

## Product datasheet for RC216305

### MGAM (NM\_004668) Human Tagged ORF Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	MGAM (NM_004668) Human Tagged ORF Clone
Tag:	Myc-DDK
Symbol:	MGAM
Synonyms:	MG; MGA
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
ORF Nucleotide Sequence:	>RC216305 ORF sequence, <b>codon optimized</b> . Due to the complexity of NM_004668, the ORF clone is codon optimized for mammalian Expression. The nucleotide sequence differs from the reference sequence, yet the amino acid sequence remains identical.

Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**CGGATCGCC**

ATGGCAAGAAAGAAGCTGAAAAATTTACTACTTTGGAGATTGTGCTCAGTGTTCTTCTGCTTGTGTTGT  
TTATCATCAGTATTGTTCTAATTGTGCTTTTAGCCAAAGAGTCACTGAAATCAACAGCCCCAGATCCTGG  
GACAACTGGTACCCAGATCCTGGGACAACCTGGTACCCAGATCCTGGAACAACCTGGTACCACACATGCT  
AGGACAACGGGTCCCCAGATCCTGGAACAACCTGGTACCACTCCTGTTTCTGCTGAATGTCCAGTGGTAA  
ATGAATTGGAACGAATTAATTGCATCCCTGACCAGCCGCAACAAGGCCACATGTGACCAACGTGGCTG  
TTGCTGGAATCCCAGGGAGCTGAAGTGTCCCTGGTCTACTATTCCAAGAATCATAGCTACCATGTA  
GAGGGCAACCTTGTCAACACAAATGCAGGATTCACAGCCCGTTGAAAAATCTGCCTTCTCACCAGTGT  
TTGGCAGCAACGTCGATAACGTCTCCTGACCGCTGAATATCAGACATCTAACAGATTTCAATTTCAAAT  
CACCGACCAACCAATAATCGCTTCGAGGTGCCCCACGAACACGTCCAATCATTAGCGGCAATGCCGCA  
GCATCTCTGACTTACCAGGTGGAGATTTCCAGACAGCCTTTTAGTATCAAAGTGACCCGGCGCAGTAATA  
ACCGAGTCTCTTCGATTCTCCATTGGGCCTTTGTTGTTGCAGATCAGTTCCTCCAACGTCCACCCG  
CCTGCCTAGTACTAACGTGTATGGCCTCGGAGAGCACGTGCACCAGCAATATCGCCACGATATGAATTGG  
AAAACCTGGCCCATCTTCAACCGCGACACCACACCTAACGGAAATGGACCAATCTGTATGGTGCACAAA  
CATTCTTCTCTGTCTGGAAGATGCATCCGGTGTGCTTTGGCGTATTTCTGATGAATTCTAACGCAAT  
GGAGGTCGTCTCAGCCGGCCCGCCATCACATACAGAACAATCGGAGGAATCCTGGATTTCTACGTG  
TTCTCGGAACACACCAGAGCAGTCTGCAAGAGTATTGGAACCTATTGGTAGCCTGCCCTGCCCT



