

Product datasheet for **SC323345**

MASTL (NM_032844) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	MASTL (NM_032844) Human Untagged Clone
Tag:	Tag Free
Symbol:	MASTL
Synonyms:	GREATWALL; GW; GWL; MAST-L; THC2
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 SC323345 sequence for NM_032844 edited (data generated by NextGen Sequencing)

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ATGGATCCCACCGCGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGC
GTGAATAGGATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTCAGCATAGTGAAGCCC
ATTAGCCGGGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGCGGCAAATGTATGCA
GTAATGGTTGTTAAAAAGCAGACATGATCAACAAAAATGACTCATCAGGTCCAAGCT
GAGAGAGATGCACCTGGCACTAAGCAAAAGCCATTCCATTGTCCATTGTATTATTTCACTG
CAGTCTGCAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCT
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GCACTGGCTCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGAC
AATATGCTTATTTCTAATGAGGGTCATATTAACCTGACGGATTTTGGCCTTTCAAAGTT
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AGACAAGATTATCAAGAACCCAGGACAAGTGTATCGCTTATCAGCTCGTTGGGATTT
AACACACCAATTGCAGAAAAAATCAAGACCCTGCAAACATCCTTTCAGCCTGTCTGTCT
GAAACATCACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAGGACACT
ACGCCTTATTCTAGCAAATTAATAAAATCATGTCTTGAACAGATTGCCTCCAACCCAGGA
ATGCCTGTGAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCC
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GAGGTGCTGAAAACGTTAGCCTCTAAAAGAAATGCTGTTGCTTTTCGAAGTTTTAACAGT
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AGAAGATCCTGTATGCCACATCAGACCCCAAATCAGATCAAGTCGGGAAGTCCATACCGA
ACTCCGAAGAGTGTGAGAAGAGGGGTGGCCCCGTTGATGATGGGCGAATTCTAGGAACC
CCAGACTACCTTGCACCTGAGCTGTTACTAGGCAGGCCCCATGGTCTGCGGTAGACTGG
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ACACCACAACAAGTATCCAGAATATTCTGAAAAGAGATATCCCTTGGCCAGAAGGTGAA
GAAAAGTTATCTGATAATGCTCAAAGTGCAGTAGAAATACTTTTAAACATTGATGATACA
AAGAGAGCTGGAATGAAAGAGCTAAAACGTCATCCTCTCTTTCAGTGTGGACTGGGAA
AATCTGCAGCATCAGACTATGCCTTTTATCCCCAGCCAGATGATGAAACAGATACCTCC
TATTTTGAAGCCAGGAATACTGCTCAGCACCTGACCGTATCTGGATTTAGTCTGTAG

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Clone variation with respect to NM_032844.3
 185 a=>t;1782 c=>t;2616 t=>c

5' Read Nucleotide Sequence:	>OriGene 5' read for mutant NM_032844 unedited CCCGCCGTTGAGCAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAA CCGTCAGAATTTTGAATACGACTCACTATAGGGCGGCCGGAATTCGGCACGAGGGGAATGGCTGCTCG CGGAGGGGCAGTGTACGCGGGCCGCTGTAGGCTGTCCAGCGATGGATCCCACCGCGGAAGCAAGAAGG AGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAGGATCGCAGTGCCAAAACCGCCCTCCATTGA GGAATTCAGCATAGTGAAGCCCATTAGCCGGGGCGCCTTCGGGAAAGTGTATCTGGGCAGAAAGCGCGC AAATTGTATGCAGTAATGTTGTTAAAAAAGCAGACATGATCAACAAAAATATGACTTCATCAGGTCCAA GCTGAGAAAGATGCACTGCACTAAGCAAAGCCATTCATTGGCCATTTGTATTAATTCAGTCAGTCCTG CAAACAATGTCTACTTGAATGGAATTTCTTATTGGGGGAGAAGGCAAGTTTCCCCTCCTAATATATGTT TTTTTGATTAAGGAGTGGCTGGGAAATATATTTCTAAGGAACAATGGCTCCAGGCTACTTCCCGACCTGG AATCCCCAAAGGGACCTGAAACCGGCATATGCTATTTTATTAAGGTCTATAAACTGACGAATTTGGCTC AAAGTACTTGGTTGGGATATATGTGTAATACCTACACACTCATGGCAACCTAGCAGATATTCGAACC AGACAGGTACCTACGCTTTGGATACCCATGCAAATAACTGCACCTAACTGTTGACTAGTTCAGCTATGC AATTGTCAGACTCATTACAAA
Kinase Domain Sequence:	>SC323345 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 ASACGMGCAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTC AGAATTTTGAATACGACTCACTATAGGGCGGCCGGAATTCGGCACGAGGGGAATGGCTGCTCGCGGAG GGGCAGTGTACGCGGGCCGCTGTAGGCTGTCCAGCGATGGATCCCACCGCGGAAGCAAGAAGGAGCCT GGAGGAGCGCGGCGACTGAGGAGGGCGTGAATAGGATCGCAGTG
Restriction Sites:	Please inquire
ACCN:	NM_032844
Insert Size:	3160 bp
OTI Disclaimer:	Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery.
	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. More info
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:

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_032844.1](#), [NP_116233.1](#)

RefSeq Size: 3084 bp

RefSeq ORF: 2637 bp

Locus ID: 84930

UniProt ID: [Q96GX5](#)

Cytogenetics: 10p12.1

Domains: pkinase, TyrKc, S_TKc

Protein Families: Druggable Genome, Protein Kinase

Gene Summary: This gene encodes a microtubule-associated serine/threonine kinase. Mutations at this locus have been associated with autosomal dominant thrombocytopenia, also known as thrombocytopenia-2. Alternatively spliced transcript variants have been described for this locus. [provided by RefSeq, Feb 2010]
Transcript Variant: This variant (2) uses an alternate in-frame splice site in the 3' coding region, compared to variant 1. This results in a shorter protein (isoform 2), compared to isoform 1. 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.