

USP7 [6His-tagged]

Deubiquitylating Enzyme

Alternate Names: Herpesvirus-Associated Ubiquitin-Specific Protease, HAUSP VMW110-associated protein

Cat. No. 64-0003-050
Lot. No. 1736

Quantity: 50 µg
Storage: -70°C

FOR RESEARCH USE ONLY

NOT FOR USE IN HUMANS



CERTIFICATE OF ANALYSIS Page 1 of 2

Background

The deubiquitylating enzymes (DUBs) regulate ubiquitin dependent signaling pathways. The activities of the DUBs include the generation of free ubiquitin from precursor molecules, the recycling of ubiquitin following substrate degradation to maintain cellular ubiquitin homeostasis and the removal of ubiquitin or ubiquitin-like proteins (UBL) modifications through chain editing to rescue proteins from proteasomal degradation or to influence cell signalling events (Komander *et al.*, 2009). There are two main classes of DUB, cysteine proteases and metalloproteases. Ubiquitin specific processing protease 7 (USP-7) is a member of the cysteine protease enzyme family and cloning of the gene in humans was first described by Everett *et al.* (1997). Overexpression of p53 and USP7 stabilizes p53 through the removal of ubiquitin moieties from polyubiquitylated p53 (Kon *et al.*, 2010). Inhibition of USP7 expression results in the accumulation and stabilisation of p53 protein. However, USP7 has been shown to stabilise mdm2 a ubiquitin ligase that promotes the degradation of p53 (Holowaty and Frappier. 2004; Krishna and Grishin. 2004). Thus USP7 appears to play multiple roles in regulating the p53/mdm2 pathway and maintaining steady-state levels of p53 in the cell. Due to the role USP7 has been shown to play in the regulation of p53 its importance as a thera-

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Physical Characteristics

Species: human

Source: *E. coli* expression

Quantity: 50 µg

Concentration: 0.5 mg/ml

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

Molecular Weight: ~130 kDa

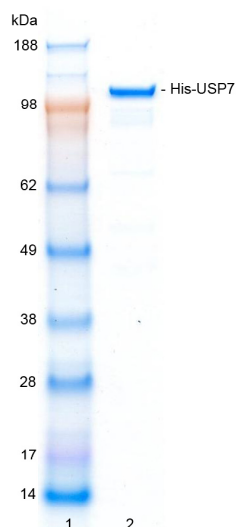
Purity: >80% by InstantBlue™ SDS-PAGE

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

Protein Sequence: Please see page 2

Quality Assurance

Purity:
4-12% gradient SDS-PAGE
InstantBlue™ staining
Lane 1: MW markers
Lane 2: 1 µg His-USP7



Protein Identification:

Confirmed by mass spectrometry.

Deubiquitylating Enzyme Assay:

The activity of His-USP7 was validated by determining the increase in fluorescence measured as a result of the enzyme catalysed cleavage of the fluorogenic substrate Ubiquitin-Rhodamine110-Glycine generating Ubiquitin and Rhodamine110-Glycine. Incubation of the substrate in the presence or absence of His-USP7 was compared confirming the deubiquitylating activity of His-USP7.



www.ubiquigent.com
Dundee, Scotland, UK

ORDERS / SALES SUPPORT

International: +1-617-245-0003
US Toll-Free: 1-888-4E1E2E3 (1-888-431-3233)
Email: sales.support@ubiquigent.com

UK HQ and TECHNICAL SUPPORT

International: +44 (0) 1382 381147 (9AM-5PM UTC)
US/Canada: +1-617-245-0020 (9AM-5PM UTC)
Email: tech.support@ubiquigent.com

Email services@ubiquigent.com for enquiries regarding compound profiling and/or custom assay development services.

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Lot-specific COA version tracker: v1.0.0

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CERTIFICATE OF ANALYSIS Page 2 of 2

Background

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peutic target for treating hematopoietic tumours has been highlighted (Cheon and Baek, 2006).

References:

Cheon KW, Baek KH (2006) HAUSP as a therapeutic target for hematopoietic tumors (review). *Int J Oncol* **28**, 1209-15.

