Cul3/Rbx1 [untagged]

E3 Ligase

Alternate Names: Cul3 = KIAA0617

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

 Cat. No.
 63-1003-025
 Quantity:

 Lot. No.
 30206
 Storage:

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CERTIFICATE OF ANALYSIS Page 1 of 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 largest class of ubiquitin E3 ligases and the enzymes of the NEDDylation pathway play a pivotal role in the activation of these, 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, DNA damage response (DDR). CRLs contain subunits including, a scaffold protein (cullin family protein), 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). Cul3 expression in human fibroblasts is induced by phorbol 12-myristate 13-acetate (PMA) and

Continued on page 2

Physical Characteristics

25 µg

-70°C

Species: human Protein Sequences: Please see page 2

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:

Cul3: ~89.0 kDa; Rbx1: ~12.3 kDa

Purity: >95% by InstantBlue™ SDS-PAGE

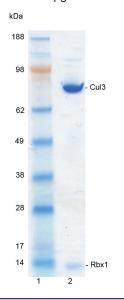
Stability/Storage: 12 months at -70°C;

aliquot as required

Quality Assurance

Purity

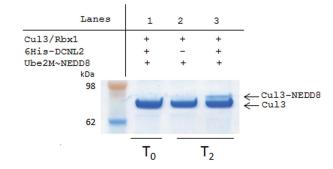
4-12% gradient SDS-PAGE InstantBlue™ staining Lane 1: MW markers Lane 2: 1 μg Cul3/Rbx1



Protein Identification:

Confirmed by mass spectrometry.

E3 Ligase Assay: The activity of Cul3/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 Cul3/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 Cul3 subunit in the presence of His-DCNL2 was demonstrated.





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Cul3/Rbx1 [untagged]

E3 Ligase

Alternate Names: Cul3 = KIAA0617

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CERTIFICATE OF ANALYSIS Page 2 of 2

Background

Continued from page 1

suppressed by salicylate (Du et al., 1998). The Cul3/Kelch like 9 (KLHL9) /Kelch like 13 (KLHL13) complex is an E3 ligase that controls the behavior of Aurora B on mitotic chromosomes and thereby coordinating mitotic progression and completion of cytokinesis (Sumara et al., 2007). Interaction of Cul3 with Kelch like 7 (KLHL7) leads to the ubiquitylation of the dopamine receptor D4 (DRD4) (Rondou et al., 2008).

References:

Du M, Sansores-Garcia L, Zu Z, Wu KK, (1998) Cloning and expression analysis of a novel salicylate suppressible gene, Hs-CUL-3, a member of cullin/Cdc53 family. *J Biol Chem* **273**, 24289-

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

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.

Mever-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, 12365-12370.

Morimoto M, Nishida T, Nagayama Y, Yasuda H. (2003) Nedd8modification of Cul1 is promoted by Roc1 as a Nedd8-É3 ligase and regulates its stability, *Biochem Biophys Res Commun* 301, 392-398

Rondou P, Haegeman G, Vanhoenacker P, Van Craenenbroeck K, (2008) BTB protein KLHL12 targets the dopamine D4 receptor for ubiquitination by a Cul3-based E3 ligase. J Biol Chem 283

Sarikas, A, Hartmann, T and Pan, ZQ (2011) The cullin protein family, Genome Biology 12, 220.

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.

Sumara I, Quadroni M, Frei C, Olma MH, Sumara G, Ricci R, Peter MA (2007) Cul3-based E3 ligase removes Aurora B from mitotic chromosomes, regulating mitotic progression and completion of cytokinesis in human cells. Dev Cell 12, 887-900.

Physical Characteristics

Continued from page 1

Protein Sequence: Cullin 3

GGSMSNLSKGTGSRKDTKMRIRAFPMTM DEKYVNSIWDLLKNAIQEIQRKNNSGLS FEELYRNAYTMVLHKHGEKLYTGLREVVTE HLINKVREDVLNSLNNNFLOTLNOAWND HQTAMVMIRDILMYMDRVYVQQNNVENVYNL GLIIFRDQVVRYGCIRDHLRQTLLDMI ARERKGEVVDRGAIRNACQMLMILGLEGRS VYEEDFEAPFLEMSAEFFQMESQKFLAEN SASVYIKKVEARINEEIERVMHCLDKSTEEP IVKVVERELISKHMKTIVEMENSGLVHM LKNGKTEDLGCMYKLFSRVPNGLKTMCECMS SYLREQGKALVSEEGEGKNPVDYIQGLLDLK SRFDRFLLESFNNDRLFKQTIAGDFEYFLN LNSRSPEYLSLFIDDKLKKGVKGLTEQE VETILDKAMVLFRFMOEKDVFERYYKOHLAR RILTNKSVSDDSEKNMISKIKTECGC **OFTSKLEGMFRDMSISNTTMDEFROHLOAT** GVSLGGVDLTVRVLTTGYWPTQSATPKC NIPPAPRHAFEIFRRFYLAKHSGRQLTLQH HMGSADLNATFYGPVKKEDGSEVGVG GAQVTGSNTRKHILQVSTFQMTILMLFN NREKYTFEEIQQETDIPERELVRALQS LACGKPTQRVLTKEPKSKEIENGHIFT VNDOFTSKLHRVKIOTVAAKOGESDPERKET ROKVDDDRKHEIEAAIVRIMKSRKKMOHNVL VAEVTQQLKARFLPSPVVIKKRIEGLIEREY LARTPEDRKVYTYVA

The residues underlined remain after cleavage and removal of the purification tag. Cullin3 (regular text): Start bold italics (amino acid residues 1-768)

Accession number: NP_003581.1

Cullin3 [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

Protein Sequence: Rbx1

MAAAMDVDTPSGTNSGAGKKRFEVKKW NAVALWAWDIVVDNCAICRNHIMDLCIEC OANOASATSEECTVAWGVCNHAFHFHCISR WLKTROVCPLDNREWEFOKYGH

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

residues 1-115)

Accession number: NP_055063.1



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