

## Product datasheet for **SC214545**

### ORP150 (HYOU1) (NM\_001130991) Human 3' UTR Clone

#### Product data:

Product Type:	3' UTR Clones
Product Name:	ORP150 (HYOU1) (NM_001130991) Human 3' UTR Clone
Symbol:	ORP150
Synonyms:	GRP-170; Grp170; HSP12A; IMD59; ORP-150; ORP150
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_001130991
Insert Size:	1435 bp



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**Insert Sequence:** >SC214545 3'UTR clone of NM\_001130991  
 The sequence shown below is from the reference sequence of NM\_001130991. The complete sequence of this clone may contain minor differences, such as SNPs.  
 Blue=Stop Codon Red=Cloning site

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GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
AAGCGGCCTTTGAAGAACGACGAACTATAACCCCACTCTGTTTTCCCAATTCATCTCCACCCCTTC
CCCCACCACTTCTATTTATTTAACATCGAGGGTTGGGGGAGGGTTGGTCTGCCCTCGGCTGGAGTTC
CTTTCTCACCCCTGTGATTTGGAGGTGTGGAGAAGGGGAAGGAGGGACAGCTCACTGGTTCCTTCTGC
AGTACCTCTGTGGTTAAAAATGGAACTGTTCTCCTCCCAAGCCCACTCCCTGTTCCTACCCATATA
GGCCCTAAATTTGGAAAAATCACTATTAATTTCTGAATCCTTTGCCTGTGGGTAGGAAGAGAATGGCT
GCCAGTGGCTGATGGTCCCGGTGATGGGAAGGGTATCAGTTGCTGGGGAGTTTCCACTTCTCTGG
TGATTGTTCCCTCCCTTCTCCTCCACCATGCGATGAGCATCCTTTCAGGCCAGTGTCTGCAGAG
CCTCAGTTACCAGTTTTGGTTTCTGAGTGCCTATCTGTGCTCTTCCCTCCCTCTGCGGGCTTCTCTGC
TCTGAGCCTCCCTCCCAATTCCCATCCAGCTCCTTCCCACTGGGTTTCTTGGCTTCCGCGAGAAA
TTGGGCAGTTCTCTGCCCTTGCCTAAAAGCCTGTACCTCTGGATTGGCGGAAGTAAATCTGGAAGGAT
TCTCACTCGTATTTCCACCCCTAGTGGCCAGAGGAGGGAGGGGCACAGTGAAGAAGGGAGCCACCAC
CTCTCCGAAGAGGAAAGCCACGTAGAGTGGTTGGCATGGGGTCCAGCATCGTGCAAGCTGTGCATAA
TCTGCATTTCCAGCAGCCTGGTACCCAGGTTCTGTAACTCCCTGCCTCCTCTCTTCTGTGTGT
TCTGCTCCTCCAGACAGAGCCTTCCCTCACCCCTGACCCCTGGGCTGACCAAAATGTGCTTTCTA
CTGTGAGTCCCTATCCCAAGATCCTGGGAAAGGAGAGACCATGGTGTGAATGTAGAGATGCCACCTCC
CTCTCTGAGGCAGCCTGTGGATGAAGGAGGAGGGTCAAGGGCTGGCCTTCTCTGTGCATCACTCTG
CTAGGTTGGGGGCCCCGACCCACCATACTACGCTAGGGAGCCCGTCCCTCCAGTATTCGCTGTAG
CAGGAGCTAGGGCTGCTGCCTCAGCTCCAAGACAAGAATGAACCTGGCTGTGTCAGTCATTTTGTCTTT
TCTTTTTTTTTTTTTTTTGGCCACATTGGCAGAGATGGGACCTAAGGGTCCACCCCTCACCCACCCC
CACCTCTCTGTATGTTTGAATCTTTTCAAGTAGCTGTTGATGCTGGTTGGACAGGTTTGTGCAAAATG
TACTTTGCTCCATTGTTAATTGAGAACTGTTTCAATAAAATATTCTTTTCTACA
ACGCGTAAGCGGCCGCGCATCTAGATTCAAGAAAATGACCGACCAAGCGACGCCCAACTGCCATCA
CGAGATTCGATTCCACCGCCCTTCTATGAAAGG
  
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**Restriction Sites:** SgfI-MluI

**OTI Disclaimer:** Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences, e.g., single nucleotide polymorphisms (SNPs).

**Components:** The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.

**RefSeq:** [NM\\_001130991.3](#)

**Summary:**

The protein encoded by this gene belongs to the heat shock protein 70 family. This gene uses alternative transcription start sites. A cis-acting segment found in the 5' UTR is involved in stress-dependent induction, resulting in the accumulation of this protein in the endoplasmic reticulum (ER) under hypoxic conditions. The protein encoded by this gene is thought to play an important role in protein folding and secretion in the ER. Since suppression of the protein is associated with accelerated apoptosis, it is also suggested to have an important cytoprotective role in hypoxia-induced cellular perturbation. This protein has been shown to be up-regulated in tumors, especially in breast tumors, and thus it is associated with tumor invasiveness. This gene also has an alternative translation initiation site, resulting in a protein that lacks the N-terminal signal peptide. This signal peptide-lacking protein, which is only 3 amino acids shorter than the mature protein in the ER, is thought to have a housekeeping function in the cytosol. In rat, this protein localizes to both the ER by a carboxy-terminal peptide sequence and to mitochondria by an amino-terminal targeting signal. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Mar 2014]

**Locus ID:**

10525

**MW:**

53.3