

# RNF8 [GST-tagged]

## E3 Ligase

**Alternate Names:** C3HC4 type zinc finger protein; KIAA0646; Ring finger protein (C3HC4 type) 8; Ring finger protein 8; UBC13/UEV-interacting ring finger protein

**Cat. No.** 63-0021-025

**Lot. No.** 30032

**Quantity:** 25 µg

**Storage:** -70°C

FOR RESEARCH USE ONLY

NOT FOR USE IN HUMANS



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). Ring Finger Protein 8 (RNF8) is a member of the E3 protein ligase family and cloning of the human gene was first described by Ishikawa *et al.* (1998). RNF8 is required for the ubiquitylation of some nuclear proteins, promoting their subsequent degradation (Kolas *et al.*, 2007). RNF8 has also been shown to interact with the E2 conjugating enzyme Ubc13 (UBE2N) recruiting BRAC1 and 53BP1 to sites of nuclear damage (Kolas *et al.*, 2007; Lok *et al.*, 2011; Santos *et al.*, 2010). RNF8 knockout mice display growth retardation and an increased pre-disposition to cancer (Li *et al.*, 2010).

### References:

Ishikawa K, Nagase T, Suyama M, Miyajima N, Tanaka A, Kotani H, Nomura N, Ohara O (1998) Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins *in vitro*. *DNA Res* 5, 169-76.

Kolas NK, Chapman JR, et al. (2007) Orchestration of the DNA-damage response by the RNF8 ubiquitin ligase. *Science* 318, 1637-40.

Li L, Halaby MJ, et al. (2010) Rnf8 deficiency impairs class switch recombination, spermatogenesis, and genomic integrity and predisposes for cancer. *J Exp Med* 207, 983-97.

Continued on page 2

### Physical Characteristics

**Species:** human

**Source:** *E. coli* expression

**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:** ~83.4 kDa

**Purity:** >80% by InstantBlue™ SDS-PAGE

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

**Protein Sequence:** Please see page 2

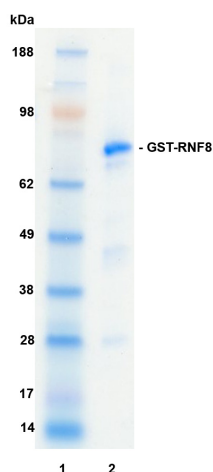
### Quality Assurance

#### Protein Identification:

Confirmed by mass spectrometry.

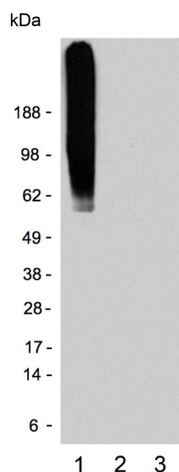
#### Purity:

4-12% gradient SDS-PAGE  
InstantBlue™ staining  
Lane 1: MW markers  
Lane 2: 1 µg GST-RNF8



#### E3 ligase assay:

The ubiquitin conjugating activity of GST-RNF8 was validated through its ability to catalyse the generation of polyubiquitin chains in the presence of the E1 activating enzyme His-UBE1, the E2 conjugating enzyme His-UBE2D4 (UbcH5d) (several E2s were tested, data generated with this E2 is provided by way of example) and ubiquitin. Incubation of GST-RNF8 for 30 minutes at 30°C in the presence of ubiquitin, His-UBE1, His-UBE2D4 and ATP (Lane 1) was compared alongside two control reactions with either ATP (Lane 2) or GST-RNF8 (Lane 3) excluded from the reaction. Ubiquitin conjugates were identified by Western blotting using an anti-ubiquitin conjugate antibody and these were observed only in the presence of both ATP and GST-RNF8.



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Lot-specific COA version tracker: v1.0.1

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CERTIFICATE OF ANALYSIS Page 2 of 2

## Background

Continued from page 1

Lok GT, Sy SM, Dong SS, Ching YP, Tsao SW, Thomson TM, Huen MS (2011) Differential regulation of RNF8-mediated Lys48- and Lys63-based poly-ubiquitylation. *Nucleic Acids Res.* [Epub ahead of print]

Santos MA, Huen MS, et al. (2010) Class switching and meiotic defects in mice lacking the E3 ubiquitin ligase RNF8. *J Exp Med* 207, 973-81.

## Physical Characteristics

Continued from page 1

### Protein Sequence:

**MSPILGYWKIKGLVQPTRLLEYLEEKY**  
**EEHLYERDEGDKWRNKKFELGLEFPN**  
**LPYYIDGDVKLTQSMAIRYIADKHMLG**  
**GCPKERAEISMLEGAVLDIRYGVSR IAY**  
**SKDFETLKVDFLSKLPEMLKMFEDRLCHK**  
**TYLNGDHSVTHPDFMLYDALDVVLYMDPM**  
**CLDAFPKLVCFKKRIEAI PQIDKYLKSSKY**  
**IAWPLQGWA TFGGGDHPPKSDLEVL FQG**  
**PLGSPEIPGSTRAAAMGEPGFVVTGDR**  
**AGGRSWCLRRVGM SAGWLLLEDGCEVT**  
**VGRGFVVTYQLVSKICPLMISRNHCV**  
**LKQNP EGQWTIMDNKSLNGVWLNRRARLE**  
**PLRVYSIHQGDYIQLGVPLENKENAEY**  
**EYEVTEEDWETIYPCLSPKNDQMI EKN**  
**KELRTRKRKFSLDEL AGPGAEGPSNLK**  
**SKINKVSCESGQPVKSQ GKGEVASTPS**  
**DNLDPKLTALEPSKTTGAPIYPGF**  
**PKVTEVHHEQKASNSSASQ RSLQM**  
**FKVTMSRILRLKIQMQEKHEAVMNVK**  
**KQTQKGN SKKVQMEQELQDLQSQ L**  
**CAEQAQQQARVEQLEKTFQEEEQHLQGLE**  
**IAQGEKDLKQQLAQA LQEHWALM EEL**  
**NRSKKDFEAI IQAKNKELEQTKEEKEK**  
**MQAQKEEVL SHMNDVLENE LQCIICSEY**  
**FIEAVTLNCAHSFCSYCIN EWMKRKIECPI**  
**CRKDIKSKTYSLVLDN CINKMVNNLSSEVK**  
**ERRIVLIRERKAKRLF**

Tag (**bold text**): N-terminal GST  
Protease cleavage site: PreScission™ (LEVL FQ▼GP)  
RNF8 (regular text): Start **bold italics** (amino acid residues 1-485)  
Accession number: NP\_003949



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