

10 Nov 1999

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The PTEN tumor suppressor acts as a phospholipid phosphatase.

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PTEN and the tumor suppressor balancing act

Tumors are formed by an abnormal proliferation of undifferentiated cells. At the molecular level, this represents a failure to adequately control cell growth and division.

In normal cells, there are many genes that code for regulatory proteins which are responsible for maintaining the delicate balance required for cell division to proceed at the right time and in the right place. Among these, proto-oncogenes stimulate the cell division cycle, while tumor suppressor genes act as brakes. When these types of genes fail to do their job, perhaps as a result of a mutation, the control mechanisms break down and cancerous growth can ensue.

Because many proto-oncogenes are kinases (enzymes that have a stimulatory effect in cell signaling pathways), the existence of a tumor suppressor gene that acts as a phosphatase (an enzyme that counteracts the action of kinases) was predicted. However, it was almost ten years after the discovery of the retinoblastoma gene - the first tumor suppressor to be described - that a gene product answering to this phosphatase description, was found.

The *PTEN* gene, located on chromosome 10q23, is missing or mutated in a variety of human cancers, including glioblastoma (a type of brain cancer), endometrial (uterine) tumors and prostate cancer, as well as in Cowden disease cells. PTEN stands for "phosphatase and tensin homolog". As well as having phosphatase activity, PTEN is similar to tensin, a protein that interacts with actin filaments at sites of intense signaling activity on the inner surface of cells known as focal adhesions.

PTEN taken from tumors often has a disabling mutation in the phosphatase domain, showing that it is important for normal PTEN function. But what might PTEN's substrate be? While, PTEN can act on both proteins and lipids *in vitro*, its favorite physiological substrate appears to be phosphatidylinositol 3,4,5-trisphosphate (PIP3), a lipid signaling molecule.

PIP3 is generated by the enzyme phosphoinositide kinase (PI3-kinase), which itself is activated by stimulatory signals emanating from the cell surface, often from focal adhesions. PIP3 activates yet another kinase called PKB/Akt - a proto-oncogene product. So if PTEN fails to deactivate PIP3 because of a mutation in its phosphatase domain, downstream signals are not switched off, and therefore PKB/Akt remains in the 'on' state. In this case, PKB/Akt can continue to stimulate downstream proteins such as transcription factors and glucose transporters, which could lead to enhanced cell growth.

PTEN is not exclusively a human protein. In the worm *Caenorhabditis elegans*, a PTEN homolog seems to

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help control lifespan and dauer formation (a hibernation state). Use of such animal models will help further investigate PTEN and could give clues to outstanding questions, such as how PTEN itself is regulated.

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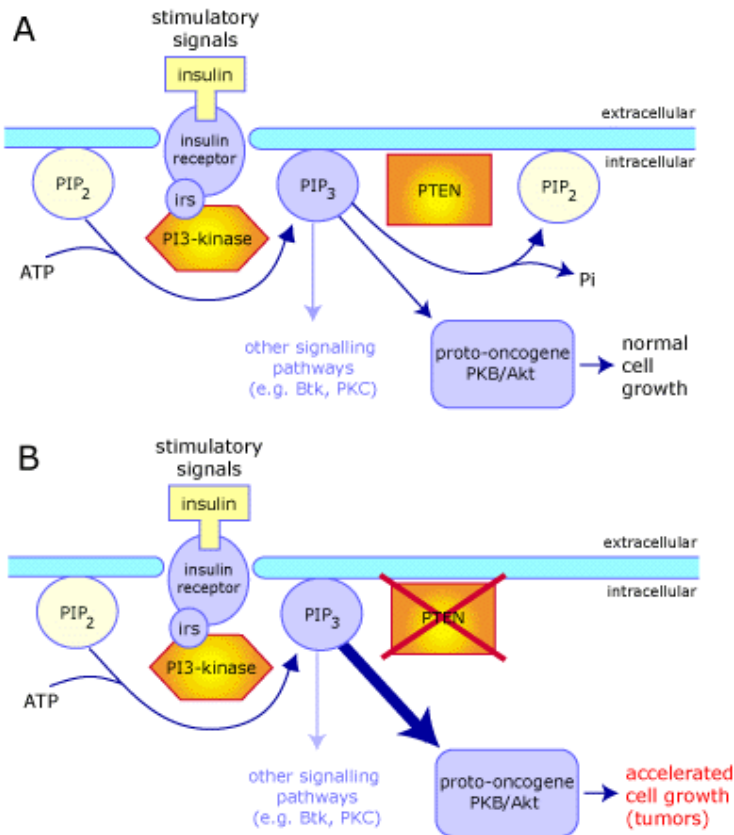


Figure 1. The PTEN tumor suppressor gene acts as a phospholipid phosphatase. (A) Under normal growth conditions, stimulatory signals from the insulin receptor activate the enzyme phosphoinositide kinase (PI3-kinase), which phosphorylates phosphatidylinositol 4,5-bisphosphate (PIP₂) to generate phosphatidylinositol 3,4,5-trisphosphate (PIP₃), a lipid signaling molecule. Downstream, PIP₃ activates several effectors, including the proto-oncogene product PKB/Akt. The role of PTEN is to dephosphorylate PIP₃, acting as a negative control on PKB/Akt activation. **(B)** If a mutation in PTEN renders it unable to carry out its phosphatase function, PIP₃ can no longer be deactivated, so continues to propagate its signal downstream. This may result in the continued activation of PKB/Akt, which, in combination with other factors, could lead to increased cell growth and possible tumor development.

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1-20 items of 97 1 page of 5

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[Figure](#)
[Blast tutorial](#)

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 PTEN interactions with focal adhesion kinase and suppression of the extracellular matrix-dependent phosphatidylinositol 3-kinase/Akt cell survival pathway.
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 Zyxin and vinculin distribution at the cell-extracellular matrix attachment complex (CMAX) in corneal epithelial tissue are actin dependent.
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 Agonist-stimulated cytoskeletal reorganization and signal transduction at focal adhesions in vascular smooth muscle cells require c-Src.
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This is the query page for a BLAST search. The sequence of PTEN protein is entered in the textbox below. The database to be searched can be selected from the following pull-down menu, as can the format that the sequence is submitted in. Click on the "Submit Query" button below the textbox to find similar sequences to this query in the database.

Database

The amino acid query sequence is [filtered](#) for low complexity regions by default.

Enter here your **amino acid sequence** as

```

LLHRGKFLK QE LDFYGEVRIKDRKGVTPSQRRYVYYSYLLAN
HLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSG
PTRREDKFMFYFEPQPLPVCVDIKVEFFHKQNKMLKDKMFFHWVN
TFFIPGPEETSEKVENGLCDQEIDSICSIERADNDKEYLVLTTLTK
NDLDKANKDKANRYFSPNFKVLYFTKTVEEPSNPEASSSTSVTPD
VSDNEPDHYRYSDTTDSDPENEPFDEDQHTQITKV
    
```


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The options below are for advanced users. In this example, the number of descriptions has been set to 100, with 50 alignments returned. If no parameters are changed or selected, then BLAST is run in default mode.

Advanced options for the BLAST server:

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Descriptions Alignments

Expect value for inclusion in PSI-BLAST iteration 1

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Query= gj5051943|gb|AAD38372.1| PTEN (403 letters) **Database:** Non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR 419,232 sequences; 128,539,543 total letters

Below are the results from a PSI-BLAST (see Altschul et al., 1997) search of the non-redundant database using PTEN as the query sequence.

The E value is a statistical measure of likelihood that the sequences listed below are truly similar to the query, rather than found by chance alone. The lower the E value, the greater the confidence that the protein found is a biologically significant match.

E-value threshold for inclusion in PSI-Blast iteration 1: 0.001

E-value threshold for inclusion in PSI-Blast iteration 2:

PSI-BLAST constructs a similarity matrix from the significant hits found in a BLAST search and uses this matrix to search the database in a second round of BLASTing. Each round of PSI-BLAST that uses the matrix to search the database is called an iteration.

Distribution of 113 Blast Hits on the Query Sequence

Mouse-over to show defline and

Color Key for Alignment Scores

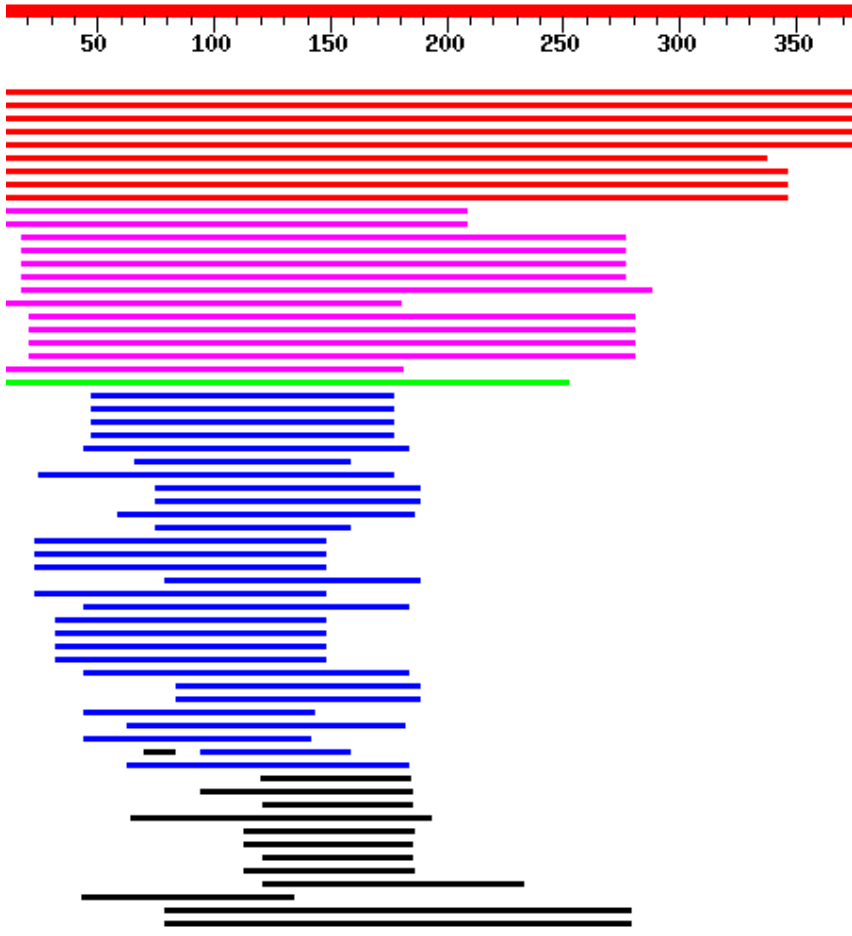
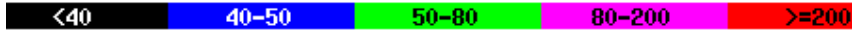


Figure legend

The above summary of the BLAST results represents proteins that match the query sequence as colored bars, with the most similar hit uppermost and appearing in red. Pink, green, blue and black bars follow, representing proteins in decreasing order of similarity. Hatched areas indicate a gap in

similarity i.e., two or more distinct regions of similarity were found within the same protein hit. Moving the mouse over the bars will display the name of the matching protein found in the textbox above.

Click [here](#) to view alignments.
Click [here](#) to see the analysis of this BLAST result.

PTEN and the tumor suppressor balancing act

The PTEN phosphatase catalytic site resembles that of inositol lipid phosphatases

Tensin <i>Gallus gallus</i> (chick)	(31%= 52%+) -VVVLHN KGNRGR LGVVVAAYM- (31%= 52%+)
PTEN <i>Homo sapiens</i> (human)	VAAIH CKAGKGR TGVMICAYL
PTEN <i>Xenopus laevis</i> (frog)	VAAIH CKAGKGR TGVMICAYL
PTEN <i>Drosophila melanogaster</i> (fruit fly)	VVAVH CKAGKGR TGTMICAYL
DAF-18 <i>Caenorhabditis elegans</i> (worm)	VIAVH CKAGKGR TGVMICALL
Dual-specificity phosphatase (human)	AIAVH CKAGLGR TGTLI-ACY
Dual-specificity phosphatase (Brewer's yeast)	KIAVH CKAGLGR TGCLIGAHL
Protein tyrosine phosphatase consensus (C-x ₅ -R)	--C-----R--
Inositol phosphatase consensus (Ref. 1)	--CK--K-R--

The phosphatase domain from the human PTEN query sequence is aligned with a selection of the proteins found using PSI-BLAST. The consensus sequences for protein tyrosine phosphatases (C-x₅-R) and inositol phosphatases (CK-x₂-K-x-R) are shown at the bottom of the figure. Both the PTENs and the dual-specificity phosphatases have the protein tyrosine phosphatase consensus sequence (red), but the PTEN sequences are distinct from the dual-specificity phosphatases because they also contain the two lysine (K) residues of the inositol phosphatase consensus (pink). While tensin is similar to PTEN over a large portion of the sequence (31% of amino acid residues are identical, 52% are similar), it contains neither the dual-specificity phosphatase nor the inositol phosphatase consensus sequence.

