

## Product datasheet for **SC301670**

### **C6ORF173 (CENPW) (NM\_001012507) Human Untagged Clone**

#### Product data:

|                           |  |
|---------------------------|--|
| Product Type:             | Expression Plasmids  |
| Product Name:             | C6ORF173 (CENPW) (NM_001012507) Human Untagged Clone   |
| Tag:                      | Tag Free   |
| Symbol:                   | C6ORF173   |
| Synonyms:                 | C6orf173; CENP-W; CUG2   |
| Mammalian Cell Selection: | None   |
| Vector:                   | <u><a href="#">pCMV6-XL5</a></u>   |
| E. coli Selection:        | Ampicillin (100 ug/mL)   |
| Fully Sequenced ORF:      | >OriGene sequence for NM_001012507 edited<br>TCGACTGAAGAAGCGTCATACGGACCGGATTGTTTTCGCTGCCCCAGTGTCCCCGGAGCT<br>TGTGTGCGATACAGAGAGCACCTCGGAAGCTGAGGCAGCTGGTACTTGACAGAGAGATG<br>GCGCTGTCGACCATAGTCTCCCAGAGGAAGCAGATAAAGCGGAAGGCTCCCCGTGGCTTT<br>CTAAAGCGAGTCTTCAAGCGAAAAGCCTCAACTTCGTCTGGAGAAAAGTGGTGACTTA<br>TTGGTCCATCTGAACTGTTTACTGTTTGTTCATCGATTAGCAGAAGAGTCCAGGACAAAC<br>GCTTGTGCGAGTAAATGTAGAGTCATTAACAAGGAGCATGACTGGCCGAGCAAAGGTA<br>ATTCTAAAGAAGAGCAGAGGTTAGAAGTCAAAGAACATATTCTTGAAAGTTATGATGCAT<br>TCTTTTGGGTGGTAACAGATCATAAAGACATTTTTTACACATCAGTTAATATGGGATTAT<br>TAAATATTGGCTATAAAAAAAAAAAAAAAAAAAAAA |
| Restriction Sites:        | NotI-NotI  |
| ACCN:                     | NM_001012507   |
| Insert Size:              | 500 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:           | The ORF of this clone has been fully sequenced and found to be a perfect match to NM_001012507.1.  |
| 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).   |



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**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\\_001012507.1](#), [NP\\_001012525.1](#)

**RefSeq Size:** 531 bp

**RefSeq ORF:** 267 bp

**Locus ID:** 387103

**UniProt ID:** [Q5EE01](#)

**Cytogenetics:** 6q22.32

**Gene Summary:** Component of the CENPA-NAC (nucleosome-associated) complex, a complex that plays a central role in assembly of kinetochore proteins, mitotic progression and chromosome segregation (By similarity). The CENPA-NAC complex recruits the CENPA-CAD (nucleosome distal) complex and may be involved in incorporation of newly synthesized CENPA into centromeres (By similarity). Part of a nucleosome-associated complex that binds specifically to histone H3-containing nucleosomes at the centromere, as opposed to nucleosomes containing CENPA. Component of the heterotetrameric CENP-T-W-S-X complex that binds and supercoils DNA, and plays an important role in kinetochore assembly. CENPW has a fundamental role in kinetochore assembly and function. It is one of the inner kinetochore proteins, with most further proteins binding downstream. Required for normal chromosome organization and normal progress through mitosis.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) uses an alternate in-frame splice site in the 5' coding region, compared to variant 1, resulting in an isoform (b) that is shorter than 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.