

# UBA7 [6His-tagged]

## E1 Activating Enzyme

Alternate Name: UBE1L

Cat. No. **61-0007-010**  
Lot. No. **30080**

Quantity: 10 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 ISGylation pathway play a pivotal role in the immune response. Three classes of enzymes are involved in the process of ISGylation an activating enzyme (E1), conjugating enzymes (E2s) and protein ligases (E3s). UBA7 is a member of the E1 activating enzyme family and cloning of the human gene was first described by Kok *et al.* (1993). The UBA7 gene has been mapped to chromosome 3p21 by high resolution fluorescence in situ hybridization (Carritt *et al.* 1992). UBA7 and UBE2L6 have been reported to function as the E1 and E2 enzymes respectively for ISG conjugation forming a thioester intermediate through Cys-131 of UBE2L6 (Takeuchi *et al.* 2005). UBA7 (Ube1L) knockout (KO) mice are deficient in ISGylation and are fertile with no obvious phenotype. (Kim *et al.* 2006). The expression of UBA7 was found to be reduced in many lung cancer cell lines and although originally thought to be a tumor suppressor gene candidate recent studies have demonstrated that UBA7 does not suppress the development of lung adenoma or thymic lymphoma in a K-rasLA2 cancer model (Kok *et al.* 1993).

#### References:

Carritt B, Kok K, van den Berg A, Osinga J, Pilz A, et al. (1992) A gene from human chromosome region 3p21 with reduced expression in small cell lung cancer. *Cancer Res* **52**, 1536-1541.

Kim KI, Yan M, Malakhova O, Luo JK, Shen MF, et al. (2006) Ube1L and protein ISGylation are not essential for alpha/beta interferon signaling. *Mol Cell Biol* **26**, 472-479.

Kok K, Hofstra R, Pilz A, van den Berg A, Terpstra P, et al. (1993) A gene in the chromosomal region 3p21 with greatly reduced expression in lung cancer is similar to the gene for ubiquitin-activating enzyme. *Proc Natl Acad Sci USA* **90**, 6071-6075.

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### Physical Characteristics

**Species:** human

**Source:** Insect sf21

**Quantity:** 10 µg

**Concentration:** 0.5 mg/ml

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

**Molecular Weight:** 116.53 kDa

**Purity:** >98% by InstantBlue™ SDS-PAGE

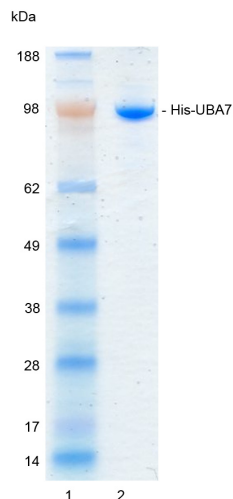
**Stability/Storage:** 12 months at -70°C; aliquot as required

**Protein Sequences:** Please see page 2

### Quality Assurance

#### Purity:

4-12% gradient SDS-PAGE  
InstantBlue™ staining  
Lane 1: MW markers  
Lane 2: 1 µg His-UBA7



#### Protein Identification:

Confirmed by mass spectrometry.

#### E1 Thioester ISG15 Loading Assay:

The activity of His-UBA7 was validated by loading ISG15 onto the active cysteine of His-UBA7. Incubation of the His-UBA7 enzyme in the presence of ISG15 and ATP at 30°C was compared at two time points, T<sub>0</sub> and T<sub>10</sub> minutes. Sensitivity of the ISG15/His-UBA7 thioester bond to the reducing agent DTT was confirmed.



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Lot-specific COA version tracker: v1.0.0

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CERTIFICATE OF ANALYSIS Page 2 of 2

### Background

Continued from page 1

Takeuchi T, Iwahara S, Saeki Y, Sasajima H, Yokosawa H (2005) Link between the ubiquitin conjugation system and the ISG15 conjugation system: ISG15 conjugation to the UbcH6 ubiquitin E2 enzyme. *J Biochem* 138, 711-719.

### Physical Characteristics

Continued from page 1

#### Protein Sequence:

**MSY YHHHHHDYDIP TTE NLY FOG**AMGS  
GIQRPTSTSSLVAAA **MDALD**ASKLL  
DEELYSRQLYVLGSPAMQRIQGARVLVS  
GLQGLGAEVAKNLVLMGVGSLTLHDPHPTCWS  
DLAAQFLLSEQDLERSRAEASQELLAQLN  
RAVQVVVHTGDITEDLLLDLDFQVVVLTAAKLE  
EQLKVGTLCHKHGVCFLAADTRGLVGLFCD  
FGEDFTVQDPTEAEP LTA A I Q H I S Q G  
SPGILTLRKGANTHYFRDGDVTFSGIEGM  
VELNDCDPRSIHVREDGSLEIGDTTTTFSRYL  
RGGAI TEVKRPKTVRHKSLDTALLQPHV  
VAQSSQEVHHAHCLHQAF CALHKFQHLHGR  
PPQPWDPVDAETVVGLARDLEPLKRTEEE  
PLEEPLDEALVRTVALSSAGVLSPMVAML  
GAVAAQEV LKAISRKFMPLDQWLYFDALD  
CLPEDGELLSPEDCALRGSRYDGGIAVF  
GAGFQEKLRROHYLLV GAGAIGCELLKV  
FALVGLGAGNSGGLTVVDMDH IERSNLSRQ  
FLFRSQDVGRPKAEVAAAAARGLNPDQVI  
PLTYPLDPTTEHIYGDNFFSRVDGVAAALDS  
FQARRYVAARCTHYLKPLLEAGTSGTWGSAT  
VFMPHVTEAYRAPASAAASEDAPYPVCT  
VRYFPSTAHTLQWARHEFEELFRLSAET  
INHHQQAHTSLADMDEPQTLTLLKPVLGVL  
RVRPQNWQDCVAWALGHWKLCFHYGIKQLL  
RHFPNKVLEDGTPFWSGPKQCPQPLEFDT  
NQDTHLLYVLAANLYAQM HGLPGSQD  
WTALRELLKLLPQDPQMAPIFASNLELA  
SASAEFGPEQQKELNKALEVWSVGPPLKPLM  
FEKDDSNFHVDFVVAASLRCONYGI  
PVNRAQSKRIVGQIIPAIATTTAAVAGLL  
GLELYKVVSGPRPRSAFRHSYLHLAENY  
LIRYMPFAPAIQTFHHLKWT SWDR LKV  
PAGQPRTLLESLLAHLQE QHGLRVRILLHG  
SALLYAAGWSPEKQAQHLPLRVTEL VQQLT  
GQAPAPGQRVVLVLELSCEGDEDDTAFFPLHYEL

Tag (bold text): N-terminal His

Protease cleavage site: TEV (**ENLYF**▼**QG**)

UBA7 (regular text): Start **bold italics** (amino acid residues 1-1012)

Accession number: NP\_003326.2



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