

Product datasheet for MC229597

Tex14 (NM_001199293) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Tex14 (NM_001199293) Mouse Untagged Clone
Tag: Tag Free
Symbol: Tex14
Synonyms: C85585
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC229597 representing NM_001199293
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCCCGGATCGCC

ATGAGACCCTGTCTACAAACAAACAAACAAACAAACATGTCTCGGGGGCTCCTTTCCAGTCCCTTGCC
 CGGTGCTGCTGGGACCTTCACAGATGACTCCCTGGAGGCTCAGCTTCACGAATACGCCAAGCAAGGGAA
 CTGCGTGAAGCTCAAGAAGATTCTAAGAAGGGAGTCTGTGTCGATGCAGTTAACACTCAGGGCCAGTCA
 GCGCTCTTTGTTGCAGCATTACTGGGCCATGTGAAATTAGTGGATGTTCTGGTGGATTATGGATCAGATC
 CAAATCACCGCTGCTTTGACGGGAGCACTCCTGTCCATGCAGCAGCCTTTTCAGGCAACCAAGTGGATCCT
 CAGTAACTGCTGACTGCAGGGGGTACCTGCGACTCCATGATGAGAAGGGTCGGAATCCACAGGCTGG
 GCCTTGACAGCAGGGAAGGATCGTAGCACTCAGATGGTGGAGTTCATGCAACGTTGACTTCACATATGA
 AGGCTATCATCCAGGGCTTCTCCTATGACCTTCTGAAGAAGATAGACTCTCCTCAGCGACTCATCGGCAG
 CCCACCCTGGTTTGGTAGCCTCATTGAGGAAGCCAAATAGTTCTCCCAACCGACAGCTTAAACCTGGA
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 TTTCTTACAGTGGCCCTACATGGTCATGACTAACCTCGTGTGGAATAGGAGCAGAGTACAGTAAGGAG
 CTGAACCTTCCCACCGTCCCCACTGTAGCAGGCTGAGGTTGGCCGACTTGTGATTGCTGAGCAGGAGC
 ACAGCAGCAACCTGCGGCATCCTAACCTGCTGCAACTGATGGCTGTATGTTTGTCCCGGACCTGGAGAA
 AATTGCGCTGGTTTACGAGCGTATCACAGTCGGCACACTGTTCAAGTGTCTCCATGAACGAAGTCCCAG
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 CTCACTTGTAAAGAAACCATAGCCTTGGGAAATTATTTAGAAGCTGATGTCAGGCTTCCGGAACCTTAC
 TATGATATTGTTAAGTCAGGAATCCATGCCAAGCAGAAGAACCGAACAATGAACCTTCAAGATATTCGTT



