

Product datasheet for **SC128030**

CDC14B (NM_003671) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	CDC14B (NM_003671) Human Untagged Clone
Tag:	Tag Free
Symbol:	CDC14B
Synonyms:	Cdc14B1; Cdc14B2; CDC14B3; hCDC14B
Vector:	<u>pCMV6-XL4</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Cell Selection:	None
Fully Sequenced ORF:	>NCBI ORF sequence for NM_003671, the custom clone sequence may differ by one or more nucleotides

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ATGAAGCGGAAAAGCGAGCGGGTTCGAGCTGGGCCGCCGCCCCCTGCTCGCGGCGCTGCTCGTCGA
CCTCGCCGGGTGTGAAGAAGATCCGCAGCTCCACGCAGCAAGACCCGCGCCGGGACCCCAAGGACGA
CGTGTACCTGGACATCACCGATCGCCTTTGTTTTGCCATTCTCTACAGCAGACCAAGAGTGCATCAAA
GTACATTATTTACAGATAGATAATGAACCTGAATATGAGAATTCTACGCAGATTTGGACCACTCAAT
TGGCAATGGTTTACAGATATTGTTGCAAGATCAATAAGAAATTAAGTCCATTACAATGTTAAGGAAGAA
AATTGTTCAATTTACTGGCTCTGATCAGAGAAAACAAGCAATGCTGCCTTCCTTGTGGATGCTACATG
GTTATATATTTGGGAGAACCCAGAAGAAGCATATAGAATTAATCTTTGGAGAGACATCCTATATTC
CTTTCAGAGATGCTGCCTATGGAAGTTGCAATTTCTACATTACACTTCTTGACTGTTTTCATGCAGTAAA
GAAGGCAATGCAGTATGGCTTCCTTAATTTCAACTCATTTAACCTTGATGAATATGAACACTATGAAAA
GCAGAAAATGGAGATTTAAATTGGATAATACCAGACCGATTTATTGCCTTCTGTGGACCTCATTCAAGAG
CCAGACTTGAAAGTGGTTACCACCAACATTCTCCTGAGACTTATATTCAATATTTAAGAATCACAATGT
TACTACCATTATTCGCTGAATAAAAGGATGTATGATGCCAAACGCTTTACGGATGCTGGCTTCGATCAC
CATGATCTTTTCTTGGCGATGGCAGCACCCCTACTGATGCCATTGTCAAAGAATTCATAGATATCTGTG
AAAATGCTGAGGGTGCCATTGCAGTACATTGCAAAGCTGGCCTTGGTCCGACGGGCACTCTGATAGCCTG
CTACATCATGAAGCATTACAGGATGACAGCAGCCGAGACCATTGCGTGGGTGAGGATCTGCAGACCTGGC
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TTCGTCAGAAGTTAAAGGGGCAGGAGAATGGACAACACAGAGCAGCCTTCTCAAACCTTCTCTGGCGT
TGATGACATTTCCATAAATGGGGTCGAGAATCAAGATCAGCAAGAACCCGAACCGTACAGTGATGATGAC
GAAATCAATGGAGTGACACAAGGTGATAGACTTCGGGCCTTGAAAAGCAGAAGACAATCCAAAACAAACG
CTATTCCTCTCACTCTCCATTTCAAGGACTAAAACAGTCTTGGCTTAA
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5' Read Nucleotide Sequence:

>OriGene 5' read for NM_003671 unedited
 GCCATGGTCGTGGCCCCCTGACGGGCCGCGCCGCCCTCCATGAAGCGGAAAAGCGAGCGG
 CCGTTCGAGCTGGGCCCGCCGCCCCCTGCTCGCGGCGCTGCTCGTGCACCTCGCCGGGT
 GTGAAGAAGATCCGCAGCTCCACGCAGCAAGACCCGCGCCCGGGACCCCAAGGACGAC
 GTGTACCTGGACATCACCAGATCGCCTTTGTTTTGCCATTCTACAGCAGACCAAGAGT
 GCATCAAATGTACATTATTTTACGATAGATAATGAACTGAATATGAGAACTTCTACGCA
 GATTTTGGACCCCTCAATCTGGCAATGGGTTACAGATATTGGTGCANGATCAATCAAGAA
 TTAAGTCCATTACAATGTTAAGGAAGAAAATCGTTCATTTTACTGGCTCTGATCAGAGA
 AAACAAGCAAATGCTGCCTTTCTTGTGGATGCTCCATGGGTATATATTTGGGGGAA
 CCCCCTGAAGAAGCCTTCAATATTAACCTTTGGAGAGACCTTCTTATTTCTTTCC
 AGAGATGCCTCCCTTTGGTATGTTGCTTTTCTCCTTACACTTCTTTGCTGTCTCTT
 GCCCCCCACCAGGGCCTGCCTCCTGGGTTTTCTGTTTTCTGTTCTCTTTTTTCTCTCC
 TTTCTCTTTTCTCCTTGTGCTCTTTCTCACCTTGCTTCTCTTCTGTGGCTCGTCT
 CCTCTCCGCCCTGCCTCTGCCTCTGTACCNGTCTCCTCGCCTCCCCCTCCTCCGACTTC
 GTTCTCTCCTTCTCGCTCGCCTCTTCTCCTTCTCCTCCCGATCTTACTTATTATCG
 CTTTTCTCGCTCTTCCACTTCAATATAACTATAA

