

Division of Signal Transduction Therapy

Clone Data Sheet

SIK1 [2 - 783]

Protein SIK1 [1 - 783]

Clone number DU 40321

Species Human

Accession number NM_17354

Tags N-terminal MBP

**Baclovirus
expressed protein**

MKIKTGARILALSALTMMFSASALAKIEEGKLVIIWINGDKGYNGLAE
VGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGY
AQSGLLAEITPDKAFQDKLYPFTWDVRYNGKLIAYPIAVEALSLIYN
KDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGG
YAFKYENKDYDIKDVGVNAGAKAGLTFLVDLIKNKHMNADTDYSIAE
AAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVL
SAGINAASPKNELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEE
LAKDPRIAATMENAQKGEIMPNI PQMSAFWYAVRTAVINAASGRQTV
EALKDAQTNSSSNNNNNNNNNNLGLEVLFOGPLGSVIMSEFSADPAGQ
GQGQKPLRVGFYDIERTLGKGNFAVVKLARHRVTKTQVAIKI IDKTR
LDSSNLEKIYREVQLMKLLNHPHI IKLYQVMETKDMLY IVTEFAKNGE
MFDYLTSHGLSENEARKKFQILSAVEYCHDHHI VHRDLKTENLLLD
GNMDIKLADFGFGNFYKSGEPLSTWCGSPPYAAPEVFEGKEYEGPQLD
IWSLGVVLYVLVCGSLPFDGPNLPTLRQRVLEGRFRIPFFMSQDCESL
IRRMLVVDPARRITIAQIRQHRWMRAEPCLPGPACPAFSAHSYTSNLG
DYDEQALGIMQTLGVDRQRTVESLQNSSYNHFAAIYYLLERLKEYRN
AQCARPGPAPRPRSSDLSGLEVPQEGLESTDPFRPALLCPQPOTLVQ
SVLQAEMDCELOSSLQWPLFFPVDASCSGVFRPRPVSPSSLLDTAISE
EARQPGLEEEQDTQESLPSSTGRRHTLAEVSTRLSPLTAPCIVVSPS
TTASPAEGTSSDSCLTFSASKSPAGLSGTPATQGLLGACSPVRLASPF
LGSQSATPVLQAQGLGGAVLLPVSFQEGRRASDTSLTQGLKAFRQQL
RKTTRTKGFLGLNKIKGLARQVCQVPASRASRGGLSPFHAPAQSPGLH
GGAAGSREGWSLLEEVLEQQRLLQLOHHPAAAPGCSQAPQAPAPFVI
APCDGPGAAPLPSTLLTSGPLLPPLLOTGASPVASAAQLLDTHLHI
GTGPTALPAVPPRLARLAPGCEPLGLLQGDCEMEDLMPCSLGTFVLV
Q

Native sequence Amino acids V2 – Q783 (end) of human SIK1.
Residue V420 of the fusion protein is equivalent to V2 of the native
enzyme. The MBP tag is located at residues 1 – 408.

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Protease cleavage PreScission site (LEVLFQGP) residues 409 – 416

