



SHANGHAI GENOMICS

Recombinant Human Cullins 5

rHuCUL5

Catalog number: 3132-09

Specifications and Use

Source	● <i>Sf9 insect cell</i>
Molecular Mass	● 94.7 kDa
Purity	● ≥ 90% as determined by SDS-PAGE
Tag	● 6 × His
Formulation	● 20mM Tris-HCl, 150mM NaCl, 0.5mM EDTA, pH7.9, 10% glycerol
Stability	● Store at -80°C. Avoid repeated freezing and thawing
Usage	● FOR RESEARCH USE ONLY. NOT FOR HUMAN USE.

Human CUL5

Cullin proteins comprise a distinct family of mediators that participate in the selective targeting of proteins for ubiquitin (Ub)-mediated proteolysis. CUL-1, which is the mammalian homolog of Cdc53 from yeast, is an integral component of the E3 ubiquitin ligase complex designated SCF. The SCF (Skp1/CUL-1/F-box protein complex) consists of Skp1 associating with both CUL-1 and an F-box protein, such as Skp2, which determines the substrate specificity of the complex. CUL-1 mediated ubiquitination results in the degradation of cell cycle proteins cyclin D, p21 and cyclin E. Another cullin, CUL-3 facilitates the degradation of cyclin E independent of SCF activity, while CUL-2 associates with the tumor suppressing protein VHL and elongin B to form VBC complexes, which structurally resemble the SCF ligase. Proteolysis also occurs by way of CUL-4 associating with Nedd-8, a ubiquitin-like protein, where it too functions as an active component of a multifunctional E3 complex. CUL-5, or vasopressin-activated, calcium-mobilizing protein (VACM-1), is also included in the cullin family as it shares substantial sequence homology with CUL-1.

Protein Sequence:

HHHHHHHDYDIPTTENLYFQAAMDPEFRANPAMATSNLLKNKGSLSLQFEDKWDFFMRPIVLKLLRQESV
TKQQWFDLFSVDVHAVCLWDDKGPAAKHQALKEDILEFIKQAQARVLSHQDDTALLKAYIVEWRKFFT
QCDILPKPFCQLEITLMGKQGSNKKSNVEDSIVRKLMLDWTNESIFSNIKNRLQDSAMKLVHAERLG
EAFDSQLVIGVRESYVNLCSNPEDKLIYRDNF EKAYLDSTERFYRTQAPSYLQQNGVQNYMKYAD
AKLKEEEKRALRYLETRRECNSVEALMECCVNALVTSFKETILAECCQGMIKRNETEKLHLMFSLMDK
VPNGIEPMLKDLEEHIIISAGLADMVAAAETITTDSEKYVEQLLTLFNRF SKLVKEAFQDDPRFLTARDK
AYKAVVNDATIFKLELPLKQKGVGLKTQPESKPELLANYCDMLLRKTPLSKKLTSEEIEAKLKEVLLV
LKYVQNKDVFMRYPYHKAHLTRRLILDISADSEIEENMVEWLREVGMPADYVNKLARMFQDIKVS
DLNQAFKEMHKNNKLALPADSVNIKILNAGAWSRSSEKVFVSLPTELEDLIPEVEEFYKKNHSGRKLH
WHHLMSNGIITFKNEVGQYDLEVTTFQLAVLFAWNQRPREKISFENLKLATELPDAELRRTLWLSLVA
FPKLRQVLLYEPQVNSPKDFTEGTLFSVNQEFSLIKNAKVQKRGKINLIGRLQLTTERMREEENEGI
VQLRILRTQEAIQIMKMRKKISNAQLQTELVEILKNMFLPQKKMIKEQIEWLIEHKYIRRESDINTFIY
MA