

Specific activity range:- To be determined

Division of Signal Transduction Therapy

Clone Data Sheet

SYK [1- 635]

Protein SYK [1 - 635]

Clone number DU 8829

Species Human

Accession number AAH01645.1

Tags N-terminal His(6)

**Baculovirus
expressed
protein**

MSYYHHHHHHHDYDIPTTENLYFQGAMGSMASGSMADSANHLPFFFGNIT
REEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHYTIEREL
NGTYAIAAGGRTHASPADLCHYHSQESDGLVCLLKPPFNRPOGVQPKTGP
FEDLKENLIREYVKQTWNLQGOALEQAIISQKPQLEKLIATTAHEKMPW
FHGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALCLLHEGKVLHYR
IDKDKTGKLSIPEGKKFDTLWQLVEHYSYKADGLLRVLTVPCKIGTQG
NVNFGGRPQLPGSHPATWSAGGIISRIKSYSFPKPGHRKSSPAQGNRQE
STVSFNPYEPPELAPWAADKGPQREALPMDTEVYESPYADPEEIRPKEVY
LDRKLLTLEDKELGSGNFGTVKKGYIQMKKVVKTVAVKILKNEANDPAL
KDELLAEANVMQQLDNPYIVRMIGICEAESWMLVMAELGPLNKYLQQ
NRHVKDKNIIELVHQVSMGMKYLEESNFFVHRDLAARNVLLVTQHYAKIS
DFGLSKALRADENYYKAQTHGKWPVKWYAPECINYYKFSSKSDVWSFGV
LMWEAFSYGQKPYRGMKGSEVTAMLEKGERMGCPAGCPREMYDLMNLCW
TYDVENRPGFAAVELRLRNYYYDVVN

Native sequence Amino acids M1 – N635 (end) of human SYK.
Residue M29 of the fusion protein is equivalent to M1 of the native
enzyme. The His(6) tag is located at residues 5 – 10.

Protease cleavage rTEV (ENLYFQG) residues 18 - 24

Cloning sites *Bam*H1 and *Not*I sites of pFastBAC HTb

Division of Signal Transduction Therapy

Nucleotide

Sequence of insert

ggatccATGGCCAGCAGCGGCATGGCTGACAGCGCCAACCACCTGCCCT
TCTTTTTTCGGCAACATCACCCGGGAGGAGGCAGAAGATTACCTGGTCCA
GGGGGGCATGAGTGATGGGCTTTATTTGCTGCGCCAGAGCCGCAACTAC
CTGGGTGGCTTCGCCCTGTCCGTGGCCACGGGAGGAAGGCACACCACT
ACACCATCGAGCGGGAGCTGAATGGCACCTACGCCATCGCCGGTGGCAG
GACCCATGCCAGCCCCGCCGACCTCTGCCACTACCACTCCCAGGAGTCT
GATGGCCTGGTCTGCCTCCTCAAGAAGCCCTTCAACCGGCCCAAGGGG
TGCAGCCCAAGACTGGGCCCTTTGAGGATTTGAAGGAAAACCTCATCAG
GGAATATGTGAAGCAGACATGGAACCTGCAGGGTCAGGCTCTGGAGCAG
GCCATCATCAGTCAGAAGCCTCAGCTGGAGAAGCTGATCGCTACCACAG
CCCATGAAAAAATGCCTTGGTTCCATGGAAAAATCTCTCGGGAAGAATC
TGAGCAAATTGTCCTGATAGGATCAAAGACAAATGGAAAGTTCTTGATC
CGAGCCAGAGACAACAACGGCTCCTACGCCCTGTGCCTGCTGCACGAAG
GGAAGGTGCTGCACTATCGCATCGACAAAGACAAGACAGGGAAGCTCTC
CATCCCCGAGGGAAAGAAGTTCGACACGCTCTGGCAGCTAGTCGAGCAT
TATTCTTATAAAGCAGATGGTTTGTTAAGAGTTCTTACTGTCCCATGTC
AAAAAATCGGCACACAGGGAAATGTTAATTTTGGAGGCCGTCCACAAC
TCCAGGTTCCCATCCTGCGACTTGGTCAGCGGGTGGAAATAATCTCAAGA
ATCAAATCATACTCCTTCCCAAAGCCTGGCCACAGAAAGTCTCCCCCTG
CCCAAGGGAACCGGCAAGAGAGTACTGTGTCAATTCAATCCGTATGAGCC
AGAACTTGCAACCCTGGGCTGCAGACAAAGGCCCCCAGAGAGAAGCCCTA
CCCATGGACACAGAGGTGTACGAGAGCCCCTACGCGGACCCTGAGGAGA
TCAGGCCCAGGAGGTTTACCTGGACCGAAAGCTGCTGACGCTGGAAGA
CAAAGAAGTGGGCTCTGGTAATTTTGGAACTGTGAAAAAGGGCTACTAC
CAAATGAAAAAAGTTGTGAAAACCGTGGCTGTGAAAATACTGAAAAACG
AGGCCAATGACCCCGCTCTTAAAGATGAGTTATTAGCAGAAGCAAATGT
CATGCAGCAGCTGGACAACCCGTACATCGTGCGCATGATCGGGATATGC
GAGGCCGAGTCCTGGATGCTAGTTATGGAGATGGCAGAACTTGGTCCCC
TCAATAAGTATTTGCAGCAGAACAGACATGTCAAGGATAAGAACATCAT
AGAAGTGGTTCATCAGGTTTCCATGGGCATGAAGTACTTGGAGGAGAGC
AATTTTGTGCACAGAGATCTGGCTGCAAGAAATGTGTTGCTAGTTACCC
AACATTATGCCAAGATCAGTGATTTTCGGACTCTCCAAAGCACTGCGTGC
TGATGAAAACTACTACAAGGCCAGACCCATGGAAAGTGGCCTGTCAAG
TGGTACGCTCCGGAATGCATCAACTACTACAAGTTCTCCAGCAAAAGCG
ATGTCTGGAGCTTTGGAGTGTGATGTGGGAAGCATTCTCCTATGGGCA
GAAGCCATATCGAGGGATGAAAGGAAGTGAAGTACCGCTATGTTAGAG
AAAGGAGAGCGGATGGGGTGCCCTGCAGGGTGTCCAAGAGAGATGTACG
ATCTCATGAATCTGTGCTGGACATACGATGTGGAAAAACAGGCCCGGATT
CGCAGCAGTGGAAGTGC GGCTGCGCAATTACTACTATGACGTGGTGAAC
taagcggccgc