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CTTACTGGGCTCTGGGTTTTTCATCTTTACGATACGAATATGGCACCCCTGGACAACATGAGGGAGGTTCGT  
 CGAACGCAACCGAGCCGCCAACTGCCGTACGACGTGCAGCAGCTGATATAGATTACATGGATGAACGG  
 CGGGACTTTACATATGACTCTGTGGATTCAAAGGCTTCCAGAATTCGTGAACGAATTCATAAATG  
 GCCAGAACTGGTAATCATCGTGGACCCCTGCTATATCCAACAACCTTCTCCTCAAGTAAACCTATGGCCC  
 ATATGACAGGGGTTGAGATATGAAGATATGGGTGAATAGTTCAGATGGAGTGACTCCACTCATTGGGGAG  
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 TTGAGCTTTTTCACAATCAAGTAGAGTTTGATGGAACTGGAATCTGGATTGATATGAATGAAGTCTCCAACCTTGT  
 TGATGGTTCGGTCTCAGGATGTTCCACAACAACCTAAATAATCCCCATTCACTCCAGAATCCTGGAT  
 GGGTACCTGTTCTGCAAGACTCTCTGTATGGATGCAAGTGCAGCACTGGGGCAAGCAGTATGACATTCACA  
 ATCTGTATGGCTACTCCATGGCGGTGCGCACAGCAGAAGCTGCCAAGACTGTGTTCCCTAAATAAGAGAAG  
 CTTTATTCTGACCCGTTTACCTTTGCGGGCTCTGGCAAGTTTGCAGCACATTGGTTAGGAGACAACACT  
 GCCACCTGGGATGACCTGAGATGGTCCATCCCTGGCGTGCTTGAAGTCAACCTTTTTGGCATCCCAATGG  
 TGGGTCTGACATATGTGGCTTTGCTTTGGACACCCCTGAGGAGCTCTGTAGGCGGTGGATGCAGTTGGG  
 TGCATTTTATCCGTTTTCTAGAAATCACAATGGCCAAGGCTACAAGGACCAGGATCTGCCTCCTTTGGA  
 GCTGACTCCCTGTGTTGAATTCCTCCAGGCACTACCTAACATCCGCTATACTCTATTGCCTACCTAT  
 ACACCCTCTTCTCCGTGCTCACAGCCGAGGGGACACGGTGGCCAGGCCCTTTTGCATGAGTTCACGA  
 GGACAACAGCACTTGGGATGTGCACCAACAGTTCTTATGGGGGCCCGGCCTCCTCATCACTCCAGTTCTG  
 GATGAAGGTGCAGAGAAAGTGTGGCATATGTGCTGATGCTGTCTGGTATGACTACGAGACTGGGAGCC  
 AAGTGAGATGGAGGAAGCAAAAAGTTCGAGATGGAACCTTCTGGAGACAAAATTGGACTTCACCTTCGAGG  
 AGGCTACATCTTCCCACACAGCAGCCAATAACAACACTCTGGCCAGTCGAAAGAACCCTCTTGGTCTT  
 ATCATTGCCCTAGATGAGAACAAAGAAGCAAAAGGAGAAGTCTTCTGGGATAATGGGGAACGAAGGATA  
 CTGTGGCCAATAAAGTGTATCTTTATGTGAGTTTCTGTCACTCAAACCGCTTGGAGGTGAATATTTT  
 ACAATCAACCTACAAGGACCCCAATAATTTAGCATTTAATGAGATTAATAATCTTGGGAGGAAACCT  
 AGCAATGTTACAGTGAACACAATGGTGTCCCAAGTCAGACTTCTCTACAGTCACTTATGATTCTAACCC  
 TGAAAGTTGCCATTATCACAGATATTGATCTTCTCCTGGGAGAAGCATACACAGTGAATGGAGCATAAA  
 GATAAGGGATGAAGAAAAATAGACTGTTACCCTGATGAGAATGGTGTCTCTGCCGAAAACCTGCACTGCC  
 CGTGGCTGTATCTGGGAGGCATCCAATCTTCTGGAGTCCCTTTTTGCTATTTTGTCAACGACCTATACT  
 CTGTCAAGTGTTCAGTATAATTCCCATGGGGCCACAGCTGACATCTCCTTAAAGTCTTCCGTTTATGC  
 CAATGCCTTCCCCTCCACACCCGTGAACCCCTTCGCCTGGATGTCACCTACCATAAGAATGAAATGCTG  
 CAGTTCAAGATTTATGATCCCAACAAGAATCGGTATGAAGTTCAGTCCCTCTGAACATACCCAGCATGC  
 CATCCAGCACCCCTGAGGGTCAACTCTATGATGTGCTCATTAAAGAAGAATCCATTTGGGATTGAAATTCG  
 CCGAAGAGTACAGGCACTATAATTTGGGACTCTCAGCTCCTTGCTTTACCTTCAGTGACATGTTTATC  
 CGCATCTCCACCCGCTTCCCTCCAAGTACCTCTATGGCTTTGGGGAAAACCTGAGCACAGGTCCTATAGGA  
 GAGACTTGGAGTGGCACACTTGGGGGATGTTCTCCCGAGACCAGCCCCAGGGTACAAGAAGAATTCCTA  
 TGGTGTCCACCCCTACTACATGGGGCTGGAGGAGGACGGCAGTGGCCATGGAGTGTCTGCTGAACAGC  
 AATGCCATGGATGTGACGTTCCAGCCCCGCTGCCTTGACATACCCGACCACAGGGGGAGTTCTGGACT  
 TTTATGTGTTCTTGGGGCCGACTCCAGAGCTTGTCAACCAGCAGTACACTGAGTTGATTGGCCGGCTGT  
 GATGGTACCTTACTGGTCTTTGGGGTCCAGCTGTGTCGCTATGGCTACCAGAATGACTCTGAGATCGCC  
 AGCTTGTATGATGAGATGGTGGCTGCCAGATCCCTTATGATGTGCAGTACTCAGACATGACTACATGG  
 AGCGGCAGCTGGACTTACCCTCAGCCCCAAGTTTGTGGGTTTCCAGCTCTGATCAATCGCATGAAGGC  
 TGATGGGATGCGGTCATCCTCATTCTGGATCCAGCCATTTCTGGCAATGAGACACAGCCTTATCCTGCC  
 TCACTCGGGCGTGGAGGATGACGTTTATCAATAACCCAAATGATGGAGACATTGTCTGGGAAAGG  
 TCTGGCCTGATTTTCTGATGTTGTTGTAATGGGTCTCTAGACTGGGACAGCCAAGTGGAGCTATATCG  
 AGCTTATGTGGCCTTCCCAGACTTTTTCCGTAATTTCAACTGCCAAGTGGTGAAGAGGGAATAGAAGAA  
 CTATAACAATCCACAGAATCCAGAGAGGAGCTTGAAGTTTGTGGCATGTGGATTGATATGAATGAAC  
 CATCAAGCTTCGTGAATGGGCAGTTTCTCCAGGCTGCAGGGACGCTCTCTGAACCACCCTCCCTACAT  
 GCCACATTTGGAGTCCAGGGACAGGGCCTGAGCAGCAAGACCCTTTGTATGGAGAGTCAAGATCCTC  
 CCAGACGGCTCCCTGGTGCAGCACTACAACGTGCAACAACCTGTATGGGTGGTCCCAGACCAGACCACAT  
 ACGAAGCCGTGCAGGAGGTGACGGGACAGCGAGGGGTCTGCATCACCCGCTCCACATTTCCCTTCTTGG  
 CCGCTGGGACAGCATTGGCTGGGAGACAACACGGCCGATGGGATCAGCTGAAGAAGTCTATCATTGGC  
 ATGATGGAGTTCAGCCTCTTGGCATATCCTATACGGGAGCAGATATCTGTGGGTTCTTTCAAGATGCTG  
 AATATGAGATGTGTGCTCGTGGATGCAGCTGGGGCCTTTTACCCTTCTCAAGAAACCACAACACCAT

