

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of TRIM28

<u>Enzyme description:-</u>	TRIM28 1-835 (full length)
<u>Clone number:-</u>	DU12450
<u>Source:-</u>	Recombinant
<u>Tag:-</u>	N-terminal GST
<u>Purification method:-</u>	GSH-Sepharose
<u>Expression level:-</u>	1 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	116278 Da
Average Mass	116346 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	5.10
<u>Purity:-</u>	60 %
<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>	

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Clone Data Sheet

Protein name GST-TRIM28

Protein TRIM28 1-835 (full length)
Synonyms TIF1B, KAP-1, KRIP-1, RNF96
Clone Number DU12450
Species Human
Accession Number Protein: Q13263 or NP_005753
Tag N-terminal GST

Aminoacid sequence
of the expressed
protein .

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGL
EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVL
DIRYGVSR IAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTH
PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA
WPLQGWQATFGGGDHPPKSDLEVLFOGPLGSPGIPGSTRAAA**MAASAAAA**
SAAAASAASGSPGPGESAGGEKRSTAP**SAAASASASAAA**SSPAGGGAEA
LELLEHCGVCRERLRPEREPRLLPCLHSACSACLGPAAPAAANSSGDGGA
AGDGTVVDCPVCKQOCFSKDIVENYFMRDSGSKAATDAQDANQCCTSCED
NAPATSYCVECSEPLCETCVEAHQRVKYTKDHTVRSTGPAKSRDGERTVY
CNVHKHEPLVLFCECDTLTCRDCQLNAHKDHQYQFLEDAVRNQRKLLAS
LVKRLGDKHATLQKSTKEVRSSI**IQVSDVQKR**VQVDVKMAILQIMKELNK
RGRVLVND**AQK**VTEGQ**QER**LERQHWTMTKI**QKHQ**EHILRFASWALESDNN
TALLSKKLIYFQLHRALKMIVDPVEPHGEMKFQWDLNAWTKSAEAFGKI
VAERPGTNSTGPAPMAPPRAPG**PLSKQ**SGSSQ**PMEVQ**EGYFGSGDDPY
SSAEPHVSGVKRSRSGEGEVSGLMRKVPRVSLERLDLDTADSQPPVFKV
FPGSTTEDYNLIVIERGAAAAATG**QPGTAPAGT**PGAPPLAGMAIVKEEET
EAAIGAPPTATEGPETK**PVLMALA**EGPGAEGPRLASPSGSTSSGLEVVAP
EGTSAPGGGGPTLDDSATICRVC**QKPGDLV**MCNQCEFCFHLDC**HLPALQD**
VPGEW**SCSLCHVLPDL**KEEDGSLSLDGADSTGVVAKLSPANQRKCERVL
LALFCHEPCRPLHQLATDSTFSLD**QPGGTL**DLTLIRARL**QEKLSPPYSSP**
QEFAQDVGRMFKQFNKLTEDKADVQSIIGLQ**RFF**ETRMNEAFGDTKFSAV
LVEPPMSLPGAGLSS**QELS**GGPGDGP

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

**DNA sequence of
insert**

GCGGCCGCGATGGCGGCCTCCGCGGGCGGCAGCCTCGGCAGCAGCGGCCTC
GGCCGCCTCTGGCAGCCCGGGCCCGGGCGAGGGCTCCGCTGGCGGGCGAAA
AGCGCTCCACCGCCCCTTCGGCCGCAGCCTCGGCCTCTGCCTCAGCCGCG
GCGTCGTGCCCCGCGGGGGGCGGGCGCCGAGGCGCTGGAGCTGCTGGAGCA
CTGCGGCGTGTGCAGAGAGCGCCTGCGACCCGAGAGGGAGCCCCGCTGC
TGCCCTGTTTGCCTCGGCCTGTAGTGCTGCTTAGGGCCCGCGGCCCC
GCCGCCGCAACAGCTCGGGGGACGGCGGGGGCGGGCGGACGGCACCGT
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GATGCGAACCAGTGCTGCACTAGCTGTGAGGATAATGCCCCAGCCACCAG
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ACCAGCGGGTGAAGTACACCAAGGACCATACTGTGCGCTCTACTGGGCCA
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ACTGCCAGCTCAATGCCACCAAGGACCACCAGTACCAGTTCTTAGAGGAT
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CACTAACTCAACAGGCCCTGCACCCATGGCCCTCCAAGAGCCCAGGGC
CCCTGAGCAAGCAGGGCTCTGGCAGCAGCCAGCCATGGAGGTGCAGGAA
GGCTATGGCTTTGGGTGAGGAGATGATCCCTACTCAAGTGCAGAGCCCCA
TGTGTCAGGTGTGAAACGGTCCCGCTCAGGTGAGGGCGAGGTGAGCGGCC
TTATGCGCAAGGTGCCACGAGTGAGCCTTGAACGCCTGGACCTGGACCTC
ACAGCTGACAGCCAGCCACCCGTCTTCAAGGTCTTCCCAGGCAGTACCAC
TGAGGACTACAACCTTATTGTTATTGAACGTGGCGCTGCCGCTGCAGCTA
CCGCCAGCCAGGGACTGCGCCTGCAGGAACCCCTGGTGCCCCACCCCTG
GCTGGCATGGCCATTGTCAAGGAGGAGGAGACGGAGGCTGCCATTGGAGC
CCCTCCTACTGCCACTGAGGGCCCTGAGACCAACCTGTGCTTATGGCTC
TTGCGGAGGGTCTGGTGCTGAGGGTCCCCGCCTGGCCTCACCTAGTGGC
AGCACCAGCTCAGGGCTGGAGGTGGTGGCTCCTGAGGGTACCTCAGCCCC
AGGTGGTGGCCCCGGAACCCCTGGATGACAGTGCCACCATTTGCCGTGTCT
GCCAGAAGCCAGGCGATCTGGTTATGTGCAACCAGTGTGAGTTTTGTTTC
CACCTGGACTGTCACCTGCCGGCCCTGCAGGATGTACCAGGGGAGGAGTG
GAGCTGCTCACTCTGCCATGTGCTCCCTGACCTGAAGGAGGAGGATGGCA
GCCTCAGCCTGGATGGTGCAGACAGCACTGGCGTGGTGGCCAAGCTCTCA
CCAGCCAACCAGCGGAAATGTGAGCGTGTACTGCTGGCCCTATTCTGTCA
CGAACCCCTGCCGCCCCCTGCATCAGCTGGCTACCGACTCCACCTTCTCCC
TGGACCAGCCCGGTGGCACCCCTGGATCTGACCCTGATCCGTGCCCGCCTC
CAGGAGAAGTTGTCACCTCCCTACAGCTCCCCACAGGAGTTTGGCCAGGA
TGTGGGCCGCGATGTTCAAGCAATTCAACAAGTTAACTGAGGACAAGGCAG
ACGTGCAGTCCATCATCGGCCTGCAGCGCTTCTTCGAGACGCGCATGAAC
GAGGCCTTCGGTGACACCAAGTTCTCTGCTGTGCTGGTGGAGCCCCCGCC
GATGAGCCTGCCTGGTGTGTCGCTGAGTTCCAGGAGCTGTCTGGTGGCC
CTGGTGTGATGGCCCTGAGCGGCCGC