

Product datasheet for **MC204570**

Bub1 (NM_009772) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Bub1 (NM_009772) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Bub1
Synonyms:	AL022991; Bub1a; C80208; D2Xrf87
Mammalian Cell Selection:	Neomycin
Vector:	PCMV6-Kan/Neo (PCMV6KN)
E. coli Selection:	Kanamycin (25 ug/mL)



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Fully Sequenced ORF:

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>BC029116
CGAGACTCGGGTTAGGGGCTGATGGGGAGTTTGGTCGGCGGCTGGTGGGGTATTTCCGCCCTGCGCGTT
TTTTCTCGTCATGGACAACCTAGAAAATGTCTTTCGCATGTTTGAAGCCCATATGCAAAGCTACACGGGT
AATGACCCACTTGGAGAAATGGGAAAAGCTTTATAAAGTGGGTAGAAGAGAAATTTTCTGACAATAAAGAA
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AACCCAGGAATTGGAACCAAGTCATCATATATATACATGTCCTGGCAGGGCATCTGGAAGCCAGGGAG
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TAGTAAATTTAACTCTCACTTTGAATCCTATTTTTTTCATACTTACTATTTATGTATGTTTAAAAAAA
TAAAGCCCATATGATATACCCAAAAAATAAAAAAAAAAAAAAAAAAAAAA
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Restriction Sites:

RsrII-NotI

ACCN:	NM_009772
Insert Size:	3180 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).
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>BC029116</u> , <u>AAH29116</u>
RefSeq Size:	3405 bp
RefSeq ORF:	3180 bp
Locus ID:	12235
UniProt ID:	<u>O08901</u>
Cytogenetics:	2 62.1 cM

Gene Summary:

Serine/threonine-protein kinase that performs 2 crucial functions during mitosis: it is essential for spindle-assembly checkpoint signaling and for correct chromosome alignment. Has a key role in the assembly of checkpoint proteins at the kinetochore, being required for the subsequent localization of CENPF, BUB1B, CENPE and MAD2L1. Required for the kinetochore localization of PLK1. Required for centromeric enrichment of AUKRB in prometaphase. Plays an important role in defining SGO1 localization and thereby affects sister chromatid cohesion. Acts as a substrate for anaphase-promoting complex or cyclosome (APC/C) in complex with its activator CDH1 (APC/C-Cdh1). Necessary for ensuring proper chromosome segregation and binding to BUB3 is essential for this function. Can regulate chromosome segregation in a kinetochore-independent manner. Can phosphorylate BUB3. The BUB1-BUB3 complex plays a role in the inhibition of APC/C when spindle-assembly checkpoint is activated and inhibits the ubiquitin ligase activity of APC/C by phosphorylating its activator CDC20. This complex can also phosphorylate MAD1L1. Kinase activity is essential for inhibition of APC/CCDC20 and for chromosome alignment but does not play a major role in the spindle-assembly checkpoint activity. Mediates cell death in response to chromosome missegregation and acts to suppress spontaneous tumorigenesis. Essential during early and later stages of embryonic development. Necessary for postimplantation embryogenesis and proliferation of primary embryonic fibroblasts and plays an important role in spermatogenesis and fertility.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) uses an alternate in-frame splice site in the mid-coding region, compared to variant 1, resulting 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.