TGGGACCAGGAGACAAGACCCTGTGCCTGGGATGTTGCTTTTGTGAATATTTCCAGAACTGCCTGCAG  
 ACCAGATACACCCTGTTGCCATATCTGTATACCTTGATGCATAAGGCCACACGGAGGGCGTCACTGTTG  
 TGGCGCCTCTGCTCCATGAGTTTGTGTACAGACCAGGTGACATGGGACATAGACAGTCAGTTCCTGCTGGG  
 CCCAGCCTTCTGGTCAAGCCTGTCTGGAGCGTAATGCCAGAAATGTCAGTGCATATTTCCCTAGAGCC  
 CGCTGGTATGATTACTACACGGGTGTGGATTAATGCAAGAGGAGAGTGAAGACCTTGCCAGCCCCTC  
 TTGACCACATTAATCTTCATGTCCGTGGGGCTACATCCTGCCCTGGCAAGAGCCTGCACGTAACACCCA  
 CTTAAGCCGCCAGAAATTCATGGGCTTCAAATTCCTTGGATGATGAAGGAACTGCTGGGGCTGGCTC  
 TTCTGGGATGATGGGCAAGCATTGATACCTATGGGAAAGGACTCTATTACTTGGCCAGCTTTTCTGCCA  
 GCCAGAATACGATGCAAAGCCATATAATTTTCAACAATTACATCACTGGTACAAATCCTTTGAAACTGGG  
 CTACATTGAAATCTGGGAGTGGCAGTGTCCCGTTACCAGTGTGAGCATCTCTGTGAGTGGCATGGTC  
 ATAACACCCTCCTTCAACAATGACCCACGACACAGGTATTAAGCATCGATGTGACTGACAGAAACATCA  
 GCCTACATAATTTTACTTCAATTGACGTGGATAAGCACTCTG

