

Division of Signal Transduction Therapy

Clone Data Sheet

SIK2 [2 - 926]

Protein SIK2 [2 - 926]

Clone number DU 16624

Species Human

Accession number NM_015191.1

Tags N-terminal GST and HA

Baculovirus expressed protein MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGL
EFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLEGAVL
DIRYGVSRIAYSKDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLNGDHVTH
PDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSSKYIA
WPLOGWQATFGGGDHPKSDLEVLFOGPLGSPNSRVDYPYDVPDYAVMAD
GPRHLQRGPVVRFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQ
LDAVNLEKIYREVQIMKMLDHPHIKLYQVMETKSMLYLVTETAKNGEIF
DYLANHGRLNESEARRKFWQILSAVDYCHGRKIVHRDLKAENLLLDNNMN
IKIADFGFGNFFKSGELLATWCGSPPYAAPEVFEQOYEGPQLDIWSMGV
VLYVLVCGALPFDGPTLPILRQVLEGRFRIPIYFMSEDCEHLIRMLVLD
PSKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQVLRMH
SLGIDQOKTIESLQNKSYNHFAAIYFLLVERLKSHRSSFPVEQRLDGRQR
RPSTIAEQTVAKAQTVGLPVTMHSNMRLLSALLPQASNVEAFSFPASG
CQAEAAFMEEECVDTPKVNGCLLDPVPPVLRKGCQSLPSNMETSIDEG
LETEGEAEEDPAHAFAEFQSTRSGORRHTLSEVTNQLVMPGAGKIFSMN
DSPSLDSVDSEYDMGSVQRDLNLFLEDNPSLKDIMLANQPSPRMTSPFISL
RPTNPAMQALSSQKREVHNRSPVSVFREGRRASDTSLTQGIVAFROHLQNL
ARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLODLASSCPQEEVSQQQ
ESVSTLPASVHPQLSPRQSLQYLOHRLQKPSLLSKAQNTCQLYCKEPP
RSLEQQLQEHRLQKRLFLQKQSQLOAYFNQMQIAESSYPQPSQQLPLPR
QETPPPSQQAPPFSLTQPLSPVLEPSSEOMQYSPFLSQYQEMQLOPLPST
SGPRAAPPLPTQLQQQQPPPPPPPPPPRQPGAAPAPLQFSYQTCELPSAA
SPAPDYPTPCQYPVDGAQQSDLTGPDCPRSPGLQEAPSSYDPLALSELPG
LFDCEMLDAVDPQHNGYVLVN

Native sequence Amino acids V2 – N926 (end) of human SIK2.
Residue V247 of the fusion protein is equivalent to V2 of the native enzyme. The GST tag is located at residues 1 – 220 and the HA tag is located at residues 238 – 246.

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Protease cleavage PreScission (LEVLFQGP) residues 221 - 229

