

Division of Signal Transduction Therapy

Clone Data Sheet

TEC [1 - 631]

Protein TEC [1 - 631]

Clone number DU 36463

Species Human

Accession number NM_003215.2

Tags N-terminal GST

**Baculovirus
expressed protein**

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTSMAIIRYIADKHNMLGGCPKERAIEISMLE
GAVLDIRYGVSR IAYS KDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY
LKSSKYIAWPLQGWQATFGGGDHPKSDLEVLVFGPLGSMNFNTILEE
ILIKRSQQKKKTSPLNYKERL FVLTKSMLTYEYEGRAEKYRKGFI DVS
KIKCVEIVKND DGVI PCQNKYPFQVVDANTLYIFAPSPQSRDLWVKK
LKEEIKNNNNIMIKYHPKFWTDGSYQCCRQTEKLAPGCEKYNLFESSI
RKALPPAPETKKRRPPPI PLEEDNSEEIVVAMYDFQAAEGHDLRLE
RGQEYLILEKNDVHWRARDKYGNEGYIPSNYVTGKKSNNLDQYEWYC
RNMNRSKAEQLLRSEDKEGGFMVRDSSQPGLYTVSLYTKFGGEGSSGF
RHYHIKETTSPKKYLAEKHAFGSIPEIEYHKHNAAGLVTRLRYPV
SVKGNAPT TAGFSYEKWEINPSELTFMRELGSGLFGVVRLGKWRAQY
KVAIKAIREGAMCEEDFIEEAKVMMKLTHPKLVQLYGVCTQOKPIYIV
TEFMERGCLLNFLRQRQGHFSRDVLLSMCQDVCEGMEYLERNSFIHRD
LAARNCLVSEAGVVKVSDFGMARYVLDDQYTSSSGAKFPVKWCPPEVF
NYSRFSSKSDVWSFGVLMWEVFTTEGRMPFEKYTNYEVVMTMVRGHRLY
QPKLASNYVVEVMLRCWQEPEGRPSFEDLLRTIDELVECEETFGR

Native sequence Amino acids M1 – R631 (end) of human TEC.

Residue M232 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage PreScission site (LEVLFQGP) residues 221 – 228

Cloning sites *Bam*H1 and *Not*1 sites of pFastBac GST

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**Nucleotide
sequence of
insert**

ggatccATGAATTTTAACTATTTTGGAGGAGATTCTTATTAAAAGG
TCACAGCAGAAAAAGAAGACATCGCCCTTAACTACAAAGAGAGACTT
TTTGTACTTACAAAGTCCATGCTAACCTACTATGAGGGTTCGAGCAGAG
AAGAAATACAGAAAGGGTTTATTGATGTTTCAAAAATCAAGTGTGTG
GAAATAGTGAAGAATGATGATGGTGTCAATCCCTGTCAAATAAGTAT
CCATTTTCAGGTTGTTTCATGATGCTAACACACTTTACATTTTTTGCACCT
AGTCCACAAAGCAGGGACCTGTGGGTGAAGAAGTTAAAAGAAGAAATA
AAGAACAACAATAATATTATGATTAAATATCATCCTAAATTTCTGGACA
GATGGAAGTTATCAGTGTGTAGACAAACTGAAAAATTAGCACCCGGA
TGTGAAAAATACAATCTTTTTGAGAGCAGTATAAGAAAAGCACTACCT
CCAGCACCAAGAAACAAAGAAGCGAAGGCCCTCCCCACCAATTCCACTA
GAAGAAGAAGATAATAGTGAAGAAATCGTTGTAGCCATGTATGATTTT
CAAGCAGCAGAAGGACATGATCTCAGATTAGAGAGAGGCCAAGAGTAT
CTCATTTTTAGAAAAGAATGATGTTTATTGGTGGAGAGCAAGAGATAAA
TATGGGAATGAAGGATATATCCCAAGTAATTACGTAACGGGAAAGAAA
TCAAACAACCTTAGATCAATATGAATGGTATTGCAGAAATATGAATAGA
AGCAAGGCAGAGCAACTCTCCGCAGTGAAGATAAAGAAGGTGGTTTTT
ATGGTAAGGGATTCCAGTCAACCAGGCTTGTACACAGTCTCCCTTTAT
ACCAAGTTTGGAGGAGAAGGTTTCATCGGGTTTTAGGCATTATCATATA
AAGGAAACAACAACATCTCAAAGAAGTATTACCTAGCTGAAAAACAT
GCTTTTGGCTCCATTCCTGAGATTATTGAATATCATAAGCACAATGCA
GCAGGACTTGTCCAGGCTTCCGGTACCCAGTTAGTGTGAAAGGGAAG
AATGCACCCACCCTGCAGGATTCAGCTATGAGAAATGGGAGATTAAC
CCTTCAGAACTGACCTTTATGAGGGAATTGGGAAGTGGACTGTTTGGGA
GTGGTGAGGCTTGGCAAATGGCGAGCCAGTACAAAGTCGCAATCAAA
GCTATTTCGGGAAGGTGCAATGTGCGAGGAGGACTTTATAGAAGAAGCT
AAAGTGATGATGAAACTGACACACCCGAAGTTAGTGCAGCTTTATGGT
GTGTGCACCCAGCAGAAACCAATATACATTGTTACTGAGTTCATGGAA
AGGGGCTGCCTTCTGAATTTCTCCGACAGAGACAAGGTCATTTTCAGT
AGAGACGTACTGCTGAGCATGTGTCAGGATGTGTGTGAAGGGATGGAG
TATCTGGAGAGAAACAGCTTCATCCACAGAGATCTGGCTGCCAGAAAT
TGTCTAGTAAGTGAGGCGGGAGTTGTAAAAGTATCTGATTTTTGGAATG
GCCAGGTATGTTCTGGATGATCAGTACACAAGTTCTTCTGGTGCCTAAG
TTTCTGTGAAGTGGTGTCCACCTGAAGTGTTTAATTACAGCCGCTTC
AGCAGCAAATCAGATGTCTGGTCATTTGGTGTTTAATGTGGGAAGTA
TTCACGGAAGGCAGAATGCCTTTTGAAAAATACACCAATTATGAAGTG
GTAACCATGGTTACTCGAGGCCACCGACTCTACCAGCCGAAGTTGGCG
TCCAACATATGTGTATGAGGTGATGCTGAGATGTTGGCAGGAGAAACCA
GAGGGAAGGCCTTCTTTTCAAGATCTGCTGCGCACAATAGATGAACCTA
GTTGAATGTGAAGAACTTTTGGGAAGAtaagcggccgc