

## *Division of Signal Transduction Therapy*

### **Standard Operation Procedure**

#### **Preparation of GST-Smurf1**

**Enzyme description:-** GST-Smurf1 1-754 (full length)

**Clone number:-** DU19628

**Source:-** Recombinant

**Tag:-** N-terminal GST

**Purification method:-** GSH-Sepharose

**Expression level:-** 0.1mg/L

**Calculated molecular mass:-**

Monoisotopic 113916

Average Mass 113986

[cysteines reduced, methionines have not been oxidised]

**Theoretical pI:-** 6.71

**Purity:-** 80%

**Enzyme storage buffer:-**

50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT

**Storage temperature:-** -80°C

**Assay:-**

Ligase assay with Ubiquitin, UBE1 and UBE2D family members. Incubate with 0.5mM Mg-ATP for 2h at 37°C and analyse by immunoblotting for Ubiquitin chain formation.

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### Clone Data Sheet

#### Protein name

**Protein** Smurf1  
**Synonyms** Smuf1  
**Clone Number** DU19628  
**Species** Human  
**Accession Number** Q9HCE7  
**Tags** N-terminal GST

Aminoacid sequence of  
the expressed protein

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELG  
LEFPNLPHYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGA  
VLDIRYGVSR IAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDH  
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS  
KYIAWPLQGWQATFGGGDHPPKSDLEVLFOGPLGSPEIPGSTRAAAMSN  
**PGTRRNGSSIKIRLTVLCAKNLAKKDFRPLDPFAKIVVDGSGQCHSTD**  
**TVKNTLDPKWNQHYDLYVGKTDSTITISVWNHKKIHKKQAGFLGCVRL**  
**SN AISRLKDTGYQRDLCKLNPSDTDAVRGQIVVSLQTRDRIGTGGSV**  
**DCRGLLENEGTVYEDSGPGRPLSCFMEEPAPYTDSTGAAAGGGNCRFVE**  
**SPSQDQRLQAQRLRNPDRVRSLOTPQNRPHGHQSPPELPEGYEQRTTVQG**  
**QVYFLHTQTGVSTWHDPRIPSPSGTIPGGDAAFLYEFLLQGHTSEPRDL**  
**NSVNCDELGPLPPGWEVRSTVSGRIYFVDHNNRTTQFTDPRLHHIMNHQ**  
**CQLKEPSQPLPLPSEGSLEDEELPAQRYERDLVQKLKVLRHLSLQQPQ**  
**AGHCRIEVSREEIFEESYRQIMKMRPKDLKKRLMVKFRGEEGLDYGGVA**  
**REWL YLLCHEMLNPYYGLFQYSTDNIYMLQINPDSSINPDHLSYFHFVG**  
**RIMGLAVFHGHYINGGFTVPFYKQLLGKPIQLSDLESVDPELHKS LVWI**  
**LENDITPVL DHTFCVEHNAFGRILQHELKPNGRNPVTEENKKEYVRLY**  
**VNWRFMRGIEAQFLALQKGFNELIPQHLLKPFDOKELELIIGGLDKIDL**  
**NDWKSNTRLKHCVADSNIVRWFQAVETFDEERRARLLQFVTGSTRVPL**  
**QGFKALQGSTGAAGPRLFTIHLIDANTDNLPKAHTCFNRIDIPPYESYE**  
**KLYEKLLTAVEETCGFAVE**

Native sequence in bold  
Protease cleavage Precission protease site underlined  
Cloning sites Not1 / Not1

