **运输方式（Shipping）** | The product is shipped with ice bag. Upon receipt, store it immediately at the temperature listed below. |
| **稳定性&储存（Stability &Storage）** | 12 months at -20°C to -80°C in lyophilized state.6 months at -20°C to -80°C under sterile conditions after reconstitution.7-10 days at 2°C to 8°C under sterile conditions after reconstitution.Please minimize freeze-thaw cycles. |
| **复溶（Reconstitution）** | Reconstitute in 10mM PBS (pH7.4) to a concentration of 0.1-1.0 mg/mL. Do not vortex. |
| **背景介绍（References）** | Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes. In addition to histones, deacetylates other proteins: plays a central role in microtubule-dependent cell motility by mediating deacetylation of tubulin. Promotes deacetylation of CTTN, leading to actin polymerization, promotion of autophagosome-lysosome fusion and completion of autophagy. Involved in the MTA1-mediated epigenetic regulation |

of ESR1 expression in breast cancer. In addition to its protein deacetylase activity, plays a key role in the degradation of misfolded proteins: when misfolded proteins are too abundant to be degraded by the chaperone refolding system and the ubiquitin-proteasome, mediates the transport of misfolded proteins to a cytoplasmic juxtanuclear structure called aggresome. Probably acts as an adapter that recognizes polyubiquitinated misfolded proteins and target them to the aggresome, facilitating their clearance by autophagy.

## 电泳图（SDS-PAGE image）




Greater than 90% as determined by reducing SDS-PAGE.

## 注意事项（Note）

For Research Use Only , Not for Diagnostic Use.