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Product datasheet for MC216502

Mgat4c (NM_001162369) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Mgat4c (NM_001162369) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Mgat4c
Synonyms:	9130411I17Rik; GntIVh
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin

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Fully Sequenced ORF:

>MC216502 representing NM_001162369
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCCGCGATCGCC

ATGCTTAAATTTTATCAAATGAAATATATTTTTCAAATATTGGATAAAATGAGATGCTTGCGAAAACGGT
CTACAGTGTCATTCTTGGGGGTTCTTGTTGTTTTTCTACTATTCATGAACTTGTACATTGAAGATAGCTA
TGTTCTGGAAGGCGACAAGCAACTTATAAGGGAAACATCGACACACCAACTTAATTCTGAACGCTATGTT
CACACTTTCAAGGATTTATCAAACTTCTCAGGAACCATAAATGTCACTTATCGCTATCTGGCTGCCACAC
CTTTACAGAGAAAACGATATCTCACAATTGGACTTTCATCAGTGAAACGAAAAAAAGGAAATTATTTACT
TGACACAATCAAGTCAATTTTTGAACAGTCCAGCTATGAAGAACTAAAGGAAATTTCAGTCGTAGTACAT
CTAGCAGACTTCAATTCATCATGGCGAGATGCCATGGTCCAAGACATTACACAGAAATTTGCCCATCATA
TTATTGCAGGAAGATTAATGGTTATACATGCTCCTGAAGAATATTATCCAGTTCTGGATGGTCTTAAAAG
AAATTACAATGACCCAGAAGATAGAGTCAGATTTCGCTCCAAGCAAAACGTAGATTATGCTTTTCTGCTA
AATTTCTGTGCCAATACTTCTGACTATTACGTGATGCTTGAAGACGATGTTCGGTGTTCCAGAAATTTCT
TAACTGCCATCAAGAAAGTCATAGCATCCTTGGAAGGAACATACTGGGTAACTCTTGAGTTCTCTAAACT
TGGCTACATTGGTAAACTCTATCATTCTCACGATCTCCCACGTCTGGCCCATTTCTTATTAATGTTCTAT
CAAGAAATGCCCTGCGATTGGCTATTGACTCATTTCCGAGGGCTGCTGGCTCAGAAAAATGTGATTCGAT
TTAAACCTTCTCTCTTTCAGCACATGGGGTATTATTCATCCTATAAAGGAACAGAGAATAAACTGAAGGA
TGATGACTTTGAAGAAGAGTCCTTTGACATCCCTGATAACCCCCCAGCGAGTTTCTACACCAACATGAAT
GTCTTTGAAAACTATGAAGCAAGCAAGGCTTACAGTAGTGTTGATGAGTATTTTTGGGGAAAGTCACCTT
CAATGGGAGATACGTTCGTTATTGTATTTGAAAATCCGATTACAATTAAAAAAATTAAAGTGAATACTGG
AACAGAGGACCGGCAGAATGACATCTTACAACATGGAGCCCTAGATGTTGGGGAAAAACTTATTTTTAGC
AAACAAATAAGACAATGTGATACTTACTTAAGACTAGGGGAATTCAAAAATGGATACTTTGAAATGTCAG
ATGTGAATCAAAAAATTCCCTTTGACATACATTGCATGAGGATATGTGTTACCAAAACACAGAAAGAATG
GCTGATAATTAGAAGCATCAGTATTTGGACTTCCTAG

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI

ACCN: NM_001162369

Insert Size: 1437 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).

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_001162369.1, NP_001155841.1
RefSeq Size:	3735 bp
RefSeq ORF:	1437 bp
Locus ID:	67569
UniProt ID:	Q9D306
Cytogenetics:	10 D1
Gene Summary:	Glycosyltransferase that participates in the transfer of N-acetylglucosamine (GlcNAc) to the core mannose residues of N-linked glycans. Catalyzes the formation of the GlcNAcbeta1-4 branch on the GlcNAcbeta1-2Manalpha1-3 arm of the core structure of N-linked glycans. Essential for the production of tri- and tetra-antennary N-linked sugar chains. Does not catalyze the transfer of GlcNAc to the Manalpha1-6 arm to form GlcNAcBeta1-4Manalpha1-6 linkage ('GnT-VI' activity) (By similarity).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (3) differs in the 5' UTR compared to variant 4. All three variants encode the same protein. 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.