

## Product datasheet for **RC403670**

### Menin (MEN1) (NM\_130799) Human Mutant ORF Clone

#### Product data:

Product Type:	Mutant ORF Clones
Product Name:	Menin (MEN1) (NM_130799) Human Mutant ORF Clone
Mutation Description:	R355W
Affected Codon#:	355
Affected NT#:	1063
Nucleotide Mutation:	MEN1 Mutant (R355W), Myc-DDK-tagged ORF clone of Homo sapiens multiple endocrine neoplasia I (MEN1), transcript variant 2 as transfection-ready DNA
Effect:	Multiple endocrine neoplasia 1
Symbol:	MEN1
Synonyms:	MEAI; SCG2
E. coli Selection:	Kanamycin (25 ug/mL)
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
Tag:	Myc-DDK
ACCN:	NM_130799
ORF Size:	1830 bp
Restriction Sites:	Sgfi-MluI



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**ORF Nucleotide Sequence:**

>RC403670 representing NM\_130799  
 Red=Cloning site Blue=ORF Green=Tags(s)

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
 GCC**CGGATCGCC**

ATGGGGCTGAAGGCCGCCAGAAGACGCTGTTCCCGCTGCGCTCCATCGACGACGTGGTGCGCCCTGTTT  
 CTGCCGAGCTGGGCCGAGAGGAGCCGGACCTGGTGCTCCTTTCCCTGGTCTGGCTTCGTGGAGCATTT  
 TCTGGCTGTCAACCGCTCATCCCTACCAACGTTCCCGAGCTCACCTTCCAGCCAGCCCCGCCCGAC  
 CCGCTGGCGGCCTCACCTACTTTCCCGTGCCGACCTGTCTATCATCGCCGCCCTCTATGCCCGTTCA  
 CCGCCAGATCCGAGGCGCCGTGACCTGTCCCTCTATCCTCGAGAAGGGGTGTCTCCAGCCGTGAGCT  
 GGTGAAGAAGTCTCCGATGTCATATGGAACAGCCTCAGCCGCTCCTACTTCAAGGATCGGGCCACATC  
 CAGTCCCTTTCAGTTCATCACAGGCACCAAATTGGACAGCTCCGGTGTGCCCTTGTGTGGTTGGG  
 CCTGCCAGGCCCTGGGTCTCCGGATGTCCACCTCGCCCTGTCTGAGGATCATGCCTGGTGTGTGG  
 GCCAATGGGGAGCAGACAGCTGAGGTACCTGGCACGGCAAGGCAACGAGGACCGAGGGCCAGACA  
 GTCAATGCCGGTGTGGCTGAGCGGAGCTGGCTGTACCTGAAAGGATCATACATGCGCTGTGACCGCAAGA  
 TGGAGGTGGCGTTCATGGTGTGTGCCATCAACCCTCCATTGACCTGCACACCGACTCGCTGGAGCTTCT  
 GCAGCTGCAGCAGAAGCTGCTCTGGCTGCTCTATGACCTGGGACATCTGGAAAGGTACCCCATGGCCTTA  
 GGGAACTGGCAGATCTAGAGGAGCTGGAGCCACCCCTGGCCGGCCAGACCCACTCACCTCTACCACA  
 AGGGCATTGCCTCAGCCAAGACCTACTATCGGGATGAACATCTACCCCTACATGTACCTGGCTGGCTA  
 CCACTGTCGAACCGCAATGTGCGGGAAGCCCTGCAGGCTGGCGGACACGGCCACTGTATCCAGGAC  
 TACAACCTACTGCTGGGAAGACGAGGAGATCTACAAGGAGTTCTTTGAAGTAGCCAATGATGTCATCCCA  
 ACCTGCTGAAGGAGGCAGCCAGCTTGTGGAGCGGGCAGGAGCGGCCGGGGGAGCAAGCCAGGCAC  
 CCAGAGCCAAGGTTCCGCCCTCCAGGACCTGAGTGCTTCGCCACCTGCTGCGATTCTACGACGGCATC  
 TGCAAATGGGAGGAGGGCAGTCCACGCCTGTGCTGCAGTGGGCTGGGCCACCTTTCTGTGCAGTCCC  
 TAGGCCGTTTTGAGGGACAGGTGCGGCAGAAGGTGCGCATAGTGAGCCGAGAGGCCGAGGCGGCCGAGGC  
 CGAGGAGCCGTGGGGCAGGAAGCCCGGAAGGCCGGCGGGGCCACGGCGGGAGTCCAAGCCAGAG  
 GAGCCCCGCCGCCAAGAAGCCAGCACTGGACAAGGGCTGGCACCGGCCAGGGTGCAGTGTGAGGAC  
 CCCCCGAAGCCTCTGGGACTGTGCTGGCACAGCCCGAGGCCCTGAAGGTGGCAGCACGGCTCAGGT  
 GCCAGCACCCGCAGCATACCACCGCCGAGGGTCCAGTGCTCACTTTCCAGAGTGAGAAGTGAAGGGC  
 ATGAAGGAGCTGCTGGTGGCCACCAAGATCAACTCGAGGCCATCAAGCTGCAACTCACGGCACAGTCCG  
 AAGTGCAGATGAAGAAGCAGAAAGTGTCCACCCTAGTACTACTCTGTCTTCTCAAGCGGCAGCG  
 CAAAGGCCTC

AG**CGGACCG**ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCC  
 TGGATTACAAGGATGACGACGA TAAGGTTTAA

**Protein Sequence:**

>RC403670 representing NM\_130799  
 Red=Cloning site Green=Tags(s)

MGLKAAQKTLFPLRSIDVVRLF AAELGREPDLVLLSLVLFVGFVEHFLAVNRVIPTNVPDLTFQSPAPD  
 PPGGLTYFPVADLSIIAALYARFTAQIRGAVDLSLYPREGGVSSREL VKKVSDVIWNSLSRSYFKDRAHI  
 QSLFSFITGKLDSSGVAVFVAVGACQALGLRDVHLAL SEDHAWVVFVGPNGEQTA EVTWHGKGNEDRRGQT  
 VNAGVAERSWL YLKGSYMRCDRKMVAFMVCAINPSIDLHTDSELELLQLQKLLWLL YDLGHLERYPMAL  
 GNLADLEEL EPTPGRPDPL TL YHKGIASAKTYRDEHI YPYMYLAGYHCRNRNVREALQAWADTATVIQD  
 YNYCWEDEE IYKEFFE VANDVIPNLLKEAASLLEAGEERPGEQSQGTQSQGSALQDPECF AHLLRFYDGI  
 CKWEEGSPTPVLHVGWATFLVQSLGRFEGQVRQKVRIVSREAEAEAEPEPWGEEAREGRRRPRRESKPE  
 EPPPPKPALDKLGTGQGAVSGPPRPPGTVAGTARGPEGGSTAQVPAPAASPPPEGPVLTQSEKMKG  
 MKELLVATKINSSAIKQLTAQSQVQMKKQKVSTPSDYTL SFLKRQRKGL

SGP**TRRRLEQKLI**SEEDLAANDILDYKDDDDKV



**Cytogenetics:** 11q13.1

**Domains:** Menin

**Protein Families:** Druggable Genome, Transcription Factors

**MW:** 67.1 kDa

**Gene Summary:** This gene encodes menin, a tumor suppressor associated with a syndrome known as multiple endocrine neoplasia type 1. Menin is a scaffold protein that functions in histone modification and epigenetic gene regulation. It is thought to regulate several pathways and processes by altering chromatin structure through the modification of histones. [provided by RefSeq, May 2019]