Cloning sites *Bam*H1 sites of pFastBac MBP

**Nucleotide
sequence of insert**

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ggatccgttatcATGTCGGAGTTCAGCGCGGACCCCGCGGGCCAGGGT  
CAGGGCCAGCAGAAGCCCTCCGGGTGGGTTTTTACGACATCGAGCGG  
ACCCTGGGCAAAGGCAACTTCGCGGTGGTGAAGCTGGCGCGGCATCGA  
GTCACCAAACGCAGGTTGCAATAAAAATAATTGATAAAACACGATTA  
GATTCAAGCAATTTGGAGAAAATCTATCGTGAGGTTTCAGCTGATGAAG  
CTTCTGAACCATCCACACATCATAAAGCTTTACCAGGTTATGGAAACA  
AAGGACATGCTTTACATCGTCACTGAATTTGCTAAAAATGGAGAAATG  
TTTGATTATTTGACTTCCAACGGGCACCTGAGTGAGAACGAGGCGCGG  
AAGAAGTTCTGGCAAATCCTGTGCGCCGTGGAGTACTGTCACGACCAT  
CACATCGTCCACCGGGACCTCAAGACCGAGAACCTCCTGCTGGATGGC  
AACATGGACATCAAGCTGGCAGATTTTGGATTTGGGAATTTCTACAAG  
TCAGGAGAGCCTCTGTCCACGTGGTGTGGGAGCCCCCGTATGCCGCC  
CCGGAAGTCTTTGAGGGGAAGGAGTATGAAGGCCCCAGCTGGACATC  
TGGAGCCTGGGCGTGGTGTGTACGTCTGGTCTGCGGTTCTCTCCCC  
TTCGATGGGCCTAACCTGCCGACGCTGAGACAGCGGGTGTGGAGGGC  
CGCTTCCGCATCCCCTTCTTCATGTCTCAAGACTGTGAGAGCCTGATC  
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ATCCGGCAGCACCGGTGGATGCGGGCTGAGCCCTGCTTGCCGGGACCC  
GCCTGCCCCGCCTTCTCCGCACACAGCTACACCTCCAACCTGGGCGAC  
TACGATGAGCAGGCGCTGGGTATCATGCAGACCTGGGCGTGGACCGG  
CAGAGGACGGTGGAGTCACTGCAAAACAGCAGCTATAACCACTTTGCT  
GCCATTTATTACCTCCTCCTTGAGCGGCTCAAGGAGTATCGGAATGCC  
CAGTGCGCCCGCCCCGGGCTGCCAGGCAGCCGCGGCTCGGAGCTCG  
GACCTCAGTGGTTTGGAGGTGCCTCAGGAAGGTCTTTCCACCGACCT  
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CGGCCCGTGTCCCAAGCAGCCTGCTGGACACAGCCATCAGTGAGGAG  
GCCAGGCAGGGGCCGGGCTAGAGGAGGAGCAGGACACGCAGGAGTCC  
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CGCTCTCCCCACTCACCGCGCCATGTATAGTCGTCTCCCCCTCCACC  
ACGGCAAGTCCTGCAGAGGGAACCAGCTCTGACAGTTGTCTGACCTTC  
TCTGCGAGCAAAGCCCCGCGGGGCTCAGTGGCACCCCGGCCACTCAG  
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GGGTGCAGTCCGCCACCCAGTGTGCAGGCTCAGGGGGGCTTGGGA  
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AAGACCACGCGGACCAAAGGGTTTCTGGGACTGAACAAAATCAAGGGG  
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GGCCTGAGCCCCCTTCCACGCCCTGCACAGAGCCAGGCCTGCACGGC  
GGCGCAGCCGGCAGCCGGGAGGGCTGGAGCCTGCTGGAGGAGGTGCTA  
GAGCAGCAGAGGCTGCTCCAGTTACAGCACACCAGCCGCGCTGCACCC
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GGCTGCTCCCAGGCCCCCAGCCGGCCCCTGCCCCGTTTGTGATCGCC
CCCTGTGATGGCCCTGGGGCTGCCCCGCTCCCCAGCACCCCTCCTCACG
TCGGGGCTCCCGCTGCTGCCGCCCCACTCCTGCAGACCGGCGCGTCC
CCGGTGGCCTCAGCGGCGCAGCTCCTGGACACACACCTGCACATTGGC
ACCGGCCCCACCGCCCTCCCCGCTGTGCCCCACCACGCCTGGCCAGG
CTGGCCCCAGGTTGTGAGCCCCTGGGGCTGCTGCAGGGGGACTGTGAG
ATGGAGGACCTGATGCCCTGCTCCCTAGGCACGTTTGTCTCCTGGTGCAG
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