

Product datasheet for RN200393

Gpx4 (NM_017165) Rat Untagged Clone

Product data:

OriGene Technologies, Inc.

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Product Type:	Expression Plasmids
Product Name:	Gpx4 (NM_017165) Rat Untagged Clone
Symbol:	Gpx4
Synonyms:	gpx-4; Gshpx-4; Phgpx; snGpx
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
Fully Sequenced ORF:	<pre>>RN200393 representing NM_017165 Red=Cloning site Blue=ORF Orange=Stop codon</pre>
	TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCC <mark>GCGATCGC</mark> C
	ATGAGCTGGGGCCGTCTGAGCCGCTTATTGAAGCCAGCACTGCTGTGCGGGGCTCTGGCTGTGCCTGGCC TGGCTGGC
	ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT ACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	Sgfl-Mlul
ACCN:	NM_017165
Insert Size:	594 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). The expression of this clone is

not guaranteed due to the nature of selenoproteins.



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ORIGENE Gpx4 (NM_017165) Rat Untagged Clone – RN200393

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:	 Centrifuge at 5,000xg for 5min. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. Close the tube and incubate for 10 minutes at room temperature. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 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:	<u>NM 017165.2, NP 058861.3</u>
RefSeq Size:	923 bp
RefSeq ORF:	594 bp
Locus ID:	29328
UniProt ID:	<u>P36970</u>
Cytogenetics:	7q11
Gene Summary:	The protein encoded by this gene belongs to the glutathione peroxidase family, members of which catalyze the reduction of hydrogen peroxide, organic hydroperoxides and lipid hydroperoxides, and thereby protect cells against oxidative damage. Several isozymes of this

which catalyze the reduction of hydrogen peroxide, organic hydroperoxides and lipid hydroperoxides, and thereby protect cells against oxidative damage. Several isozymes of this gene family exist in vertebrates, which vary in cellular location and substrate specificity. This isozyme has a high preference for lipid hydroperoxides and protects cells against membrane lipid peroxidation and cell death. It is also required for normal sperm development; thus, it has been identified as a 'moonlighting' protein because of its ability to serve dual functions as a peroxidase, as well as a structural protein in mature spermatozoa. Disruption of this gene in mouse spermatocytes is associated with male infertility. This isozyme is also a selenoprotein, containing the rare amino acid selenocysteine (Sec) at its active site. Sec is encoded by the UGA codon, which normally signals translation termination. The 3' UTRs of selenoprotein mRNAs contain a conserved stem-loop structure, designated the Sec insertion sequence (SECIS) element, that is necessary for the recognition of UGA as a Sec codon, rather than as a stop signal. Transcript variants resulting from alternative splicing or use of alternate promoters have been described to encode isoforms with different subcellular localization. Pseudogenes of this locus have been identified on chromosomes 1, 10 and 14. [provided by RefSeq, Jan 2019]

Transcript Variant: This variant (1) represents the predominant transcript and encodes the canonical isoform A (also known as phGPx or the L-form), which is localized to the mitochondria (PMID:9988735). Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.

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