

Product datasheet for **MC226959**

Zap70 (NM_001289612) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Zap70 (NM_001289612) Mouse Untagged Clone
Tag: Tag Free
Symbol: Zap70
Synonyms: mrtle; mur; S; Srk; ZAP-; ZAP-70
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC226959 representing NM_001289612
Red=Cloning site **Blue**=ORF **Orange**=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**GCGATCGCC**

ATGCCCATGGACACAAGTGTGTACGAGAGTCCCTACAGCGACCCTGAGGAACTCAAAGACAAGAAGCTCT
TCCTGAAGCGAGAGAATCTCCTCGTGGCGGACATCGAGCTTGGCTGTGGCACTTTGGCTCCGTGCGCCA
GGGAGTCTATCGCATGCGCAAGAAGCAGATTGACGTGGCCATCAAGGTGCTGAAGCAGGGCACAGAGAAG
GCCGACAAAGATGAGATGATGCGAGAGGCCAGATCATGCACCAGCTCGACAACCCTACATCGTGCGGC
TCATCGGCGTGTGCCAGGCAGAAGCACTCATGCTGGTCATGGAGATGGCGGGAGGCGGGCCCTGCACAA
GTTCTGCTGGGAAAGAAGGAGGAGATCCCTGTGAGCAATGTGGCTGAACTGCTGCACCAGGTGGCCATG
GGCATGAAGTATTTGGAGGAGAAAACTTTGTGCACCGCGACCTGGCAGCCCGCAATGTTCTACTGGTCA
ATCGGCACTATGCCAAGATCAGCGACTTTGGCCTGTCCAAAGCCCTGGGTGCTGACGACAGCTATTACAC
AGCCCGGTCTGCAGGGAAGTGGCCTCTGAAGTGGTACGCGCCAGAGTGCATCAACTTTCGGAAGTTCTCC
AGCCGCAGTGACGTCTGGAGCTATGGGGTACCATGTGGGAGGCCTTCTCCTATGGCCAGAAGCCCTACA
AGAAAATGAAGGGCCCCGAGGTCTGGACTTCATCAAGCAGGGTAAGAGGATGGAATGTCCGCGGAGTG
TCCTCCTGAGATGTATGCACTTATGAGTGACTGCTGGATCTACAAGTGGGAGGATCGCCCCGACTTCTCG
ACTGTGGAACAACGTATGCGGAACTATTACTACAGCCTGGCCAGCCGGGCGGAGGACCCCCACAGTGTG
AACAGGTGGCCGAGGCTGCATGTGG**TGA**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001289612
Insert Size: 939 bp



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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:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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_001289612.1 , NP_001276541.1
RefSeq Size:	1343 bp
RefSeq ORF:	939 bp
Locus ID:	22637
UniProt ID:	P43404
Cytogenetics:	1 15.41 cM
Gene Summary:	<p>This gene encodes a member of the protein tyrosine kinase family. The encoded protein is essential for development of T lymphocytes and thymocytes, and functions in the initial step of T lymphocyte receptor-mediated signal transduction. A mutation in this gene causes chronic autoimmune arthritis, similar to rheumatoid arthritis in humans. Mice lacking this gene are deficient in alpha-beta T lymphocytes in the thymus. In humans, mutations in this gene cause selective T-cell defect, a severe combined immunodeficiency disease characterized by a selective absence of CD8-positive T lymphocytes. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jan 2014]</p> <p>Transcript Variant: This variant (2) contains a 5' terminal exon that extends past a splice site that is used in variant 1. This variant differs in the 5' UTR, lacks a portion of the 5' coding region and initiates translation at a downstream start codon compared to variant 4. The encoded isoform (TZK, also known as truncated ZAP kinase; PMID 14985102) has a shorter N-terminus compared to isoform b. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p>