ATATTCTGAAGAATGACTTAAAGGAATTTATTGGAGCTCAGAAAACCTCAGCCAACCGAGAGCCCCAGAGG
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 CCAGACTTGGACATCAAGGAACTAAAGGAAATGGGTAGTCAGCCCCATTACCTACAGATCACTCCTTTT
 TCACTGTAAAACCAACTAGCTCCTCAGACCTAGATTCAAGTCTGTCAGCCCAGAAACCTGACAAATGC
 AAATGTTCTTCTCCTCTGCTGCATGTCTGGCAGAAGAGGTGAGGAGCCCCACTGCAAGTCAGGACAGC
 CTCTGCAGCTTTGAAATCAATGAGATCTACTCAGGCTGCTTGACACTGGGAACTGACAAGGAGGAAGAT
 GTCTGGGACTGCTGCTTACCTGAGGGGGATAGACCAAACCGAGGAGATGAGCTGCCATCCCTGGAAAG
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 CCAGAGAAGCCAAGGGCAAAACGAGCAGCTGGTCCAAGACTGATGAGTATGTCAGTAAGTGTGTGTGAA
 TCTGAAGATTTACAGGTGATGATGCAGCAGAGCGCTGAGTGGCTGAGGAAGCTTGAGCAGGAGGTAGAG
 GAGCTCGAGTGGGCACAGAAGGAGCTGGACAGTCACTGCAGCAGTTTGCGGGATGCTTCATTAAGTTTG
 CAAATGCCAAGTCCAGCCGGCTGAGGCCCTCCATCTTTGGCCTATCTTCTCCTGTTATGCAATTACC
 AGGGCTCAAGCAGCCTGAAAATGGTGGCACCTGGTTAACCTAGCAAGGTCTCCAGGAAATGAGAGAGAG
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 AATAGTAGGAGTATGGCGTCTGTGCTTCTGAAATCTATGCTACTAAGTCAAGAAATATGAGGATAATG
 GAGAGGCACACTTGAAATGGAGATTGGCAGTAAAAGAAATGGCAGAGAAAGCAGTTTCCGGACAGCTCTT
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 CCACGGCCCCAATTAGAGTCTGAGAGCACAGAATGGCAGCACATTTAGAAATACCAGAGGGAAAATG
 ATGAGCCCAAAGGAAATACGAAGTTTGGCAAAAATGGACAACAGTACTGTGACAAGAACAAGCACAGCAG
 ATGGACAGGCCTCCAGCGCTTCACTGGTATTAGATACCCATTCTCAGAAAACCGAGCAGCCAGAGCAG
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 CAAATTAACACGCACCAACTAGTGCCAGTACCCCGCTAAGCCAGAGTCGATTTCTTCAGCTGCTAGT
 CACTATGAAGACTGCCTTAAAAATACCACATTTTCAATGTTAAAAGAGGATCTACATTTTGTGGAATGGCC
 AAGAAGCTATGAGAACTTTGTCTGCCAAATTTACAACGTCCGAGAGAGAGCTAAGAGCCTGGAATCACT
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 GGCTCTTCTAACGTTTTCTGCGGCATTTGTAACATCAACTCATGCTACCAAGAGGAAGAGCCTACCCAGAG
 AACTGGCAGAAGCCACTCTCAACAGCATCTTGATGAGCTTCCACCACCAGCTCAGGAGCTACTTGATGA
 AATTGAGCAACTGAAGCAGCAGCAGGTCTCATCCCTGGCGTCACATGAGAACACGGCACGTGATCTGAGT
 GTCATAACAAGGATAAGAAGCATTGGAAGAACAAGAAACCAACAGTAGTAAAGACAGCAGTTTCTTT
 CCAGCAGAGAAATTCAGGATCTGGAAGATACAGAGAGAGCTCATTCTTCTTGTGAGGACCTGGAAAG
 ATCTCTGCAGTCACCTGAGGAGAACACGGCACTGCTGGACCCTACCAAGGGCTCTACAAGGGAGAAAAAA
 AACAAAGATCAAGACGTTGTTGAGCAGAAGAGAAAAAGAAAGAAAGCATCAAGCCAGAGAGAAGGGAGT
 CAGACAGCTCCCTAGGGACCTTGAAGAAGATGAACTAAAACCCTGTTTTTGAAGCGACTGGGTTGGTC
 CGAACCTTCCAGGATAATTGTGCTGGATCAGAGCGACTTGTGAGACTGA

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
 ACCN: NM_001199293
 Insert Size: 4389 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_001199293.1</u> , <u>NP_001186222.1</u>
RefSeq Size:	4795 bp
RefSeq ORF:	4389 bp
Locus ID:	83560
UniProt ID:	<u>Q7M6U3</u>
Cytogenetics:	11 C
Gene Summary:	<p>Required both for the formation of intercellular bridges during meiosis and for kinetochore-microtubule attachment during mitosis. Intercellular bridges are evolutionarily conserved structures that connect differentiating germ cells and are required for spermatogenesis and male fertility. Acts by promoting the conversion of midbodies into intercellular bridges via its interaction with CEP55: interaction with CEP55 inhibits the interaction between CEP55 and PDCD6IP/ALIX and TSG101, blocking cell abscission and leading to transform midbodies into intercellular bridges. Also plays a role during mitosis: recruited to kinetochores by PLK1 during early mitosis and regulates the maturation of the outer kinetochores and microtubule attachment. Has no protein kinase activity in vitro.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (1) represents the longer transcript and it encodes the longer protein (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.</p>