

Product datasheet for MC229689

Scn9a (NM_001290674) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Scn9a (NM_001290674) 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:	>MC229689 representing NM_001290674 Red=Cloning site Blue=ORF Orange=Stop codon

CTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCCGGCGC
GCC

ATGGCGATGTTGCCTCCGCCAGGACCTCAGAGCTTCGTTCACTTCACAAAACAGTCCCTTGCCTCATTG
AACACGCATTTCTGAAGAAAAAGCCAAGGACACAAAGATGAAAAGAAAGATGATGAGGAAGAAGTCC
CAAGCCCAGTAGTGACTTGAAGCAGGTAACAGCTACCTTCATCTACGGAGACATCCCCGGGAATG
GTGTCAGAGCCCCCTGGAGGACCTGGACCAATACTATGCAGACAAAAAACTTTTATAGTATTGAACAAAG
GGAAAGCAATCTTCCGTTTCAACGCCACCCCTGCTTGTACATGCTGTCTCCCTTCAGTCCCTCAGAAG
AATATCTATTAAGATTTAGTGCCTTATTTCAGCATGCTAATCATGTGCACAATTCTGACAACTGC
ATATTCATGACCATGAGCAACCCCTCAGATTGGACAAAAACGTAGAGTACACTTTTACTGGGATATATA
CTTTTGAATCACTCATAAAAAATCCTTGCAAGAGGCTTTTGCCTGGGCGAATTCACCTTCCCTCGTGACCC
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TCAGCTCTTCGAACTTTCAGAGCTTTGAGAGCTTTGAAAATTTCTGTAATTCAGGACTAAAAACCA
TCGTGGGGCCCTGATCCAATCAGTGAAGAAGCTCTGACGTCATGATCCTCACTGTGTCTGTCTCAG
TGTGTTGCACATAATTGGACTACAATGTTTATGGCAACTTGAAGCATAAATGTTTCCGGAAGGACCTT
GAGCAGAATGAAACATTAGAAAAGCATCATGAGTACTGCTGAGAGTGAAGAAGAATTGAAAAGATTTTTT
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TTCTTGGCCTTGTTCGGCTAATGACTCAGGACTACTGGGAGAACCTTTTCAACAGACTGCGTGTCTG
CTGGCAAAACCTACATGATTTTCTTTGTCGTGGTGATTTTCTGGGATCCTTTTACCTGATAAACTTGAT
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GCTGAGCTCAAAGAGTGCCAAGGAGAGAAGAAACCGAAGAAAGAAAAAAGAAAGCTGTCCAGTGGC
GAGGAAAAGGGTATGATGAGAAGCTGTCCAAGTCAGGGTCAGAGGAAAGCATCCGAAAGAAAAGCTTCC



