

Product datasheet for **MC229096**

Tyro3 (NM_001290800) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Tyro3 (NM_001290800) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Tyro3
Synonyms:	A1323366; Brt; Dtk; Etk-2; etk2/tyro3; Rse; Sky; Tif; tk19-1; TK19-2
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin



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Fully Sequenced ORF: >MC229096 representing NM_001290800
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGATCGCC**

ATGGACGACAAACTGGAAAACACTCTGGGAAGATGGGCTGGGAGAATGGTCTTTCGATAGGAGAATACT
 TGGCGATTAAAGCCTGAAGCTCATGGGCGCCCAAGTGAAGATGACCGTGTCTCAGGGCAGCCAGTGAA
 GCTCAACTGCAGCGTGGAGGGATGGAGGACCTGACATCCACTGGATGAAGGATGGCACCCTGGTCCAG
 AATGCAAGCCAGGTGTCCATCTCCATCAGCGAGCACAGCTGGATTGGCTTACTCAGCCTAAAGTCAGTGG
 AACGGTCTGATGCTGGCCTGACTGGTGCCAGGTGAAGGATGGGGAGGAAACCAAGATTTCTCAGTCAGT
 ATGGCTCACTGTCGAAGGTGTGCCATTCTCACAGTGGAAACAAAAGTCTGGCGGTGCCACCCAATGCC
 CCTTTTCAGTGTCTTGTGAGGCTGTGGTCTCCAGAACCCGTAACCATTTACTGGTGGAGAGGACTCA
 CTAAGGTTGGGGACCTGCTCCCTCTCCCTCTGTTTTAAATGTGACAGGAGTGACCCAGCGCACAGAGTT
 TTCTTGTGAAGCCGCAACATAAAAAGGCTGGCCACTTCCCAGCAGCCATTGTTCCGCTTCAAGCACCG
 CCTGCAGCTCCTTTCAACACCACAGTAAACAACGATCTCCAGCTACAACGCTAGCGTGGCCTGGGTGCCAG
 GTGCTGACGGCCTAGCTCTGCTGCATTCTGTACTGTACAGGTGGCACACGCCCCAGGAGAATGGGAGGC
 CCTTGCTGTTGTGGTTCCTGTGCCACCTTTTACCTGCCTGCTTCGGAACCTGGCCCTGCCACCAACTAC
 AGCCTTAGGGTGCCTGTGCCAATGCCTTGGGCCCTTCTCCCTACGGCGACTGGGTGCCCTTTCAGACAA
 AGGGCCTAGCGCCAGCCAGAGCTCCTCAGAATTTCCATGCCATTCTGACCGACTCAGGCCTTATCCTGGA
 ATGGGAAGAAGTATTCTGAGGACCTGGGGAAGGCCCTAGGACCTATAAGCTGTCTGGGTCCAA
 GAAAATGGAACCCAGGATGAGCTGATGGTGAAGGACCAGGGCCAATCTGACCGACTGGATCCCCAGA
 AGGACCTGATTTGCGTGTGTGCCTCCAATTGGTGTGAGGCGCTGGAGTCCAGCTGGTGGT
 GTCTTCTCATGACCATGCAGGGAGGCAGGGCCCTCCCCACAGCCGCACATCTGGGTGCCCTGTGGTCTG
 GGCGTGTCCACGCCCTGATCACAGCTGCTGCCTTGGCCCTCATCTGCTTCGGAAGAGACGCAAGGAGA
 CGCGTTTCGGGAAGCCTTTGACAGTGTATGGCCGAGGGGAGCCAGCTGTACACTTCCGGGCAGCCCG
 ATCTTTCAATCGAGAAAGCCTGAACGCATTGAGGCCACATTGGATAGCCTGGGCATCAGCGATGAATTG
 AAGGAAAAGCTGGAGGATGTCTCATTCCAGAGCAGCAGTTACCCTCGGTGGATGTTGGGCAAAGGAG
 AGTTTGGATCAGTGGGAAGCCAGCTAAAGCAGGAAGATGGCTCCTTCGTGAAAGTGGCAGTGAAGAT
 GCTGAAAGCTGACATCATTGCCTCAAGCAGCATAGAAGAGTTCCTCCGGGAAGCAGCTTGCATGAAGGAG
 TTTGACCATCCACACGTGGCCAAGCTTGTGGGGTGGAGCTCCGGAGCAGGGCTAAAGGTCGTCTCCCA
 TTCCCATGGTTCATCTGCCCTCATGAAACATGGAGACTTGACAGCCTTCTGCTCGCCTCCCGAATCGG
 GGAGAACCCTTTAACCTGCCCTCCAGACCCTGGTCCGGTTCATGGTGGACATTGCCTGTGGCATGGAG
 TACCTGAGCTCCCGAACTTCATCCACCAGACCTAGCAGCTCGGAATTGCATGTGGCCGAGGACATGA
 CAGTGTGTGGCTGATTTTGGACTCTCTCGGAAAATCTATAGCGGGGACTATTATCGTCAGGGCTGTGC
 CTCAAATGGCCGTCAAGTGGCTGGCCCTGGAGAGCTGGCTGACAACCTGTATACTGTACACAGTGT
 GTGTGGCCTTCGGGTGACCATGTGGGAGATCATGACTCGTGGGCAGACGCCATATGCTGGCATTGAAA
 ATGCCGAGATTTAACTACCTCATCGGCGGAACCCCTGAAGCAGCCTCCGGAGTGCATGGAGGAAGT
 GTATGATCTCATGTACCAGTGTGGAGCGCCGACCCCAAGCAGCGCCCAAGCTTACGTGTCTGCGAATG
 GAACTGGAGAACATTCTGGGCCACTGTCTGTGCTGTCCACCAGCCAGGACCCCTGTACATCAACATTG
 AGAGAGCTGAGCAGCCTACTGAGAGTGGCAGCCCTGAGGTCCACTGTGGAGAGCGATCCAGCAGCGAGGC
 AGGGGACGGCAGTGGCGTGGGGCAGTAGGTGGCATCCCCAGTACTCTCGGTACATCTCAGCCCCGGA
 GGGCTATCCGAGTACCAGGGCAGCTGGAGCAGCAGCCAGAAAGCCCTCAATGAGAACCAGAGGCTGT
 TGTTGCTGCAGCAAGGGCTACTGCCTCACAGTAGCTGT**TAA**

