# Cul2/Rbx1 [untagged]

E3 Ligase

Alternate Names: Cul2=Cullin2

Rbx1 = HRT1, Regulator of cullins 1, Ring finger protein 75, RNF75, ROC1, ZYP protein

 Cat. No.
 63-1004-025
 Quantity:
 25 μg

 Lot. No.
 30215
 Storage:
 -70 °C

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**CERTIFICATE OF ANALYSIS Page 1 of 2** 

Protein Sequences: Please see page 2

## **Background**

The enzymes of the ubiquitylation pathway play a pivotal role in a number of cellular processes including the regulated and targeted proteasome-dependent degradation of substrate proteins. Three classes of enzymes are involved in the process of ubiquitylation; activating enzymes (E1s), conjugating enzymes (E2s) and protein ligases (E3s). Cullin-RING-Ligases (CRLs) are one of the largest classes of ubiquitin E3 ligases and the enzymes of the NEDDylation pathway play a pivotal role in the activation of these CRLs. Akin to ubiquitylation, the E1 activating enzyme (APP-BP1/UBA3 heterodimer) and the E2 conjugating enzymes (UBE2M or UBE2F) are involved in mammalian NEDDylation of the Cullin Ring Ligases (CRLs) (Meyer-Schaller et al., 2009: Huang et al., 2011: Morimoto et al., 2003). The human Cullin1-5 genes were first described by Kipreos et al. (1996). Cullin RING ligases (CRL) comprise the largest subfamily of ubiquitin ligases which are activated by Neddylation. CRLs are involved in cell cycle regulation, DNA replication and the DNA damage response (DDR). CRLs consist of several subunits including, a scaffold protein (cullin) and a Ring finger protein: either Rbx1 (Cul1-4) or Rbx2 (Cul5) that binds a ubiquitin E2 Ube2M or Ube2F respectively (Sarikas et al., 2011; Skowyra et al., 1997). The first CRL to be identified was named Skp1/Cullin or Cdc53/F-box (SCF) from Saccharomyces cerevisiae. Many CRL E3 ligases have additional linker proteins such as Elongin B/C associated with Cul2 and DDB1 associated with Cul4. The Elongin B/C-Cul2 or Cul5-SOCS box (ECS) family also be-

Continued on page 2

## **Physical Characteristics**

Species: human

Source: Insect (Sf21)

Quantity: 25 µg

Concentration: 0.5 mg/ml

Formulation: 50 mM HEPES pH 7.5,

150 mM sodium chloride, 2 mM dithiothreitol, 10% glycerol

Molecular Weight:

Cul2: ~87.1 kDa; Rbx1: ~12.3 kDa

Purity: >75% by InstantBlue™ SDS-PAGE

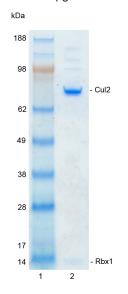
Stability/Storage: 12 months at -70°C;

aliquot as required

# **Quality Assurance**

#### **Purity:**

4-12% gradient SDS-PAGE InstantBlue™ staining Lane 1: MW markers Lane 2: 1 µg Cul2/Rbx1



### **Protein Identification:**

Confirmed by mass spectrometry.

E3 Ligase Assay: The activity of Cul2/Rbx1 was validated indirectly through its ability to act as a substrate for Neddylation in the presence of the NEDD8 E3 ligase His-DCNL2 and thioester-loaded His-UBE2M-NEDD8. Incubation of Cul2/Rbx1 and thioester loaded His-UBE2M-NEDD8 in the presence or absence of His-DCNL2 at  $4^{\circ}\text{C}$  was compared at two time points  $T_{_0}$  and  $T_{_2}$  minutes. Neddylation of the Cul2 subunit in the presence of His-DCNL2 was demonstrated.

Lanes	1	2	3
Cul2/Rbx1	+	+	+
6His-DCNL2	+	-	+
Ube2M~NEDD8	+	+	+
kDa			
98			
62	-	_	-
	$T_0$	•	Γ <sub>2</sub>



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Lot-specific COA version tracker: v1.0.0

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## Background

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longs to the CRL superfamily (Kile et al., 2002). SCF and ECS ubiquitin ligases have structural similarities in that both contain Rbx1 or Rbx2 as a RING finger protein and Cul1, Cul2 or Cul5 as a scaffold protein (Kile et al., 2002; Kamura et al., 2004). The von Hippel-Lindau (VHL) complex is a ubiquitin ligase which targets the Hypoxia Inducible Factor alpha (HIFα) family of transcription factors for proteasomal degradation. The complex comprises pVHL, the Cul2/Rbx1 subunit and the BC box protein Elongin B/C. Loss of functional pVHL protein prevents the oxygen dependent degradation of HIF1α resulting in constitutive expression of HIF dependent genes and consequently VHL disease (Okumura et al., 2012).