[Back to BLAST result](#)

Human PTEN was used to search the non-redundant protein sequence database using the PSI-BLAST program [3] with standard parameters. Sequences included in the multiple alignment of the phosphatase domain were selected from output from the first iteration. The multiple sequence alignment was constructed using ClustalW [4].

[1] Maehama, T. and Dixon, J.E. (1999) PTEN: a tumour suppressor that functions as a phospholipid phosphatase *Trends Cell Biol.* 9, 125-128

[2] Fauman, E.B. and Saper, M.A. (1996) Structure and function of the protein tyrosine phosphatases *Trends Biochem. Sci.* 21, 413-417

[3] Altschul, S. F. et al. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* 25, 3389-402

[4] Higgins, D. G., Thompson, J. D. and Gibson, T. J. (1996) Using CLUSTAL for multiple sequence alignments. *Methods Enzymol.* 266, 383-402

About the alignments

Use of human PTEN protein as the query sequence finds several PTEN homologs in a number of different organisms, the eponymous tensin from chicken, and several protein phosphatases. Some of the protein phosphatases have been demonstrated by experiment, while others have been identified on the basis of sequence analysis alone.

The match with the top score is to itself (reassuringly) - the lower the e-value or the higher the score, the higher the chance that the similarity is biologically relevant. Clicking on the scores will take you to the alignments for each of the top ten hits (as requested in our query). Clicking on the ID numbers on the left will display the sequence record at the NCBI site.

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or

Click [here](#) to see the analysis of this BLAST search.

Sequences with E-value BETTER than threshold

Sequences producing significant alignments:	Score	E
	(bits)	Value
ref NP_000305.1 PPTEN phosphatase and tensin homolog (mutated ...	799	0.0
sp O08586 PTEN_MOUSE PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN...	798	0.0
gi 2772900 (AF017185) protein tyrosine phosphatase and tensin h...	795	0.0
gi 2655025 (AF019083) phosphatase and tensin homolog 2 [Homo sa...	777	0.0
gb AAD46165.1 AF144732_1 (AF144732) protein/lipid phosphatase P...	688	0.0
gi 2407318 (AF017999) putative protein tyrosine phosphatase hom...	662	0.0
gb AAD45364.1 AF161259_1 (AF161259) PTEN3 [Drosophila melanogas...	272	5e-72
gb AAD45362.1 AF161257_1 (AF161257) PTEN1 [Drosophila melanogas...	272	5e-72
gb AAD45363.1 AF161258_1 (AF161258) PTEN2 [Drosophila melanogas...	272	5e-72
gi 2702362 (AF036706) contains similarity to Gallus gallus card...	184	9e-46
emb CAA10315 (AJ131181) DAF-18 protein [Caenorhabditis elegans...	184	9e-46
pir A57075 tensin - chicken (fragment) > gi 63805 emb CAA79215 ...	136	4e-31
sp Q04205 TENS_CHICK TENSIN > gi 619577 (M96625) cardiac muscle ...	136	4e-31
pir A54970 tensin, cardiac muscle - chicken	136	4e-31
pir S27939 tensin - chicken > gi 212752 (M74165) tensin [Gallus...	131	1e-29
dbj BAA83027.1 (AB028998) KIAA1075 protein [Homo sapiens]	131	1e-29
emb CAA22831 (AL035226) protein-tyrosine phosphatase [Schizosa...	121	9e-27
ref NP_005246.1 PGAK cyclin G associated kinase > gi 2506080 db ...	117	2e-25
sp P97874 GAK_RAT CYCLIN G-ASSOCIATED KINASE > gi 1902913 dbj BA ...	116	4e-25
dbj BAA32318 (AB007942) KIAA0473 protein [Homo sapiens]	110	2e-23
sp Q27974 AUXI_BOVIN AUXILIN > gi 2136718 pir S68983 auxilin - ...	108	7e-23
sp P53916 YNM8_YEAST HYPOTHETICAL 50.2 KD PROTEIN IN CPT1-SPC98...	85	1e-15
sp P91301 YLPK_CAEEL HYPOTHETICAL 30.3 KD PROTEIN F46F11.3 IN C...	71	1e-11
dbj BAA09533 (D55715) phosphoprotein phosphatase [Saccharomyce...	46	7e-04
gi 171183 (M61194) CDC14 [Saccharomyces cerevisiae]	46	7e-04
emb CAA52971 (X75077) putative protein tyrosine phosphatase [S...	46	7e-04
sp Q00684 CC14_YEAST PROBABLE PROTEIN-TYROSINE PHOSPHATASE CDC1...	46	7e-04

Sequences with E-value WORSE than threshold

sp P80994 VH01_RACVI PROTEIN-TYROSINE PHOSPHATASE (LATE PROTEIN...	44	0.002
ref NP_003454.1 PPTP4A1 Protein tyrosine phosphatase IVA1 > gi ...	44	0.002
gi 1125812 (U42846) Similar to protein-tyrosine phosphatase. [C...	43	0.003
gi 1246236 (L48937) ptp-IV1b, PTP-IV1 gene product [Homo sapiens]	43	0.003
ref NP_003470.1 PPTP4A2 Protein tyrosine phosphatase IVA2 > gi ...	43	0.003
sp P29352 PTN8_MOUSE HEMATOPOIETIC CELL PROTEIN-TYROSINE PHOSPH...	43	0.004
emb CAA07417 (AJ007016) protein tyrosine phosphatase [Rattus n...	43	0.004
pir I68523 protein tyrosine phosphatase - human (fragment) > gi ...	43	0.006
ref NP_003662.1 PCDC14B S. cerevisiae CDC14 homolog, gene B > g...	43	0.006
gb AAC16661.1 (AF064104) Cdc14B2 phosphatase [Homo sapiens]	43	0.006
gb AAC16662.2 (AF064105) Cdc14B3 phosphatase [Homo sapiens]	43	0.006
sp P33064 VH01_VARV PROTEIN-TYROSINE PHOSPHATASE > gi 419331 pir...	42	0.007
gb AAD15415 (AC006024) similar to Cdc14B1 phosphatase; similar...	42	0.007
sp P20495 VH01_VACCC PROTEIN-TYROSINE PHOSPHATASE (LATE PROTEIN...	42	0.010
ref NP_003663.1 PCDC14A S. cerevisiae CDC14 homolog, gene A > g...	42	0.010
gi 2992632 (AF035645) mPRL-3 [Mus musculus]	42	0.010
gb AAC16659.1 (AF064102) Cdc14A2 phosphatase [Homo sapiens]	42	0.010
gb AAC16660.1 (AF064103) Cdc14A3 phosphatase [Homo sapiens]	42	0.010
gb AAD49217.1 (AF122013) dual-specificity phosphatase [Homo sa...	42	0.010
gi 3406430 (AF041434) hPRL-3 [Homo sapiens]	41	0.013
dbj BAA03003 (D13903) MPTPdelta [Mus musculus]	41	0.017
sp P07239 VH01_VACCV PROTEIN-TYROSINE PHOSPHATASE (LATE PROTEIN...	41	0.017
sp P24656 PTP_NPVAC PROTEIN-TYROSINE PHOSPHATASE (BVP) > gi 9303...	41	0.022
bbs 126561 BVP-protein tyrosine phosphatase [Autographa califor...	41	0.022
gi 2062356 (U64896) protein-tyrosine phosphatase [Anagrapha fal...	41	0.022
gb AAD31775.1 AF124517_2 (AF124517) H1L homolog [sheeppox virus]	41	0.022
dbj BAA08253 (D45413) brain-enriched membrane-associated prote...	40	0.029

gb AAC63820.1 (L33180) PTP=Phosphotyrosine Phosphatase=AcMNPV ...	40	0.038
gb AAD14737 (AF125960) contains similarity to dual specificity...	39	0.049
gi 450583 (L22437) protein tyrosine phosphatase [Gallus gallus]...	39	0.085
dbj BAA82559.1 (AB019126) sPTPR2B [Ephydatia fluviatilis]	39	0.085
gi 3300096 (AF063249) glomerular mesangial cell receptor protei...	38	0.11
sp P18052 PTPA_MOUSE PROTEIN-TYROSINE PHOSPHATASE ALPHA PRECURS...	38	0.15
pir JC1285 protein-tyrosine-phosphatase (EC 3.1.3.48), recepto...	38	0.15
sp Q03348 PTPA_RAT PROTEIN-TYROSINE PHOSPHATASE ALPHA PRECURSOR...	38	0.15
pdb 1YFO A Chain A, Receptor Protein Tyrosine Phosphatase Alpha...	38	0.15
prf 1701300A protein Tyr phosphatase [Homo sapiens]	38	0.19
ref NP_002827.1 PPTPRA protein tyrosine phosphatase, receptor ...	38	0.19
emb CAA37447 (X53364) tyrosine phosphatase precursor [Homo sap...	38	0.19
ref NP_002831.1 PPTPRF protein tyrosine phosphatase, receptor ...	38	0.19
emb CAA38065 (X54130) protein-tyrosine phosphatase [Homo sapiens]	38	0.19
sp P18433 PTPA_HUMAN PROTEIN-TYROSINE PHOSPHATASE ALPHA PRECURS...	38	0.19
gi 533265 (L32180) tyrosine phosphatase [Rabbit fibroma virus]	38	0.19
gi 205131 (M60103) leukocyte common antigen related protein [Ra...	37	0.25
bbs 104679 LAR, leukocyte common antigen-related protein=transm...	37	0.25
gi 392566 (U00477) LAR receptor-linked tyrosine phosphatase [Ra...	37	0.25
pir S46216 leukocyte antigen-related protein precursor - rat >...	37	0.25
prf 1711408A protein Tyr phosphatase LAR [Homo sapiens]	37	0.25
emb CAA58537 (X83546) leukocyte common antigen-related protein...	37	0.25
pir A56493 leukocyte common antigen-related protein (LAR) - ra...	37	0.25
ref NP_002833.1 PPTPRH protein tyrosine phosphatase, receptor ...	37	0.25
pir A57068 protein-tyrosine-phosphatase (EC 3.1.3.48), recepto...	37	0.25
dbj BAA24090 (AB009903) PTEN/MMAC1 [Homo sapiens]	37	0.25
emb CAA38068 (X54133) protein-tyrosine phosphatase [Homo sapiens]	37	0.33
ref NP_002830.1 PPTPRD protein tyrosine phosphatase, receptor ...	37	0.33
emb CAA63304 (X92546) stpA [Salmonella typhi]	37	0.33
gi 1519054 (U63293) protein tyrosine phosphatase SptP [Salmonel...	37	0.33
dbj BAA20333 (D78610) protein tyrosine phosphatase epsilon C [...	37	0.33
gi 2702271 (AC003033) unknown protein [Arabidopsis thaliana]	37	0.33
gi 4100632 (AF001846) lymphoid phosphatase LyP1 [Homo sapiens]	37	0.33
gi 4100634 (AF001847) lymphoid phosphatase LyP2 [Homo sapiens]	37	0.33
sp P16621 LAR_DROME PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR...	36	0.43
gi 483922 (U09135) protein tyrosine phosphatase alpha [Xenopus ...	36	0.43
ref NP_003575.1 PDUSP11 dual specificity phosphatase 11 (RNA/R...	36	0.43
emb CAA20521.1 (AL031369) putative protein [Arabidopsis thaliana]	36	0.43
gb AAD23008.1 AC006585_3 (AC006585) putative protein [Arabidop...	36	0.43
dbj BAA82558.1 (AB019125) sPTPR4 [Ephydatia fluviatilis]	36	0.43
pir C54689 protein-tyrosine-phosphatase (EC 3.1.3.48), recepto...	36	0.56
gi 2695655 (AF017083) receptor tyrosine phosphatase [Hirudo med...	36	0.56
gi 2731378 (U28739) similar to calcium channel protein and prot...	36	0.56
gi 2731379 (U28739) C17G10.4c [Caenorhabditis elegans] >gi 2738...	36	0.56
gi 2731380 (U28739) similar to calcium channel protein and prot...	36	0.56
gi 4056425 (AC005322) ESTs gb H36249, gb AA59732 and gb AA65121...	36	0.56

Alignments

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ref|NP_000305.1|PPTEN| phosphatase and tensin homolog (mutated in multiple advanced
cancers 1) >gi|2811005|sp|O00633|PTEN_HUMAN
PROTEIN-TYROSINE PHOSPHATASE PTEN (MUTATED IN MULTIPLE
ADVANCED CANCERS 1) >gi|1916326 (U92435) MMAC1 [Canis
familiaris] >gi|1916328 (U92436) MMAC1 [Homo sapiens]
>gi|1916352 (U93051) putative protein tyrosine
phosphatase [Homo sapiens] >gi|2039370 (U96180) protein
tyrosine phosphatase [Homo sapiens] >gi|2197039
(AF000734) putative protein tyrosine phosphatase [Homo
sapiens] >gi|4240387 (AF067844) PTEN [Homo sapiens]
>gi|5051943|gb|AAD38372.1| (AF143315) PTEN [Homo
sapiens]
Length = 403

