UBE2M (Ubc12) [GST-tagged]

E2 - NEDD8 Conjugating Enzyme

Alternate Names: Nedd8-conjugating enzyme Ubc12, UBC-RS2, UBC12

Cat. No. Lot. No.	62-0088-020 1840

The enzymes of the NEDDylation

pathway play a pivotal role in a number

of cellular processes including the in-

direct regulation and targeting of sub-

strate proteins for proteasomal degra-

dation. Three classes of enzymes are

involved in the process of NEDDyla-

tion; the ubiquitin-like activating en-

zyme APP-BP1/Uba3 (E1), the ubiq-

uitin-like conjugating enzymes (E2s)

and protein ligases (E3s). UBE2M is

a member of the E2 conjugating en-

zyme family and the cDNA for Hu-

man UBE2M was first described by

Osaka et al. (1998) and shares 42%

sequence identity with yeast UBE2M.

A trapped ubiquitin like activation

complex has been described for the NEDD8 pathway comprising, the E1

APP-BP1/Uba3, two NEDD8 mole-

cules, UBE2M and MgATP. Thioester

linkage of NEDD8 to APP-BP1-Uba3

results in an alternate E1 conforma-

tion that exposes two NEDD8 binding

sites on the E2 enzyme. After transfer

of the non-covalently bound NEDD8

to the E2, an alternate E1 conforma-

tion allows the release of the thioester

bound NEDD8 product. Transference

of the NEDD8 thioester linkage be-

tween E1 and E2 enzymes in this way

can induce a conformational change

and alter downstream signalling in the

NEDD8 ubiquitin-like (Ubl) cascade (Huang et al., 2007). The interaction

of different E2 enzymes with different Cullin RING E3 Ligases (CRLs)

has been determined; for example

Quantity: 20 µg Storage: -70°C

NOT FOR USE IN HUMANS

FOR RESEARCH USE ONLY

Background

Physical Characteristics

Species: human

Source: E. coli expression

Quantity: 20 µg

Concentration: 1 mg/ml

Formulation: 50 mM HEPES pH 7.5. 150 mM sodium chloride, 2 mM dithiothreitol, 10% glycerol

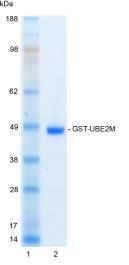
Molecular Weight: ~49 kDa

Purity: >98% by InstantBlue™ SDS-PAGE

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

Quality Assurance

4-12% gradient SDS-PAGE Lane 2: 1 µg GST-UBE2M



Protein Sequence:

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEH LYERDEGDKWRNKKFELGLEFPNLPYYIDGD VKLTQSMAIIRYIADKHNMLGGCPKERAEISMLE GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEM LKMFEDRLCHKTYLNGDHVTHPDFMLYDALDV VLYMDPMCLDAFPKLVCFKKRIEAIPQIDKY **LKSSKYIAWPLQGWQATFGGGDHPPKSD**LEV LFQGPLGSPGIPGSTRAAA**M**IKLFSLKQQKKEEE SAGGTKGSSKKASAAQLRIQKDINELNLPKTCD ISFSDPDDLLNFKLVICPDEGFYKSGKFVFS FKVGQGYPHDPPKVKCETMVYHPNIDLEGNVCL NILREDWKPVLTINSIIYGLQYLFLEPNPED PLNKEAAEVLQNNRRLFEQNVQRSMRGGYIGSTY FERCLK

Tag (bold text): N-terminal GST Protease cleavage site: PreScission™ (LEVLFQ▼GP) UBE2M (regular text): Start bold italics (amino acid residues 1-183) Accession number: AAH58924

Protein Identification:

Confirmed by mass spectrometry.

E2-NEDD8 Thioester Loading Assay:

The activity of GST-UBE2M was validated by loading E1 APP-BP1/Uba3 activated NEDD8 onto the active cysteine of the GST-UBE2M E2 enzyme via a transthiolation reaction. Incubation of the APP-BP1/Uba3 and GST-UBE2M enzymes in the presence of NEDD8 and ATP at 30°C was compared at two time points, T_0 and T_{10} minutes. Sensitivity of the NEDD8/GST-UBE2M thioester bond to the reducing agent DTT was confirmed.



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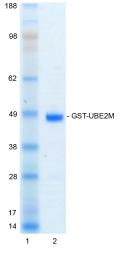
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Lot-specific COA version tracker: v1.0.0



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Purity: InstantBlue[™] staining Lane 1: MW markers kDa



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1840

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Storage:

CERTIFICATE OF ANALYSIS Page 2 of 2

Background

Cat. No.

Lot. No.

Continued from page 1

UBE2M/RBX1 and UBE2F/RBX2 can interact with such ligases. This reveals the functional importance of hierarchical expansion of the NEDD8 conjugation system in establishing selective CRL activation (Huang *et al.*, 2009). Following ionizing irradiation of a human esophageal cancer cell line a cDNA microarray screen found UBE2M to be upregulated suggesting a role for UBE2M in esophageal cancer (Bo *et al.*, 2004).

References:

Bo H, Ghazizadeh M, Shimizu H, Kurihara Y, Egawa S, Moriyama Y, Tajiri T, Kawanami O (2004) Effect of ionizing irradiation on human esophageal cancer cell lines by cDNA microarray gene expression analysis. *J Nippon Med Sch* **71**, 172-80.

Huang DT, Ayrault O, *et al.* (2009) E2-RING expansion of the NEDD8 cascade confers specificity to cullin modification. *Mol Cell* **33**, 483-95.

Huang DT, Hunt HW, Zhuang M, Ohi MD, Holton JM, Schulman BA (2007) Basis for a ubiquitin-like protein thioester switch toggling E1-E2 affinity. *Nature* **445**, 394-8.

Osaka F, Kawasaki H, Aida N, Saeki M, Chiba T, Kawashima S, Tanaka K, Kato S (1998) A new NEDD8-ligating system for cullin-4A. *Genes Dev* **12**, 2263-8.



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