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Product datasheet for SC336348

ZWILCH (NM_001287823) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	ZWILCH (NM_001287823) Human Untagged Clone
Tag:	Tag Free
Symbol:	ZWILCH
Synonyms:	hZwilch; KNTC1AP
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)

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Fully Sequenced ORF:

>SC336348 representing NM_001287823.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

GTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTA
CCGAGGAGATCTGCCGCCGCGATCGCCGGCGCGCCC
ATGGCTCACAATCCTAATATGACCCATTTGAAGATTAATCTGCCAGTTACTGCCCTTCCTCCCCTTTGG
GTAAGATGTGACAGTTCAGATCCTGAAGGTACTTGTTGGCTAGGAGCTGAGCTTATCACAACAAACAAC
AGCATTACAGGAATTGTCTTATATGTGGTCAGTTGTAAAGCTGATAAAAATTATTCTGTAAATCTTGAA
AACCTAAAAAATTTACACAAGAAAAGACATCACTTGTCTACTGTAACATCCAAAGGCTTTGCCCAGTAT
GAGCTCTTTAAGTCCTCTGCCTTGGATGATACAATCACAGCATCACAAACTGCGATCGCTTTGGATATT
TCCTGGAGTCCTGTGGATGAGATTCTTCAAATCCCTCCACTCTCTTCAACTGCAACTCTGAATATTAAA
GTGGAATCAGGAGAGCCCAGAGGTCCTTTGAATCATCTCTACAGAGAACTGAAATTTCTTCTTGTTTTG
GCTGATGGTTTGAGGACTGGTGTCACTGAATGGCTCGAGCCCCTGGAAGCAAAATCTGCTGTTGAACTT
GTTCAGGAATTTCTGAATGACTTAAATAAGCTGGATGGATTTGGTGATTCTACAAAAAAAGACACTGAG
GTTGAGACCTTGAAGCATGACACTGCTGCAGTCGATCGTTCCGTCAAGCGTCTTTTCAAAGTTCGGAGT
GATCTTGATTTTGCTGAGCAACTGTGGTGCAAAATGAGCAGTAGTGTGATTTCATACCAAGACTTGGTG
AAGTGTTTCACATTGATCATCCAGAGTCTACAACGTGGTGATATACAGCCATGGCTCCATAGTGGAAGT
AACAGTTTACTAAGTAAGCTCATTCATCAGTCTTATCATGGAACCATGGACACAGTTTCTCTCAGTGGG
ACTATTCCAGTTCAAATGCTTTTGGAAATTGGTTTGGACAAACTAAAGAAAGATTATATCAGTTTTTTC
ATAGGTCAGGAACTTGCATCTTTGAATCATTTGGAATACTTCATTGCTCCATCAGTAGATATACAAGAA
CAGGTTTATCGTGTCCAAAAACTCCACCATATTCTAGAAATATTAGTCAGTTGCATGCCTTTCATTAAA
TCTCAACATGAACTCCTCTTTTCTTTAACACAGATCTGCATAAAGTATTACAAACAAAATCCTCTTGAT
GAGCAACACATTTTTCAGCTGCCAGTCAGACCAACTGCTGTAAAGAACTTATATCAAAGTGAGAAGCCA
CAGAAATGGAGAGTGGAAATATATAGTGGTCAAAAGAAGATTAAGACAGTTTGGCAACTGAGTGACAGC
TCACCCATAGACCATCTGAATTTTCACAAACCTGATTTTTCGGAATTAACACTAAACGGTAGCCTGGAA
GAAAGGATATTCTTTACTAACATGGTTACCTGCAGCCAGGTGCATTTCAAGTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites: AscI-MluI

ACCN: NM_001287823

Insert Size: 1434 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_001287823.1

RefSeq Size:	3152 bp
RefSeq ORF:	1434 bp
Locus ID:	55055
UniProt ID:	Q9H900
Cytogenetics:	15q22.31
MW:	54.2 kDa
Gene Summary:	Essential component of the mitotic checkpoint, which prevents cells from prematurely exiting mitosis. Required for the assembly of the dynein-dynactin and MAD1-MAD2 complexes onto kinetochores. Its function related to the spindle assembly machinery is proposed to depend on its association in the mitotic RZZ complex (PubMed:15824131).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (4) lacks an internal exon, compared to variant 1. This difference results in predicted translation initiation at a downstream in-frame start site through ribosomal re-initiation or leaky scanning. The encoded isoform (2) is shorter than isoform 1. Variants 2, 3, and 4 encode the same protein. 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.