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Score = 799 bits (2042), Expect = 0.0
Identities = 378/403 (93%), Positives = 378/403 (93%)

```

Query: 1  MTAAIKEIVSRNKRKYQEDGFDDLDTYIYPNIIAMGFPAERLEGVYRNNIDVVRFLLDSK 60
Sbjct: 1  MTAAIKEIVSRNKRKYQEDGFDDLDTYIYPNIIAMGFPAERLEGVYRNNIDVVRFLLDSK 60

Query: 61  HKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCELDLQWLSEDDNHVA 120
Sbjct: 61  HKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCELDLQWLSEDDNHVA 120

Query: 121  AIHCKAGKGRGTVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGGVTIPSRQRYVYVYYSY 180
Sbjct: 121  AIHCKAGKGRGTVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGGVTIPSRQRYVYVYYSY 180

Query: 181  LLKNHLDYRFPVALLFHKMMFETIPMFSGGTCNPQFVVCQKVKIYSSNSGPTRRREDKFMY 240
Sbjct: 181  LLKNHLDYRFPVALLFHKMMFETIPMFSGGTCNPQFVVCQKVKIYSSNSGPTRRREDKFMY 240

Query: 241  FEFPQPLPVCVDIKVEFFHKQNKMLKKDKMFHFVWNTFFFIPGPEETSEKVENGLSCDQEI 300
Sbjct: 241  FEFPQPLPVCVDIKVEFFHKQNKMLKKDKMFHFVWNTFFFIPGPEETSEKVENGLSCDQEI 300

Query: 301  DSICSIERANDNKEYLVLTLTXXXXXXXXXXXXXXXXRYFSPNFVKVLYFTKTVVEEPSNPEAX 360

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DSICSIERADNDKEYLVLT LT RYFSPNFKVKLYFTKTVEEPSNPEA
Sbjct: 301 DSICSIERADNDKEYLVLT LT KNDLKDANKDKANRYFSPNFKVKLYFTKTVEEPSNPEAS 360
Query: 361 XXXXXXXXXXXXNEPDHYRSDTTSDPENEPFDEQHTQITKV 403
NEPDHYRSDTTSDPENEPFDEQHTQITKV
Sbjct: 361 SSTSVPDVSNDNEPDHYRSDTTSDPENEPFDEQHTQITKV 403

[sp|008586|PTEN_MOUSE](#) PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN (MUTATED IN MULTIPLE
ADVANCED CANCERS 1) >gi|1916330 (U92437) MMAC1 [Mus
musculus]
Length = 403

Score = 798 bits (2038), Expect = 0.0
Identities = 377/403 (93%), Positives = 378/403 (93%)

Query: 1 MTAIKEIVSRNKRRYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDVVRFLDSK 60
MTAIKEIVSRNKRRYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDVVRFLDSK
Sbjct: 1 MTAIKEIVSRNKRRYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDVVRFLDSK 60
Query: 61 HKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVA 120
HKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVA
Sbjct: 61 HKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVA 120
Query: 121 AIHCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTPSQRRYVYVYYSY 180
AIHCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTPSQRRYVYVYYSY
Sbjct: 121 AIHCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTPSQRRYVYVYYSY 180
Query: 181 LLKNHLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQKVKIYSSNSGPTREDDKFMY 240
LLKNHLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQKVKIYSSNSGPTREDDKFMY
Sbjct: 181 LLKNHLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQKVKIYSSNSGPTREDDKFMY 240
Query: 241 FEFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLCDQEI 300
FEFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLCDQEI
Sbjct: 241 FEFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLCDQEI 300
Query: 301 DSICSIERADNDKEYLVLT LT XXXXXXXXXXXXRYFSPNFKVKLYFTKTVEEPSNPEAX 360
DSICSIERADNDKEYLVLT LT RYFSPNFKVKLYFTKTVEEPSNPEA
Sbjct: 301 DSICSIERADNDKEYLVLT LT KNDLKDANKDKANRYFSPNFKVKLYFTKTVEEPSNPEAS 360
Query: 361 XXXXXXXXXXXXNEPDHYRSDTTSDPENEPFDEQHTQITKV 403
NEPDHYRSDTTSDPENEPFDEQHTQITKV
Sbjct: 361 SSTSVPDVSNDNEPDHYRSDTTSDPENEPFDEQHSQITKV 403

[gi|2772900](#) (AF017185) protein tyrosine phosphatase and tensin homolog/mutated
in multiple advanced cancers protein [Rattus norvegicus]
Length = 403

Score = 795 bits (2032), Expect = 0.0
Identities = 376/403 (93%), Positives = 377/403 (93%)

Query: 1 MTAIKEIVSRNKRRYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDVVRFLDSK 60
MTAIKEIVSRNKRRYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDVVRFLDSK
Sbjct: 1 MTAIKEIVSRNKRRYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDVVRFLDSK 60
Query: 61 HKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVA 120
HKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVA
Sbjct: 61 HKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVA 120
Query: 121 AIHCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTPSQRRYVYVYYSY 180
AIHCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTPSQRRYVYVYYSY
Sbjct: 121 AIHCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTPSQRRYVYVYYSY 180
Query: 181 LLKNHLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQKVKIYSSNSGPTREDDKFMY 240
LLKNHLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQKVKIYSSNSGPTREDD MY
Sbjct: 181 LLKNHLDYRPVALLFHKMMFETIPMFSGGTCNPQFVVCQKVKIYSSNSGPTREDDKLMY 240
Query: 241 FEFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLCDQEI 300
FEFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLCDQEI
Sbjct: 241 FEFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFVWNTFFIPGPEETSEKVENGSLCDQEI 300
Query: 301 DSICSIERADNDKEYLVLT LT XXXXXXXXXXXXRYFSPNFKVKLYFTKTVEEPSNPEAX 360
DSICSIERADNDKEYLVLT LT RYFSPNFKVKLYFTKTVEEPSNPEA
Sbjct: 301 DSICSIERADNDKEYLVLT LT KNDLKDANKDKANRYFSPNFKVKLYFTKTVEEPSNPEAS 360
Query: 361 XXXXXXXXXXXXNEPDHYRSDTTSDPENEPFDEQHTQITKV 403
NEPDHYRSDTTSDPENEPFDEQHTQITKV
Sbjct: 361 SSTSVPDVSNDNEPDHYRSDTTSDPENEPFDEQHSQITKV 403

[gi|2655025](#) (AF019083) phosphatase and tensin homolog 2 [Homo sapiens]
Length = 403

Score = 777 bits (1984), Expect = 0.0
Identities = 369/402 (91%), Positives = 372/402 (91%)

Query: 2 TAIKEIVSRNKRRYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDVVRFLDSKH 61
TAIKEIVSRNKRRYQEDGFDDLTYIY NIIAMGFPAERLEGVYRNNIDVVRFLDSKH

Sbjct: 2 TAIKEIVSRNKRKYQEDGFDDLTYIYLNIIAMGFPAERLEGVYRNNIDDVVRFLDSKH 61
Query: 62 KNHYKIYNLCAERHYDTAKFNCRVAQYPPFEDHNPQLELIKPFCELDQWLSEDDNHVA 121
KNHYKI+NLCAERHYDTAK N RVAQYPPFEDHNPQLELIKPFCELDQWLSEDDNHVA
Sbjct: 62 KNHYKIHNLCAERHYDTAKSNRYRVAQYPPFEDHNPQLELIKPFCELDQWLSEDDNHVA 121
Query: 122 IHCKAGKGRGTGMICAYLLHRGKFLKAQEALDFYGEVTRDCKGVTIPSQRRYVYYSYL 181
IHCKAGKGRGTG+MICAYLLHRGKFLKAQEALDFYGEVTRDCKGVTIPSQRRYVYYSYL
Sbjct: 122 IHCKAGKGRGTGMICAYLLHRGKFLKAQEALDFYGEVTRDCKGVTIPSQRRYVYYSYL 181
Query: 182 LKNHLDYRVPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTREDKFMFY 241
+KNHLDYRVPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTREDKFMFY
Sbjct: 182 VKNHLDYRVPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTREDKFMFY 241
Query: 242 EFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHWNTFFIPGPEETSEKVENGLCDQEID 301
EFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHWNTFFIPGPEETSEKVENGLCDQEID
Sbjct: 242 EFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHWNTFFIPGPEETSEKVENGLCDQEID 301
Query: 302 SICSIERADNDKEYLVLTLTXXXXXXXXXXXXXXXXRYFSPNFVKVLYFTKTVEEPSNPEAX 361
SICSIERADNDKEYLVLTLT RYFSPN KVKLYFTKTVEEPSNPEA
Sbjct: 302 SICSIERADNDKEYLVLTLTKNLDLTKANKDKANRYFSPNVKLYFTKTVEEPSNPEASS 361
Query: 362 XXXXXXXXXXXXNEPDHYRSDTTSDPENEPFDEDQHTQITKV 403
NEPDHYRSDTTSDPENEPFDEDQHTQITKV
Sbjct: 362 STSVTPDVSDNEPDHYRSDTTSDPENEPFDEDQHTQITKV 403

[gb|AAD46165.1|AF144732_1](#) (AF144732) protein/lipid phosphatase Pten [*Xenopus laevis*]
Length = 402

Score = 688 bits (1755), Expect = 0.0
Identities = 333/404 (82%), Positives = 353/404 (86%), Gaps = 3/404 (0%)

Query: 1 MTAIKEIVSRNKRKYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSK 60
MTAIKEIVSRNKRKYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSK
Sbjct: 1 MTAIKEIVSRNKRKYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSK 60
Query: 61 HKNHYKIYNLCAERHYDTAKFNCRVAQYPPFEDHNPQLELIKPFCELDQWLSEDDNHVA 120
HKNHYKIYNLCAERHYDT KF+CRVAQYPPFEDHNPQLELIKPFCELDQ LSE+N VA
Sbjct: 61 HKNHYKIYNLCAERHYDTNFKSCRVAQYPPFEDHNPQLELIKPFCELDQLSENE-VA 119
Query: 121 AIHCKAGKGRGTGMICAYLLHRGKFLKAQEALDFYGEVTRDCKGVTIPSQRRYVYYSY 180
AIHCKAGKGRGTGMICAYLLHRGKF +AQEALDFYGEVTRDCKGVTIPSQRRYVYYSY
Sbjct: 120 AIHCKAGKGRGTGMICAYLLHRGKFPRAQEALDFYGEVTRDCKGVTIPSQRRYVYYSY 179
Query: 181 LLKNHLDYRVPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTREDKFM 240
LLKN L+YRPV LLFHK+ FETIPMFSG TCNPQFVV QLKVKI++S +GP +R +K MY
