Product datasheet for MC226729

Aptx (NM_001025445) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Aptx (NM_001025445) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Aptx
Synonyms:	2410016G21Rik; AA388047; FHA-HIT
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC226729 representing NM_001025445 Red=Cloning site Blue=ORF Orange=Stop codon TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCCGCGATCGCC ATGGGGGTCAACCCCACCAGCATTGACTCGGGCGTCATCGGGAAGGACCAAGAGAAGAAGCTGCTGCCTG GTCAGGTTCTCCACATGGTGAATGGACTTTATCCATACATCGTAGAGTTTGAGGAAGTGGCAGAGAGCCC TAACCTAACACAGAGGAAGAGAAAGAGGTCAGACTGTGATAGTGAGGAGATGGAAGCTGAGTCTGGGACA GGGCTGGCACCTGGGAGCAGCCCCAGCCAGTGCTCTGTGTCCCCTAAGAAGGACAAGAATGGAGCCACCA AAAAGGAATCACTGGGCCACTGGAGTCAAGGCTTGAAGATGTCTATGAAAGACCCCAAAATGCAGGTTTA CAAAGACGACCAGGTGGTGGTGATTAAGGATAAATACCCCAAGGCCCGTCACCACTGGCTGGTCTTACCG TGGGCCTCCATTTCCAGTCTGAAGGTTGTGACCAGTGAACACCTTGAACTTCTCAAACATATGCACGCTG TGGGGGAGAAGGTGATAGCAGATTTTGCTGGATCCAGCAAACTGCGCTTCCGATTGGGCTACCATGCCAT TCCCAGCATGAGCCACGTACATCTTCATGTGATCAGCCAGGATTTTGATTCTCCTTGCCTTAAAAACAAA AAGCATTGGAATTCTTTTAATACAGAATACTTTCTGGAATCACAAGCTGTGATCAAGATGGTTCAGGAAG CCGGCAGAGTGACTGTTAAAGATGGCACTTGTGAGCTCTTGAAGCTGCCTCTCCGTTGCCATGAGTGTCA GCAGCTGCTGCCTTCCATCCCGCAGCTGAAAGAGCACCTCAGGAAGCACTGGGGCGGGTGA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-MluI
ACCN:	NM_001025445
Insert Size:	831 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).
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:	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:	NM_001025445.2, NP_001020616.1
RefSeq Size:	5549 bp
RefSeq ORF:	831 bp
Locus ID:	66408
UniProt ID:	Q7TQC5
Cytogenetics:	4 A5
Gene Summary:	DNA-binding protein involved in single-strand DNA break repair, double-strand DNA break repair and base excision repair. Resolves abortive DNA ligation intermediates formed either at base excision sites, or when DNA ligases attempt to repair non-ligatable breaks induced by reactive oxygen species. Catalyzes the release of adenylate groups covalently linked to 5'-phosphate termini, resulting in the production of 5'-phosphate termini that can be efficiently rejoined (PubMed:16964241). Also able to hydrolyze adenosine 5'-monophosphoramidate (AMP-NH(2)) and diadenosine tetraphosphate (ApppppA), but with lower catalytic activity (By similarity). Likewise, catalyzes the release of 3'-linked guanosine (DNAppG) and inosine (DNAppI) from DNA, but has higher specific activity with 5'-linked adenosine (AppDNA) (By similarity).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (3) uses an alternate splice site in the 5' coding region and initiates translation at a downstream start codon, compared to variant 1. It encodes isoform c, which has a shorter N-terminus compared to 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.