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGATT  
 ACAAGGATGACGACGATAAGGTTTAA

**Protein Sequence:**

>RC216305 representing NM\_004668  
 Red=Cloning site Green=Tags(s)

MARKKLLKFFTTLEIVLSVLLLVLFIIISIVLIVLLAKESLKSTAPDPGTTGTPDPGTTGTPDPGTTGTTTHA  
 RTTGPPDPGTTGTPVSAECPVNELERINCIPDQPPTKATCDQRGCCWNPQAVSVWPCYYSKNHSYHV  
 EGNLVNTNAGFTARLKNLPSSPFGSNVDNVLTAEYQTSNRFHFKLTDQTNRFVEVPHEHVQVQSFSGNAA  
 ASLTYQVEISRQPFSEIKVTRRSNNRVLFDSSIGPLLFADQFLQLSTRLPSTNVYGLGEHVHQYRHRDMNW  
 KTWPIFNDRDTPNGNLTLYGAQTFFLCELEASGLSFGVFLMNSNAMEVVLQPAPAITYRTIGGILDYFV  
 FLGNTPEQVQVEYLELIGRPALPSYWALGFHLSRYEYGLDNMREVVERNRAAQLPYDVQHADIDYMDER  
 RDFTYDSVDFKGFPEFVNELHNNQKLVIIIVDPAISNNSSSSKPYGYPDRGSDMKIWNSSDGVTPILGE  
 VWPGQTVFPDYTPNCAVWWTKEFELFHNQVEFDGIWIDMNEVSNFVDSVSGCSTNNLNNPFTPRILD  
 GYLFCKTLCMDAVQHWKQYDIHNLGYSMAVATAEAAKTVFPNKRSEILTRSTFAGSGKFAHWLGDNT  
 ATWDDLRSWIPGVLEFNLFGIPMVGPDICGFALDTPPEELCRRWMLGAFYFYSRNHNGQYKQDQDPASFG  
 ADSLNLSSRHYLNIRYTLPLYLTLFFRAHSRGDVARPLLHEFYEDNSTWDVHQFLWGPGLLITPVL  
 DEGAEKVMAYVPDAVWYDYETGSQVRWRKQKVEMLPGDKIGLHLRGGYIFPTQQPNTTTLASRKNPLGL  
 IIALDENKEAKGELFWDNGETKDTVANKVYLLCEFVSVTQNRLEVNISQSTYKDPNNLAFNEIKILGTEEP  
 SNTVVKHNGVPSQTSPTVYDSNLKVAIITDIDLLGEAYTVEWSIKIRDEEKIDCYPDENGASAENCTA  
 RGCWEASNSSGVPFCYFVNDLYSVSDVQYNHSHGATADISLKSSVYANAFSTPVPNPLRLDVTYHKNEML  
 QFKIYDPNKNRYEVPVPLNIPSMPSSTPEGLYDVLIKKNPFGIEIRRKSTGTIIWDSQLLGFTFSDMFI  
 RISTRLPSKYL YGFGETEHRSYRRDLEWHTWGMFSRDQPPGYKKNYGVHPYMGLEEDGSAHGVLNLS  
 NAMDVTFQPLPALTYRTTGGVLDYVFLGPTPELVTQYTELIGRPVMVPYWSLGFQLCRYGYQNDSEIA  
 SLYDEMVAQIPYDVQYSDIDYMERQLDFTLSPKFAGFPALINRMKADGMRVILILDPAISGNETQYPYA  
 FTRGVEDDVFYKYPNDGDIVWGKVPDFPDVVVNGSLDWDVQVELYRAYVAFPDFFRNSTAKWWWREIEE  
 LYNNPQNPERSLKFDGMWIDMNEPSSFVNGAVSPGCRDASLNHPPYMPHLESRRGLSSKTLCMESQQIL  
 PDGSLVQHYNVHNLVYGSQTRPTYEAVQEVTGQRGVVITRSTFPSSGRWAGHWLGDNTAAWDQLKKSIIIG  
 MMEFSLFGISYTGADICGFFQDAEYEMCVRWMQLGAFYFYSRNHNTIGTRRQDPVSWDVAFVNISRTVLQ  
 TRYTLPLYLTLMHKAHTEGTVVRPLLHEFVSDQVTWIDSQFLGPAFLVSPVLERNARNVTAYFPRA  
 RWYDYTYGVDINARGWKTLPAPLDHNLHVRGGYILPWQEPALNTHLSRQKFMGFKIALDDEGTAGGWL  
 FWDDGQSIDTYGKGLYLLASFSASQNTMQSHIIFNNYITGTNPLKLGYIEIHWGVGSVPVTSVSVISVSGMV  
 ITPSFNNDPTTQVLSIDVTRNLSLHNFSTLWISTL