Sbjct: 180 LLKNSLEYRVPVLLFHKIEFETIPMFSGTCNPQFVVYQLKVKIFTSTAGP-KRAEKLMY 238
Query: 241 FEPQPLPVCGDIKVEFFHKQNKMLKKDKMFHWNTFFIPGPEETSEKVENGLC-DQE 299
F+FPQPLPVCGDIKVEFFHKQNK++K+KMFHWNTFFIPGPEE SEKVENGL +L +QE
Sbjct: 239 FDPQPLPVCGDIKVEFFHKQNKVMKKEKMFHWNTFFIPGPEEYSEKVENGLVGEQE 298
Query: 300 IDSICSIERADNDKEYLVLTLTXXXXXXXXXXXXXXXXRYFSPNFVKVLYFTKTVEEPSNPEA 359
+D I S ER+DNDKEYL L LT R FSPNFVKVLYFTKTVEEPSNPEA
Sbjct: 299 LDGIYSTERSDNDKEYLVLTALTKNDLTKANKDKANRLFSPNFVKVLYFTKTVEESSNSEA 358
Query: 360 XXXXXXXXXXXXNEPDHYRSDTTSDPENEPFDEDQHTQITKV 403
NEPDHYRSDTTSDPENEPFDEDQ TQITKV
Sbjct: 359 SSSTSVTPDVSDNEPDHYRSDTTSDPENEPFDEDQITQITKV 402

[gi|2407318](#) (AF017999) putative protein tyrosine phosphatase homologue [*Homo sapiens*]
Length = 338

Score = 662 bits (1690), Expect = 0.0
Identities = 315/337 (93%), Positives = 319/337 (94%)

Query: 2 TAIKEIVSRNKRKYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKH 61
TAIKEIVSRNKRKYQEDGFDDLTYIY NIIAMGFPAERLEGVYRNNIDDVVRFLDSKH
Sbjct: 2 TAIKEIVSRNKRKYQEDGFDDLTYIYLNIIAMGFPAERLEGVYRNNIDDVVRFLDSKH 61
Query: 62 KNHYKIYNLCAERHYDTAKFNCRVAQYPPFEDHNPQLELIKPFCELDQWLSEDDNHVA 121
KNHYKI+NLCAERHYDTAK N RVAQYPPFEDHNPQLELIKPFCELDQWLSEDDNHVA
Sbjct: 62 KNHYKIHNLCAERHYDTAKSNRYRVAQYPPFEDHNPQLELIKPFCELDQWLSEDDNHVA 121
Query: 122 IHCKAGKGRGTGMICAYLLHRGKFLKAQEALDFYGEVTRDCKGVTIPSQRRYVYYSYL 181
IHCKAGKGRGTG+MI AYLLHRGKFLKAQEALDFYGEVTRDCKGVTIPSQRRYVYYSYL
Sbjct: 122 IHCKAGKGRGTGIMIYAYLLHRGKFLKAQEALDFYGEVTRDCKGVTIPSQRRYVYYSYL 181
Query: 182 LKNHLDYRVPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTREDKFMFY 241
+KNHLDYRVPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKI+YSSNSGPTREDKFMFY
Sbjct: 182 VKNHLDYRVPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTREDKFMFY 241
Query: 242 EFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHWNTFFIPGPEETSEKVENGLCDQEID 301
EFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHWNTFFIPGPEETSEKVENGLCDQEID
Sbjct: 242 EFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHWNTFFIPGPEETSEKVENGLCDQEID 301

Query: 302 SICSIERADNDKEYLVLTTLTXXXXXXXXXXXXRYFS 338
SICSIERADNDKEYLVLTTLT RYFS
Sbjct: 302 SICSIERADNDKEYLVLTTLTKNDLKDANKANRYFS 338

[gb|AAD45364.1|AF161259_1](#) (AF161259) PTEN3 [Drosophila melanogaster]
Length = 509

Score = 272 bits (687), Expect = 5e-72
Identities = 154/357 (43%), Positives = 205/357 (57%), Gaps = 40/357 (11%)

Query: 1 MTAIIKEIVSRNKRRYQEDGFDDLDTYIYPNIIAMGFPA-ERLEGVYRNNIDDVVRFLDS 59
M+ +I+ +VS+ + RY+E G+DLDLTYI NIIAMG+PA ++LEG++RN ++DV + L+
Sbjct: 8 MSNVIRNVVSKKRIRYKEKGYDLDLTYINDNIIAMGYAPADKLEGLFRNRLEDFVKLLEE 67

Query: 60 KHKNHKYIYNLCERHYDTAKFNCRVAQYPPFEDHNPQLELIKPFCELDLQWLSEDDNHV 119
H HYKIYNLC+ER YD AKF RVA YPF+DHNPP +ELI+ FC D+D WL ED ++V
Sbjct: 68 NHAQHYYKIYNLCSERSYDVAKFRGRVAVYPPFDDHNPPTIELIQRFCSDVDMWLKEDSSNV 127

Query: 120 AAHCKAGKGRGTGMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTTIPSQRRYVYYYS 179
A+HCKAGKGRGTG MICAYL+ G A EAL +Y E RT+D+KGVTTIPSQRRYV Y+S
Sbjct: 128 VAVHCKAGKGRGTGMICAYLVFSGIKKSADEALAWYDEKRTKDRKGVTTIPSQRRYVQYFS 187

Query: 180 YLLKNHLDYRYPVALLFHKMMFETIPMFGSGTGNPQFVVCQKVKIYSS--NSGPTRE-- 235
L+ + + Y V+L ++ F S N V C + V S+ N+ P R +
Sbjct: 188 KLVCSVPYKSVSLNVEIRFSE----SSCVQLGMVECSISVLHDSATENAKPDRKTL 243

Query: 236 ---DKFMYFEFPQPLPVCVDIKVEFFHKQNKMLKKDKMF-HFWVNTFFIPGPEETSEKV 290
K +PV GD+K E K DK+ HFW+NTFF V
Sbjct: 244 PIDFQKSFVLTIKPSPVSGDVKFELTKK-----SPDKIICHFWLNTFF-----V 288

Query: 291 ENGLCDQEIDSICSIERADNDKEYLVLTTLTXXXXXXXXXXXXRYFSPNFVKLYF 347
N S C+ +D + TL+ + FS FK+ + F
Sbjct: 289 RNYSPCE-----SDGTVNKYIHTLSKSEIDDVHKDSEHKRFSEEFKISIVF 334

[gb|AAD45362.1|AF161257_1](#) (AF161257) PTEN1 [Drosophila melanogaster]
Length = 418

Score = 272 bits (687), Expect = 5e-72
Identities = 154/357 (43%), Positives = 205/357 (57%), Gaps = 40/357 (11%)

Query: 1 MTAIIKEIVSRNKRRYQEDGFDDLDTYIYPNIIAMGFPA-ERLEGVYRNNIDDVVRFLDS 59
M+ +I+ +VS+ + RY+E G+DLDLTYI NIIAMG+PA ++LEG++RN ++DV + L+
Sbjct: 8 MSNVIRNVVSKKRIRYKEKGYDLDLTYINDNIIAMGYAPADKLEGLFRNRLEDFVKLLEE 67

Query: 60 KHKNHKYIYNLCERHYDTAKFNCRVAQYPPFEDHNPQLELIKPFCELDLQWLSEDDNHV 119
H HYKIYNLC+ER YD AKF RVA YPF+DHNPP +ELI+ FC D+D WL ED ++V
Sbjct: 68 NHAQHYYKIYNLCSERSYDVAKFRGRVAVYPPFDDHNPPTIELIQRFCSDVDMWLKEDSSNV 127

Query: 120 AAHCKAGKGRGTGMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTTIPSQRRYVYYYS 179
A+HCKAGKGRGTG MICAYL+ G A EAL +Y E RT+D+KGVTTIPSQRRYV Y+S
Sbjct: 128 VAVHCKAGKGRGTGMICAYLVFSGIKKSADEALAWYDEKRTKDRKGVTTIPSQRRYVQYFS 187

Query: 180 YLLKNHLDYRYPVALLFHKMMFETIPMFGSGTGNPQFVVCQKVKIYSS--NSGPTRE-- 235
L+ + + Y V+L ++ F S N V C + V S+ N+ P R +
Sbjct: 188 KLVCSVPYKSVSLNVEIRFSE----SSCVQLGMVECSISVLHDSATENAKPDRKTL 243

Query: 236 ---DKFMYFEFPQPLPVCVDIKVEFFHKQNKMLKKDKMF-HFWVNTFFIPGPEETSEKV 290
K +PV GD+K E K DK+ HFW+NTFF V
Sbjct: 244 PIDFQKSFVLTIKPSPVSGDVKFELTKK-----SPDKIICHFWLNTFF-----V 288

Query: 291 ENGLCDQEIDSICSIERADNDKEYLVLTTLTXXXXXXXXXXXXRYFSPNFVKLYF 347
N S C+ +D + TL+ + FS FK+ + F
Sbjct: 289 RNYSPCE-----SDGTVNKYIHTLSKSEIDDVHKDSEHKRFSEEFKISIVF 334

[gb|AAD45363.1|AF161258_1](#) (AF161258) PTEN2 [Drosophila melanogaster]
Length = 511

Score = 272 bits (687), Expect = 5e-72
Identities = 154/357 (43%), Positives = 205/357 (57%), Gaps = 40/357 (11%)

Query: 1 MTAIIKEIVSRNKRRYQEDGFDDLDTYIYPNIIAMGFPA-ERLEGVYRNNIDDVVRFLDS 59
M+ +I+ +VS+ + RY+E G+DLDLTYI NIIAMG+PA ++LEG++RN ++DV + L+
Sbjct: 8 MSNVIRNVVSKKRIRYKEKGYDLDLTYINDNIIAMGYAPADKLEGLFRNRLEDFVKLLEE 67

Query: 60 KHKNHKYIYNLCERHYDTAKFNCRVAQYPPFEDHNPQLELIKPFCELDLQWLSEDDNHV 119
H HYKIYNLC+ER YD AKF RVA YPF+DHNPP +ELI+ FC D+D WL ED ++V
Sbjct: 68 NHAQHYYKIYNLCSERSYDVAKFRGRVAVYPPFDDHNPPTIELIQRFCSDVDMWLKEDSSNV 127

Query: 120 AAHCKAGKGRGTGMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTTIPSQRRYVYYYS 179
A+HCKAGKGRGTG MICAYL+ G A EAL +Y E RT+D+KGVTTIPSQRRYV Y+S
Sbjct: 128 VAVHCKAGKGRGTGMICAYLVFSGIKKSADEALAWYDEKRTKDRKGVTTIPSQRRYVQYFS 187

Query: 180 YLLKNHLDYRYPVALLFHKMMFETIPMFGSGTGNPQFVVCQKVKIYSS--NSGPTRE-- 235
L+ + + Y V+L ++ F S N V C + V S+ N+ P R +
Sbjct: 188 KLVCSVPYKSVSLNVEIRFSE----SSCVQLGMVECSISVLHDSATENAKPDRKTL 243

Query: 236 ----DKFMYFEFPQPLPVCGDIKVEFFHKQNKMLKKDKMF-HFWVNTFFIPGPEETSEKV 290
K +PV GD+K E K DK+ HFW+NTFF V
Sbjct: 244 PIDFQKSFVLTIKPSPVSGDVKFEFTKK-----SPDKIICHFWLNTFF-----V 288

Query: 291 ENGSLCDQEIDSICSIERADNDKEYLVLTLTXXXXXXXXXXXXXRYFSPNFVKLYF 347
N S C+ +D + TL+ + FS FK+ + F
Sbjct: 289 RNYSPCE-----SDGTVNKYIHTLSKSEIDDVHKDSEHKRFSEEFKISIVF 334

[gi|2702362](#) (AF036706) contains similarity to Gallus gallus cardiac muscle tensin (GB:M96625) [Caenorhabditis elegans]
Length = 965

Score = 184 bits (463), Expect = 9e-46
Identities = 90/207 (43%), Positives = 126/207 (60%), Gaps = 1/207 (0%)

Query: 4 IIKEIVSRNKRRYQEDGFDLDTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKH-K 62
I + VS N+ R + DLD YI IIA+G+PA +E +RN+ +FL +H K
Sbjct: 48 IFRTAVSSNRCRTEYQNIIDLDCAYITDRIIAIGYPATGIEANFRNSKVQTTQQFLTRRHGK 107

Query: 63 NHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVAAI 122
+ K++NL +YD F+ V + DH+PP LEL+ PFC + +WL DD HV A+
Sbjct: 108 GNVKVFNLRGYYDADNFDGNVICFDMTDHHPSPLELMAPPFCREAKEWLEADDKHVI 167

Query: 123 HCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTTIPSQRRYVYYSYLL 182
HCKAGKGRGVMICA L++ + ++ LD+Y +RT++ KGVTTIPSQRRY+YYY L
Sbjct: 168 HCKAGKGRGVMICALLIYINFYSPRQILDYYSIIRTKNKGVTTIPSQRRYVYYHKL 227

Query: 183 KNHLDYRVPVALLFHKMMFETIPMFSGG 209
+ L+Y P+ + + E P GG
Sbjct: 228 ERELNYLPLRMQLIGVYVERPPKTWGG 254

[emb|CAA10315](#) (AJ131181) DAF-18 protein [Caenorhabditis elegans] >[gi|4050032](#)
(AF098286) DAF-18 [Caenorhabditis elegans]
>[gi|4512113|gb|AAD21620.1](#) (AF126286) PTEN
phosphatidylinositol 3' phosphatase homolog DAF-18
[Caenorhabditis elegans]
Length = 962

Score = 184 bits (463), Expect = 9e-46
Identities = 90/207 (43%), Positives = 126/207 (60%), Gaps = 1/207 (0%)

Query: 4 IIKEIVSRNKRRYQEDGFDLDTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKH-K 62