### References:

Huang G, Kaufman A J, Ramanathan Y, Singh B (2011) SCCRO (DCUN1D1) promotes nuclear translocation and assembly of the neddylation E3 complex. J Biol Chem 286, 10297-10304.

Kamura T, Maenaka K, Kotoshiba S, Matsumoto M, Kohda D, Conaway RC, Conaway JW, Nakayama KI (2004) VHL-box and SOCS-box domains determine binding specificity for Cul2-Rbx1 and Cul5-Rbx2 modules of ubiquitin ligases. Genes Dev

Kile BT, Schulman BA, Alexander WS, Nicola NA, Martin HM, Hilton DJ (2002) The SOCS box: a tale of destruction and degradation. Trends Biochem Sci 27, 235-41.

Kipreos ET, Lander LE, Wing JP, He WW, Hedgecock EM (1996) cul-1 is required for cell cycle exit in *C. elegans* and identifies a novel gene family. *Cell* **85**, 829-839.

Meyer-Schaller N, Chou YC, Sumara I, Martin DD, Kurz T, Katheder N, Hofmann K, Berthiaume LG, Sicheri F, Peter M.(2009) The human Dcn1-like protein DCNL3 promotes Cul3 neddylation at membranes. Proc Natl Acad Sci U S A 106, 12365-

Morimoto M, Nishida T, Nagayama Y, Yasuda H (2003) Nedd8-modification of Cul1 is promoted by Roc1 as a Nedd8-E3 ligase and regulates its stability. Biochem Biophys Res Commun 301, 392-398.

Okumura F, Matsuzaki M, NakatsukasaK, Kamura T (2012) The Role of Elongin BC-Containing Ubiquitin Ligases. Front Oncol

Skowyra D, Craig KL, Tyers M, Elledge SJ, Harper JW (1997) Fbox proteins are receptors that recruit phosphorylated substrates to the SCF ubiquitin-ligase complex. Cell 91, 209-219.

## **Physical Characteristics**

25 µg

-70°C

Continued from page 1

## Protein Sequence: Cullin 2

GSMSLKPRVVDFDETWNKLLTTIKAVVM LEYVERATWNDRFSDIYALCVAYPEPLGER LYTETKIFLENHVRHLHKRVLESEEQV LVMYHRYWEEYSKGADYMDCLYRYLNTOFIK KNKLTEADLQYGYGGVDMNEPLMEIGELALD MWRKLMVEPLQAILIRMLLREIKNDRGGEDP NQKVIHGVINSFVHVEQYKKKFPLKFYQEIF ESPFLTETGEYYKQEASNLLQESNCSQYMEKV LGRLKDEEIRCRKYLHPSSYTKVIHECOORM VADHLQFLHAECHNIIRQEKKNDMANMYVLL RAVSTGLPHMIQELQNHIHDEGLRATSNLTQEN MPTLFVESVLEVHGKFVQLINTVLNGDQHF MSALDKALTSVVNYREPKSVCKAPELLAKY CDNLLKKSAKGMTENEVEDRLTSFITVFKYID DKDVFOKFYARMLAKRLTHGLSMSMDSEEAM TNKLKOACGYEFTSKLHRMYTDMSVSADLNN KFNNFIKNODTVIDLGISFOIYVLOAGAW PLTQAPSSTFAIPQELEKSVQMFELFYSQHFS GRKLTWLHYLCTGEVKMNYLGKPYVAMVTTYQ MAVLLAFNNSETVSYKELQDSTQMNEKELTK TIKSLLDVKMINHDSEKEDIDAESSFSLNMNF SSKRTKFKITTSMQKDTPQEMEQTRSAVDEDRK MYLOAATVRIMKARKVLRHNALTOEVISOS RARFNPSISMIKKCIEVLIDKQYIERSQASA DEYSYVA

The residues underlined remain after cleavage and removal of the purification tag. Cullin2 (regular text): Start bold italics (amino acid residues 1-745) Accession number: AAH09591.1

## Protein Sequence: Rbx1

**M**AAAMDVDTPSGTNSGAGKKRFEVKKW NAVALWAWDIVVDNCAICRNHIMDLCIEC OANOASATSEECTVAWGVCNHAFHFHCISR WLKTROVCPLDNREWEFOKYGH

Rbx1 (regular text): Start bold italics (amino acid

residues 1-108)

Accession number: NP 055063.1

Cullin2 [Dac tagged] / Rbx1 was cleaved with TEV protease [6His tagged]. The Dac tag and TEV protease [6His-Tagged] were removed by capturing on amp sepharose and nickel resin respectively.



Dundee, Scotland, UK

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