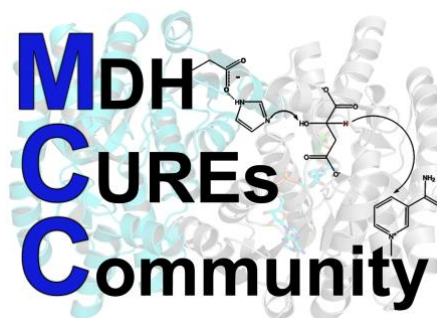


# MCC Protein/Clone Information Sheet wgMDH



**Protein Name:** Glyoxysomal Malate Dehydrogenase (wg MDH)

**Organism:** Watermelon (*Citrullus lantus*) **Plasmid Name:** pQE60 wgMDH

**Clone/Plasmid History:** Originally cloned by [Gietl C et. al. \(1996\) BBA 1274, 48-58](#) into pQE60 vector with the His affinity tag on the C terminus of MDH. This is the mature watermelon glyoxyl MDH (wgMDH) without presequence. This construct does NOT have the transit peptide (mqpipdvnr iarisahlp pksqmeessa Irrancr) and instead has an added Met as the start codon after removal of transit peptide sequence. wgMDH, was prepared by PCR using the NcoI- and BglII-site and cloned into the same vector. wgMDH is cloned between the restriction sites NcoI and BglII; the NcoI-site also provided the start codon. The necessary restriction sites at the 5'-end and 3'-end of the cDNA sequence were added by PCR. Either during cloning or in subsequent manipulations, the NcoI site (C/CATGG) was mutated to CTATGG, destroying the NcoI cut site. *Biochimica et Biophysica Acta* 1274 (1996) 48-58. And *FEBS Journal* 272 (2005) 643-654.

**NCBI / Gene Accession Number:** [M33148.1](#) (shown with transit peptide)

**Plasmid Map:** Downloadable file will include:

- Amp resistance in pQE60 construct (use 100 µg/ml), Promotor (for bacterial or mammalian), Sequencing primers, RBS and Kozak sequence, History of cloning, Annotated start and stop of protein all located on snapgene file

**NCBI Protein Sequence Accession:** [P19446.1](#) (shown with precursor transit peptide)

**UniProt Protein Page:** [MDHG\\_CITLA](#)

**RCSB PDB Page:** [1SEV](#) (with transit peptide) [1SMK](#) (mature form)



**Key Publications:** Plant glyoxysomal but not mitochondrial malate dehydrogenase can fold without chaperone assistance, Gietl et al.

Organelle and translocatable forms of glyoxysomal malate dehydrogenase: The effect of the N-terminal presequence, Cox et al.

**Available Mutations:** Over 80 prepared. See MCC website for list.

**Protein Notes:** Transit peptide (aa 1-36) required for entry into glyoxasomes and is cleaved as mature format. wgMDH is a 320 amino acid protein as a functional homodimer. Mature wgMDH monomer mw = 34.5 kDa.

**Recommended Protocols:** Enzyme Activity Assay / Protein Expression / Protein Purification

**Clone FAQ and Important Points:** High protein expression at 37°F 1mM IPTG for 3-4 hour induction. ~0.25-0.8 mg per ml of culture. pQE60 (Qiagen) is a low copy plasmid and will not give high yields of DNA preps. Amp Resistant. Do not freeze thaw purified protein – stability test of proteins in glycerol needed. Stable at 4°C for several days in elution buffer with minimal loss of activity. Stable at 4°C for 1-4 weeks dialyzed against (10 mM KPi, 150 mM NaCl, 0.1 mM EDTA, pH 8.0). Long term storage -20 to -80°C (10 mM K-phosphate, 0.1 mM EDTA, 20% glycerol, pH 8.0). Concentrations approaching 1-1.25 mg/ml will precipitate over a short time. Dilute immediately after purification and before dialysis to 1 mg/ml or less. See MDH Stability Datasheet for more information. Expected Km 146µM for NADH and 76 µM for OAA, (additional info from key publications – see above). Purification easily performed in column or batch format.

See Snap Gene File for details.

Amino Acid Coding Sequence:

MAKGGAPGFKVAILGAAGGIGQPLAMLMKMNPLVSVLHLYDVVNAPGVTADISHMDTGAVVRGFLGQQQLEAALTGMDLIIVPAGVPRKPG  
MTRDDLKINAGIVKTLCEGIAKCCPRAIVNLISNPVNSTVPIAAEVFKKAGTYDPKRLLGVTMLDVVRANTFVAEVLGLDPRDVPVVGHHAGV  
TILPLLSQVKPPSSFTQEEISYLDRIQNGGTEVVEAKAGAGSATLSMAYAAVKFADACLRLRGLRGDAGVIECAFVSSQVTELPFFASKVRLGRNGIEE  
VYSLGPLNEYERIGLEKAKKELAGSIEKGVSFIRSRSHHHHHH\*

Coding Region for MDH Plasmid Sequence:

ATGGCTAAAGGCGGAGCTCCCGGGTTCAAAGTCGCAATACTTGGCGCTGCCGGTGGCATTGGCCAGCCCCTTGCATGTTGATGAAGATG  
AATCCTCTGGTTTCTGTTCTACATCTATATGATGTAGTCAATGCCCTGGTGTACCGCTGATATTAGCCACATGGACACGGGTGCTGTGGTG  
CGTGGATTCTTGGGGCAGCAGCAGCTGGAGGCTGCGCTTACTGGCATGGATCTTATTATAGTCCCTGCAGGTGTTCCCTCGAAAACCAGGAA  
TGACGAGGGATGATCTGTTCAAAATAAACGCAGGAATTGTCAAGACTCTGTGTGAAGGGATTGCAAAGTGTGTCCAAGAGCCATTGTCAA  
CCTGATCAGTAATCCTGTGAACTCCACCGTGCCCATCGCAGCTGAAGTTTTCAAGAAGGCTGGAATTATGATCCAAAGCGACTTCTGGGAG  
TTACAATGCTCGACGTAGTCAGAGCCAATACCTTTGTGGCAGAAGTATTGGGTCTTGATCCTCGGGATGTTGATGTTCCAGTTGTTGGCGGT  
CATGCTGGTGTAAACATTTTGGCCCTTCTATCTCAGGTGAAGCCTCCAAGTCTTTACACAAGAAGAGATTAGTTACCTGACTGATAGGATT  
CAAAATGGTGGAAACAGAAGTTGTGAGGCCAAAGCAGGAGCTGGTTCAGCAACTCTCTCAATGGCTTATGCTGCCGTTAAGTTTGCAGATG  
CATGCCTCAGGGGCTTAAGAGGAGATGCTGGTGTGATTGAATGCGGTTTTGTGCTTCTCAGGTGACTGAACTTCCATTCTTTGCATCAAAA  
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GAGTTGGCAGGAAGCATTGAGAAGGGAGTTTCTTCATCAGAAGCAGATCTCATCACCATCACCATCACTAA