

Fig2-09 cDNA information (A2)

Stop codon: S strands for presence of stop codon; L strands for not presence of stop codon.

cDNA information

C-NT2RP4000259

Clone ID	FLJ ID	Accession No.
NT2RP4000259	FLJ14777	AK027683

1228 bp A 328 C 330 G 280 T 282 N 0 (0X)

[ORF](#) [BLAST](#) [Pfam](#) [PROSITE](#) [PSORT](#) [SignalP](#)

ORF

ORF	Start	End	Len(aa)	Stop codon	ATGPr	Identity to Kozak rule
1	40	603	187	S	0.90	KK

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>C-NT2RP4000259
MVAATYAAALLLLAAACAAQDEQDFYDFKAVNIRKILYSLEKRYGYSVLYVVAASECGFT
DQHYRALDQLDRDLGPHFNYLAFPCNDFGQDEPDSNKEIESFARTYSVSPFMFSK IAY
TGTGAHPAFKYLADTSGKEPTNFWIKYLYAPDGVYVANDPTVYSVEEYRPIALYRKL I
LLKREDL

>C-NT2RP4000259
CTCTTTGCCCTCGCGAAGCCGCGCCACCTCCGGAACAAGCCATGGTGGGGCGGACGGTGGCA
GGGGGCTGGCTGCTGCTGCTGCTGGCTGGCGCTCGCGCAGCAGGAGCAGACTGTACGAC
TTCAAGGGGCTCAACATCCGGGGCAACTGGTGTGGTGGAGAGTACCGCGGATCGGTG
TCCCTGGTGGTGAATGCTGGCAGCGAGTGGCGCTTACAGACAGCAGCAGTACCGAGCCCTG
CAGCAGCTGGAGCGAGACCTGGGGCCCAACACTTTAAGCTGCTGCTTCCCTGCCAAG
CAGTTGGCCCAACGAGCCTGACAGCAACAGAGATGAGAGCTTTGCCCGCCGACC
TACAGTGTCTCAATCCCATGTTAAGAAATTGCAAGTTCAGCTCAGCGGACTGCTGCCATCCT
GCCCTCAAGTACCTGGCCAGACTTCTGGGAAGAGCCACCCTGGAATCTTGGGAAGTAC
CTAGTAGCCCGAGATGGAAAGGTGTAGGGGCTTGGGACCAACTGTGTGCTGAGGAG
GTGACAGCCCAAGATCACAGCCTGTGAGGAAGCTCATCTACTGAAGCCGAGAGACTTA
TAAACCCAGGCTGCTCCTCCACACCTCATCCCGCCACCTGTGTGGGGCTGACCAAT
GCAAACTCAAAATGGTCTTCAAAAGGAGAGACCACTGACTCCTCCTTACTCTTAT
GCCATTGGTCCCATCTTCTGTGGGGAAAAATGTAGTATTTGATTTTGAATCTT
ACAGCAACAATAGGAACCTCCTGGCAATGAGAGCTCTTGACCAAGTGAATCACCAGCGGA
TACCAAGCTGCTTCCCAACAAAAATGTGGCAATAGAGATATCAAGCAATAATCTCC
CACCACCAAGCTTCTGAACTGGGACCAATGATTAACCTCATAGGCTGTTGTGAGGATTA
GGATCAAAATACCTGTCAAAAGTGGCTAGGCAAGTGGCAGCAATAGGAGGATTCATGAA
CATTTTTGCATATAAACCAAAAATAACTGTATCAATAAAAACTGCATCCCAACATG
AATTTCCAGCGGATGATAATCCAGCCAAAGTTAGTTGTTGTTATTTCTCTGTATTA
TTTTCTTATTACAAAAAATGCAAGTTCATTGTATAAATCCCAACAATACCTCAGCAT
ATAAAAAAAAATGAAAGTATCCTCCTC
```

BLAST

SwissProt

Top hit

Definition: Glutathione peroxidase 7 prec
Acc: Q86SL4
Keyword: Oxidoreductase; Peroxidase; S
OMIM No:
E-value: 1e-106
Consensus Len:187
Identity: 100

Second hit

Definition: Glutathione peroxidase 7 prec
Acc: Q89LJ6
Keyword: Oxidoreductase; Peroxidase; S
OMIM No:
E-value: 2e-95
Consensus Len:166
Identity: 89

Third hit

Definition: Probable phospholipid hydropo
Acc: O48648
Keyword: Mitochondrion; Oxidoreductase
OMIM No:
E-value: 3e-30
Consensus Len:86
Identity: 40

Refseq

Top hit

Definition: glutathione peroxidase 7 [Homo
Acc: NP_058511.2
LOCUS ID: 2882
OMIM No:
E-value: 1e-106
Consensus Len:187
Identity: 100

Second hit

Definition: glutathione peroxidase 7 [Mus
Acc: NP_077180.1
LOCUS ID: 67905
OMIM No:
E-value: 8e-96
Consensus Len:166
Identity: 89

Third hit

Definition: glutathione peroxidase 4 [Homo
Acc: NP_002076.1
LOCUS ID: 2879
OMIM No: 188322
E-value: 2e-26
Consensus Len:95
Identity: 44

Pfam

Pfam1

Pfam ID: PF00255.9
Pfam Name: GSHPx
Pfam Description: Glutathione peroxidase
IN..EN(aa): 24..133
E-Value: 4.9e-48
InterProID: IPR000889

PROSITE

Prosit1

Second tree info: Glutathione peroxidases active sit
PDOC No: PDOC00396
Third tree info: GLUTATHIONE_PEROXID_1
PS No: PS00460
IN..EN(aa): 45..60
E-value: 1E-9.02
Quality: Medium quality motif.

Prosit2

Second tree info: Glutathione peroxidases signature
PDOC No: PDOC00396
Third tree info: GLUTATHIONE_PEROXID_2
PS No: PS00763
IN..EN(aa): 82..89
E-value: 1E-8.85
Quality: Medium quality motif.

PSORT

Psort1

Signal: Yes
Cleavage site(aa):21

SignalP

Signal peptide: YES
Cleavage site(aa):19

SOSUI

Number of Transmembrane: 2
Transmembrane1
N Terminal: 1
C Terminal: 23

Transmembrane2
N Terminal: 36
C Terminal: 58

GO

GO1

GO No: GO:0004601
Category: Molecular Function
Term: peroxidase activity
Tree:
molecular_function
->antioxidant activity
->peroxidase activity

GO2

GO No: GO:0004602
Category: Molecular Function
Term: glutathione peroxidase activity
Tree:
molecular_function
->antioxidant activity
->peroxidase activity
->glutathione peroxidase activity

GO3

GO No: GO:0004602
Category: Molecular Function
Term: glutathione peroxidase activity
Tree:
molecular_function
->catalytic activity
->oxidoreductase activity
->oxidoreductase activity, acting on peroxide as acceptor
->peroxidase activity
->glutathione peroxidase activity

ATGPr: Assessing protein coding region integrity
(A.A. Salamov, T. Nishikawa, M.B. Swindells (1998)
Assessng protein coding region integrity in cDNA
sequencing projects. *Bioinformatics*, 14, 384-390)