Cloning sites *Sal1* and *Not1* sites in pFastBAC GST

Nucleotide sequence of insert gtcgactaccatac gatgtgccagattacgccGTCATGGCGGATGGCCC
GAGGCACTTGCAGCGCGGGCCGGTCCGGGTGGGGTTCTACGACATCGAGG
GCACGCTGGGCAAGGGCAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGG
ATCACCAAGACGGAGGTGGCAATAAAAAATAATCGATAAGTCTCAGCTGGA
TGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACAAATAATGAAAATGT
TAGACCACCCTCACATAATCAAACCTTATCAGGTAATGGAGACCAAAAGT
ATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAATTTTTGACTA
TCTTGCTAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATTTCT
GGCAAATCCTGTCTGCTGTTGATTATTGTCATGGTCGGAAGATTGTGCAC
CGTGACCTCAAAGCTGAAAATCTCCTGCTGGATAACAACATGAATATCAA
AATAGCAGATTTTCGGTTTTGGAAATTTCTTTAAAAGTGGTGAAGTCTGG
CAACATGGTGTGGCAGCCCCCTTATGCAGCCCCAGAAGTCTTTGAAGGG
CAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCT
TTATGTCCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAA
TTTTGAGGCAGAGGGTTCTGGAAGGAAGATTCCGGATTCGGTATTTTCATG
TCAGAAGATTGCGAGCACCTTATCCGAAGGATGTTGGTCCTAGACCCATC
CAAACGGCTAACCATAGCCCCAAATCAAGGAGCATAAATGGATGCTCATAG
AAGTTCCGTGCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAATGAG
CCATCCATCGGGGAGTTAATGAGCAGGTTCTGCGACTGATGCACAGCCT
TGGAATAGATCAGCAGAAAACCATTTGAGTCTTTGCAGAACAAGAGCTATA
ACCACTTTGCTGCCATTTATTTCTTGTGGTGGAGCGCCTGAAATCACAT
CGGAGCAGTTTCCAGTGGAGCAGAGACTTGATGGCCGCCAGCGTCCGGCC
TAGCACCATTGCTGAGCAAACAGTTGCCAAGGCACAGACTGTGGGGCTCC
CAGTGACCATGCATTCACCGAACATGAGGCTGCTGCGATCTGCCCTCCTC
CCCCAGGCATCCAACGTGGAGGCCTTTTCATTTCCAGCATCTGGCTGTCA
GGCGGAAGCTGCATTCATGGAAGAAGAGTGTGTGGACACTCCAAAGGTCA
ATGGCTGTCTGCTTGACCCTGTGCCTCCTGTCTGGTGCAGGAGGGATGC
CAGTCACTGCCCAGCAACATGATGGAGACCTCCATTGACGAAGGGCTGGA
GACAGAAGGAGAGGGCCGAGGAAGACCCCGCTCATGCCTTTGAGGCATTTT
AGTCCACACGCAGCGGGCAGAGACGGCACACTCTGTGAGAAGTGACCAAT
CAACTGGTCGTGATGCC TGGGGCAGGGAAAATTTTCTCCATGAATGACAG
CCCCTCCCTTGACAGTGTGGACTCTGAGTATGATATGGGGTCTGTTTCAGA
GGGACCTGAACTTTCTGGAAGACAACCCTTCCCTTAAGGACATCATGTTA
GCCAATCAGCCTTCACCCCGCATGACATCTCCCTTCATAAGCCTGAGACC
TACCAACCCAGCCATGCAGGCTCTGAGCTCCCAGAAAACGAGAGGTCCACA
ACAGGTCTCCAGTGAGCTTTCAGAGAGGGCCGCAGAGCATCAGATACCTCC
CTCACCCAGGGAATTGTAGCATTTAGACAACATCTTCAGAATCTGGCTAG
AACCAAAGGAATTCTAGAGTTGAACAAAGTGCAGTTGTTGTATGAACAAA
TAGGACCGGAGGCAGACCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAG
GACCTTGCTAGCAGCTGCCCTCAGGAAGAAGTTTCTCAGCAGCAGGAAAG
CGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCTGTCCCCACGGCAGA
GCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCAGCCTTCTG
TCAAAGGCCCAGAACACCTGTCAGCTTTATTGCAAAGAACCACCGCGGAG

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CCTTGAGCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTC
TTCAGAAGCAGTCTCAACTGCAGGCCTATTTTAATCAGATGCAGATAGCA
GAGAGCTCCTACCCACAGCCAAGTCAGCAGCTGCCCTTCCCCGCCAGGA
GACTCCACCGCCTTCTCAGCAGGCCCCACCGTTCAGCCTGACCCAGCCCC
TGAGCCCCGTCTGGAGCCTTCCTCCGAGCAGATGCAATACAGCCCTTTC
CTCAGCCAGTACCAAGAGATGCAGCTTCAGCCCCTGCCCTCCACTCCGG
TCCCCGGGCTGCTCCTCCTCTGCCACGCAGCTACAGCAGCAGCAGCCGC
CACCGCCACCACCCCTCCACCACCACGACAGCCAGGAGCTGCCCCAGCC
CCCTTACAGTTCCTATCAGACTTGTGAGCTGCCAAGCGCTGCTTCCCC
TGCGCCAGACTATCCCACTCCCTGTCAGTATCCTGTGGATGGAGCCAGC
AGAGCGACCTAACGGGGCCAGACTGTCCCAGAAGCCCAGGACTGCAAGAG
GCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTT
TGATTGTGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCC
TGGTGAATtagcggccgc