

Product datasheet for **MC227727**

Brap (NM_001289543) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Brap (NM_001289543) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Brap
Synonyms:	3010002G07Rik; BRAP2; IMP
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin



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Fully Sequenced ORF: >MC227727 representing NM_001289543
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGGATCGCC**

ATGACCTCCCTAAAAGAAGACGTTTCGGCGCAGTGCCATGTGTGTCTCACCGTCCCTGCCACCATGA
CCAGTCATGACCTTATGAAGTTTGTGCCCCATTCAATGATGTAATTGAACAAATGAAAATCATCAGGGA
CTCTACTCCGAATCAGTACATGGTACTGATCAAGTTCAGTGCGCAGGCTGATGCAGACAGTTTCTACATG
GCGTGCAATGGCCGCGAGTTCAACTCAATCGAAGATGACGTCTGCCAGCTGGTCTATGTGGAAAGGGCTG
AAGTGCTGAAATCTGAAGATGGCGCCAGCTCCCCGTGATGGACCTGACGGAGCTGCCAAAGTGCAGTGT
GTGTCTGGAGCGGATGGACGAGTCTGTGAATGGCATCCTCACCACCCTCTGCAACCACAGCTTCCATAGT
CAGTGTCTGCAGCGGTGGGATGACACCACGTGCCTGTGTGCCGATACTGTCAAACGCCAGAGCCAGTGG
AAGAAAACAAATGTTTTGAGTGTGGTGTCCAGGAAAACCTCTGGATTTGTTAATATGCGGCCACATAGG
CTGTGGGCGGTACGTGAGTCGGCATGCTTACAAGCACTTTGAGGAGACCCAGCACACATACGCCATGCAG
CTACCAACCATCGAGTCTGGGACTATGCTGGAGATAATTATGTCCATCGACTGGTTGCAAGCAAGACGG
ATGGAAAGATCGTTACAGTACGAGTGTGAGGGCGACACCTGCCAGGAAGAGAAGATAGATGCCTTACAGTT
AGAGTACTCGTACCTGTTGACAAGCCAGCTGGAATCGCAGCGGATATACTGGGAGAACAAAATCGTGCGC
ATAGAGAAGGACACGGCAGAGGAGATTAACAACATGAAGACCAAGTTTAAAGAGACCATCGAGAAGTGTG
ACAGCCTGGAGCTCAGGCTCAGTGACCTCCTGAAGGAGAAGCAGTCTGTGGAAAGGAAGTGTACCCAGCT
GAACACCAGAGTGGCCAAGCTCAGCACGGAGCTGCAGGAGGAGCAGGAGCTGAACAAGTGTCTGCGGCC
AACCAGCTGGTGTCTGAGAACCAGCTCAAGGAGGAGGAGAAGCTGCTGAAGGAGACCTGTGCCAGAAAG
ACCTGCAGATCACCGAGATCCAGGAGCAGCTGCGCGATGTCATGTTCTACCTGGAGACACAGCAGCAGAT
CAGCCACCTGCCTGCGGAGACGAGGAGGAGATCCAGGAAGGCCAGATCAACATCGCCATGGCCTCAGCG
CCCAACCCACCCTCTCCGGGGCCGGTGGGAAGCTGCAGTCCAGAAAGGGCCGAGCAAGAGGGGCAAGT
GA

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: Sgfl-Mlul

ACCN: NM_001289543

Insert Size: 1332 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:

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_001289543.1](#), [NP_001276472.1](#)

RefSeq Size: 3541 bp

RefSeq ORF: 1332 bp

Locus ID: 72399

Cytogenetics: 5 F

Gene Summary: Negatively regulates MAP kinase activation by limiting the formation of Raf/MEK complexes probably by inactivation of the KSR1 scaffold protein. Also acts as a Ras responsive E3 ubiquitin ligase that, on activation of Ras, is modified by auto-polyubiquitination resulting in the release of inhibition of Raf/MEK complex formation. May also act as a cytoplasmic retention protein with a role in regulating nuclear transport (By similarity).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) lacks an exon in the 5' coding region and initiates translation at a downstream in-frame start codon, compared to variant 1. The encoded isoform (2) has a shorter N-terminus than 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.