

Product datasheet for **SC336626**

CATSPER2 (NM_001282309) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: CATSPER2 (NM_001282309) Human Untagged Clone
Tag: Tag Free
Symbol: CATSPER2
Vector: pCMV6-Entry (PS100001)
Fully Sequenced ORF: >SC336626 representing NM_001282309.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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ATGGCCGCTTACCAACAAGAAGAGCAGATGCAGCTTCCCCGAGCTGATGCCATTCGTTACAGTCTCATC
GATACTTTCTCTCTCATTGAGCATTGCAAGGCTTGAGCCAAGCTGTGCCGCGGCACACTATCAGGGAG
TACTTGATCCTTCCCGCCAGAAGAACTTGATTGGGAGATCAACACCAGCTAGTGCCTTCTCTATA
AAGCCTCAGCGTATAGAACAGATTTACATGCCAGAGGCTGTTGAGCAGGCTTCATGTGCGCTGCAGT
CAGAGGCCACCTCTTTCTTTGTGGGCCGGATGGGTCCTTGAGTGTCTCTCTTCAAAAACATCATCATC
TTCTGGTCTTTTGAATACGATCATATTGATGGTTGAAATAGAATTGCTGGAATCCAAAATACCAAA
CTATGGCCATTGAAGCTGACCTTGGAGGTGGCAGCTTGGTTTATCTTGCTTATTTTCATCCTGGAGATC
CTTCTTAAGTGGCTATCCAACCTTTCTGTTTTCTGGAAGAGTGCCTGGAATGTCTTTGACTTTGTTGT
ACCATGTTGTCCCTGCTTCCCGAGGTTGTGGTATTGGTAGGGTAACAGGCCAATCGGTGTGGCTCAG
CTTCTGAGGATCTGCCGGTGTGAGGTCTCTCAAACCTTGCACAATCCGTCAAATTCAAATATT
ATTTTGGTCTGGTCAAGAGCCTCAAGAGCATGACCTTCTCTTGTGCTGCTCATCTTCTTCTAC
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CATGTGTTCTTCTCGGACCTCCGAATCCCTGGTAACAGTGTCATTCTCTTACCTTGGATCATTGG
TATGCACTGCTCAGGACGTCTGGAAGGTGCCTGAAGTCAGTCGCATCTTCAAGCAGCATCTATTTATC
CTTTGGTTGTTGCTTGGCTCCATTATCTTTGAAAGTATCATAGTAGCCATGATGGTTACTAACTTTCAG
AATATCAGGAAAGAGCTGAATGAGGAGATGGCGCTCGGGAGGTTGAGCTCAAAGCTGACATGTTCAAG
CGGCAGATCATCCAGAGGAGAAAAACATGTCACATGAAGCACTGACGTCAGCCATAGCAAAAATAGAG
GACAGAGGAGCTAGTCAACAAAGGGAAAGTTGGACTTATCAGAAGTGTCTGAAGTAGAGTCAATTAT
GGTGCCACTGAAGAGGATTTAATAACATCTGCATCAAAAACAGAAGAGACCTTGTCAAAAAGAGAGAG
TACCAGTCTTCTCCTGTGTCTCCTCCACATCCTTCTTCTTCTTCTTCTTCTGAAATCCAGATTTTCT
GAATCTATTGGTCGTTTGGACTGGGAGACTCTTGTGCACGAAAATCTGCCGGGCTAATGGAAATGGAT
CAGGATGACCGTGTGGCCAGAGACTCACTTCCGATATTTTGAAGTGTAGAAAAGCTTCAAGTAT
AACCTAGAGGAACGTAAGAAGTTACAAGAGTTTGCAGTGCAGGCACTGATGAACTTGAAGACAAGTAA
  
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Restriction Sites: SgfI-MluI
ACCN: NM_001282309
Insert Size: 1587 bp



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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:	<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_001282309.1</u>
RefSeq Size:	1840 bp
RefSeq ORF:	1587 bp
Locus ID:	117155
UniProt ID:	<u>Q96P56</u>
Cytogenetics:	15q15.3
Protein Families:	Druggable Genome, Ion Channels: Other, Transmembrane
MW:	61.9 kDa
Gene Summary:	<p>This gene encodes a member of a family of cation channel proteins that localize to the flagellum of spermatozoa. Defects at this locus causes male infertility. Alternatively spliced transcript variants have been observed at this locus. Readthrough transcription originates upstream of this locus in diphosphoinositol pentakisphosphate kinase 1 pseudogene 1 and is represented by GeneID:110006325. Related pseudogenes are found next to this locus on chromosome 15 and on chromosome 5. [provided by RefSeq, Mar 2017]</p> <p>Transcript Variant: This variant (6) differs in the 5' UTR and uses an alternate in-frame splice site in the 3' coding region compared to variant 2. The encoded isoform (1) is shorter than isoform 2. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p>