TRTRPLEQKLISEEDLAANDILDYKDDDDKV

**Restriction Sites:**

SgfI-MluI

**Cloning Scheme:**


ACCN: NM\_004668

ORF Size: 5571 bp

OTI Disclaimer: 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 clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.

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.

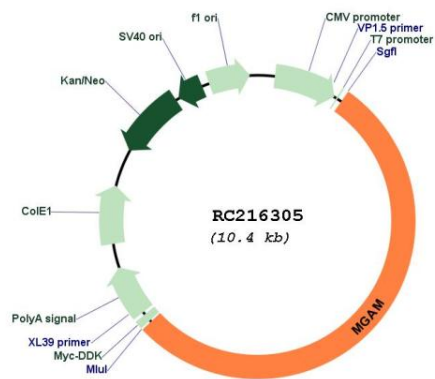
RefSeq: [NM\\_004668.2](#), [NP\\_004659.2](#)

RefSeq Size: 6513 bp

RefSeq ORF: 5574 bp

**Locus ID:** 8972  
**UniProt ID:** [O43451](#)  
**Cytogenetics:** 7q34  
**Protein Families:** Druggable Genome, Transmembrane  
**Protein Pathways:** Galactose metabolism, Metabolic pathways, Starch and sucrose metabolism  
**MW:** 209.9 kDa  
**Gene Summary:** This gene encodes maltase-glucoamylase, which is a brush border membrane enzyme that plays a role in the final steps of digestion of starch. The protein has two catalytic sites identical to those of sucrase-isomaltase, but the proteins are only 59% homologous. Both are members of glycosyl hydrolase family 31, which has a variety of substrate specificities. [provided by RefSeq, Jul 2008]

### Product images:



Circular map for RC216305