AG**CGGACCG**ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCC
 TGGATTACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-RsrII
ACCN: NM_001290800

Insert Size:	2631 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:	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:	<u>NM_001290800.1</u> , <u>NP_001277729.1</u>
RefSeq Size:	4469 bp
RefSeq ORF:	2631 bp
Locus ID:	22174
UniProt ID:	<u>P55144</u>
Cytogenetics:	2 59.97 cM

Gene Summary:

Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding to several ligands including TULP1 or GAS6. Regulates many physiological processes including cell survival, migration and differentiation. Ligand binding at the cell surface induces dimerization and autophosphorylation of TYRO3 on its intracellular domain that provides docking sites for downstream signaling molecules. Following activation by ligand, interacts with PIK3R1 and thereby enhances PI3-kinase activity. Activates the AKT survival pathway, including nuclear translocation of NF-kappa-B and up-regulation of transcription of NF-kappa-B-regulated genes. TYRO3 signaling plays a role in various processes such as neuron protection from excitotoxic injury, platelet aggregation and cytoskeleton reorganization. Plays also an important role in inhibition of Toll-like receptors (TLRs)-mediated innate immune response by activating STAT1, which selectively induces production of suppressors of cytokine signaling SOCS1 and SOCS3.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) contains alternative 5' exon structure, and it thus differs in its 5' UTR and initiates translation from an alternative start codon, compared to variant 1. The encoded isoform (B) has a distinct N-terminus and is shorter than isoform A. 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.