

Division of Signal Transduction Therapy

Clone Data Sheet

MAP4K1 [1 – 821]

Protein MAP4K1 [1 – 821]

Clone number DU 32902

Species Human

Accession number NM_001042600.2

Tags N-terminal GST

**Baculovirus
expressed protein**

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAETSMLEGA
VLDIRYGVSRIAYSKDFETLKVDLFLSKLPEMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS
KYIAWPLQGWQATFGGGDHPPKSDLEVLVLFQGPLGSPGIPGSTRAAAMDV
VDPDIFNRDPRDHYDLLQRLGGGTYGEVFKARDKVS GDLVALKMKVMEP
DDDVSTLQKEILILKTCRHANIVAYHGSYLWLQKLWICMEFCGAGSLQD
IYQVTGSLSELQISYVCREVLQGLAYLHSQKKIHRDIKGANILINDAGE
VRLADFGISAQIGATLARRLSFIGTPYWMAPEVA AVALKGGYNELCDIW
SLGITAIELAELOPPLFDVHPLRVLFLMTKSGYQPPRLKEKKGWSAAFH
NFIKVTTLTKSPKKRPSATKMLSHQLVVSQPGLNRGLILDLLDKLKNPGKG
PSIGDIEDEEPELPPAIPRRIRSTRSSSLGIPDADCCRRHMEFRKLRG
METRPPANTARLQPPRDLRSSSPRKQLSESSDDDDYDDVDIPTPAEDTPP
PLPPKPKFRSPSDEGPGSMGDDGQLSPGVLVRCASGPPPN SPRGPPPS
TSSPHLTAHSEPSLWNPPSRELDKPPLLPPKKEKMKRKGCALLVKLFNG
CPLRIHSTAATHPSTKDQHLLLGAEEGIFILNRNDQEATLEMLFPSRT
TWVYSINNVLM SLSGKTPHLYSHSILGLLERKETRAGNPIAHISPHRLL
ARKNMVSTKIQDTKGCRAACVAEGASSGGPFLCGALET SVVLLQWYQPM
NKFLLRQVLFPLPTPLSVFALLTGPGSELPAVCIGVSPGRPGKSVLFH
TVRFGALSCWL GEMSTEHRGPVQVTQVEEDMVMVLM DGSVKLV TPEGSP
VRGLRTP EIPMTEAVEAVAMVGGQLQAFWKHG VQVWALGSDQLLQELRD
PTLTFRLLGSPRPVVVETRPVDDPTAPSNLYIQE

Native sequence Amino acids M1 – E821 (end) of human MAP4K1.
Residue M243 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 *Not1* sites into pFastBacDual GST-2

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Nucleotide Sequence of Insert:

