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SUMO2 Human

Description: SUMO2 Human Recombinant produced in E.Coli is a single, non-glycosylated polypeptide chain containing 93 amino acids and having a molecular mass of 10.6 kDa. The SUMO-2 is purified by proprietary chromatographic techniques.

Synonyms: Small ubiquitin-related modifier 2, SUMO-2, Ubiquitin-like protein SMT3B, SMT3 homolog 2, Sentrin-2, HSMT3, SUMO-3, SUMO2, SMT3B, SMT3H2, MGC117191.

Source: Escherichia Coli.

Physical Appearance: Sterile filtered colorless solution.

Amino Acid Sequence:

MADEKPKEGVKTENNDHINLKVAGQDGSVVQFKIKRHTPLSKLMKAYCERQGLSMRQIRFRFDG QPINETDTPAQLEMEDEDTIDVFQQQTGG.

Purity: Greater than 95.0% as determined by:(a) Analysis by RP-HPLC.(b) Analysis by SDS-PAGE.

Formulation:

The SUMO2 containing 20 mM Tris-HCl buffer (pH 8.0)

Stability:

Can be stored at +4C for 1 week. For long term storage, below -20C.Please prevent freeze-thaw cycles.

Usage:

NeoBiolab's products are furnished for LABORATORY RESEARCH USE ONLY. The product may not be used as drugs, agricultural or pesticidal products, food additives or household chemicals.

Introduction:

Small Ubiquitin-like Modifiers (SUMOs) are a family of small, related proteins that can be enzymatically attached to a target protein by a post-translational modification process termed sumoylation. Unlike ubiquitination, which targets proteins for degradation, sumoylation participates in a number of cellular processes, such as nuclear transport, transcriptional regulation, apoptosis, and protein stability. All SUMO proteins share the conserved ubiquitin domain and the C-terminal diglycine cleavage/attachment site. Human SUMO2, also known as Sentrin2 and SMT3B is synthesized as a 95 amino acid (aa), 11 kDa propeptide that contains a two aa C-terminal prosegment, and an 18 aa N-terminal protein interacting region (aa 33 -50). Following prosegment cleavage, the C-terminal glycine is enzymatically attached to a lysine on a target protein. Human SUMO2 shares 100% sequence identity to SUMO-2 from mouse. SUMO2 also has very high sequence homology to SUMO3 and SUMO4, 86 % and 85%, respectively. SUMO2 shares only 44% sequence identity to SUMO1.

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