Everett RD, Meredith M, Orr A, Cross A, Kathoria M, Parkinson J (1997) A novel ubiquitin-specific protease is dynamically associated with the PML nuclear domain and binds to a herpesvirus regulatory protein. *EMBO J* **16**, 1519-30.

Holowaty MN, Frappier L (2004) HAUSP/USP7 as an Epstein-Barr virus target. *Biochem Soc Trans* **32**, 731-2.

Komander D, Clague MJ, Urbe S (2009) Breaking the chains: structure and function of the deubiquitinases. *Nat Rev Mol Cell Biol* **10**, 550-63.

Kon N, Kobayashi Y, Li M, Brooks CL, Ludwig T, Gu W (2010) Inactivation of HAUSP in vivo modulates p53 function. *Oncogene* **29**, 1270-9.

Krishna SS, Grishin NV (2004) The finger domain of the human deubiquitinating enzyme HAUSP is a zinc ribbon. *Cell Cycle* **3**, 1046-9.

Physical Characteristics

Continued from page 1

Protein Sequence:

M G S S H H H H H S S G L E V L F Q G P G S M N
HQQQQQQKAGEQQQLSEPEDMEMEAGDTD
DPPRITQNPVINGNVALSDGHNTAEEDMED
DTSWRSEATFQFTVERFSRLSESVLSPP
CFVRNLPWKIMVMPRFYPDRPHQKSVGF
FLQCNAESDSTSWSCHAQAVLKIINYRD
DEKFSRRISHLFFHKENDWGFSNFMAWSEVT
DPEKGFIDDDKVTFEVQADAPHGVAWDSK
KHTGYVGLKNQGATCYMNSLLQTLFFTNQL
RKAVYMPTEGDDSSKSVPLALQRFVYELQHS
DKPVGTKKLTKSFGWETLDSFMQHDVQEL
CRVLLDNVENKMGTCVEGTIPKLFGRKM
VSYIQCKEVDYRSDRREYDIQLS IKGK
KNIFESFVDYVAVEQLDGNKYDAGEHGLQE
AEKGVKFLTLPPVLHLQLMRFMYDPQTDQNI
KINDRFEFPEQLPLDEFLOKTDPKDPANYIL
HAVLVHSGDNHGGHYVVYLNPKGDGKW
CKFDDDVVSRCTKEEAIEHNYGGHDDLS
VRHCTNAYMLVYIRESKLSEVLQAVTDHDI
PQQLVERLQEEKRIEAKRKRQE AHL YMQVQ
IVAEDQFCGHQGNMDEEKVKYTVFKVLKNS
SLAEFVQSLSQTMGFPPQDQIRLWPMQARSNGT
KRPAMLDNEADGNKTMIELSDNENPWTIFLET
VDPELAASGATLPKFDKDHVMLFLKMYDPK
TRSLNYCGHIYTPISCKIRDLLPVMCDRAG
FIQDTSLILYEEVKPNLTERIQDYDVSLDKA
LDELMDGDIIVFQKDDPENDNSELPTAKEY
FRDLYHRVDVIFCDKTI PNDPGFVVTLNRM
NYFQVAKTVAQRLNTDPMLLQFFKSQGYRDG
PGNPLRHNYEGLRDLLOFFKPRQPKKLYY
QQLKMKITDFENRRSFKCIWLSQFREEEIT
LYPDKHGCVRDLL EEC K KAVELG EKASGKL
RLLEIVSYKIIIGVHQEDELLECLSPATSRT
FRIEEIPLDQVIDKENEMLVTVAHFHKEV
FGTFGIPFLLRHQGEHFREVMKRIQSLLD
DIQEKEFEKFKFAIVMTGRHQY INE DEYE VN
LKDFEPQPGNMSHPRPWLGLDHFNKAPKRSRY
TYLEKAIKIHN*

Tag (bold text): N-terminal His

Protease cleavage site: PreScission™ (LEVL FQ▼GP)

USP7 (regular text): Start **bold italics** (amino acid residues 1-1102)

Accession number: CAA96580



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Dundee, Scotland, UK

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