3' Read Nucleotide Sequence:

>OriGene 3' genomic read for NM_003671 unedited
 TTACATGATTGTAATTATACAACCTTCCACTATTCGATATTTTGTATAAAACCAGTTACA
 ACCCACAAAGATTTTCAAATGTGACAATATGTATCAAACACATACATATGCAAAGTTTAC
 ACGCCATTAGGAAGCTTTATCTTAAAAATACCTTCAGGAAAAATAAACATTCATTCAACCA
 GTTCTCTTGGCTTTAAAAAATATGATTAGAAATATACGCTGTAAAAAATAAAGACAA
 TGATTGATCAATACTGATCAGTTACATTTTAAACTTTTAAATAATCTGTACATGAGTGCA
 GGTANATAAAAGTCTGCACATTATTAATAGAAAAGTGCAGTACTATCATCGGATGAACA
 TGCTGTGACAAACCCTACCAGTAATTCAGGAGTAATTTCTCCCGAGTTAGGTGACA
 CGTCCAGTGTAAACCACATCTGGCGTCTGCGCCCTTCGCGCTTCCACCCCGTTAC
 CGTGTGTCATGCGTGCCTCCCTCCCTCCCTATTGACGCGCTCTGCTTCTCATGCATCCTCT
 GATTCCTGACCCCACTCCGCCCGCGCTTCTCCCTCCTTGCCATCTCCTTCTTCTCTCC
 TCGGCCCTACGCCTTCCCTTCTCCCTCAGCCCCCCCCCGCCTGCTGTGTTTTTTTCCCC
 CGTGTACCATGCTCCTCCCCCCCCGCTCCCCCTCACATATCCGCCTTCTCATCCC
 CCTTCTTTTCCCTCCCTCGCCTCCACTTCCCCCCCCCCCCCTTCTCCCCCTCCC
 CCCCCCGCGCCACTCTTTTCTGCTCGCGCTCACGCCCCGCCCCCTCCTCTCCGCGTTC
 TTCGCCAGTTTCTTCTCTTTCCCCCTCCGCTCCTTATTCTTCTTTCTTTTCTTTT
 CCCTTTCTTTTCTTTTCCCATCCCGTCCCTTTTCTCCTCTCCCCCTCCGGGCCGG
 TTCTCCCTCTTCTCTCC

Restriction Sites:

NotI-NotI

ACCN:

NM_003671

Insert Size:

4700 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:

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_003671.2](#), [NP_003662.1](#)

RefSeq Size: 5472 bp

RefSeq ORF: 5472 bp

Locus ID: 8555

UniProt ID: [O60729](#)

Cytogenetics: 9q22.32-q22.33

Domains: Y_phosphatase, DSPc, PTPc_motif

Protein Families: Druggable Genome, Phosphatase

Protein Pathways: Cell cycle

Gene Summary: The protein encoded by this gene is a member of the dual specificity protein tyrosine phosphatase family. This protein is highly similar to *Saccharomyces cerevisiae* Cdc14, a protein tyrosine phosphatase involved in the exit of cell mitosis and initiation of DNA replication, which suggests the role in cell cycle control. This protein has been shown to interact with and dephosphorylates tumor suppressor protein p53, and is thought to regulate the function of p53. Alternative splice of this gene results in 3 transcript variants encoding distinct isoforms. [provided by RefSeq, Jul 2008]

Transcript Variant: This variant (1) lacks an alternate in-frame exon, compared to variant 2, resulting in a shorter protein (isoform 1) that lacks an internal segment in the C-terminal region, compared to isoform 2. 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.