

# SMURF2 [GST-tagged]

## E3 Ligase

Alternate Names: SMAD specific E3 ubiquitin protein ligase 2, MGC138150

Cat. No. 63-0046-025  
Lot. No. 30231

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). Smad-Specific E3 Ubiquitin Protein Ligase 1 (SMURF2) is a member of the E3 protein ligase family and cloning of the human gene was first described by Kavsak *et al.* (2000). SMURF2 is a HECT domain ubiquitin E3 ligase that has been shown to regulate cell polarity, senescence and tumor suppression (Blank *et al.*, 2012). Immunoprecipitation studies have demonstrated that SMURF2 interacts with RNF11 through the binding of the WW domain 2 and 3 of SMURF2 to the PY motif of RNF11. RNF11 was also found to interact with Ube2D1 in this complex and ubiquitylation of both SMURF2 and RNF11 was detected. (Subramaniam *et al.*, 2003). Knock down of SMURF2 in human tumour cell lines results in increased levels of RNF20 and ubiquitylation of the RNF20 substrate histone H2B (Blank *et al.*, 2012). SMURF2 knockout mice appear normal until early adulthood, when a large number of them develop tumours of all types (Blank *et al.*, 2012).

### References:

Blank M, Tang Y, Yamashita M, Burkett SS, Cheng SY *et al.* (2012) A tumor suppressor function of Smurf2 associated with controlling chromatin landscape and genome stability through RNF20. *Nature Med* 18, 227-234.

Continued on page 2

## Physical Characteristics

**Species:** human

**Source:** *E. coli*

**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

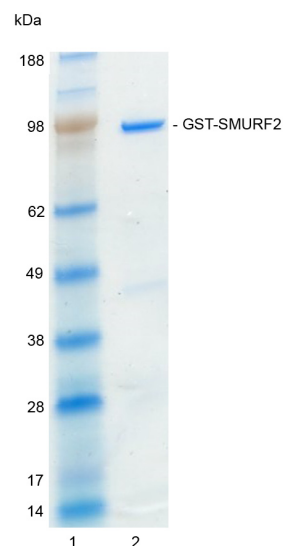
**Stability/Storage:** 12 months at -70°C;  
aliquot as required

**Protein Sequence:** Please see page 2

## Quality Assurance

### Purity:

4-12% gradient SDS-PAGE  
InstantBlue™ staining  
Lane 1: MW markers  
Lane 2: 1 µg GST-SMURF2



### Protein Identification:

Confirmed by mass spectrometry.



**E3 ligase assay:** The ubiquitin conjugating activity of GST-SMURF2 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-UBE2D3 (UbcH5c) (several E2s were tested, data generated with this E2 is provided by way of example) and ubiquitin. Incubation of GST-SMURF2 for 60 minutes at 30°C in the presence of ubiquitin, His-UBE1, His-UBE2D3 and ATP (Lane 1) was compared alongside two control reactions with either ATP (Lane 2) or GST-SMURF2 (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-SMURF2.



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Lot-specific COA version tracker: v1.0.0

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## Background

Continued from page 1

Kavsak P, Rasmussen RK, Causing CG, Bonni S *et al.* (2000) Smad7 binds to Smurf2 to form an E3 ubiquitin ligase that targets the TGF-beta receptor for degradation. *Molec Cell* 6, 1365-1375.

Subramaniam V, Li H, Wong M, Kitching R, Attisano L, Wrana J, Zubovits J, Burger AM, Seth A (2003) The RING-H2 protein RNF11 is overexpressed in breast cancer and is a target of Smurf2 E3 ligase. *Brit J Cancer* 89, 1538-1544.

## Physical Characteristics

Continued from page 1

### Protein Sequence:

**MSPILGYWKIKGLVQPTRLLLEYLEEKY**  
**EEHLYERDEGDKWRNKKFELGLEFPN**  
**LPYYIDGDVKLTQSMAIIRYIADKHNMLG**  
**GCPKERAEISMLEGAVLDIRYGVSRIAY**  
**SKDFETLKVDFLSKLPEMLKMFEDRLCHK**  
**TYLNGDHVTHPDFMLYDALDVVLYMDPM**  
**CLDAFPKLVCFKKRIEAIPOIDKYLKSSKY**  
**IAWPLQGWQATFGGGDHPKSDLEVLVQ**  
**PLGSPEIPGSTRAAAMSNPGRRRNGPVKLR**  
**LTVLCAKNLVKKDFRRLPDPFAKVVDGS**  
**GQCHSTDVKNLDPKWNQHYDLYIGKSDS**  
**VTISVWNHKKIHKKQGAGFLGCVRLLSNAIN**  
**RLKDTGYQRLDLCKLGPNDNDTVRGQIVVS**  
**LQSRDRIGTGGQVVDCSRFLDNDLPDGWEER**  
**RTASGRIQYLNHITRRTQWERPTRPASEY**  
**SSPGRPLSCFVDENTPISGTNGATCGQSS**  
**DPRLAERRVRSQRHRNYMSRTHLHTPP**  
**DLPEGYEQRTTQQGQVYFLHTQTGVSTWH**  
**DPVRPRDLSNINCEELGPLPPGWEIRN**  
**TATGRVYFVDHNNRRTQFTDPRLSANL**  
**HLVLRNQQLKDDQQQVVS LCPDDTE**  
**CLTVPRYKRDVQKLIKLRQELSQQQPQAGH**  
**CRIEVSREEIFEESYRQVMKMRPKDLWKRL**  
**MIKFRGEEGLDYGGVAREWLYLLSHEMLN**  
**PYYGLFQYSRDDIYTLQINPDSAVNPEHLSY**  
**FHFVGRIMGMAVFHGHYIDGGFTLPFYKQLL**  
**GKSITLDDMELVDPDLHNSLVWILENDIT**  
**GVL DHTFCVEHNAYGEIQHELKPNGK**  
**SIPVNEENKKEYVRLYVNWRFRLGIEAQFLA**  
**LQKGFNEVIPQHLLKTFDEKELELIICGLG**  
**KIDVNDWKVNTLKHCTPDSNIVKFWKAV**  
**EFFDEERRARLLQFVTGSSRVPLQGFKALQ**  
**GAGPRLFTIHQIDACTNNLPKAHTCFNRID**  
**IPPYESYEKLYEKLLTAIEETCGFAVE**

Tag (**bold text**): N-terminal GST

Protease cleavage site: PreScission™ (LEVLVQ▼GP)

SMURF2 (regular text): Start **bold italics** (amino acid residues 1-748)

Accession number: AAG45422.1



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