

Product datasheet for MC229687

Scn9a (NM_001290675) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Scn9a (NM_001290675) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Scn9a
Synonyms:	mKIAA4197; Nav1.7; PN1
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
Fully Sequenced ORF:	>MC229687 representing NM_001290675 Red=Cloning site Blue=ORF Orange=Stop codon

CTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCCGGCGC
GCC

ATGGCGATGTTGCCTCCGCCAGGACCTCAGAGCTTCGTTCACTTCACAAAACAGTCCCTTGCCTCATTG
AACACGCATTTCTGAAGAAAAAGCCAAGGACACAAAGATGAAAAGAAAGATGATGAGGAAGAAGTCC
CAAGCCCAGTAGTGACTTGAAGCAGGTAACAGCTACCTTCATCTACGGAGACATTCCTCCGGGAATG
GTGTCAGAGCCCCCTGGAGGACCTGGACCAATACTATGCAGACAAAAAACTTTTATAGTATTGAACAAAG
GGAAAGCAATCTTCCGTTTCAACGCCACCCCTGCTTTGTACATGCTGTCTCCCTTCAGTCCCTCAGAAG
AATATCTATTAAGATTTTAGTGCCTCCTTATTGAGCATGCTAATCATGTGCACAATTCTGACAACTGC
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TCAGCGTTGAGAACATTCAGAGTTCTCCGAGCATTGAAAACAATATCAGTCATTCAGGACTAAAAACCA
TCGTGGGGCCCTGATCCAATCAGTGAAGAAGCTCTGACGTCATGATCCTCACTGTGTTCTGTCTCAG
TGTGTTGCACATAATTGGACTACAATGTTTATGGGCAACTTGAAGCATAAATGTTTCCGGAAGGACCTT
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TTCTTGGCCTTGTTCGGCTAATGACTCAGGACTACTGGGAGAACCTTTTCAACAGACACTGCGTGCTG
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GCTGAGCTCAAAGAGTGCCAAGGAGAGAAGAAACCGAAGAAAGAAAAAAGCAGAAAGCTGTCCAGTGGC
GAGGAAAAGGGTATGATGAGAAGCTGTCCAAGTCAGGGTCAGAGGAAAGCATCCGAAAGAAAAGCTTCC



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ATCTCGGCGTGGAAAGGGACCACCGGGCCAGGAAAAGAGGCTGTCCACCCCAACCAGTCACTCAG
 CATTCTGGTGGTCTTGTCTTCTGCCAGGCGCAGCAGCAGAACAAGTCTCTTCAGTTTTAAGGGGCGAGGA
 AGAGATCTGGGATCTGAAACGGAATTTGCTGATGATGAGCATAGCATTTTTGGAGACAACGAGAGCAGAA
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 CCCACCAGTGTGCCGGTGAACGGGAAGATGCACAGTGCAGTGGACTGCAATGGCGTGGTGTGCTTGT
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 GTGCTGTGTGGGAGTGGATAGAGACCATGTGGGACTGCATGGAGTTGCGGGCCAGACCATGTGCCTTA
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 TTCCTTAGTCTGACAATCTTACAGCAATTGAAGAAGACACCGACGCAAAACACCTCCAGATTGCAGTG
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 CCTCTGCCAGGAGAAGAGGAGGCAGAAGCTGAGCCTATCAATGCAGATGAGCCCGAAGCCTGTTTTACAG
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 CATCCGGAAGACCTGCTACAGGATAGTGGAGCACAGCTGGTTGAAAGCTTCATTGTTCTCATGATCCTG
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 CCCTAAGAGCTTTGTCTAGATTTGAAGGAATGAGGGTAGTGGTCAACGCACTCATAGGAGCAATCCCTTC
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 GCTGGCAAGTCTATGAGTGTGTTAACACCACAGATGGCTCACGATTTTCTGTATCTCAAGTTGCAAACC
 GTTCTGAGTGTGTTGCCCTGATGAATGTTAGTGGAAATGTGCGATGGAAAAACCTGAAAGTAAACTTCGA
 TAACGTTGGACTTGGTTACCTGTCGCTGCTTCAAGTTGCAACGTTCAAGGGCTGGATGGATATTATGAT
 GCAGCAGTTGACTCTGTTAATGTAATGCACAACCAATATATGAATACAACCTCTACATGTACATTTATT
 TTGTCATCTTCATCATCTTTGGCTCATTCTTCACTTTGAACTTGTTCATTGGTGTATCATCGATAATTT
 CAACCAACAGAAGAAGAGCTTGGAGGTCAAGATATCTTTATGACAGAAGAACAGAAGAAATACTATAAT
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 GCATATTTGACTTAGTGACAAAACCAAGCTTTTGTATACCCATCATGGTTCTTATCTGCCTCAATATGGT
 AACCATGATGGTAGAAAAAGAGGGGCAAACTGACTACATGAGTTTTGTGCTATACTGGATCAACGTGGTC
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 GATGGAACATTTTGTGTTTGTGGTAGTGATCCTCTCCATTGTAGGAATGTTTCTCGCTGAGATGATAGA
 GAAGATTTTCGTGTCTCCTACCCTGTTCCGAGTCACTCGCTGGCCAGGATTGGACGAATCTACGCTG
 ATCAAAGGCGCAAGGGGATCCGCACGCTGCTCTTTGCTCTGATGATGTCCCTTCTGCGCTGTTCAACA
 TCGGCCTCCTGCTTTTCTCGTCATGTTTATCTACGCCATCTTTGGGATGTCCAACCTTGGCTACGTTAA
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 ATCACCACCTCTGCGGGCTGGATGGACTGCTGGCCCCATCCTCAACAGTGCACCTCCTGACTGTGACC
 CAAAAAGGTTCAACCAGGAAGTTCAGTGGAAAGGGGACTGTGAAATCCATCTGTGGAAATTTTCTACTT

