

Product datasheet for **SC315437**

MYH (MUTYH) (NM_001048173) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	MYH (MUTYH) (NM_001048173) Human Untagged Clone
Tag:	Tag Free
Symbol:	MUTYH
Synonyms:	MYH
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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Fully Sequenced ORF: >SC315437 representing NM_001048173.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

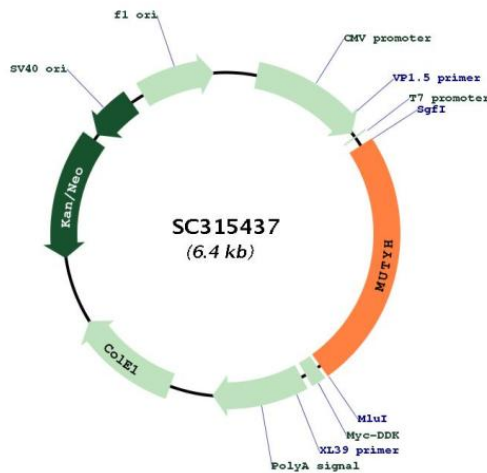
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Restriction Sites:

Sgfl-MluI

Plasmid Map:



ACCN:

NM_001048173

Insert Size:	1566 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).
OTI Annotation:	This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.
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:	<ol style="list-style-type: none">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_001048173.1
RefSeq Size:	1791 bp
RefSeq ORF:	1566 bp
Locus ID:	4595
UniProt ID:	Q9UIF7
Cytogenetics:	1p34.1
Protein Families:	Druggable Genome, Stem cell - Pluripotency
Protein Pathways:	Base excision repair
MW:	57.4 kDa

Gene Summary:

This gene encodes a DNA glycosylase involved in oxidative DNA damage repair. The enzyme excises adenine bases from the DNA backbone at sites where adenine is inappropriately paired with guanine, cytosine, or 8-oxo-7,8-dihydroguanine, a major oxidatively damaged DNA lesion. The protein is localized to the nucleus and mitochondria. This gene product is thought to play a role in signaling apoptosis by the introduction of single-strand breaks following oxidative damage. Mutations in this gene result in heritable predisposition to colorectal cancer, termed MUTYH-associated polyposis (MAP). Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Apr 2017]

Transcript Variant: This variant (gamma3) contains a distinct 5' UTR and uses an alternate in-frame splice site in the 5' coding region, compared to variant alpha5. These differences cause translation initiation at a downstream start codon and result in a protein (isoform 4) that is shorter than isoform 5. Variants beta3, gamma3 and beta5 encode the same isoform 4, which has been shown to localize to the nucleus.