

NEDD8 Human

Description: NEDD8 Human Recombinant fused with 37 amino acid His tag at N-terminus produced in E.Coli is a single, non-glycosylated, polypeptide chain containing 113 amino acids (1-76 a.a.) and having a molecular mass of 12.8 kDa. The NEDD8 is purified by proprietary chromatographic techniques.

Catalog #: ENPS-403

For research use only.

Synonyms: Nedd-8, FLJ43224, MGC104393, MGC125896, MGC125897, NEDD8, Ubiquitin-like protein Nedd8, Neddylin, Neural precursor cell expressed developmentally down-regulated protein 8.

Source: Escherichia Coli.

Physical Appearance: Sterile Filtered colorless solution.

Amino Acid Sequence: MHHHHHHMKI EEGKLVIWIN GDKGYNGLAE VGKKFEKDTG
IKVTVEHPDK LEEKFPQVAA TGDGPDIIIFW AHDRFGGYAQ SGLLAEITPD KAFQDKLYPF
TWDVRYNGK LIAYPIAVEA LSLIYNKDLL PNPPKTWEEI PALDKELKAK GKSALMFNLQ
EPYFTWPLIA ADGGYAFKYE NGKYDIKDVG VDNAGAKAGL TFLVDLIKNN HMNADTDYSI
AEAFAFNKGET AM

Purity: Greater than 95.0% as determined by SDS-PAGE.

Formulation:

The NEDD8 solution contains 20mM Tris pH 8.0, 50mM NaCl, 0.5mM DTT & 10% glycerol.

Stability:

NEDD8 although stable 4°C for 4 weeks, should be stored desiccated below -18°C. For long term storage it is recommended to add a carrier protein (0.1% HSA or BSA). 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:

NEDD8 is part of the ubiquitin family. Human NEDD8 shares 60% amino acid sequence homology to ubiquitin. The NEDD8 system is essential for the regulation of protein degradation pathways involved in cell cycle progression, morphogenesis and tumorigenesis. NEDD8 is involved in cell cycle control and embryogenesis. Covalent attachment to its substrates requires prior activation by the E-1 complex UbE1c- appbp1 and linkage to the E-2 enzyme UbE2m. Attachment of NEDD8 to cullins activates their associated E-3 ubiquitin ligase activity, and thus promotes polyubiquitination and proteasomal degradation of cyclins and other regulatory proteins.

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