

Division of Signal Transduction Therapy

Clone Data Sheet

IRAK1 [1 - 712]

Protein IRAK1 [1 - 712]

Clone number DU 8915

Species Human

Accession number NM_001569.3

Tags N-terminal His(6)

Baculovirus expressed protein

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELG
LEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAETSMLEGA
VLDIRYGVSR IAYS KDFETLKVDFLSKLP EMLKMFEDRLCHKTYLNGDH
VTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKYLKSS
KYIAWPLQGWQATFGGGDHPPKSDLEVLFOGPLGSPGIPGSTRAAAMAG
GPGGPEPAAPGAQHFLYEVPWVMCRFYKVMDALEPADWCQFAALIVRD
QTELRLCERSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIITA
WHPPAPLPSPGTTAPRPSSIAPAEAEAWSPRKLPSASTFLSPAFP GS
QTHSGPELGLVPSASLWPPPPSPAPSS TKPGPESSVSLLOGARPF PFC
WPLCEISRGT HNFSEELKIGEGGF GCVYRAVMRNTVYAVKRLKENADLE
WTAVKQSF LTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLE
DRLHCQTQAC PPLSWPQRDILLGTARAIQFLHQDSPSLIHGD IKSSNV
LLDERLTPKLGDFGLARFSRFAGSSPSQSSMVAR TQTVRGTLAYLPEEY
IKTGRLAVD TDTSFGVVVLETLAQRAVKTHGARTKYLKDLVEEEAEE
AGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDPRPGPCPPELGLGL
GQLACCC LHRRAKRRPMTQVYERLEKLQAVVAGVPGHWEAASCIP PPS
QENSYVSSTGRAHSGAAPWQPLAAPSGASAQAAEQ LQRGPNQPVE SDES
LGGLSAALRSWHLTPSCPLDPAPLREAGCPQGD TAGESSWGSGPGSRPT
AVEGLALGSSASSSSEPPQIIINPARQK MVQKLALYEDGALDSLQL LSS
SSLPGLGLEQDRQGPEESDEFQS

Native sequence Amino acids M1 – S712 (end) of human IRAK1.
Residue M1 of the fusion protein is equivalent to M243 of the native enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage PreScission (LEVLFOGP) residues 221 - 229

Cloning sites *Not1* sites in pFastBAC GST

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**Nucleotide
sequence of insert**

gcggccgcgATGGCCGGGGGGCCGGGCCCGGGGAGCCCGCAGCCCCCG
GCGCCAGCACTTCTTGTACGAGGTGCCGCCCTGGGTCATGTGCCGCTT
CTACAAAGTGATGGACGCCCTGGAGCCCGCCGACTGGTGCCAGTTCGCC
GCCCTGATCGTGCGGACCAGACCGAGCTGCGGCTGTGCGAGCGCTCCG
GGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCG
TGTGGCCGACCTGGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCG
CGGGACATCATCACAGCCTGGCACCCCTCCCGCCCCGCTTCCGTCCCCAG
GCACCACTGCCCCGAGGCCAGCAGCATCCCTGCACCCGCCGAGGCCGA
GGCCTGGAGCCCCCGAAGTTGCCATCCTCAGCCTCCACCTTCTCTCC
CCAGCTTTTCCAGGCTCCCAGACCCATTCAGGGCCTGAGCTCGGCCTGG
TCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCCCTT
TTCTACCAAGCCAGGCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCC
CGCCCCCTTCCGTTTTGCTGGCCCCTCTGTGAGATTTCCCGGGCACCC
ACAACCTTCTCGGAGGAGCTCAAGATCGGGGAGGGTGGCTTTGGGTGCGT
GTACCGGGCGGTGATGAGGAACACGGTGTATGCTGTGAAGAGGCTGAAG
GAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCCTGACCG
AGGTGGAGCAGCTGTCCAGGTTTCGTACCCAAACATTGTGGACTTTGC
TGGCTACTGTGCTCAGAACGGCTTCTACTGCCTGGTGTACGGCTTCCCTG
CCCAACGGCTCCCTGGAGGACCGTCTCCACTGCCAGACCCAGGCCTGCC
CACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTGGGTACAGCCCG
GGCAATTCAGTTTCTACATCAGGACAGCCCCAGCCTCATCCATGGAGAC
ATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGCACCCCAAGCTGG
GAGACTTTGGCCTGGCCCGGTTTCAGCCGCTTTGCCGGGTCCAGCCCCAG
CCAGAGCAGCATGGTGGCCCGGACACAGACAGTGCGGGGCACCCCTGGCC
TACCTGCCCCGAGGAGTACATCAAGACGGGAAGGCTGGCTGTGGACACGG
ACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGCTGGTTCAGAG
GGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGAAAGACCTGGTG
GAAGAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGCA
CACTGCAAGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCAT
GCAGATCTACAAGAAGCACCTGGACCCAGGCCCGGGCCCTGCCACCT
GAGCTGGGCCTGGGCCTGGGCCAGCTGGCCTGCTGCTGCCTGCACCGCC
GGGCCAAAAGGAGGCCTCCTATGACCCAGGTGTACGAGAGGCTAGAGAA
GCTGCAGGCAGTGGTGGCGGGGGTGCCCGGGCATTGGGAGGCCGCCAGC
TGCATCCCCCCTTCCCCGCAGGAGAACTCCTACGTGTCCAGCACTGGCA
GAGCCACAGTGGGGCTGCTCCATGGCAGCCCCCTGGCAGCGCCATCAGG
AGCCAGTGCCAGGCAGCAGAGCAGCTGCAGAGAGGCCCCCAACCAGCCC
GTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGCCCTGCGCTCCT
GGCACTTGACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGC
CGGCTGTCTCAGGGGGACACGGCAGGAGAATCGAGCTGGGGGAGTGGC
CCAGGATCCCGGCCACAGCCGTGGAAGGACTGGCCCTTGGCAGCTCTG
CATCATCGTCGTCAGAGCCACCGCAGATTATCATCAACCCTGCCCGACA
GAAGATGGTCCAGAAGCTGGCCCTGTACGAGGATGGGGCCCTGGACAGC
CTGCAGCTGCTGTGTCAGCTCCCTCCAGGCTTGGGCCTGGAACAGG
ACAGGCAGGGGCCCGAAGAAAGTGATGAATTTAGAGCtgagcggccgc