

Standard Operating Procedure

Preparation of active MerTK [557 - 882]

Substrate:-
GGMEDIEYFMGGKKK Final concentration: 300 μM

MRC PPU Reagents and Services

Clone Data Sheet

MerTK [557 – 882]

Protein MerTK [557 – 882]

Clone number DU 47368

Species Human

Accession number NM_006343.3

Tags N-terminal GST

**Baculovirus
expressed protein**

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLE
GAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY
LKSSKYIAWPLQGWQATFGGGDHPPKSDLEVLFGQPLGSMRRAIELTL
HSLGVSEELQNKLEDVVIDRNLLILGKILGEGEFGSVMEGNLKQEDGT
SLKVAVKTMKLDNSSQREIEEFLSEAACMKDFSHPNVIRLLGVCIEMS
SQGIPKPMVILPFMKYGDHLTYLLYSRLETGPKHIPLQTLLKFMVDIA
LGMEYLSNRNFLHRDLAARNCMLRDDMTVCVADFGLSKKIYSGDYRQ
GRIAKMPVKWIAIESLADRVYTSKSDVWAFGVTMWEIATRGMPYPGV
QNHMYDYLLHGHRLKQPEDCLDELYEIMYSCWRTPDRPTFSVLRL
QLEKLLESPLDVRNQADVIVNTQLLESSE

Native sequence Amino acids R557 – E882 (end residue is M999) of human MerTK. Residue R233 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage PreScission (LEVLFQGP) residues 221 - 228

Cloning sites *Bam*H1 - *Not*I sites of pFastBac GST

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Nucleotide sequence of insert

ggatccATGCGGCGAGCCATTGAACTTACCTTACATAGCTTGGGAGTC
AGTGAGGAACTACAAAATAAACTAGAAGATGTTGTGATTGACAGGAAT
CTTCTAATTCTTGAAAAATTCTGGGTGAAGGAGAGTTTGGGTCTGTA
ATGGAAGGAAATCTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCA
GTGAAGACCATGAAGTTGGACAACCTCTCACAGCGGGAGATCGAGGAG
TTTCTCAGTGAGGCAGCGTGCATGAAAGACTTCAGCCACCCAAATGTC
ATTGACTTCTAGGTGTGTGTATAGAAATGAGCTCTCAAGGCATCCCA
AAGCCCATGGTAATTTTACCCTTCATGAAATACGGGGACCTGCATACT
TACTTACTTTATTCCCGATTGGAGACAGGACCAAAGCATATTCCTCTG
CAGACACTATTGAAGTTCATGGTGGATATTGCCCTGGGAATGGAGTAT
CTGAGCAACAGGAATTTTCTTCATCGAGATTTAGCTGCTCGAAACTGC
ATGTTGCGAGATGACATGACTGTCTGTGTTGCGGACTTCGGCCTCTCT
AAGAAGATTTACAGTGGCGATTATTACCGCCAAGGCCGCATTGCTAAG
ATGCCTGTTAAATGGATCGCCATAGAAAGTCTTGCAGACCGAGTCTAC
ACAAGTAAAAGTGATGTGTGGGCATTTGGCGTGACCATGTGGGAAATA
GCTACGCGGGGAATGACTCCCTATCCTGGGGTCCAGAACCATGAGATG
TATGACTATCTTCTCCATGGCCACAGGTGTAAGCAGCCCGAAGACTGC
CTGGATGAACTGTATGAAATAATGTACTCTTGCTGGAGAACCGATCCC
TTAGACCGCCCCACCTTTTCAGTATTGAGGCTGCAGCTAGAAAAACTC
TTAGAAAGTTTGCCTGACGTTTCGGAACCAAGCAGACGTTATTTACGTC
AATACACAGTTGCTGGAGAGCTCTGAGtgagcgggccgc