I + VS N+ R + DLD YI IIA+G+PA +E +RN+ +FL +H K
Sbjct: 48 IFRTAVSSNRCRTEYQNIIDLDCAYITDRIIAIGYPATGIEANFRNSKVQTTQQFLTRRHGK 107

Query: 63 NHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVAAI 122
+ K++NL +YD F+ V + DH+PP LEL+ PFC + +WL DD HV A+
Sbjct: 108 GNVKVFNLRGYYDADNFDGNVICFDMTDHHPSPLELMAPPFCREAKEWLEADDKHVI 167

Query: 123 HCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTTIPSQRRYVYYSYLL 182
HCKAGKGRGVMICA L++ + ++ LD+Y +RT++ KGVTTIPSQRRY+YYY L
Sbjct: 168 HCKAGKGRGVMICALLIYINFYSPRQILDYYSIIRTKNKGVTTIPSQRRYVYYHKL 227

Query: 183 KNHLDYRVPVALLFHKMMFETIPMFSGG 209
+ L+Y P+ + + E P GG
Sbjct: 228 ERELNYLPLRMQLIGVYVERPPKTWGG 254

[pir||A57075](#) tensin - chicken (fragment) >[gi|63805|emb|CAA79215](#) (Z18529) tensin
[Gallus gallus] >[gi|212755](#) (L06662) tensin [Gallus
gallus]
Length = 1792

Score = 136 bits (338), Expect = 4e-31
Identities = 82/264 (31%), Positives = 140/264 (52%), Gaps = 5/264 (1%)

Query: 18 EDGFDLDTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKNHYKIYNLCAERHYD 77
E +LDL YI IIA+ +P+ E +R+N+ +V L SKH ++Y ++NL +ER +D
Sbjct: 110 ESSCELDLVYITERIIAVSYPTAEQSPFRSNLREVAHMLKSKHGDNVYLFNL-SERRHD 168

Query: 78 TAKFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVAAIHCKAGKGRGVMICA 137
+K + +V + + D + P LE I C+ +D WL+ ++V +H K +GR GV++ A
Sbjct: 169 ISKLHPKVLDFGWPDLHTPALEKICISICKAMDTWLNAAAHHNVVVLHNKGNRGRGLGVVAA 228

Query: 138 YLLHRGKFLKAQEALDFYGEVTRDKKGVTTI--PSQRRYVYYSYLLKNHLDYRVPVALLF 195
Y+ + A +ALD + R + K V + PSQ+RY++Y+S LL + L
Sbjct: 229 YMHYSNISASADQALDRFAMKRFYEDKVVVPGQPSQKRYIHYFSGLLSGSIKMNKPLFL 288

Query: 196 HKMMFETIPMF--SGGTCNPQFVVCQLKVKIYSSNSGPTREDKFMFEPQP--LPVCGDI 253
H ++ IP F S G C P + Q +Y+S + + + +P L + GDI
Sbjct: 289 HHVIMHGIPNFESKGGCRPFLKIYQAMQPVYTSGIYVQVQDSQTGICITIEPGLLLKGD 348

Query: 254 KVEFFHKQNKMLKKDKMFHFWVNT 277
++ +HK+ + +D +F +T
Sbjct: 349 LLKCYHKKFRSPTRDVI FRVQFHT 372

Sbjct: 117 ERRWDLDTYVTERILAAAFPARPDEQRHRGHLRELAHVLSKHRDKYLLFNLSEKRH-D 175
Query: 78 TAKFNCRVAQYPPFDHNPQLELIKPFCELDQWLSEDDNHVAIIHCKAGKGRGTGMICA 137
+ N +V + + + + P L+ + C+ ++ WLS D HV ++CK KG+ GV++ A
Sbjct: 176 LTRLNPKVQDFGWPELHAPLDKLCISICKAMETWLSADPQHVVVLYCKGNKGLGVIVSA 235
Query: 138 YLLHRGKFLKAQEALDFYGEVTRDCKKGV--IPSQRRYVYYSYLLKNHLDYRPVALLF 195
Y+ + A+AL + + K T PSQRRY+ Y+S LL + L
Sbjct: 236 YMHYSKISAGADQALATLTMRFCEDEKQVATELQPSQRRYISYFSGLLSGSIRMNSSLPLFL 295
Query: 196 HKMMFETIPMFSGGT-CNPQFVVCQLKVKIYSSN---SGPTRREDKFMFEFPQLPVC 250
H ++ +P F GT P + Q +Y+S +GP ++ + L +
Sbjct: 296 HVVLIPLMLPAFEPGTGFQPFLLKIYQSMQLVYTSGVYHIAGPGPQQ---LCISLEPALLLK 352
Query: 251 GDKVEFFHKQNKMLKKDKMFHFVNTFFIPGPEETSEK 289
GD+ V +HK + + +F +T I GP+ T K
Sbjct: 353 GDVMVTCYHKGGRGTRTLVFRVQFHTCTIHGPQLTFPK 391

[emb|CAA22831](#) (AL035226) protein-tyrosine phosphatase [Schizosaccharomyces pombe]
Length = 348

Score = 121 bits (301), Expect = 9e-27
Identities = 69/184 (37%), Positives = 104/184 (56%), Gaps = 7/184 (3%)

Query: 4 IIKEIVSRNKRYYQEDGFD----LDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLD 58
I++ +VSR ++ +++ + LD+ YI +IAM PA + +YRN+ DV ++L
Sbjct: 3 ILRSVSVSRGRKGLKQKVNRSFAYLDMVYITSKVIAMSTPAAGIHKLYRNEDELDFVKYLT 62
Query: 59 SKHKNHKYIYNLCAERH-YDTAKFNCRVAQYPPFDHNPQLELIKPFCELDQWLSEDDN 117
++ K+++ + NLCAE Y F V Y F+DHNPP L + ++D
Sbjct: 63 TQLKDNWILLNLCAEETVYHLELFKPNVINYGFQDHNPPPLFLWAIVMNMDALFQTQPL 122
Query: 118 HVAIIHCKAGKGRGTGMICAYLLHRGKFLKAQEALDFYGEVTRDCKKGVTIIPSQRRYVY 177
+HCKAGKGRGT +IC+YL+ G L A+++L+ Y E R G+TI SQ RYVY
Sbjct: 123 LTLVVHCKAGKGRGTGTICSYLVAFFG-LTAKQSLEYTEKRMVRGHGLTISSQIRVYVY 181
Query: 178 YSYL 181
L
Sbjct: 182 IEIL 185

[ref|NP_005246.1|PGAK](#) cyclin G associated kinase >gi|2506080|dbj|BAA22623| (D88435) HsGAK
[Homo sapiens]
Length = 1311

Score = 117 bits (290), Expect = 2e-25
Identities = 77/278 (27%), Positives = 133/278 (47%), Gaps = 27/278 (9%)

Query: 22 DLDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKNHKYIYNLCAERHYDTAKF 81
DLD+YI I M FPAAE +E +NNI+DV FLDSKH HY +YNL + R Y ++F
Sbjct: 407 DLDISYITSRIAIVMSFPAEGVESALKNNIEDVRLFLDSKHPGHYAVYNL-SPRTYRPSRF 465
Query: 82 NCRVAQYPPFDHNPQLELIKPFCELDQWLSEDDNHVAIIHCKAGKGRGTGMICAYLLH 141
+ RV++ + P L + C ++ WL +D +V +HC G+ + V +C++L
Sbjct: 466 HNRVTECGWAARRAPHLHTLYNICRNMHAWLRQDHKNVCVVHCMDGRAASAVAVCSFLCF 525
Query: 142 RGKFLKAQEALDFYGEVTRDCKKGVTIIPSQRRYV-YYSYLLKNHLDYRPVALLFHKMMF 200
F A+ A+ + R G+ PS +RY+ Y + + + +L ++
Sbjct: 526 CRLFSTAEAAVYMF--MKRCPPGIW-PSHKRYIEYVCDMVAEEPITPHSKPILVRAVVM 582
Query: 201 ETIPMFSGGTGTCNPQFVVCQLKVKIYSSN---SGPTRREDKFMFE-----FPQLPVC 250
+P+FS Q C+ ++Y + + ++ DK F+ P + V
Sbjct: 583 TPVPLFS-----KQSGCRPFCEVYVGDERVASTSQEYDKMRDFKIEDGKAVIPLGVTVQ 637
Query: 251 GDKVEFFHKQNKM-----LKKDKMFHFVNTFFIP 281
GD+ + +H ++ + + KMF +T F+P
Sbjct: 638 GDVLIVIIYHARSTLGGRLQAKMASMKMFQIQFHTGFVP 675

[sp|P97874|GAK_RAT](#) CYCLIN G-ASSOCIATED KINASE >gi|1902913|dbj|BAA18911| (D38560)
cyclinG-associated kinase [Rattus norvegicus]
Length = 1305

Score = 116 bits (287), Expect = 4e-25
Identities = 79/274 (28%), Positives = 128/274 (45%), Gaps = 19/274 (6%)

Query: 22 DLDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKNHKYIYNLCAERHYDTAKF 81
DLD+YI I M FPAAE +E +NNI+DV FLD+KH HY +YNL + R Y +KF
Sbjct: 405 DLDISYITSRIAIVMSFPAEGVESAIKNNIEDVRLFLDAKHPGHYAVYNL-SPRIYRASKF 463
Query: 82 NCRVAQYPPFDHNPQLELIKPFCELDQWLSEDDNHVAIIHCKAGKGRGTGMICAYLLH 141
+ RV + + P L + C + WL ED +V +HC G+ + V +CA+L
Sbjct: 464 HNRVTECGWAVRRAPHLHSLYTLCRSMHAWLRDHRNVCVVHCMDGRAASAVAVCAFLCF 523
Query: 142 RGKFLKAQEALDFYGEVTRDCKKGVTIIPSQRRYV-YYSYLLKNHLDYRPVALLFHKMMF 200
F A+ A+ + R G+ PS +RY+ Y + + + +L ++
Sbjct: 524 CRLFSTAEAAVYMF--MKRCPPGIW-PSHKRYIEYVCDMVAEEPITPHSKPMLVKSVMV 580

Query: 201 ETIPMFS--GGTCNPQFVVCQLKVKIYSSNSGPTRRREDKFMFYFE----FPQPLPVCGLDIK 254
+P+FS C P F + + ++ S R +F + P + V GD+
Sbjct: 581 TPVPLFSKQRNGCRP-FCEVYVGEERVTTSQEYDRMKEFKIEDGKAVIPLGITVQGDVL 639

Query: 255 VEFFHKQNKM-----LKKDKMFHFVWNTFFIP 281
+H ++ + + KMF +T F+P
Sbjct: 640 TIIYHARSTLGGRLQAKMASMKMFQIQFHTGFVP 673

[dbj|BAA32318|](#) (AB007942) KIAA0473 protein [Homo sapiens]
Length = 913

Score = 110 bits (273), Expect = 2e-23
Identities = 77/275 (28%), Positives = 132/275 (48%), Gaps = 21/275 (7%)

Query: 22 DLDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKHNYKIYNLCAERHYDTAKF 81
DLD TY+ II M FP + ++ +RN +DD+ FLDS+H +HY +YNL + + Y TAKF
Sbjct: 63 DLDFTYVTSRIIIVMSFPLDNVDIGFRNQVDDIRSFLDSRHLHDHYTVYNL-SPKSYRTAKF 121

Query: 82 NCRVAQYPFEDHNPQLELIKPFCELDLQWLSEDDNHVAAIHCKAGKGRGTGMICAYLLH 141
+ RV++ + P L + C ++ WL ++ +V +HC G+ + +++ A +
Sbjct: 122 HSRVSECSWPIRQAPSLHNLFAVCRNMYNLLQNPKNVVCVHCLDGRAASSILVGAMFIF 181

Query: 142 RGKFLKAQEALDFYGEVTRDCKGVTI-PSQRRYVYYSYLLKNHLDYRP--VALLFHKM 198
+ A+ + + G+ + PS RRY+ Y LL + YRP L +
Sbjct: 182 CNLYSTPGPAI----RLLYAKRPGIGLSPSHRRYLGYMCDLLADK-PYRPHFKPLTIKSI 236

Query: 199 MFETIPMFS--GGTCNPQFVVCQLKVKIYSSNSGPTRRREDKFMFY--FEFPQPLPVCGLDI 253
IP F+ C P V + KIYS+ + R ++ + P + V GD+
Sbjct: 237 TVSPVFFFKQRNGCRPYCDVLIGETKIYSTCTDFERMKEYRVQDGKIFIPLNITVQGDV 296

Query: 254 KVEFFHKQNKM-----LKKDKMFHFVWNTFFIP 281
V +H ++ + + ++F +T FIP
Sbjct: 297 VVSMYHLRSTIGSRLQAKVINTQIFQLQFHTGFIP 331

[sp|Q27974|AUXI_BOVIN](#) AUXILIN >gi|2136718|pir||S68983 auxilin - bovine >gi|485269
(U09237) auxilin [Bos taurus]
Length = 910

Score = 108 bits (268), Expect = 7e-23
Identities = 75/275 (27%), Positives = 132/275 (47%), Gaps = 21/275 (7%)

Query: 22 DLDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKHNYKIYNLCAERHYDTAKF 81
DLD TY+ II M FP + ++ +RN +DD+ FLDS+H +HY +YNL + + Y TAKF
Sbjct: 60 DLDFTYVTSRIIIVMSFPLDSVDIGFRNQVDDIRSFLDSRHLHDHYTVYNL-SPKSYRTAKF 118

Query: 82 NCRVAQYPFEDHNPQLELIKPFCELDLQWLSEDDNHVAAIHCKAGKGRGTGMICAYLLH 141
+ RV++ + P L + C ++ WL ++ +V +HC G+ + +++ A +
Sbjct: 119 HSRVSECSWPIRQAPSLHNLFAVCRNMYNLLQNPKNVVCVHCLDGRAASSILVGAMFIF 178

Query: 142 RGKFLKAQEALDFYGEVTRDCKGVTI-PSQRRYVYYSYLLKNHLDYRP--VALLFHKM 198
+ A+ + + G+ + PS RRY+ Y LL + YRP L +
