

MASP2 (NM_139208) Human cDNA Clone

Specifications

SKU	Description
SC110196	Homo sapiens mannan-binding lectin serine peptidase 2 (MASP2), transcript variant 2 as transfection-ready DNA NM_139208.1, 10ug

OriGene Data

Vector:	pCMV6-XL4	Insert Size: 780	Restriction Site: NotI-NotI
Sequence Data:	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 Disclaimer:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials. Every lot of primer is tested to provide clean sequencing of OriGene TrueClones.		
Product Components:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials. Every lot of primer is tested to provide clean sequencing of OriGene TrueClones.		
Protein Families:	Secreted Protein	Protease	
	Druggable Genome		
Protein Pathways:	Complement and coagulation cascades		

Reference Data

RefSeq: NM_139208.1 , NP_631947	RefSeq Size: 738	RefSeq ORF: 558
Synonyms: MAP19; MASP-2; MASP1P1; sMAP		
LocusID: 10747	Cytogenetic: 1p36.3	Domains: CUB, EGF_CA, EGF

Summary: The Ra-reactive factor (RARF) is a complement-dependent bactericidal factor that binds to the Ra and R2 polysaccharides expressed by certain enterobacteria. Alternate splicing of this gene results in two transcript variants encoding two RARF components that are involved in the mannan-binding lectin pathway of complement activation. The longer isoform is cleaved into two chains which form a heterodimer linked by a disulfide bond. The encoded proteins are members of the trypsin family of peptidases. [provided by RefSeq, Jul 2008].

Transcript Variant: This variant (2), also called MAp19, differs in the 3' UTR and 3' coding region compared to variant 1, resulting in a frameshift and upstream stop codon. Isoform 2 has a unique C-terminus and lacks the serine protease catalytic domain, compared to isoform 1.

[5' Read Nucleotide Sequence](#)

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>OriGene 5' read for NM_139208 unedited
TTATGTAATCCGACTTACTATAGNNGCGCGCCGCAATTCGGCACCAGGCCAGCTGGAC
GGGCACACCATGAGGCTGCTGACCCCTCTGGGCTTCTGTGTGGCTCGGTGGCCACCCCT
TTGGGCCCGAAGTGGCCTGAACCTGTGTTCCGGGCGCCTGGCATCCCCGGCTTTCCAGGG
GAGTATGCCAATGACCAGGAGCGGGCTGGACCTGACTGCACCCCCGGCTACCGCTG
CGCCTCTACTTCAACCCACTTCGACCTGGAGCTTCCACCTCTGCGAGTACGACTTCGTC
AAGCTGAGCTCGGGGGCCAAGGTGCTGGCCACGCTGTGCGGGCAGGAGACAGACACG
GACATTGACGAGTGCCAGGTGGCCCCGGGAGAGGCGCCACCTGCGACCACTGCCAC
AACCACCTGNGCGGTTTCTACTGCTCCTGCCGCGCAGGCTACGTCCTGCACGTAACAG
CGCACCTGCTCAGAGCAGACCTTAGCCTCCCTGGAGCTCCGGCCTGCCAGCAGGTC
AGAAGCCAGAGCCAGCCTGCTGGCCTCAGCTCCGGGTGGGCTGAGATGGCTGTGCCCA
ACTTCCATTACCCACCATGAGCCATAATTAACCTGGCCCCACCCANTAAAAA
ANAAAAAACCCGACTTAGATTGGCCCGCGCTCATAGCTGTTTCTGAAAAATCCCGGG
TGGCATCCCTTGAACCCCTCCAGAGCCTTCTGCTGCCCTGNAAGTTGCTCCCGTGCCAC
CACCTGNCCATAAATAGGTGCATCATTGTCTGACAGGGCTCCTAAATACGTGCCG
GGCGCGGGGGCCCTTACCCCT
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[3' Read Nucleotide Sequence](#)

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>OriGene 3' read for NM_139208 unedited
NNAAGATNTTTACTCTGNACCGCGGNCCCGCATTNANGATCGAGTTTTTTTTTTTTTTT
TTTTTTTGGGGTGGGGCCGGTTTATATGGGTCCTGGGGGTGAATGGGAGTTGGGGCAC
AGCCATCTCAGCCCAACCCGGAGCTGAGGCCAGCAGGCTGGCTCTGGCTTCTGACCTGCT
GGGACGGCCGGAGCTCCAGGGGAGGCTAGAGGCTCTGCTCTGAGCAGGTGCGCTTGTAC
GGTGCAAGACGTAGCTGCGCGGAGGAGCAGTAGAAACCGCCAGGTGGTGTGGCAGT
GGTGGTCCGCAAGTGGGGCCCTCTCCCGGGCCACCTGGCACTCGTCAATGTCCTCGGCTG
CATAGAGGCTCGAAACCCGTGAACGCTTCTCCTTGGAGTAGTCGGAGCGGAAGGTAA
TGTCAGGCTGGAGCCAGCAGTAGAAAAGTGTCTTGGCAGGGGGCCCGCTCCGTGTCTG
TGCTCTCCTGCCCGCACAGGCTGGCCAGCACCTTGGCCCCGAGCTCAGTTGACGAAGT
CGTACTCGCAGAGGTGGGAGGCTCCAGGTCGAAGTGGTGAAGTAAAGGCGCAGGCGGT
AGCCGGGGGTGCACTAGGTCAGGTCAGCCGCTCCTGGTCATTGGCATACTCCCTGGAA
AGCCGGGGGATGCCAGGCGCCGACACAGGTTAGGCCACTTCGGGCCCAAGGGGGGTGG
CCACCAGCCACACAGAAGGCCNAGNAGGTCAGCAGCTCATGGTGTGCCGCTCCAGCT
GGCCTGGTCCGANATCCGGCCGCTATAGTGAGTCGTATACAAATTTCTGACGGTCACTA
ACGAGCTCTGCTATATAGACTNCCACGTAACGCTACGCCATTGCGTACGGGGCGGGGTA
TACGACATTG
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