

Product datasheet for **SC323420**

SYK (NM_003177) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	SYK (NM_003177) Human Untagged Clone
Tag:	Tag Free
Symbol:	SYK
Synonyms:	IMD82; p72-Syk
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)



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Fully Sequenced ORF: >OriGene ORF within SC323420 sequence for NM_003177 edited (data generated by NextGen Sequencing)

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ATGGCCAGCAGCGGCATGGCTGACAGCGCCAACCACTGCCCTTCTTTTTCGGCAACATC
ACCCGGGAGGAGGCAGAAAGATTACCTGGTCCAGGGGGCATGAGTGATGGGCTTTATTTG
CTGCGCCAGAGCCGCAACTACCTGGGTGGCTTCGCCCTGTCCGTGGCCCACGGGAGGAAG
GCACACCACTACACCATCGAGCGGGAGCTGAATGGCACCTACGCCATCGCCGGTGGCAGG
ACCCATGCCAGCCCCGACCTCTGCCACTACCACTCCCAGGAGTCTGATGGCCTGGTC
TGCCCTCCTCAAGAAGCCCTTCAACCGGCCCAAGGGGTGCAGCCAAGACTGGGCCCTTT
GAGGATTTGAAGGAAAACCTCATCAGGGAATATGTGAAGCAGACATGGAACCTGCAGGT
CAGGCTCTGGAGCAGGCCATCATCAGTCAGAAGCCTCAGCTGGAGAAGCTGATCGCTACC
ACAGCCCATGAAAAAATGCCTTGGTTCCATGAAAAAATCTCTCGGAAGAATCTGAGCAA
ATTGCTCTGATAGGATCAAAGACAAATGGAAAGTTCTGATCCGAGCCAGAGACAACAAC
GGCTCCTACGCCCTGTGCCTGCTGCACGAAGGGAAGGTGCTGACTATCGCATCGACAAA
GACAAGACAGGGAAGCTCTCCATCCCCGAGGAAAGAAGTTCGACACGCTCTGGCAGCTA
GTCGAGCATTATTCTTATAAAGCAGATGGTTTGTAAAGAGTTCTTACTGTCCCATGTCAA
AAAATCGGCACACAGGGAATGTTAATTTTGGAGGCCGTCCACAACCTCCAGTTCCCAT
CCTGCGACTTGGTCAGCGGGTGAATAATCTCAAGAATCAAATCATACTCTCCCAAAG
CCTGGCCACAGAAAGTCTCCCTGCCCAAGGGAACCGGCAAGAGAGTACTGTGTCATTC
AATCCGTATGAGCCAGAACTTGCACCCTGGGCTGCAGACAAGGCCCCAGAGAGAAGCC
CTACCCATGGACACAGAGGTGTACGAGAGCCCCCTACGCGGACCCCGAGGAGATCAGGCC
AAGGAGGTTTACCTGGACCGAAAGCTGCTGACGCTGGAAGACAAGAAGTGGGCTCTGGT
AATTTTGGAACTGTAAAAAGGGCTACTACCAAATGAAAAAGTTGTGAAAACCGTGGCT
GTGATGATACTGAAAAACGAGGCCAATGACCCCGCTCTTAAAGATGAGTTATTAGCAGAA
GCAAATGTCATGCAGCAGCTGGACAACCCGTACATCGTGCAGGATGATCGGGATATGCGAG
GCCGAGTCTGGATGCTGGTTATGGAGATGGCAGAACTGGTCCCCTCAATAAGTATTTG
CAGCAGAACAGACATGTCAAGGATAAGAACATCATAGAAGTGGTTCATCAGGTTTCCATG
GGCATGAAGTACTTGGAGGAGAGCAATTTTGTGCACAGAGATCTGGTGCAGAAATGTG
TTGCTAGTTACCCAACATTACGCCAAGATCAGTGATTTCCGACTTTCCAAAGCACTGCGT
GCTGATGAAAACACTACAAGGCCAGACCCATGGAAAGTGGCCTGTCAAGTGGTACGCT
CCGGAATGCATCAACTACTACAAGTTCTCCAGCAAAGCGATGTCTGGAGCTTTGGAGTG
TTGATGTGGGAAGCATTCTCCTATGGGCAGAAGCCATATCGAGGGATGAAAGGAAGTGAA
GTCACCGCTATGTTAGAGAAAGGAGAGCGGATGGGGTGCCTGCAGGGTGTCCAAGAGAG
ATGTACGATCTCATGAATCTGTGCTGGACATACGATGTGAAAAACAGGCCCGGATTCCGA
GCAGTGGAACTGCGGCTGCGCAATTACTACTATGACGTGGTGAACATA
    