Sbjct: 179 CNLYSTPGPAV----RLLYAKRPGIGLSPSHRRYLGYMCDLLADK-PYRPHFKPLTIKSI 233

Query: 199 MFETIPMFS--GGTCNPQFVVCQLKVKIYSSNSGPTRRREDKFMFY--FEFPQPLPVCGLDI 253
+P F+ C P V + KIY++ + R ++ + P + V GD+
Sbjct: 234 TVSPVFFFKQRNGCRPYCDVLIGETKIYTTCADFERMKEYRVQDGKIFIPLSITVQGDV 293

Query: 254 KVEFFHKQNKM-----LKKDKMFHFVWNTFFIP 281
V +H ++ + + ++F +T FIP
Sbjct: 294 VVSMYHLRSTIGSRLQAKVINTQIFQLQFHTGFIP 328

[sp|P53916|YNM8_YEAST](#) HYPOTHETICAL 50.2 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION
>gi|1078297|pir||S55155 probable tyrosine phosphatase
YNL128w - yeast (Saccharomyces cerevisiae)
>gi|854509|emb|CAA86897| (Z46843) tyrosine phosphatase
(putative) [Saccharomyces cerevisiae]
>gi|1302064|emb|CAA96010| (Z71404) ORF YNL128w
[Saccharomyces cerevisiae]
Length = 434

Score = 84.7 bits (206), Expect = 1e-15
Identities = 64/234 (27%), Positives = 107/234 (45%), Gaps = 58/234 (24%)

Query: 4 IIKEIVSRNKRRYQED-GFDLDTYIYPNIIAMGFPAERLEGV-YRNNIDDVVRFLDSKH 61
++K+I+S ++ + D G LD++YI N+I +P + YRN++DD++ FL H
Sbjct: 22 LMKKILSLPMKTKNDIGRLDISYILVNLIVCSYPVNTYPKLLYRNSLDDLILFLTVYH 81

Query: 62 -KNHYKIYNLCAERHYDTAKFN-----CRVAQYPFE----- 91
K +++I+N E+ K N + FE
Sbjct: 82 KGKGNFRIFNFRGKEDSDYKDNLDLIGIAAKFESKDFEIQELRSTLINDGKIPISPIDLET 141

Query: 92 -----DHNPPQLELIKPFCELDLQWLSEDDNHVAAIHCKAGKGRGTG 132
DH PP EL++ + ++ +LS N VA +HC+ GKGR+G
Sbjct: 142 RTLVEEETNNVICERIGWLDHFPFPPFELLEIVDGIENYLSVSKNRVAVLHCRMKGKGRSG 201

Query: 133 VMICAYLLHRGKFLKAQ--EALDFYGEVTR--DKKGVTIPSQRRYVYYSYLL 182

++ AYL+ K+L+ EA + + R + GVTIPSQ RY+ Y+ + +
Sbjct: 202 MITVAYLM--KYLQCLPEARLIFMQARFKYGMTNGVTTIPSQRLRLRYHEFFI 252

[sp|P91301|YLPK_CABEL](#) HYPOTHETICAL 30.3 KD PROTEIN F46F11.3 IN CHROMOSOME I >gi|1825644
(U88173) similar to chicken tensin (SP:Q04205)
[Caenorhabditis elegans]
Length = 264

Score = 71.4 bits (172), Expect = 1e-11
Identities = 56/255 (21%), Positives = 112/255 (42%), Gaps = 20/255 (7%)

Query: 4 IIKEIVSRNKRRYQEDGFDDLTYIYPNIIAMGFPAERLEGVYRNNDVVVFLDSKHKH 63
+++++ + K + +++G ++ YI +I + +E E + ++ + + H
Sbjct: 15 LVEKLRKQKMKDRKEGVQVE--YITSRLIVLSTSETSERKFVESLLKASQQIQNAHNK 72

Query: 64 HYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCELDQWLSEDDNHVAAIH 123
H +++N+ RH ++ + +P E P LE + C++LDQW+ E ++A I
Sbjct: 73 HIRVWNVSQRRHDISSSLDAIPFGWPSE--TAPSLEKLCITCKNLDQWMLHPLNIAVIF 130

Query: 124 CKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDK--KGVTTIPSQRRYVYYSYL 181
CK G R +++ A++ +D + R ++ PS +RY+ Y+S L
Sbjct: 131 CKGGLERCAIVVNAFMRFNAISATDDSVDRFSMQRFSEFLGPDGPPSYKRYLGYFSSL 190

Query: 182 LKNHLDYRVPVALLFHKMM---FETIPMFSGGTCNPQFVVCQKVKIYSSNSGPTREDKF 238
L + L H ++ FE I +F + + V +Y S + + K
Sbjct: 191 LSGRISVNSDPLYLHNIILTFEPINVF-----LKIYERLVPVYQSKTVALNKSSK- 241

Query: 239 MYFEFPQPLPVCEDI 253
FE L + GDI
Sbjct: 242 --FEMDGLKLRGDI 254

[dbj|BAA09533|](#) (D55715) phosphoprotein phosphatase [Saccharomyces cerevisiae]
Length = 551

Score = 45.7 bits (106), Expect = 7e-04
Identities = 37/131 (28%), Positives = 59/131 (44%), Gaps = 19/131 (14%)

Query: 48 NNIDVVVFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCE 107
NN+ VVR + H + K + +H D FED P L ++K F
Sbjct: 221 NNVQLVVRL--NSHLYNKKHFEDIGIQHLDLI-----FEDGTCPDLSIVKNFVGA 268

Query: 108 LDQWLSEDDNHVAAIHCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGV 167
+ + A+HCKAG GRTG +I A+L++ F A E + F +R G+
Sbjct: 269 AETIIKRGK--IAVHCKAGLGRGCLIGAHLIYTYGF--TANECIGFLRFIR---PGMV 321

Query: 168 IPSQRRYVYYY 178
+ Q+ ++Y +
Sbjct: 322 VGPQQHWLYLH 332

[gi|171183|](#) (M61194) CDC14 [Saccharomyces cerevisiae]
Length = 423

Score = 45.7 bits (106), Expect = 7e-04
Identities = 37/131 (28%), Positives = 59/131 (44%), Gaps = 19/131 (14%)

Query: 48 NNIDVVVFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCE 107
NN+ VVR + H + K + +H D FED P L ++K F
Sbjct: 93 NNVQLVVRL--NSHLYNKKHFEDIGIQHLDLI-----FEDGTCPDLSIVKNFVGA 140

Query: 108 LDQWLSEDDNHVAAIHCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGV 167
+ + A+HCKAG GRTG +I A+L++ F A E + F +R G+
Sbjct: 141 AETIIKRGK--IAVHCKAGLGRGCLIGAHLIYTYGF--TANECIGFLRFIR---PGMV 193

Query: 168 IPSQRRYVYYY 178
+ Q+ ++Y +
Sbjct: 194 VGPQQHWLYLH 204

[emb|CAA52971|](#) (X75077) putative protein tyrosine phosphatase [Saccharomyces cerevisiae]
Length = 326

Score = 45.7 bits (106), Expect = 7e-04
Identities = 37/131 (28%), Positives = 59/131 (44%), Gaps = 19/131 (14%)

Query: 48 NNIDVVVFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCE 107
NN+ VVR + H + K + +H D FED P L ++K F
Sbjct: 126 NNVQLVVRL--NSHLYNKKHFEDIGIQHLDLI-----FEDGTCPDLSIVKNFVGA 173

Query: 108 LDQWLSEDDNHVAAIHCKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVTRDKKGV 167
+ + A+HCKAG GRTG +I A+L++ F A E + F +R G+
Sbjct: 174 AETIIKRGK--IAVHCKAGLGRGCLIGAHLIYTYGF--TANECIGFLRFIR---PGMV 226

Query: 168 IPSQRRYVYYY 178
+ Q+ ++Y +
Sbjct: 227 VGPQQHWLYLH 237

[sp|Q00684|CC14_YEAST](#) PROBABLE PROTEIN-TYROSINE PHOSPHATASE CDC14 >gi|1084834|pir||S56283
protein-tyrosine-phosphatase (EC 3.1.3.48) CDC14 - yeast
(Saccharomyces cerevisiae) >gi|836783|dbj|BAA09267.1|
(D50617) cell division control protein 14 [Saccharomyces
cerevisiae] >gi|893423|dbj|BAA08039| (D44602) cell
division control protein [Saccharomyces cerevisiae]
Length = 551

Score = 45.7 bits (106), Expect = 7e-04
Identities = 37/131 (28%), Positives = 59/131 (44%), Gaps = 19/131 (14%)

Query: 48 NNIDVVRFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCE 107
NN+ VVR + H + K + +H D FED P L ++K F
Sbjct: 221 NNVQLVVRLL--NSHLYNKKHFEDIGIQHLDLI-----FEDGTCPLSIVKNFVGA 268
Query: 108 LDQWLSSEDDNHVAIHCAGKAGRTGVMICAYLLHRGKFLKAQEALDFYGEVTRTRDKKGV 167
+ + A+HCAG GRTG +I A+L++ F A E + F +R G+
Sbjct: 269 AETIIRGGK--IAVHCAGLGRGCLIGAHLLIYTYGF--TANECIGFLRFIR----PGMV 321
Query: 168 IPSQRRYVYYY 178
+ Q+ ++Y +
Sbjct: 322 VGFQHHWLYLH 332

[sp|P80994|VH01_RACVI](#) PROTEIN-TYROSINE PHOSPHATASE (LATE PROTEIN H1)
>gi|477715|pir||B47452 dual specificity phosphatase (EC
3.1.3.-) VH1 - raccoonpox virus
Length = 171

Score = 44.1 bits (102), Expect = 0.002
Identities = 41/145 (28%), Positives = 65/145 (44%), Gaps = 12/145 (8%)

Query: 45 VYRNNIDVVRFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPF 104
VY N + + S+ K Y I NL ++ Y N + P D ++ +
Sbjct: 34 VYLGNYKNAMEAPSSSEVKFKY-ILNLTMDK-YSFTNSNINI IHVPMVDDTSTDISI---Y 88
Query: 105 CEDLDQWLSSEDD--NHVAIHCAGKAGRTGVMICAYLLHRGKFLKAQEALDF-YGEVTR 161
+D+ +LS+ D N +HC AG R+G MI AYL+ + K ++ L F Y R
Sbjct: 89 FDDITAFLEKCDQRNEPVLVHCAAGVNRSGAMILAYLMSKNK--ESSPLYFLYVYHSMR 146
Query: 162 DKKGVTI--PSQRRYVYYYSYLLKN 184
D +G + PS +R + + KN
Sbjct: 147 DLRGAFVENPSFKRQIEKYVIDKN 171

[ref|NP_003454.1|PPTP4A1](#) Protein tyrosine phosphatase IVA1 >gi|1083833|pir||A56059
protein-tyrosine-phosphatase (EC 3.1.3.48) PRL-1 - rat
>gi|530162 (L27843) tyrosine phosphatase [Rattus rattus]
>gi|177755|gb|AAB40597.1| (U48296) protein tyrosine
phosphatase PTPCAAX1 [Homo sapiens] >gi|1814024 (U84411)
protein tyrosine phosphatase [Mus musculus] >gi|2961199
(AF051160) tyrosine phosphatase [Homo sapiens]
Length = 173

Score = 44.1 bits (102), Expect = 0.002
Identities = 32/103 (31%), Positives = 48/103 (46%), Gaps = 20/103 (19%)

Query: 67 IYNLCAERHYDTA---KFNCRVAQYPFEDHNPPQLELIKPFCELDQWLS-----EDD 116
I +C E YDT K V +PF+D PP +++ D WLS E+
Sbjct: 45 IVRVC-EATYDITLVEKEGIVHLDWPFDDGAPPSNQIV-----DDWLSLVKIKFREEP 96
Query: 117 NHVAIHCAGKAGRTGVMICAYLLHRGKFLKAQEALDFYGEV 159
A+HC AG GR V++ L+ G +K ++A+ F + R
Sbjct: 97 GCCIAVHCVAGLGRAPVLVALALIEGG--MKYEDAVQFIRQKR 137

[gi|1125812](#) (U42846) Similar to protein-tyrosine phosphatase. [Caenorhabditis
elegans] >gi|3152650 (AF063401) putative prenylated
protein tyrosine phosphatase [Caenorhabditis elegans]
Length = 190

Score = 43.4 bits (100), Expect = 0.003
Identities = 37/156 (23%), Positives = 67/156 (42%), Gaps = 9/156 (5%)

Query: 26 TYIYPNIIAMGFPAERLEGVYRNNIDVVRFLDSKHKHNYKIYNLCAERHYDTAKFN--- 82
