

Division of Signal Transduction Therapy

Clone Data Sheet

CSK [1 - 450]

Protein CSK [1 - 450]

Clone number DU 1500

Species Human

Accession number NM_004383.2

Tags N-terminal GST

**Bacterially
expressed protein**

MSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFEL
GLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNMLGGCPKERAIEISMLE
GAVLDIRYGVSR IAYS KDFETLKVDFLSKLPPEMLKMFEDRLCHKTYLN
GDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPOIDKY
LKSSKYIAWPLQGWQATFGGGDHPKSDLVPRGSMSAI**QAAWPSGTEC**
IAKYNFHGTAEQDLPFCKGDVLTIVAVTKDPNWKAKNKVGREGIIPA
NYVQKREGVKAGTKLSLMPWFHGKITREQAERLLYPPETGLFLVREST
NYPGDYTL CVSCDGKVEHYRIMYHASKLSIDEEVYFENLMQLVEHYTS
DADGLCTRLIKPKVMEGTVAQAQDEFYRSGWALNMKELKLLQTIKGEF
GDVMLGDYRGNKVAVKCIKNDATAQAFLAEASVMTQLRHSNLVQLLGV
IVEEKGLYIVTEYMAKGS LVDYLRSRGRSVLGGDCLLKFSLDVCEAM
EYLEGNNFVHRDLAARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPV
KWTAPEALREKKFSTKSDVVSFGILLWEIYSFGRVPYPRIPKDVVPR
VEKGYKMDAPDGCPPAVYEV MKNCWHLDAAMRPSFLQLREOLEHIKTH
ELHL

Native sequence Amino acids M1 – L450 (end) of human CSK.

Residue M227 of the fusion protein is equivalent to M1 of the native enzyme. The GST tag is located at residues 1 – 220.

Protease cleavage Thrombin site (LVPRGS) residues 221 – 226

Cloning sites *Bam*H1 sites of pGex4T1

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**Nucleotide
sequence of
insert**

ggatccATGTCAGCAATACAGGCCGCCTGGCCATCCGGTACAGAATGT
ATTGCCAAGTACAACCTCCACGGCACTGCCGAGCAGGACCTGCCCTTC
TGCAAAGGAGACGTGCTCACCATTGTGGCCGTCACCAAGGACCCCAAC
TGGTACAAAGCCAAAAACAAGGTGGGCCGTGAGGGCATCATCCCAGCC
AACTACGTCCAGAAGCGGGAGGGCGTGAAGGCGGGTACCAAACCTCAGC
CTCATGCCTTGGTTCCACGGCAAGATCACACGGGAGCAGGCTGAGCGG
CTTCTGTACCCGCCGGAGACAGGCCTGTTCCCTGGTGCGGGAGAGCACC
AACTACCCCGGAGACTACACGCTGTGCGTGAGCTGCGACGGCAAGGTG
GAGCACTACCGCATCATGTACCATGCCAGCAAGCTCAGCATCGACGAG
GAGGTGTACTTTGAGAACCTCATGCAGCTGGTGGAGCACTACACCTCA
GACGCAGATGGACTCTGTACGCGCCTCATTA AACCAAAGGTCATGGAG
GGCACAGTGGCGGCCAGGATGAGTTCTACCGCAGCGGCTGGGCCCTG
AACATGAAGGAGCTGAAGCTGCTGCAGACCATCGGGAAGGGGGAGTTC
GGAGACGTGATGCTGGGCGATTACCGAGGGAACAAAGTCGCCGTCAAG
TGCATTAAGAACGACGCCACTGCCCAGGCCTTCTGGCTGAAGCCTCA
GTCATGACGCAACTGCGGCATAGCAACCTGGTGCAGCTCCTGGGCGTG
ATCGTGGAGGAGAAGGGCGGGCTCTACATCGTCACTGAGTACATGGCC
AAGGGGAGCCTTGTGGACTACCTGCGGTCTAGGGGTCGGTCAGTGCTG
GGCGGAGACTGTCTCCTCAAGTTCTCGCTAGATGTCTGCGAGGCCATG
GAATACCTGGAGGGCAACAATTTTCGTGCATCGAGACCTGGCTGCCCGC
AATGTGCTGGTGTCTGAGGACAACGTGGCCAAGGTCAGCGACTTTGGT
CTCACCAAGGAGGCGTCCAGCACCCAGGACACGGGCAAGCTGCCAGTC
AAGTGGACAGCCCCTGAGGCCCTGAGAGAGAAGAAATCTCCACTAAG
TCTGACGTGTGGAGTTTCGGAATCCTTCTCTGGGAAATCTACTCCTTT
GGGCGAGTGCCTTATCCAAGAATTCCCCTGAAGGACGTCGTCCCTCGG
GTGGAGAAGGGCTACAAGATGGATGCCCCCGACGGCTGCCCGCCCGCA
GTCTATGAAGTCATGAAGA ACTGCTGGCACCTGGACGCCGCCATGCGG
CCCTCCTTCTACAGCTCCGAGAGCAGCTTGAGCACATCAAACCCAC
GAGCTGCACCTGTGACGGCTGGCCTCCGCCTGGGTCATGGGCCTGTGG
GGACTgaacctggaagatcatggacggatcc