

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of TRAF2

<u>Enzyme description:-</u>	TRAF2 2-501 (end)
<u>Clone number:-</u>	DU43745
<u>Source:-</u>	insect recombinant
<u>Tag:-</u>	cleaved from Dac-TEV-
<u>Purification method:-</u>	Ampicillin-Sepharose
<u>Expression level:-</u>	0.5mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	55982 Da
Average Mass	55927 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	8.21
<u>Purity:-</u>	50%
<u>Enzyme storage buffer:-</u>	
50mM HEPES pH 7.5, 150mM NaCl, 0.03% Brij35, 1mM TCEP	
<u>Storage temperature:-</u>	-80°C
<u>Assay:-</u>	

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Clone Data Sheet

TRAF2

<u>Protein</u>	TRAF2 2-501
<u>Synonyms</u>	TRAP3
<u>Clone Number</u>	DU43745
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q12933
<u>Tags</u>	cleaved from N-terminal Dac-
Aminoacid sequence of the expressed protein	GGSAASVTPPGSLELLQPGFSKTLGKLEAKYLCSACRNVLRRPFQAQCG HRYCSFCLASILSSGPQNC AACVHEGIYEEGISILESSAFP DNAARREVES LPAVCPDGDCTWKGT LKEYESCHEGRCPLMLTECPACKGLVRLGKERHLEH ECPERSLS CRHCRAPCCGADVKAHHEVCPKFLPTCDGCGKKKI PREKFQDHV KTCGKCRVPCR FHAIGCLETVEGEKQEQEHEVQWLREHLAMLLSSVLEAKPLL GDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTAEACSRQHRLD QDKIEALSSKVQQLERSIGL KDLAMADLEQKVLEMEASTYDGVFIWKISDFA RRRQEA VAGRI PAIFSPAFYTSRYGYKMCLRIYLN GDGTGRGTHLSLFFVVM KGPNDALLRWP FNQVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIA SGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL
Native sequence	in bold
Protease site	TEV-protease
Cloning sites	BamH1 / NotI

**DNA sequence of
the insert**

GGATCCGCTGCAGCTAGCGTGACCCCCCTGGCTCCCTGGAGTTGCTACA
GCCCCGGCTTCTCCAAGACCCTCCTGGGGACCAAGCTGGAAGCCAAGTACC
TGTGCTCCGCCTGCAGAAACGTCCTCCGCAGGCCCTTCCAGGCGCAGTGT
GGCCACCGGTACTGCTCCTTCTGCCTGGCCAGCATCCTCAGCTCTGGGCC
TCAGAACTGTGCTGCCTGTGTTACGAGGGCATATATGAAGAAGGCATTT
CTATTTTAGAAAAGCAGTTCGGCCTTCCCAGATAATGCTGCCCGCAGGGAG
GTGGAGAGCCTGCCGGCCGTCTGTCCCAGTGATGGATGCACCTGGAAGGG
GACCTGAAAGAATACGAGAGCTGCCACGAAGGCCGCTGCCCGCTCATGC
TGACCGAATGTCCCGCGTGCAAAGGCCTGGTCCGCCTTGGTAAAAGGAG
CGCCACCTGGAGCACGAGTGCCCGGAGAGAAGCCTGAGCTGCCGGCATTG
CCGGGCACCCTGCTGCGGAGCAGACGTGAAGGCCACACGAGGTCTGCC
CCAAGTTCCTTAACCTGTGACGGCTGCGGCAAGAAGAAGATCCCCCGG
GAGAAGTTTCAGGACCACGTCAAGACTTGTGGCAAGTGTGAGTCCCTTG
CAGATTCACGCCATCGGCTGCCCTCGAGACGGTAGAGGGTGAGAAACAGC
AGGAGCACGAGGTGCAGTGGCTGCGGGAGCACCTGGCCATGCTACTGAGC
TCGGTGCTGGAGGCAAAGCCCCCTTGGGAGACCAGAGCCACGCGGGGTC
AGAGTCCTGCAGAGGTGCGAGAGCCTGGAGAAGAAGACGGCCACTTTTG
AGAACATTGTCTGCGTCCTGAACCGGGAGGTGGAGAGGGTGGCCATGACT
GCCGAGGCCTGCAGCCGGCAGCACCGGCTGGACCAAGACAAGATTGAAGC
CCTGAGTAGCAAGGTGCAGCAGCTGGAGAGGAGCATTGGCCTCAAGGACC
TGGCGATGGCTGACTTGGAGCAGAAGGTCTTGGAGATGGAGGCATCCACC
TACGATGGGGTCTTCATCTGGAAGATCTCAGACTTCGCCAGGAAGCGCCA
GGAAGCTGTGGCTGGCCGCATACCCGCCATCTTCTCCCCAGCCTTCTACA
CCAGCAGGTACGGCTACAAGATGTGTCTGCGTATCTACCTGAACGGCGAC
GGCACCGGGCGAGGAACACACCTGTCCCTCTTCTTTGTGGTGTGAAGGG
CCCGAATGACGCCCTGCTGCGGTGGCCCTTCAACCAGAAGGTGACCTTAA
TGCTGCTCGACCAGAATAACCGGGAGCACGTGATTGACGCCCTCAGGCC
GACGTGACTTCATCCTCTTTTCAGAGGCCAGTCAACGACATGAACATCGC
AAGCGGCTGCCCCCTTCTGCCCCGTCTCCAAGATGGAGGCAAAGAATT
CCTACGTGCGGGACGATGCCATCTTCATCAAGGCCATTGTGGACCTGACA
GGGCTCTAAGCGGCCGCGC