TY P + + R R N + +++ K+ + E YDT
Sbjct: 18 TYFKPAPSEIAWGMRFLLITDRPNSSIQSYIEELEKKGARAVRVRVCEPTYDTLALKEAG 77
Query: 83 CRVAQYPFEDHNPPQLELIKPFCELDQWLSSEDDNHVAIHCAGKAGRTGVMICAYLLHR 142
V + F D +PP E+IK + + E + A+HC AG GR V++ L+
Sbjct: 78 IDVLDWQFSDGSPPPPEVIKSWFQLCMTSFKEHPDKSIAVHCVAGLGRAPVLVAIALIEA 137
Query: 143 GKFLKAQEALDFYGEVTRTRDKKGVTTIPSQRRYVYYY 178
G +K ++A++ +RT+ ++G Q +++ Y
Sbjct: 138 G--MKYEDAVEM---IRTQ-RRGALNQKQKFLETY 167

[gi|1246236](#) (L48937) ptp-IV1b, PTP-IV1 gene product [Homo sapiens]
Length = 167

Score = 43.4 bits (100), Expect = 0.003
Identities = 32/117 (27%), Positives = 54/117 (45%), Gaps = 11/117 (9%)

Query: 76 YDTA---KFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVAIHCAGKGRGTG 132
YD A K V +PF+D PP +++ + L E+ A+HC AG GR
Sbjct: 50 YDKAPVEKEGIHVLDPFDGAPPPNQIVDDWLNLLKTKFREEPGCCVAVHCVAGLGRAP 109

Query: 133 VMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTTIPSQRRYVYYSYLLKNHLDYR 189
V++ L+ G +K ++A+ F + R +G + ++ +Y Y K L +R
Sbjct: 110 VLVALALIECG--MKYEDAVQFIRQKR---RGAF--NSKQLLYLEKYRPMRLRFR 158

[ref|NP_003470.1|PPTP4A2](#) Protein tyrosine phosphatase IVA2 >gi|894159 (U14603)
protein-tyrosine phosphatase [Homo sapiens]
>gi|1777757|gb|AAB40598.1| (U48297) protein tyrosine
phosphatase PTPCAAX2 [Homo sapiens] >gi|1817730 (L48723)
protein tyrosine phosphatase [Homo sapiens] >gi|2992630
(AF035644) mPRL-2 [Mus musculus]
Length = 167

Score = 43.4 bits (100), Expect = 0.003
Identities = 32/117 (27%), Positives = 54/117 (45%), Gaps = 11/117 (9%)

Query: 76 YDTA---KFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVAIHCAGKGRGTG 132
YD A K V +PF+D PP +++ + L E+ A+HC AG GR
Sbjct: 50 YDKAPVEKEGIHVLDPFDGAPPPNQIVDDWLNLLKTKFREEPGCCVAVHCVAGLGRAP 109

Query: 133 VMICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTTIPSQRRYVYYSYLLKNHLDYR 189
V++ L+ G +K ++A+ F + R +G + ++ +Y Y K L +R
Sbjct: 110 VLVALALIECG--MKYEDAVQFIRQKR---RGAF--NSKQLLYLEKYRPMRLRFR 158

[sp|P29352|PTN8_MOUSE](#) HEMATOPOIETIC CELL PROTEIN-TYROSINE PHOSPHATASE 70Z-PEP
>gi|538546|pir||B44390 protein-tyrosine-phosphatase (EC
3.1.3.48), nonreceptor type 8 - mouse >gi|200523
(M90388) protein tyrosine phosphatase [Mus musculus]
Length = 802

Score = 43.0 bits (99), Expect = 0.004
Identities = 45/138 (32%), Positives = 65/138 (46%), Gaps = 16/138 (11%)

Query: 60 KHKNHKYIYNLCAERHYDTAK-FNCRVAQYPFEDHN-PPQLELIKPFCELDLQWLEDDN 117
K K+ YKI L A+ + +T + +P DH+ P ++ I D+ + EDD
Sbjct: 164 KKKSDYKIRTLKAKFNNEIRIIYQFHYKNWP--DHDVPSIDPILQLIWDW-RCYQEDDC 220

Query: 118 HVAIHCAGKGRGTGMVICA----YLLHRGKFLKAQEALDFYGEVTRDKKGVTTIPSQR 172
IHC AG GRTGV ICA LL G K + E+RT ++ + +Q
Sbjct: 221 VPICIHCSAGCGRTGV-ICAVDYTWMLLKDGIIIPKNFSVFNLIQEMRT--QRPSTVQTQE 277

Query: 173 RYVYYSYLL---KNHLD 187
+Y YS +L K H+D
Sbjct: 278 QYELVYSAVLELFRHMD 295

[emb|CAA07417|](#) (AJ007016) protein tyrosine phosphatase [Rattus norvegicus]
Length = 167

Score = 43.0 bits (99), Expect = 0.004
Identities = 26/87 (29%), Positives = 42/87 (47%), Gaps = 5/87 (5%)

Query: 76 YDTA---KFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVAIHCAGKGRGTG 132
YD A K V +PF+D PP +++ + L E+ A+HC AG GR
Sbjct: 50 YDKAPVEKEGIHVLDPFDGAPPPNQIVDDWLNLLKTKFREEPGCCVAVHCVAGLGRAP 109

Query: 133 VMICAYLLHRGKFLKAQEALDFYGEVR 159
V++ L+ G +K ++A+ F + R
Sbjct: 110 VLVALALIECG--MKYEDAVQFIRQKR 134

[pir||I68523](#) protein tyrosine phosphatase - human (fragment) >gi|1008854
(L39000) protein tyrosine phosphatase [Homo sapiens]
Length = 154

Score = 42.6 bits (98), Expect = 0.006
Identities = 29/110 (26%), Positives = 51/110 (46%), Gaps = 8/110 (7%)

Query: 80 KFNCRVAQYPFEDHNPQLELIKPFCELDLQWLEDDNHVAIHCAGKGRGTGMICAYL 139
K V +PF+D PP +++ + L E+ A+HC AG GR V++ L
Sbjct: 44 KEGIHVLDPFDGAPPPNQIVDDWLNLLKTKFREEPGCCVAVHCVAGLGRAPVLVALAL 103

Query: 140 LHRGKFLKAQEALDFYGEVTRDKKGVTTIPSQRRYVYYSYLLKNHLDYR 189
+ G +K ++A+ F + R +G + ++ +Y Y K L +R
Sbjct: 104 IECG--MKYEDAVQFIRQKR---RGAF--NSKQLLYLEKYRPMRLRFR 145

[ref|NP_003662.1|PCDC14B](#) S. cerevisiae CDC14 homolog, gene B >gi|2662463 (AF023158) tyrosine

phosphatase [Homo sapiens]
Length = 459

Score = 42.6 bits (98), Expect = 0.006
Identities = 36/133 (27%), Positives = 62/133 (46%), Gaps = 15/133 (11%)

Query: 24 DLTYYIPN-IIAMGFPAERLE---GVYRNNIDVVRFLDSKHKHNYKIYNLCAERHYDTA 79
DL +I P+ IA P R G ++++ + +++ K+ N I L +R YD
Sbjct: 215 DLNWIIPDRFIAFCGPHSRARLESGYHQHSPETYIQYF--KNHNVTTIIRL-NKRMYDAK 271

Query: 80 KFNCRVAQYP---FEDHNPPQLELIKPFCELDLQWLSEDDNHVAIHCAGKAGRTGVMIC 136
+F + F D + P ++K F + + E+ A+HCKAG GRTG +I
Sbjct: 272 RFTDAGFDHDLFFADGSTPTDAIVKEFLD-----ICENAEGAIHVHCKAGLGRGTGLIA 326

Query: 137 AYLLHRGKFLKAQ 149
Y++ + A+
Sbjct: 327 CYIMKHYRMTAAE 339

[gb|AAC16661.1](#) (AF064104) Cdc14B2 phosphatase [Homo sapiens]
Length = 498

Score = 42.6 bits (98), Expect = 0.006
Identities = 36/133 (27%), Positives = 62/133 (46%), Gaps = 15/133 (11%)

Query: 24 DLTYYIPN-IIAMGFPAERLE---GVYRNNIDVVRFLDSKHKHNYKIYNLCAERHYDTA 79
DL +I P+ IA P R G ++++ + +++ K+ N I L +R YD
Sbjct: 215 DLNWIIPDRFIAFCGPHSRARLESGYHQHSPETYIQYF--KNHNVTTIIRL-NKRMYDAK 271

Query: 80 KFNCRVAQYP---FEDHNPPQLELIKPFCELDLQWLSEDDNHVAIHCAGKAGRTGVMIC 136
+F + F D + P ++K F + + E+ A+HCKAG GRTG +I
Sbjct: 272 RFTDAGFDHDLFFADGSTPTDAIVKEFLD-----ICENAEGAIHVHCKAGLGRGTGLIA 326

Query: 137 AYLLHRGKFLKAQ 149
Y++ + A+
Sbjct: 327 CYIMKHYRMTAAE 339

[gb|AAC16662.2](#) (AF064105) Cdc14B3 phosphatase [Homo sapiens]
Length = 471

Score = 42.6 bits (98), Expect = 0.006
Identities = 36/133 (27%), Positives = 62/133 (46%), Gaps = 15/133 (11%)

Query: 24 DLTYYIPN-IIAMGFPAERLE---GVYRNNIDVVRFLDSKHKHNYKIYNLCAERHYDTA 79
DL +I P+ IA P R G ++++ + +++ K+ N I L +R YD
Sbjct: 215 DLNWIIPDRFIAFCGPHSRARLESGYHQHSPETYIQYF--KNHNVTTIIRL-NKRMYDAK 271

Query: 80 KFNCRVAQYP---FEDHNPPQLELIKPFCELDLQWLSEDDNHVAIHCAGKAGRTGVMIC 136
+F + F D + P ++K F + + E+ A+HCKAG GRTG +I
Sbjct: 272 RFTDAGFDHDLFFADGSTPTDAIVKEFLD-----ICENAEGAIHVHCKAGLGRGTGLIA 326

Query: 137 AYLLHRGKFLKAQ 149
Y++ + A+
Sbjct: 327 CYIMKHYRMTAAE 339

[sp|P33064|VH01_VARV](#) PROTEIN-TYROSINE PHOSPHATASE >gi|419331|pir||I36845 dual
specificity phosphatase (EC 3.1.3.-) Vh1 - variola virus
>gi|62360|emb|CAA47583| (X67119) H1L COP [Variola virus]
>gi|262443|bbs|125277 (S55844) H1L [variola major virus,
India-1967, Peptide, 171 aa] [Variola major virus]
>gi|297264|emb|CAA49025| (X69198) I1L [Variola virus]
>gi|439002 (L22579) homolog of vaccinia virus CDS H1L
(protein phosphatase); putative [variola major virus]
>gi|1143689|emb|CAA53838| (X76264) ORF2L [Variola virus]
>gi|5830645|emb|CAB54684.1| (Y16780) J1L protein
[variola minor virus] >gi|745202|prf||2015436CU I1L gene
[Variola major virus]
Length = 171

Score = 42.2 bits (97), Expect = 0.007
Identities = 41/145 (28%), Positives = 64/145 (43%), Gaps = 12/145 (8%)

Query: 45 VYRNNIDVVRFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPF 104
VY N + + S+ K Y + NL ++ Y N + P D I +
Sbjct: 34 VYLGNYKNAMNAPSSEVKFKY-VLNLTMDC-YTLPNSNINIIHIPLVDDTTTD---ISKY 88

Query: 105 CEDLDQWLSEDD--NHVAIHCAGKAGRTGVMICAYLLHRGKFLKAQEALDF-YGEVTRR 161
+D+ +LS+ D N +HC AG R+G MI AYL+ + K ++ L F Y R
Sbjct: 89 FDDVTAFLSKCDQRNEPVLVHCVAGVNRSGAMILAYLMSKNK--ESSPMLYFLYVYHSMR 146

Query: 162 DKKGVTI--PSQRRYVYYSYLLKN 184
D +G + PS +R + + KN
Sbjct: 147 DLRGAFVENPSFKRQIEKYVIDKN 171

[gb|AAD15415](#) (AC006024) similar to Cdc14B1 phosphatase; similar to AF064104
(PID:g3136332) [Homo sapiens]

Length = 447

Score = 42.2 bits (97), Expect = 0.007
Identities = 36/133 (27%), Positives = 62/133 (46%), Gaps = 15/133 (11%)

Query: 24 DLTYYIPN-IIAMGFPAERLE---GVYRNNIDVVFRFLDSKHKHNYKIYNLCAERHYDTA 79
DL +I P+ IA P R G +++ + +++ K+ N I L +R YD
Sbjct: 185 DLNWIIPDRFIAFCGPHSRARLESQYHQSPETIYQF--KNHNVTIIRL-NKRMVDAK 241

Query: 80 KFNCRVAQYP---FEDHNPPQLELIKPFCELDQWLSEDDNHVAAIHCKAGKGRGTGMVIC 136
+F + F D + P ++K F + + E+ A+HCKAG GRTG +I
Sbjct: 242 RFTDAGFDHDLFFADGSTPTDAIVKRFLD----ICENAEGAIHVHCKAGLGRGTGLIA 296