**DNA sequence of  
insert**

GCGGCCGCTATGTCTGAACCCCGGGACACGCAGGAACGGCTCCAGCATCA  
AGATCCGTCTGACAGTGTATGTGCCAAGAACCTTGCAAAGAAAGACTT  
CTTCAGGCTCCCTGACCCTTTTGCAAAGATTGTCGTGGATGGGTCTGGG  
CAGTGCCACTCAACCGACACTGTGAAAAACACATTGGACCCAAAGTGGAA  
ACCAGCACTATGATCTATATGTTGGGAAAACGGATTTCGATAACCATTAG  
CGTGTGGAACCATAAGAAAATTCACAAGAAACAGGGAGCTGGCTTCCTG  
GGCTGTGTGCGGCTGCTCTCCAATGCCATCAGCAGATTAAGATAACCG  
GATAACCAGCGTTTGGATCTATGCAAATAAACCCCTCAGATACTGATGC  
AGTTCGTGGCCAGATAGTGGTCAGTTTACAGACACGAGACAGAATAGGA  
ACCGGCGGCTCGGTGGTGGACTGCAGAGGACTGTTAGAAAATGAAGGAA  
CGGTGTATGAAGACTCGGGCCCTGGGAGGCCGCTCAGCTGCTTCATGGA  
GGAACCAGCCCCTTACACAGATAGCACCGGTGCTGCTGCTGGAGGAGGG  
AATTGCAGGTTTCGTGGAGTCCCCAAGTCAAGATCAAAGACTTCAGGCAC  
AGCGGCTTCGAAACCCTGATGTGCGAGGTTCACTACAGACGCCCCAGAA  
CCGACCACACGGCCACCAGTCCCCGGAAGTGCCTGAAAGGCTACGAACAA  
AGAACAACAGTCCAGGGCCAAGTTTACTTTTTGCATACACAGACTGGAG  
TTAGCACGTGGCACGACCCAGGATACCAAGTCCCTCGGGGACCATTCC  
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TCTGAGCCAGAGACCTTAACAGTGTGAACTGTGATGAACTTGGACCAC  
TGCCGCCAGGCTGGGAAGTCAAGTACAGTTTCTGGGAGGATATATTT  
TGTAGATCATAATAACCGAACAAACCAGTTTACAGACCCAAGGTTACAC  
CACATCATGAATCACCAGTGCCAACTCAAGGAGCCAGCCAGCCGCTGC  
CACTGCCAGTGAGGGCTCTCTGGAGGACGAGGAGCTTCCTGCCAGAG  
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TCGCTTCAGCAGCCCCAAGCTGGTCATTGCCGCATCGAAGTGTCCAGAG  
AAGAAATCTTTGAGGAGTCTTACCGCCAGATAATGAAGATGCGACCGAA  
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GATTACGGTGGTGTGGCCAGGGAGTGGCTTTACTTGTGTGCCATGAAA  
TGCTGAATCCTTATTACGGGCTCTTCCAGTATTCTACGGACAATATTTA  
CATGTTGCAAATAAATCCGGATTCTTCAATCAACCCCGACCATTGTCT  
TATTTCCACTTTGTGGGGCGGATCATGGGGCTGGCTGTGTTCCATGGAC  
ACTACATCAACGGGGCTTCACAGTGCCCTTCTACAAGCAGCTGCTGGG  
GAAGCCCATCCAGCTCTCAGATCTGGAATCTGTGGACCCAGAGCTGCAT  
AAGAGCTTGGTGTGGATCCTAGAGAACGACATCACGCCTGTACTGGACC  
ACACCTTCTGCGTGGAACACAACGCCTTCGGGCGGATCCTGCAGCATGA  
ACTGAAACCCAATGGCAGAAATGTGCCAGTACAGAGGAGAATAAGAAA  
GAATACGTCCGGTTGTATGTAACCTGGAGGTTTATGAGAGGAATCGAAG  
CCCAGTTCTTAGCTCTGCAGAAGGGGTTCAATGAGCTCATCCCTCAACA  
TCTGCTGAAGCCTTTTGACCAGAAGGAACTGGAGCTGATCATAGGCGGC  
CTGGATAAAAATAGACTTGAACGACTGGAAGTCAACACGCGGCTGAAGC  
ACTGTGTGGCCGACAGCAACATCGTGCGGTGGTTCTGGCAAGCGGTGGA  
GACGTTTCGATGAAGAAAGGAGGGCCAGGCTCCTGCAGTTTGTGACTGGG  
TCCACGCGAGTCCCGCTCCAAGGCTTCAAGGCTTTGCAAGGTTCTACAG  
GCGCGGCAGGCCCCGGCTGTTCAACCATCCACCTGATAGACGCGAACAC  
AGACAACCTTCCGAAGGCCATACCTGCTTTAACCGGATCGACATTCCA  
CCATATGAGTCCATGAGAAGCTCTACGAGAAGCTGCTGACAGCCGTGG  
AGGAGACCTGCGGGTTTGCTGTGGAGTGAAGCGGCCG