

Product datasheet for MC225390

Nipbl (NM_201232) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Nipbl (NM_201232) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Nipbl
Synonyms:	Idn3
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
Fully Sequenced ORF:	>MC225390 representing NM_201232 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGGATCGC**C

ATGAATGGGGATATGCCCATGTCCCCATAACTACGCTTGCGGGGATTGCTAGTCTTACGGACCTCCTGA
ACCAGCTGCCTCTCCATCTCCTTTACCTGCTACAACACAAAGAGCCTCCTCTTAATTCACGAATAGC
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 TGGATTACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-RsrII
 ACCN: NM_201232
 Insert Size: 8076 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:	NM_201232.2 , NP_957684.1
RefSeq Size:	10762 bp
RefSeq ORF:	8076 bp
Locus ID:	71175
UniProt ID:	Q6KCD5
Cytogenetics:	15 A1
Gene Summary:	<p>Plays an important role in the loading of the cohesin complex on to DNA (PubMed:29094699). Forms a heterodimeric complex (also known as cohesin loading complex) with MAU2/SCC4 which mediates the loading of the cohesin complex onto chromatin. Plays a role in cohesin loading at sites of DNA damage. Its recruitment to double-strand breaks (DSBs) sites occurs in a CBX3-, RNF8- and RNF168-dependent manner whereas its recruitment to UV irradiation-induced DNA damage sites occurs in a ATM-, ATR-, RNF8- and RNF168-dependent manner (By similarity). Along with ZNF609, promotes cortical neuron migration during brain development by regulating the transcription of crucial genes in this process. Preferentially binds promoters containing paused RNA polymerase II. Up-regulates the expression of SEMA3A, NRP1, PLXND1 and GABBR2 genes, among others (PubMed:28041881).[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (b) differs in the 3' coding region and 3' UTR, compared to variant 1. The encoded isoform (b) has a shorter and distinct C-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.</p>