OriGene Technologies, Inc.
9620 Medical Center Drive, Ste 200
Rockville, MD 20850, US
Phone: +1-888-267-4436
https://www.origene.com
techsupport@origene.com
EU: info-de@origene.com
CN: techsupport@origene.cn

Product datasheet for SC217221

EML1 (NM_001008707) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	EML1 (NM_001008707) Human 3' UTR Clone
Symbol:	EML1
Synonyms:	BH; ELP79; EMAP; EMAP-1; EMAPL
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_001008707
Insert Size:	1978 bp

View online »

Insert Sequence:

>SC217221 3'UTR clone of NM_001008707
The sequence shown below is from the reference sequence of NM_001008707. The complete sequence of this clone may contain minor differences, such as SNPs.
Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
ACAAGCATCATGCAGTGGCGCGTCATTTAGTACCCACCGAGAGCTGTGGGGAGCAGCATGGGCAAGGAA
GACACAGACTCGCATTACCCTTGGTCACTGTGATTTCTGTTTTGTTTAAAAAATTCTTACAAACCTCAG
GAAAACTGTGCCCTCCGCCGGCTACCTTAGCTTAGCGTGTCAGCGGGCGCCACAGCGGATCAGCGGTTC
CGTGTTCACTTTTGTTGTACAATATATGACACAGTGCACATTGAATACCAACAAGGTTGCAACGTTTAC
ATTATAGCCACATCAACAGAAGTAACTGGTATATTCTTAGTAACTTTTCTATGAACTCTTCAAAAATGG
TCACAGAATGCCTTTTAAAACATTGTATATAATCTTCACTGTTTCACCATCTAGCTTGCTAAGTCAAAT
ATTTATGATGATAATGAGGTACTGAACCACGATGGCTGTTGAGGAATTGGTCCTAAAAGGACAGATCAC
TTCAGAAGAGTGAATAACTGATTTGCACAGCTGAATCAGGAGACACAAAGATGAGACTGTGTTTGGTTA
CATTTTCCAAAGTTTCATTGCATTCTCCCTTGGGGAGGCTGTGAGAGAGGGCTTGTATCCCTCTTGTGC
TAAGCAGACTCTACTCCTAACTGACTTCAATATTTCAGCAGGGTACACAGGCGTTTCCAAGTTTCAGTG
ACACCGTCCTGCCTAACCAGATGCGGTCAGCCTCTTCACACCCACCTGGCTTGCATCCCCCATCCCTTG
TTCACACGCCCTGATTCACGGTGAGACATTTTGCCACCTTCTTGTGTATATTACTTGGCATGAGATGAT
ATTGTACTTGTATAGGATTCTAGCAATTCATAATAAATATGTAAGACTAGGCTTTACTGTCTTATGCTT
ATGGACATTGTATATTTGTATTTTATGACCAAGTAGACCAAGTCAGAAAGATCTCTCTCGAGCGTACCA
TAAACCTGCAGAGAGAAGTCTCGAAAGGCTCCACCAGGTACCAAGGGCAGCTGCTTTTCCTGTCTTTTG
TGCATGGGCGACCCATTACAGTATGAGATAAGATTGAGTTCTGATGCGTTAAACGGAGGTGGCAGAAAT
TTGTCAAGAAGGCCTTATCCATTTCGATTGTGTGACAGATTGAAATTTATTGTTTACATTGGGGAATGT
ATCTCAAATTTTTAAATAGAAGAGTAATAAACAGACTTTAAAGCAAATATTAAGATTTTTACTCATTCA
AGGCAAGTAAATGAATGGAATTATCTGAGCTCTATGGCACTGGTTGTTTAGAGTGACTGATGAAGTGCA
ACTTTCAAAAACATTTTTGATGACATCACCAGCCTACTGCAGAAGTGCAGGGCACCAGTAAACACCATG
TATTATTGAAGATGAATCTGTTTGTATGTATCCTTGTCAAATATATTCTATAATGAAATAAAATCTGAA
AAGTGGATTTCTTATTGACCTATATTCATGAAAGCATATAAATTAAAATATTTAAAATTAGATATGATT
CACACTATATTCTGTTTCATATGCAGATTTTATTCTCACCTGGGCCATTTGCAGATGAGACTGTAGTTT
GCAGATGAGACTGTAGTTTGCAGATGGCGTGGAAGCATTCATCAGGGGAGATAACCATAAAGGATTTGG
CCTAATTACCATACTCAATTGTCAGTTTACGTGGTTTTGTGAATACTGGCAAAAGCAATTGTTTTTAAA
TTAACAATGGAGAGAATGATAAGATGAGGGAAGGAAAAGGCATTCATTATTGACTTACATGTCAGTAAG
GTCTGCTTTTATTTCTATGTACTCCTGTTTGCCAAGCTCAATAATGGACAAAGGATACAAACACACACA
CATCTACTATTTTAGATAAATGTACTGTTATATATATATGTAAACTACTATTGCTCTCTTTATAATGAT
TAATCACTTTATTATGAATGAATGAATGAATTTGATGGATTTAAAA
ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA
CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: SgfI-MluI

OTI Disclaimer: Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).

Components: The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.

RefSeq: NM_001008707.2

Summary: Human echinoderm microtubule-associated protein-like is a strong candidate for the Usher syndrome type 1A gene. Usher syndromes (USHs) are a group of genetic disorders consisting of congenital deafness, retinitis pigmentosa, and vestibular dysfunction of variable onset and severity depending on the genetic type. The disease process in USHs involves the entire brain and is not limited to the posterior fossa or auditory and visual systems. The USHs are catagorized as type I (USH1A, USH1B, USH1C, USH1D, USH1E and USH1F), type II (USH2A and USH2B) and type III (USH3). The type I is the most severe form. Gene loci responsible for these three types are all mapped. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2008]

Locus ID: 2009

MW: 76.9