TGTCAGCTACATCATCATATCCTTCCTGGTTGGTGAACATGTACATTGCTGTCATCCTGGAGAACTTC
AGCGTTGCCACAGAAGAAAGTACTGAGCCCTGAGTGAGGACGACTTTGAGATGTTCTACGAAGTCTGGG
AGAAGTTCGACCCTGACGCCACCCAGTTCATAGAGTTCTGCAAGCTCTGACTTTGACGAGCCCTGGA
TCCTCCCCTCCTCATCGCAAAGCAAACAAGTCCAGCTCATTGCCATGGACCTGCCATGGTGAGTGGA
GACCGCATCCACTGCCTGGACATCTTATTTGCTTTTACAAAGCGGGTCTGGGCGAGACGGAGAGATGG
ATTCCTTCGTTACAGATGGAAGAAAGTTTATGTCAGCCAATCCTTCTAAAGTGTCTATGAGCCCAT
CACAAACCACACTGAAGCGAAAACAAGAGGATGTATCTGCGACTATCATTACGCGTGTACAGACGGTAC
CGCCTTAGGCAAAACGTCAAGAATATATCAAGTATATATATAAAAGATGGAGACAGAGATGACGATTTGC
CCAATAAAGAAGATATAGTTTTTGTATAATGTTAACGAGAAGTCAAGTCCAGAAAAGACAGATGCAACAGC
CTCTACCATCTCTCCACCTTCTATGACAGTGTCAAAAGCCAGATCAAGAGAAATATGAAACAGACAAA
ACGGAGAAGGAAGACAAAGAGAAAGACGAAAGCAGGAAA TAG

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	Ascl-Mlul
ACCN:	NM_001290675
Insert Size:	5922 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:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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:	<u>NM_001290675.1, NP_001277604.1</u>
RefSeq Size:	9832 bp
RefSeq ORF:	5922 bp
Locus ID:	20274
Cytogenetics:	2 39.13 cM

Gene Summary:

Mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium-selective channel through which Na(+) ions may pass in accordance with their electrochemical gradient (PubMed:15123669). It is a tetrodotoxin-sensitive Na(+) channel isoform. Plays a role in pain mechanisms, especially in the development of inflammatory pain (PubMed:15314237).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) lacks an in-frame exon but contains an alternate in-frame exon in the 5' coding region, and also contains an alternate in-frame splice site in the central coding region, compared to variant 1. The resulting isoform (b) is shorter than isoform a.

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.