SMURF1 [GST-tagged]

E3 Ligase

Alternate Names: E3 ubiquitin ligase SMURF1; Smad ubiquitination regulatory factor 1; KIAA1625

Cat. No. 63-0027-025 Quantity: 25 μg **Lot. No. 30028** 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). Smad-Specific E3 Ubiquitin Protein Ligase 1 (SMURF1) is a member of the E3 protein ligase family and cloning of the human gene was first described by Zhu et al. (1999). SMURF1 is a HECT domain ubiquitin E3 ligase that has been shown to regulate the cell polarity and protrusive activity and motility of tumour cells. Atypical protein kinase C-zeta (PKCζ), an effector of the Cdc42/Rac1-PAR6 polarity complex, recruits SMURF1 to cellular protrusions where it controls the local level of Rho A through degradation of the Rho A in the lamellipodia and filopodia of the cell (Wang et al., 2003). SMURF1 is also a negative regulator of the Bone Morphogenetic Protein (BMP) signalling pathway mediating the ubiquitylation and degradation of SMAD1 and SMAD5 (Zhu et al., 1999). More recently SMURF1 has been shown to ubiquitylate and degrade Krüppel-like factor 2 (KLF2) a transcription factor essential for normal lung development (Xie et al., 2011).

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Physical Characteristics

Species: human **Protein Sequence:** Please see page 2

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: ~114 kDa

Purity: >90% by InstantBlue™ SDS-PAGE

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

aliquot as required

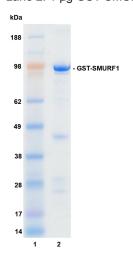
Quality Assurance

Protein Identification:

Confirmed by mass spectrometry.

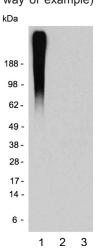
Purity:

4-12% gradient SDS-PAGE InstantBlue™ staining Lane 1: MW markers Lane 2: 1 µg GST-SMURF1



E3 ligase assay:

The ubiquitin conjugating activity of GST-SMURF1 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-UBE2D2 (UbcH5b) (several E2s were tested, data generated with this E2 is provided by way of example) and ubiquitin. Incubation of GST-



SMURF1 for 30 minutes at 30°C in the presence of ubiquitin, His-UBE1, His-UBE2D2 and ATP (Lane 1) was compared alongside two control reactions with either ATP (Lane 2) or GST-SMURF1 (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-SMURF1.

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Lot-specific COA version tracker: v1.0.1

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CERTIFICATE OF ANALYSIS Page 2 of 2

Background

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References:

Wang HR, Zhang Y, Ozdamar B, Ogunjimi AA, Alexandrova E, Thomsen GH, Wrana JL (2003) Regulation of cell polarity and protrusion formation by targeting RhoA for degradation. *Science* **302**. 1775-9.

Xie P, Tang Y, Shen S, Wang Y, Xing G, Yin Y, He F, Zhang L (2011) Smurf1 ubiquitin ligase targets Kruppel-like factor KLF2 for ubiquitination and degradation in human lung cancer H1299 cells. *Biochem Biophys Res Commun* 407, 254-9.

Zhu H, Kavsak P, Abdollah S, Wrana JL, Thomsen GH (1999) A SMAD ubiquitin ligase targets the BMP pathway and affects embryonic pattern formation. *Nature* **400**, 687-93.

Physical Characteristics

Continued from page 1

Protein Sequence:

MSPILGYWKIKGLVQPTRLLLEYLEEKY EEHLYERDEGDKWRNKKFELGLEFPN LPYYIDGDVKLTQSMAIIRYIADKHN MLGGCPKERAEISMLEGAVLDIRYGVS RIAYSKDFETLKVDFLSKLPEMLKMFE DRLCHKTYLNGDHVTHPDFMLYDALDV VLYMDPMCLDAFPKLVCFKKRIEAIPO IDKYLKSSKYIAWPLQGWQATFGGGDHP PKSDLEVLFQGPLGSPEIPGSTRAAAM SNPGTRRNGSSIKIRLTVLCAKNLAKKDF FRLPDPFAKIVVDGSGQCHSTDTVKNTLD PKWNOHYDLYVGKTDSITISVWNHKKIHK KQGAGFLGCVRLLSNAISRLKDTGYQRLD LCKLNPSDTDAVRGQIVVSLQTRDRIGT GGSVVDCRGLLENEGTVYEDSGPGRPLSCF MEEPAPYTDSTGAAAGGGNCRFVESP SQDQRLQAQRLRNPDVRGSLQTPQNRPH GHQSPELPEGYEQRTTVQGQVYFLHTQT GVSTWHDPRIPSPSGTIPGGDAAFLYE FLLOGHTSEPRDLNSVNCDELGPLPPGW EVRSTVSGRIYFVDHNNRTTOFTDPRLH HIMNHQCQLKEPSQPLPLPSEGSLEDEEL PAQRYERDLVQKLKVLRHELSLQQPQAGH CRIEVSREEIFEESYRQIMKMRPKDLK KRLMVKFRGEEGLDYGGVAREWLYLLCHEM LNPYYGLFQYSTDNIYMLQINPDSSIN PDHLSYFHFVGRIMGLAVFHGHYING GFTVPFYKOLLGKPIOLSDLESVDPEL HKSLVWILENDITPVLDHTFCVEHNAF GRILQHELKPNGRNVPVTEENKKEYVRLY VNWRFMRGIEAQFLALQKGFNELIPQHLLK PFDQKELELIIGGLDKIDLNDWKSN TRLKHCVADSNIVRWFWQAVETFDEER RARLLQFVTGSTRVPLQGFKALQGST GAAGPRLFTIHLIDANTDNLPKAHTCFNRID **IPPYESYEKLYEKLLTAVEETCGFAV**

Tag (**bold text**): N-terminal GST Protease cleavage site: PreScission™ (<u>LEVLFQ▼GP</u>) SMURF1 (regular text): Start **bold italics** (amino acid

residues 1-757)

Accession number: NP_065162.1



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

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