Query: 137 AYLLHRGKFLKAQ 149
Y++ + A+
Sbjct: 297 CYIMKHYRMTAAE 309

[sp|P20495|VH01_VACCC](#) PROTEIN-TYROSINE PHOSPHATASE (LATE PROTEIN H1)
>gi|93441|pir||A42514 dual specificity phosphatase (EC
3.1.3.-) VH1 - vaccinia virus (strain Copenhagen)
>gi|335436 (M35027) H1L; putative [Vaccinia virus]
Length = 171

Score = 41.8 bits (96), Expect = 0.010
Identities = 41/145 (28%), Positives = 64/145 (43%), Gaps = 12/145 (8%)

Query: 45 VYRNNIDVVFRFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPF 104
VY N + + S+ K Y + NL ++ Y N + P D I +
Sbjct: 34 VYLGNYKNAMDAPSSVVKFY-VLNLTMK-YTLPNSNINIIHIPLVDDTTD---ISKY 88

Query: 105 CEDLDQWLSEDD--NHVAAIHCKAGKGRGTGMVICAYLLHRGKFLKAQEALDF-YGEVTR 161
+D+ +LS+ D N +HC AG R+G MI AYL+ + K ++ L F Y R
Sbjct: 89 FDDVTAFLSKCDQRNEPVLVHCAAGVNRSGAMILAYLMSKNK--ESSPMLYFLVYHSMR 146

Query: 162 DKKGVTI--PSQRRYVYYSYLLKN 184
D +G + PS +R + + KN
Sbjct: 147 DLRGAFVENPSFKRQIEIKYVIDKN 171

[ref|NP_003663.1|PCDC14A](#) S. cerevisiae CDC14 homolog, gene A >gi|2662417 (AF000367) cdc14
homolog [Homo sapiens]
Length = 580

Score = 41.8 bits (96), Expect = 0.010
Identities = 32/121 (26%), Positives = 51/121 (41%), Gaps = 21/121 (17%)

Query: 33 IAMGFPAERLEGVY---RNNIDVVFRFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQY 88
I G+P E + ++N+ VVR +K K + HYD
Sbjct: 186 IENGYPLHAPAEYFPYFKKHNVTAIVRL--NKKIYEAKRFTDAGFEHYDLF----- 234

Query: 89 PFEDHNPPQLELIKPFCELDQWLSEDDNHVAAIHCKAGKGRGTGMVICAYLLHRGKFLKA 148
F D + P +++ F + E+ A+HCKAG GRTG +I Y++ +F A
Sbjct: 235 -FIDGSTPSDNIVRRFLN-----ICENTEAGIAVHCKAGLGRGTGLIACYVMKHYRFTA 288

Query: 149 Q 149
+
Sbjct: 289 E 289

[gi|2992632](#) (AF035645) mPRL-3 [Mus musculus]
Length = 173

Score = 41.8 bits (96), Expect = 0.010
Identities = 28/105 (26%), Positives = 48/105 (45%), Gaps = 8/105 (7%)

Query: 85 VAQYPFEDHNPPQLELIKPFCELDQWLSEDDNHVAAIHCKAGKGRGTGMVICAYLLHRGK 144
V +PF+D PP ++++ + L D +HC AG GR V++ L+ G
Sbjct: 65 VVDWPFDDGAPPVPGKVVEDWLSLLKAKFYNDPGSCVLVHCVAGLGRAPVLVALALIESG- 123

Query: 145 FLKAQEALDFYGEVTRDCKKGVTIQPSQRRYVYYSYLLKNHLDYR 189
+K ++A+ F R K+ I S ++ Y Y K L ++
Sbjct: 124 -MKYEDAIQF-----IRKRRGAINS-KQLTYLEKYRQRLRFK 161

[gb|AAC16659.1](#) (AF064102) Cdc14A2 phosphatase [Homo sapiens]
Length = 623

Score = 41.8 bits (96), Expect = 0.010
Identities = 32/121 (26%), Positives = 51/121 (41%), Gaps = 21/121 (17%)

Query: 33 IAMGFPAERLEGVY---RNNIDVVFRFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQY 88
I G+P E + ++N+ VVR +K K + HYD
Sbjct: 200 IENGYPLHAPAEYFPYFKKHNVTAIVRL--NKKIYEAKRFTDAGFEHYDLF----- 248

Query: 89 PFEDHNPPQLELIKPFCELDQWLSEDDNHVAAIHCKAGKGRGTGMVICAYLLHRGKFLKA 148
F D + P +++ F + E+ A+HCKAG GRTG +I Y++ +F A
Sbjct: 249 -FIDGSTPSDNIVRRFLN-----ICENTEAGIAVHCKAGLGRGTGLIACYVMKHYRFTA 302

Query: 149 Q 149

+
Sbjct: 303 E 303

[gb|AAC16660.1](#) (AF064103) Cdc14A3 phosphatase [Homo sapiens]
Length = 383

Score = 41.8 bits (96), Expect = 0.010
Identities = 32/121 (26%), Positives = 51/121 (41%), Gaps = 21/121 (17%)

Query: 33 IAMGFPAERLEGVY---RNNIDVVRFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQY 88
I G+P E + ++N+ VVR +K K + HYD
Sbjct: 200 IENGYPLHAPEAYFPYFKKHNVTA VVRL--NKKIYEAKRFTDAGFEHYDLF----- 248

Query: 89 PFEDHNPPQLELIKPFCELDLQWLSEDDNHVAAIHCKAGKGRGTGMICAYLLHRGKFLKA 148
F D + P +++ F + E+ A+HCKAG GRTG +I Y++ +F A
Sbjct: 249 -FIDGSTPSDNIVRRFLN-----ICENTEGAI AVHCKAGLGRGTGLIACYVMKHYRFTA 302

Query: 149 Q 149
+
Sbjct: 303 E 303

[gb|AAD49217.1](#) (AF122013) dual-specificity phosphatase [Homo sapiens]
Length = 594

Score = 41.8 bits (96), Expect = 0.010
Identities = 32/121 (26%), Positives = 51/121 (41%), Gaps = 21/121 (17%)

Query: 33 IAMGFPAERLEGVY---RNNIDVVRFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQY 88
I G+P E + ++N+ VVR +K K + HYD
Sbjct: 200 IENGYPLHAPEAYFPYFKKHNVTA VVRL--NKKIYEAKRFTDAGFEHYDLF----- 248

Query: 89 PFEDHNPPQLELIKPFCELDLQWLSEDDNHVAAIHCKAGKGRGTGMICAYLLHRGKFLKA 148
F D + P +++ F + E+ A+HCKAG GRTG +I Y++ +F A
Sbjct: 249 -FIDGSTPSDNIVRRFLN-----ICENTEGAI AVHCKAGLGRGTGLIACYVMKHYRFTA 302

Query: 149 Q 149
+
Sbjct: 303 E 303

[gi|3406430](#) (AF041434) hPRL-3 [Homo sapiens]
Length = 173

Score = 41.4 bits (95), Expect = 0.013
Identities = 28/105 (26%), Positives = 49/105 (46%), Gaps = 8/105 (7%)

Query: 85 VAQYPFEDHNPPQLELIKPFCELDLQWLSEDDNHVAAIHCKAGKGRGTGMICAYLLHRGK 144
V +PF+D PP +++++ + + E A+HC AG GR V++ L+ G
Sbjct: 65 VVDWPFDDGAPP PGKVVEDWLSLVKAKFCEAPGSCVAVHCVAGLGRAPVLVALALIESG- 123

Query: 145 FLKAQEALDFYGEVTRDKKGV TIPSQRRYVYYSYLLKNHLDYR 189
+K ++A+ F R K+ I S ++ Y Y K L ++
Sbjct: 124 -MKYEDAIQF----IRKRRGRINS-KQLTYLEKYRPKQRLRFK 161

[dbj|BAA03003](#) (D13903) MPTdelta [Mus musculus]
Length = 1291

Score = 41.0 bits (94), Expect = 0.017
Identities = 32/123 (26%), Positives = 55/123 (44%), Gaps = 6/123 (4%)

Query: 64 HYKIYNLCAERHYDTAKFNCRVAQYP-FEDHNPPQLELIKPFCELDLQWLSEDDNHVAAI 122
H ++C + + K R Q+ + DH P+ P Q L D +
Sbjct: 872 HILCPDICTLNNGSSEKRVQRQFTAWPDHGVPEHPTVPVPSFLTESQNLHPPDAGPMV 931

Query: 123 HCKAGKGRGTGMICA-YLLHRGKFLKAQEALDFYGEVTRDKKGV TIPSQRRYVYYSY 180
HC AG GRTG I +L R +K ++ +D YG V R ++ + ++ +Y++ +
Sbjct: 932 HCSAGVGRGTGCFVIDAMLER---IKHEKTVDIYGHVTLMRAQRNYMVQTEDQYIFIHDA 988

Query: 181 LLK 183
LL+
Sbjct: 989 LLE 991

[sp|P07239|VH01_VACCV](#) PROTEIN-TYROSINE PHOSPHATASE (LATE PROTEIN H1)
>gi|74345|pir||QQVZH1 dual specificity phosphatase (EC 3.1.3.-) VH1 - vaccinia virus (strain WR) >gi|335742 (M13209) 19 kDa late protein [Vaccinia virus]
>gi|2772707 (U94848) protein tyrosine/serin phosphatase [Vaccinia virus]
Length = 171

Score = 41.0 bits (94), Expect = 0.017
Identities = 30/102 (29%), Positives = 46/102 (44%), Gaps = 7/102 (6%)

Query: 45 VYRNNIDVVRFLDSKHKHNYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPF 104

VY N + + S+ K Y + NL ++ Y N + P D I +
Sbjct: 34 VYLGNYKNAMDAPSSSEVKFKY-VLNLTMDK-YTLPNSNINIIHIPLVDDTTTD---ISKY 88

Query: 105 CEDLDQWLSEDD--NHVAAIHCKAGKGRGTVMICAYLLHRGK 144

+D+ +LS+ D N +HC AG R+G MI AYL+ + K

Sbjct: 89 FDDVTAFLSKCDQRNEPVLVHCAAGVNRSGAMILAYLMSKNK 130

[sp|P24656|PTP_NPVAC](#) PROTEIN-TYROSINE PHOSPHATASE (BVP) >gi|93039|pir||A40781 dual
specificity phosphatase (EC 3.1.3.-) BVP - Autographa
californica nuclear polyhedrosis virus >gi|332493
(M96763) protein tyrosine phosphatase [Autographa
californica nuclear polyhedrosis virus]
>gi|559070|gb|AAA66631| (L22858) protein tyrosine
phosphatase [Autographa californica
nucleopolyhedrovirus]
Length = 168

Score = 40.6 bits (93), Expect = 0.022
Identities = 19/65 (29%), Positives = 36/65 (55%), Gaps = 2/65 (3%)

Query: 95 PPQLELIKPFCELDQWLSEDDNHVAAIHCKAGKGRGTVMICAYLLHRGKFLKAQEALDF 154
PP+ +++ F + + ++ + + +HC G RTG M+C YL+H + QEA+D

Sbjct: 91 PPE-SIVQEFIDTVKEFTEKCPGMLVGVHCTHGINRTGYMVCRYLMHT-LGIAPQEAI DR 148

Query: 155 YGEVR 159

+ + R

Sbjct: 149 FEKAR 153

CPU time: 47.72 user secs. 0.64 sys. secs 48.36 total secs.

Database: Non-redundant GenBank CDS
translations+PDB+SwissProt+SPupdate+PIR
Posted date: Oct 22, 1999 4:05 PM
Number of letters in database: 128,539,543
Number of sequences in database: 419,232

Lambda	K	H
0.321	0.139	0.429

Gapped Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 108738379

Number of Sequences: 419232

Number of extensions: 4644913

Number of successful extensions: 8434

Number of sequences better than 10.0: 181

Number of HSP's better than 10.0 without gapping: 66

Number of HSP's successfully gapped in prelim test: 115

Number of HSP's that attempted gapping in prelim test: 8301

Number of HSP's gapped (non-prelim): 241

length of query: 403

length of database: 128539543

effective HSP length: 52

effective length of query: 351

effective length of database: 106739479

effective search space: 37465557129

effective search space used: 37465557129

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

S1: 41 (21.8 bits)

S2: 71 (32.1 bits)