

Product datasheet for MC209269

Qk (NM_001159516) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Tag:	Tag Free
Symbol:	Qk
Synonyms:	1110003F05Rik; 1500005P18; l(17)-lWis; l17Wisl; Qkl
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC209269 representing NM_001159516 Red=Cloning site Blue=ORF Orange=Stop codon TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCCGCGATCGCC ATGGTCGGGGAAATGGAACGAAGGAGAAGCCGAAGCCACCCAGATTATTTGATGCAGCTGATGAACG ACAAGAAGCTCATGAGCAGCCTGCCCAACTTCTGCGGGATCTTCAACCACCTCGAGCGGCTGCTGGACGA AGAAATTAGCAGAGTACGGAAGACATGTACAATGACACGTTAAATGGCAGTACAGAGAAAAGAAGTGCA GAATTGCCTGACGCGGTGGGACCCATTGTTCAAGTACAAGAGAACTTTATGTGCTGTAAAGAATACC CTGATTTTAAATTTTGTGGGAGAATCCTTGGACCTAGAGGACTTACAGCTAAACAACCTGAAGCAGAAAC GGGATGTAATAATGGTCCGAGGCAAGGCTCAATGAGGGATAAAAAGAAGGAGGAGCAAAATAGAGGC AAGCCCAATTGGGAGCATCTAAATGAAGACTTACATGTAATCACTGTGAAGATGCTCAGAACAGAG CAGAAATCAAGCTGAAGAGAGCGGTTGAAGAAGTGAAGAAGTTACTGGTACCTGCGGCTGAAGGTGAAGA CAGCCTGAAGAAGATGCAGCTGATGGAGCTTGCAATTCTGAATGGCACCTACAGAGACGCCAACATTAAA TCACCAGCCCTTGCCCTTTCTCTTGAGCAACTGCCAGGCTGCTCCAAGGATCATCACTGGGCCTGCGC CTGTCTCCACAGCTGCTCTGCGTACACCTACGCCAGCTGGCCCTACCATAATGCCTTTGATCAGACA AATACAGACCGCTGTCATGCCAAACGGAACCTCACCCTGCTGCAATAGTCCCTCCAGGCCTGAA GCTGGGTTAATCTACACCCCTATGAATACCCCTACACATTGGCACCAGCTACATCAATCCTTGAGTACC CTATTGAACCCAGTGGTGTGTAGGTATGGCTTCCCAACGAAAGGCTAA ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_001159516



Insert Size:	960 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).
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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	<u>NM_001159516.1</u> , <u>NP_001152988.1</u>
RefSeq Size:	5438 bp
RefSeq ORF:	960 bp
Locus ID:	19317
UniProt ID:	<u>Q9QYS9</u>
Cytogenetics:	17 7.75 cM

Gene Summary:

RNA-binding protein that plays a central role in myelination (PubMed:10864952, PubMed:11917126). Also required for visceral endoderm function and blood vessel development (PubMed:11892011, PubMed:16470614). Binds to the 5'-NACUAAY-N(1,20)-UAAAY-3' RNA core sequence (PubMed:16041388). Acts by regulating pre-mRNA splicing, mRNA export, mRNA stability and protein translation, as well as cellular processes including apoptosis, cell cycle, glial cell fate and development (PubMed:10535969, PubMed:12467586, PubMed:11297509, PubMed:11917126, PubMed:15568022). Required to protect and promote stability of mRNAs such as MBP and CDKN1B which promotes oligodendrocyte differentiation (PubMed:10535969, PubMed:15568022). Participates in mRNA transport by regulating the nuclear export of MBP mRNA (PubMed:12467586). May also play a role in smooth muscle development (PubMed:14706070).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) differs in the 3' UTR and coding sequence compared to variant 1. The resulting isoform (2) has a shorter and distinct C-terminus compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.