gcggccgcgATGGACGTCGTGGACCCTGACATTTTCAATAGAGACCCCCG
GGACCACTATGACCTGCTACAGCGGCTGGGTGGCGGCACGTATGGGGAAG
TCTTTAAGGCTCGAGACAAGGTGTCAGGGGACCTGGTGGCACTGAAGATG
GTGAAGATGGAGCCTGATGATGATGTCTCCACCCTCAGAAGGAAATCCT
CATATTGAAAACCTGCCGGCACGCCAACATCGTGGCCTACCATGGGAGTT
ATCTCTGGTTGCAGAACTCTGGATCTGCATGGAATTCTGTGGGGCTGGT
TCTCTCCAGGACATCTACCAAGTGACAGGCTCCCTGTCAGAGCTCCAGAT
TAGCTATGTCTGCCGGGAAGTGCTCCAGGGACTGGCCTATTTGCACTCAC
AGAAGAAGATACACAGGGACATCAAGGGAGCTAACATCCTCATCAATGAT
GCTGGGGAGGTGAGATTGGCTGACTTTGGCATCTCGGCCCAGATTGGGGC
TACACTGGCCAGACGCCCTCTCTTTCATTGGGACACCCACTGGATGGCTC
CGGAAGTGGCAGCTGTGGCCCTGAAGGGAGGATAACAATGAGCTGTGTGAC
ATCTGGTCCCTGGGCATCACGGCCATCGAACTGGCCGAGCTACAGCCACC
GCTCTTTGATGTGCACCCTCTCAGAGTTCTCTTCCTCATGACCAAGAGTG
GCTACCAGCCTCCCCGACTGAAGGAAAAAGGCAAATGGTTCGGCTGCCCTC
CACAACCTTCATCAAAGTCACTCTGACTAAGAGTCCCAAGAAACGACCCAG
CGCCACCAAGATGCTCAGTCATCAACTGGTATCCCAGCCTGGGCTGAATC
GAGGCCTGATCCTGGATCTTCTTGACAAACTGAAGAATCCCGGGAAAGGA
CCCTCCATTGGGGACATGAGGATGAGGAGCCCGAGCTACCCCTGCTAT
CCCTCGGCGGATCAGATCCACCCACCGCTCCAGCTCTCTGGGGATCCCAG
ATGCAGACTGCTGTTCGGCGGCACATGGAGTTCAGGAAGCTCCGAGGAATG
GAGACCAGACCCCCAGCCAACACCGCTCGCCTACAGCCTCCTCGAGACCT
CAGGAGCAGCAGCCCCAGGAAGCAACTGTCAGAGTCGTCTGACGATGACT
ATGACGACGTGGACATCCCCACCCCTGCAGAGGACACACCTCCTCCACTT
CCCCCAAGCCCAAGTTCCGTTCTCCATCAGACGAGGGTTCCTGGGAGCAT
GGGGGATGATGGGCAGCTGAGCCCCGGGGTGTGGTCCGGTGTGCCAGTG
GGCCCCACCAAACAGCCCCGTCCTGGGCCTCCCCATCCACCAGCAGC
CCCACCTCACCGCCCATTCAGAACCCTCACTCTGGAACCCACCCTCCCG
GGAGCTTGACAAGCCCCACTTCTGCCCCCCAAGAAGGAAAAGATGAAGA
GAAAGGGATGTGCCCTTCTCGTAAAGTTGTTCAATGGCTGCCCCCTCCGG
ATCCACAGCACGGCCGCCTGGACACATCCCTCCACCAAGGACCAGCACCT
GCTCCTGGGGCAGAGGAAGGCATCTTTATCCTGAACCGGAATGACCAGG
AGGCCACGCTGGAAATGCTCTTTCCTAGCCGACTACGTGGGTGTACTCC
ATCAACAACGTTCTCATGTCTCTCTCAGGAAAGACCCCCACCTGTATTC
TCATAGCATCCTTGGCCTGCTGGAACGGAAAGAGACCAGAGCAGGAAACC
CCATCGCTCACATTAGCCCCACCGCCTACTGGCAAGGAAGAACATGGTT
TCCACCAAGATCCAGGACACCAAAGGCTGCCGGGCGTGCTGTGTGGCGGA
GGGTGCGAGCTCTGGGGGCCCGTTCCCTGTGCGGTGCATTGGAGACGTCCG
TTGTCTTGCTTCAGTGGTACCAGCCATGAACAAATTCCTGCTTGTCCGG
CAGGTGCTGTTCCCACTGCCGACGCCTCTGTCCGTGTTCCGCGCTGCTGAC
CGGGCCAGGCTCTGAGCTGCCCGCTGTGTGCATCGGCGTGAGCCCCGGG
GGCCGGGGAAGTCGGTGCTCTTCCACACGGTGCCTTTGGCGCGCTCTCT
TGCTGGCTGGGCGAGATGAGCACCGAGCACAGGGGACCCGTGCAGGTGAC
CCAGGTAGAGGAAGATATGGTGATGGTGTGATGGATGGCTCTGTGAAGC
TGGTGACCCCGAGGGGTCCCCAGTCCGGGGACTTCGCACACCTGAGATC
CCCATGACCGAAGCGGTGGAGCCGTGGCTATGGTTGGAGGTCAGCTTCA
GGCCTTCTGGAAGCATGGAGTGCAGGTGTGGGCTCTAGGCTCGGATCAGC
TGCTACAGGAGCTGAGAGACCCACCCCTCACTTCCGTCTGCTTGGCTCC
CCCAGGCCTGTAGTGGTGGAGACACGCCAGTGGATGATCCTACTGCTCC
CAGCAACCTCTACATCCAGGAAtgagcggccgc

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