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Product datasheet for MC219722

Spast (NM_016962) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Spast (NM_016962) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Spast
Synonyms:	mKIAA1083; Spg4
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin

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Fully Sequenced ORF:

>MC219722 representing NM_016962
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCCGCGATCGCC

ATGAGTTCTCCGGCCGGACGACGGAAGAAGAAAGGCTCGGGCGGCGCGAGCCCGGCGCCCGCCAGGCCTC
CGCCCCCCGCCGCGGTCCCCGCCCCTGCCGCCGGCCCGGCCCCTGCGGCCGGCTCGCCGCCTAAGCGGAA
CCCGTCTTCTTTCTCGTCCCCGCTGGTCGTCGGCTTCGCCCTGCTGCGCCTGCTGGCCTGCCACCTGGGG
CTCCTCTTCGCGTGGCTCTGCCAGCGCTTCTCCCGCGCCCTCATGGCCGCCAAGAGGAGCTCCGGGACCG
CGCCGGCGCCCGCCTCGCCCTCGCCCCCAGAGCCCGGACCGGGTGGCGAGGCCGAGAGCGTCCGCGTCTT
CCACAAGCAGGCCTTCGAGTACATCTCCATTGCCCTGCGCATCGACGAGGAAGAGAAAGGACAGAAGGAA
CAAGCTGTGGAATGGTATAAGAAAGGTATCGAAGAACTGGAAAAAGGAATCGCTGTTATAGTTACGGGCC
AAGGTGAACAGTATGAAAGAGCTAGACGTCTTCAAGCCAAAATGATGACTAATTTAGTTATGGCCAAGGA
CCGTTTACAACTTCTAGAGAAGCTGCAACCAGTTTTGCAATTTTCCAAGTCACAGACGGACGTCTATAAC
GAGAGTACTAACCTGACATGCCGCAATGGACATCTCCAGTCAGAAAGTGGAGCAGTTCCGAAGAGGAAAG
ACCCCTTAACACATGCTAGTAATTCATTGCCTCGATCAAAAACTGTCCTGAAAAGTGGCTCCGCAGGGCT
CTCCGGTCACCACAGGGCGCCTAGTTGCAGTGGTTTGTCCATGGTTTCTGGAGCAAGACCGGGACCTGGT
CCTGCAGCTACCACACATAAGGGTACTCCAAAACCAAATAGAACCAACAAACCTTCTACTCCCACAACTG
CAGTTCGGAAAAAGAAAGACTTGAAAAATTTTAGGAATGTGGACAGCAATCTTGCTAACCTTATAATGAA
TGAAATTGTTGACAATGGGACAGCTGTTAAGTTTGATGACATAGCCGGGCAGGAGCTGGCAAAGCAAGCG
CTGCAGGAGATTGTCATCCTTCCTTCTCTGCGGCCTGAGTTGTTCACAGGGCTCAGAGCTCCTGCTAGAG
GCTTGTTACTCTTCGGTCCGCCAGGAAACGGAAAAACAATGCTGGCTAAAGCAGTAGCTGCAGAGTCTAA
TGCGACCTTTTTCAACATAAGTGCTGCCAGTTTAACTTCAAAATATGTGGGAGAAGGAGAGAAATTGGTG
AGAGCTCTCTTTGCTGTGGCTCGAGAACTTCAACCATCTATAATTTTTATAGATGAAGTTGACAGTCTTT
TGTGTGAGAGACGGGAAGGGGAGCACGACGCTAGCAGACGGCTAAAGACGGAATTTTTAATAGAATTTGA
CGGGGTGCAATCTGCTGGAGATGACAGAGTACTTGTAATGGGTGCAACTAACAGGCCCCAAGAGCTTGAT
GAAGCTGTTCTCAGGCGTTTCATTAAACGGGTATATGTGTCCTTACCAAATGAGGAGACAAGACTCCTTC
TGCTTAAAAACCTGTTGTGTAAACAAGGAAGTCCACTGACCCAAAAAGAACTCGCACAGCTTGCTAGAAT
GACCGATGGATACTCTGGAAGTGATCTGACCGCTTTGGCCAAGGATGCAGCCCTGGGTCCTATCCGAGAA
CTGAAGCCAGAGCAGGTGAAGAATATGTCTGCCAGTGAGATGAGAAATATTCGATTATCTGACTTCACAG
AATCCTTAAAAAAGATAAAACGCAGTGTGAGTCCTCAGACCTTAGAAGCATACATACGCTGGAACAAGGA
TTTTGGAGACACCACTGTTTAA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI

ACCN: NM_016962

Insert Size: 1842 bp

OTI Disclaimer:	Due to the inherent nature of this plasmid, standard methods to replicate additional amounts of DNA in E. coli are highly likely to result in mutations and/or rearrangements. Therefore, OriGene does not guarantee the capability to replicate this plasmid DNA. Additional amounts of DNA can be purchased from OriGene with batch-specific, full-sequence verification at a reduced cost. Please contact our customer care team at custsupport@origene.com or by calling 301.340.3188 option 3 for pricing and delivery. The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. More info
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.
RefSeq:	NM_016962.2, NP_058658.2
RefSeq Size:	4693 bp
RefSeq ORF:	1842 bp
Locus ID:	50850
UniProt ID:	Q9QYY8
Cytogenetics:	17 E2

Gene Summary:

ATP-dependent microtubule severing protein that specifically recognizes and cuts microtubules that are polyglutamylated (PubMed:19141076 PubMed:20530212). Preferentially recognizes and acts on microtubules decorated with short polyglutamate tails: severing activity increases as the number of glutamates per tubulin rises from one to eight, but decreases beyond this glutamylation threshold (By similarity). Severing activity is not dependent on tubulin acetylation or detyrosination (By similarity). Microtubule severing promotes reorganization of cellular microtubule arrays and the release of microtubules from the centrosome following nucleation (By similarity). It is critical for the biogenesis and maintenance of complex microtubule arrays in axons, spindles and cilia (By similarity). SPAST is involved in abscission step of cytokinesis and nuclear envelope reassembly during anaphase in cooperation with the ESCRT-III complex (By similarity). Recruited at the midbody, probably by IST1, and participates in membrane fission during abscission together with the ESCRT-III complex (By similarity). Recruited to the nuclear membrane by IST1 and mediates microtubule severing, promoting nuclear envelope sealing and mitotic spindle disassembly during late anaphase (By similarity). Required for membrane traffic from the endoplasmic reticulum (ER) to the Golgi and endosome recycling (By similarity). Recruited by IST1 to endosomes and regulates early endosomal tubulation and recycling by mediating microtubule severing (By similarity). Probably plays a role in axon growth and the formation of axonal branches (PubMed:18234839).[UniProtKB/Swiss-Prot Function]
Transcript Variant: This variant (2) uses an alternate in-frame splice site in the 5' coding region compared to variant 1. This results in a shorter protein (isoform 2) compared to isoform 1.
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.