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ATCTCGGCGTGAAGGGCACCACCGGGCCAGGAAAAGAGGCTGTCCACCCCAACCAGTCACCACTCAG
 CATTTCGTGGGTCCTTGTTTTCTGCCAGGCGCAGCAGCAGAACAAGTCTCTTCAGTTTTAAGGGGCGAGGA
 AGAGATCTGGGATCTGAAACGGAATTTGCTGATGATGAGCATAGCATTTCAGGAGACAACGAGAGCAGAA
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 GGTCTGAACCTGTTTCTGGCTTATTACTGAGTTCCTTAGTTCGACAATCTTACAGCAATTAAGAA
 GACACCGCAGCAAACAACCTCCAGATTGCAGTGGCCAGAATAAAAGAGGGATCAATTATGTGAAACAGA
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 GGAGAATATGAACACAGAAGAGCTTAGCAGTACTCAGATAGTACTACAGCAAAGAGAGACGGAACCGA
 TCAAGTCTTTCAGAGTGCAGCACAGTTGATAAACCCTCTGCCAGGAGAAGAGGAGGAGCAGAAGCTGAGCCTA
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 CTAATATTTAGCATCATGGGAGTCAATCTGTTTGTGGCAAGTCTATGAGTGTGTTAACACCACAGATG
 GCTCACGATTTTCTGTATCTCAAGTTGCAAACCTTCTGAGTGTGTTTGCCTGATGAATGTTAGTGGAAA
 TGTGCGATGGAAAACCTGAAAGTAACTTCGATAACGTTGGACTTGGTTACCTGTGCTGCTTCAAGTT
 GCAACGTTCAAGGGCTGGATGGATATTATGTATGCAGCAGTTGACTCTGTTAATGTAATGCACAACCAA
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 GAACCTGTTTATTGTTGTCATCATCGATAATTTCAACCAACAGAAGAAGCTTGGAGTCAAGATATC
 TTTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAGAAGCTGGGGTCCAAGAAACCACAAAAAC
 CAATTCGAGGCCAGGGAACAAATTCGAAGGATGCATATTTGACTTAGTGACAAACCAAGCTTTTGTATAT
 CACCATCATGGTCTTATCTGCCTCAATATGGTAACCATGATGGTAGAAAAAGAGGGGCAAACTGACTAC
 ATGAGTTTTGTGCTATACTGGATCAACGTGGTCTTCATCATCCTGTTCACTGGGGAGTGTGTGCTGAAGC
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 CATTGTAGGAATGTTTCTCGCTGAGATGATAGAGAAGTATTTCTGTCTCCTACCCTGTTCCGAGTCATT
 CGCCTGGCCAGGATTGGACGAATCCTACGCTGATCAAAGGCGCAAGGGGATCCGACGCTGCTCTTTG
 CTCTGATGATGTCCCTTCTGCGCTGTTCAACATCGGCCTCCTGCTTTTCTCGTCATGTTTCACTACGC
 CATCTTTGGGATGTCCAACCTTGGCTACGTTAAAAAGGAAGCTGGAATTAATGACATGTTCAACTTTGAG
 ACCTTCGGCAACAGCATGATCTGCCTGTTCCAAATCACCACCTCTGCGGGCTGGGATGGACTGCTGGCCC
 CCATCCTCAACAGTGCACCTCCTGACTGTGACCAAAAAAGGTTACCCAGGAAGTTCAGTGAAGGGGA

CTGTGGAATCCATCTGTGGGAATTTTCTACTTTGTCAGCTACATCATCATATCCTTCCTGGTTGTGGT
AACATGTACATTGCTGTCATCCTGGAGAACTTCAGCGTTGCCACAGAAGAAAGTACTGAGCCCCTGAGTG
AGGACGACTTTGAGATGTTCTACGAAGTCTGGGAGAAGTTCGACCCTGACGCCACCCAGTTCATAGAGTT
CTGCAAGCTCTGACTTTGCAGCAGCCCTGGATCCTCCCCTCCTCATCGCAAAGCCAAACAAGTCCAG
CTCATTGCCATGGACCTGCCATGGTGAAGTGGAGACCGCATCCACTGCCTGGACATCTTATTTGCTTTTA
CAAAGCGGGTCTGGGCGAGAGCGGAGAGATGGATTCCTTCGTTACAGATGGAAGAAAGGTTTATGTC
AGCCAATCCTTTAAAGTGTCTATGAGCCCATCACAAACCACACTGAAGCGAAAACAAGAGGATGTATCT
GCGACTATCATTACAGCGTCTTACAGACGGTACCGCCTTAGGCAAAACGTCGAAGAATATATCAAGTATAT
ATATAAAGATGGAGACAGAGATGACGATTTGCCCAATAAAGAAGATATAGTTTTTGATAATGTTAACGA
GAACTCAAGTCCAGAAAAGACAGATGCAACAGCCTCTACCATCTCTCCACCTTCTATGACAGTGCACA
AAGCCAGATCAAGAGAAATATGAAACAGACAAAACGGAGAAGGAAGACAAAGAGAAAGACGAAAGCAGGA
AATAG

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	Ascl-Mlul
ACCN:	NM_001290674
Insert Size:	5955 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_001290674.1, NP_001277603.1</u>
RefSeq Size:	9865 bp
RefSeq ORF:	5955 bp
Locus ID:	20274
UniProt ID:	<u>Q62205</u>
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 (1) represents the longer transcript and encodes the longer 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.