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Product datasheet for SC204216

HSPA6 (NM_002155) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	HSPA6 (NM_002155) Human 3' UTR Clone
Symbol:	HSPA6
Synonyms:	HSP70B'
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_002155
Insert Size:	334 bp
Insert Sequence:	>SC204216 3'UTR clone of NM_002155 The sequence shown below is from the reference sequence of NM_002155. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC ACCGGCCCCATCATTGAGGAGGTTGATTGAATGGCCCTTCGTGATAAGTCAGCTGTGACTGTCAGGGCT ATGCTATGGGCCTTCTAGACTGTCTTCTATGATCCTGCCCTTCAGAGATGAACTTTCCCTCCAAAGCTA GAACTTTCTTCCCAGGATAACTGAAGTCTTTTGACTTTTTGCGGGGAGGGCGGTTCATCCTCTTCTGCT TCAAATAAAAAGTCATTAATTTATTAAAACTTGTGTGGCACTTTAACATTGCTTTCACCTATATTTTGT GTACTTTGTTACTTGCATGTATGAATTTTGTTATGTAAAATATAGTTATAGACCTAAA ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG
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_002155.5

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Summary: Molecular chaperone implicated in a wide variety of cellular processes, including protection of the proteome from stress, folding and transport of newly synthesized polypeptides, activation of proteolysis of misfolded proteins and the formation and dissociation of protein complexes. Plays a pivotal role in the protein quality control system, ensuring the correct folding of proteins, the re-folding of misfolded proteins and controlling the targeting of proteins for subsequent degradation. This is achieved through cycles of ATP binding, ATP hydrolysis and ADP release, mediated by co-chaperones. The affinity for polypeptides is regulated by its nucleotide bound state. In the ATP-bound form, it has a low affinity for substrate proteins. However, upon hydrolysis of the ATP to ADP, it undergoes a conformational change that increases its affinity for substrate proteins. It goes through repeated cycles of ATP hydrolysis and nucleotide exchange, which permits cycles of substrate binding and release (PubMed:26865365).[UniProtKB/Swiss-Prot Function]

Locus ID: 3310

MW: 12.1