

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of GST-Smurf2

<u>Enzyme description:-</u>	Smurf 2 1-748
<u>Clone number:-</u>	DU19879
<u>Source:-</u>	Recombinant
<u>Tag:-</u>	N-terminal GST-tag
<u>Purification method:-</u>	GSH-Sepharose
<u>Expression level:-</u>	0.1mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	113998
Average Mass	114069
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	7.89
<u>Purity:-</u>	60% -70%
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	

Division of Signal Transduction Therapy

Clone Data Sheet

Protein name

Protein Smurf 2 1-748
Synonyms
Clone Number DU19879
Species Human
Accession Number Protein: Q9HAU4 DNA: NM_022739.3
Tags N-terminal GST

Aminoacid sequence of the expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEELHYERDEGDKWRNKKFELGLEF
PNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRY
GVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLY
DALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIAWPLOGWQA
TFGGGDHPPKSDLEVLFOGPLGSPEIPGSTRAAAMS**NPGGRRNGPVKLRLTV**
LCAKNLVKKDFRRLPDPFAKVVDGSGQCHSTDTVKNTLDPKWNQHYDLYIG
KSDSVTISVWNHKKIHKKQGAGFLGCVRLLSNAINRLKDTGYQRDLCKLGP
NDNDTVRGQIVVSLQSRDRIGTGGQVDCSRLFDNDLDPGWEERRTASGRIQ
YLNHITRRTQWERPTRPASEYSSPGRPLSCFVDENTPISGTNGATCGOSSDP
RLAERRVRSQRHRNYMSRTHLHTPPDLPEGYEQRTTQQGQVYFLHTQTGVST
WHDPRVPRDLSNINCEELGPLPPGWEIRNTATGRVYFVDHNNRTQFTDPRL
SANLHLVLRQNLKDQQQQVSLCPDDECTVPRYKRDVQKLKILRQE
LSQQQPQAGHCRIEVSREEIFEESYRQVMKMRPKDLWKRLMIKFRGEEGLDY
GGVAREWLYLLSHEMLNPYYGLFQYSRDDIYTLOINPDSAVNPEHLSYFHFV
GRIMGMAVFHGHYIDGGFTLPFYKQLLGSITLDDMELVDPDLHNSLVWILE
NDITGVL DHTFCVEHNAYGEIIQHELKPNGKSI PVNEENKKEYVRLYVNWRF
LRGIEAQFLALQKGFNEVIPQHLLKTFDEKELELIICGLGKIDVNDWKVNT
LKHCTPDSNIVKFWKAVEFFDEERRARLLOFVTGSSSRVPLQGFKALQGAAG
PRLFTTIHQIDACTNNLPKAHTCFNRIDIPPYESYEKLYEKLLTAIEETCGFA
VE

Native sequence Smurf 2 full length in bold
Protease cleavage Precission Protease site underlined
Cloning sites Not 1 / Not 1