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Clone variation with respect to NM_003177.5
 1205 a=>t;1206 a=>g

5' Read Nucleotide Sequence:

>OriGene 5' read for mutant NM_003177 unedited

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ACCGCCCGTCTGAGCAACGGGCGGTAGGCGCTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGT
GAACCGTCAGAAATTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGGCACGAGGCGGGAAACGAC
GCGCTGCTTTTCATGCCCTTCTTGTCTACCTTCATCGGCCGAGGTAAAAGTGTGAAACCATGTGAATA
AAATACAGGTGGACACCTGCGCAGGTGTGTGCCCTCCGGCCCCTGAAGCATGGCCAGCAGCGGCATGGCT
GACAGCGCAACCACTGCCCTTCTTTTTCTGCAACATCACCCCGGGAGGAGGCATAAGATTACCTGGGT
GGAGGTGGGGCATGAGTGATGGGCTTAATTAGGTTCCCCATAAGCCGGAATTCACAGTGGGGGGGAGGC
GGGGGCTCCGGCCGAAAGAGGGGGCCTGCCATTCCCTGCCGTGGCTTAAATTTTGGGGGGGAGGGTC
CGGAGAA
    
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Kinase Domain Sequence:	>SC323420 kinase domain raw sequence. By performing BLASTX analysis with this sequence against NCBI reference protein database, you can confirm the presence of the kinase-deficient mutation GACTGGGCTCTGGTATTTTGGACTGTGAAAAGGGCTACTACCAAATGAAAAAGTTGTGAAAACCGTGGC TGTGATGATACTGAAAAACGAGGCCAATGACCCCGCTCTTAAAGATGAGTTATTAGCAGAAGCAAATGTC ATGCAGCAGCTGGACAACCCGTACATCGTGC GGATGATCGGGATATGCGAGGCCGAGTCTGGATGCTGG TTATGGAGATGGCAGAACTTGGTCCCCTCAATAAGTATTTGCAGC
Restriction Sites:	Please inquire
ACCN:	NM_003177
Insert Size:	2660 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
OTI Annotation:	This kinase-deficient mutant clone was generated by created by site-directed mutagenesis from the corresponding wild-type clone. See details in "Application of active and kinase-deficient kinome collection for identification of kinases regulating hedgehog signaling." Cell. 2008 May p536-548.
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	<ol style="list-style-type: none">1. Centrifuge at 5,000xg for 5min.2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.3. Close the tube and incubate for 10 minutes at room temperature.4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	NM_003177.3 , NP_003168.2
RefSeq Size:	2672 bp
RefSeq ORF:	1908 bp
Locus ID:	6850
UniProt ID:	P43405
Cytogenetics:	9q22.2
Domains:	pkinase, SH2, TyrKc, S_TKc
Protein Families:	Druggable Genome, Protein Kinase
Protein Pathways:	B cell receptor signaling pathway, Fc epsilon RI signaling pathway, Fc gamma R-mediated phagocytosis, Natural killer cell mediated cytotoxicity

Gene Summary:

This gene encodes a member of the family of non-receptor type Tyr protein kinases. This protein is widely expressed in hematopoietic cells and is involved in coupling activated immunoreceptors to downstream signaling events that mediate diverse cellular responses, including proliferation, differentiation, and phagocytosis. It is thought to be a modulator of epithelial cell growth and a potential tumour suppressor in human breast carcinomas.

Alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Mar 2010]

Transcript Variant: This variant (1) represents the longest transcript and encodes the longer isoform (Syk(L)). Both variants 1 and 3 encode the same isoform. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.