

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of TRAF3

<u>Enzyme description:-</u>	TRAF3 1-569 (end)
<u>Clone number:-</u>	DU24564
<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	64448 Da
Average Mass	64488Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	8.72
<u>Purity:-</u>	70%
<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

TRAF3

<u>Protein</u>	TRAF3
<u>Synonyms</u>	CAP-1, CRAF1
<u>Clone Number</u>	DU24564
<u>Species</u>	Human
<u>Accession Number</u>	Protein: Q13114
<u>Tags</u>	cleaved from N-terminal Dac-
Aminoacid sequence of the expressed protein	GGSMESSKKMDSPGALQTNPPLKLHTDRSAGTPVVFVPEQGGYKEKFVKTVED KYKCEKCHLVLCSPKQTECGHRFCESMAALLSSSSPKCTACQESIVKDKVF KDNCKREILALQIYCRNESRGCAEQMLGHELLVHLKNDCHFELPCVRPDC KEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCP HKCSVQTLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAV QHVNLLKEWSNSLEKKVSLQNESVEKNKSIQSLHNQICSFEIEIERQKEML RNNESKILHLQVIDSQAEKLELDKEIRPFRQNWEEADSMKSSVESLQNRV TELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETAS YNGVLIWKIRDYKRRKQEAVMGKTLISLQSPFYTYGYFGYKMCARVYLNQDGM GKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMMLMDQSSRRHLGDAFKPDPN SSSFKKPTGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVDTSDLDP
Native sequence	in bold
Protease site	TEV-protease
Cloning sites	BamH1

**DNA sequence of
the insert**

GGATCCATGGAGTCGAGTAAAAAGATGGACTCTCCTGGCGCGCTGCAGAC
TAACCCGCCGCTAAAGCTGCACACTGACCGCAGTGCTGGGACGCCAGTTT
TTGTCCCTGAACAAGGAGGTTACAAGGAAAAGTTTGTGAAGACCGTGGAG
GACAAGTACAAGTGTGAGAAGTGCCACCTGGTGCTGTGCAGCCCCGAAGCA
GACCGAGTGTGGGCACCGCTTCTGCGAGAGCTGCATGGCGGCCCTGCTGA
GCTCTTCAAGTCCAAAATGTACAGCGTGTCAAGAGAGCATCGTTAAAGAT
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ATCTGCTGGTGCATTTAAAAAATGATTGCCATTTTGAAGAACTTCCATGT
GTGCGTCCCTGACTGCAAAGAAAAGGCTTTGAGGAAAGACCTGCGAGACCA
CGTGGAGAAGGCGTGTAAATACCGGGAAGCCACATGCAGCCACTGCAAGA
GTCAGGTTCCGATGATCGCGCTGCAGAAACACGAAGACACCGACTGTCCC
TGCGTGGTGGTGTCTTCCCTCACAAGTGCAGCGTCCAGACTCTCCTGAG
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GAAATTGAAATTGAGAGACAAAAGGAAATGCTTCGAAATAATGAATCCAA
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ATTAAAGATGATACAATTTTTTATTAAAGTCATAGTGGATACTTCCGATCT
GCCCCATCCCTGAGCGGCCGC