**DNA sequence of
insert**

GCGGCCGCTATGTCTAACCCCGGAGGCCGGAGGAACGGGCCCGTCAAGCTGC
GCCTGACAGTACTCTGTGCAAAAAACCTGGTGAAAAAGGATTTTTTCCGACT
TCCTGATCCATTTGCTAAGGTGGTGGTTGATGGATCTGGGCAATGCCATTCT
ACAGATACTGTGAAGAATACGCTTGATCCAAAGTGAATCAGCATTATGACC
TGTATATTGGAAAGTCTGATTCAGTTACGATCAGTGTATGGAATCACAAGAA
GATCCATAAGAAACAAGGTGCTGGATTTCTCGGTTGTGTTTCGTCTTCTTTCC
AATGCCATCAACCGCCTCAAAGACACTGGTTATCAGAGGTTGGATTATGCA
AACTCGGGCCAAATGACAATGATACAGTTAGAGGACAGATAGTAGTAAGTCT
TCAGTCCAGAGACCGAATAGGCACAGGAGGACAAGTTGTGGACTGCAGTCGT
TTATTTGATAACGATTTACCAGACGGCTGGGAAGAAAGGAGAACCGCCTCTG
GAAGAATCCAGTATCTAAACCATATAACAAGAACTACGCAATGGGAGCGCCC
AACACGACCGGCATCCGAATATTCTAGCCCTGGCAGACCTCTTAGCTGCTTT
GTTGATGAGAACACTCCAATTAGTGGAACAAATGGTGCAACATGTGGACAGT
CTTCAGATCCAGGCTGGCAGAGAGGAGATCAGGTCACAACGACATAGAAA
TTACATGAGCAGAACACATTTACATACTCCTCCAGACCTACCAGAAGGCTAT
GAACAGAGGACAACGCAACAAGGCCAGGTGTATTTCTTACATACACAGACTG
GTGTGAGCACATGGCATGATCCAAGAGTGCCAGGGATCTTAGCAACATCAA
TTGTGAAGAGCTTGGTCCATTGCCTCCTGGATGGGAGATCCGTAATACGGCA
ACAGGCAGAGTTTATTTCTGTTGACCATAACAACAGAACAACACAATTTACGG
ATCCTCGGCTGTCTGCTAACTTGCATTTAGTTTTAAATCGGCAGAACCAATT
GAAAGACCAACAGCAACAGCAAGTGGTATCGTTATGTCCTGATGACACAGAA
TGCCTGACAGTCCCAAGGTACAAGCGAGACCTGGTTCAGAAACTAAAAATTT
TGCGGCAAGAACTTTCCAACAACAGCCTCAGGCAGGTCATTGCCGCATTGA
GGTTTCCAGGGAAGAGATTTTTTGAGGAATCATATCGACAGGTCATGAAAATG
AGACCAAAAAGATCTCTGGAAGCGATTAATGATAAAATTTCTGGGAGAAGAAG
GCCTTGACTATGGAGGCGTTGCCAGGGAATGGTTGTATCTCTTGTACATGA
AATGTTGAATCCATACTATGGCCTCTCCAGTATTCAAGAGATGATATTTAT
ACATTGCAGATCAATCCTGATTCTGCAGTTAATCCGGAACATTTATCCTATT
TCCACTTTGTTGGACGAATAATGGGAATGGCTGTGTTTCATGGACATTATAT
TGATGGTGGTTTTCACATTGCCTTTTTTATAAGCAATTGCTTGGGAAGTCAATT
ACCTTGGATGACATGGAGTTAGTAGATCCGGATCTTCACAACAGTTTAGTGT
GGATACTTGAGAATGATATTACAGGTGTTTTGGACCATACCTTCTGTGTTGA
ACATAATGCATATGGTGAAATTATTCAGCATGAACTTAAACCAAATGGCAAA
AGTATCCCTGTTAATGAAGAAAATAAAAAAGAATATGTCAGGCTCTATGTGA
ACTGGAGATTTTTTACGAGGCATTGAGGCTCAATTCTTGGCTCTGCAGAAAGG
ATTTAATGAAGTAATTCACAACATCTGCTGAAGACATTTGATGAGAAGGAG
TTAGAGCTCATTATTTGTGGACTTGGAAAGATAGATGTTAATGACTGGAAGG
TAAACACCCGGTTAAAAACTGTACACCAGACAGCAACATTGTCAAATGGTT
CTGGAAAGCTGTGGAGTTTTTTGATGAAGAGCGACGAGCAAGATTGCTTCAG
TTTGTGACAGGATCCTCTCGAGTGCCTCTGCAGGGCTTCAAAGCATTGCAAG
GTGCTGCAGGCCCGAGACTCTTTACCATACACCAGATTGATGCCTGCACTAA
CAACCTGCCGAAAGCCCACACTTGCTTCAATCGAATAGACATTCCACCCTAT
GAAAGCTATGAAAAGCTATATGAAAAGCTGCTAACAGCCATTGAAGAAACAT
GTGGATTTGCTGTGGAATGAGCGGCCGC