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NCBI Coffee Break

27 July 2000

Article reference:
CB15.270700
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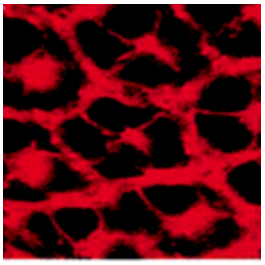

The *Drosophila* homolog of human *TSC2* is a gene called *gigas*. which, when mutated, causes cells to enlarge.

Click on figure for more information.

Tuberous Sclerosis Complex in flies too?

Tuberous sclerosis complex (TSC) affects as many as 1 in 6000 newborns. Although named in 1880 for the firm, potato-like nodules that form in the cerebral cortex, few organs escape the benign tumors - hamartomas - that also sprout in the kidneys, lungs, heart, eyes, and skin. The first clinical signs of TSC include seizures, mental retardation, and skin lesions. However, symptoms can be so subtle that they go undetected for many years.

One-third of TSC patients inherit a defective copy of either the *TSC1* gene (chromosome 9q34) or the *TSC2* gene (chromosome 16p13.3). The remaining two-thirds acquire the disease by spontaneous mutation of either gene, probably very early in embryonic development. Since no individual lacking functional copies of both genes has ever been found, it is believed that such a condition is lethal to the embryo.

The product of the *TSC1* gene, hamartin, shows no overall sequence similarity to any known protein, although it contains an extensive coiled-coil region near its carboxyl end. Coiled-coil domains often provide a binding surface for protein-protein interactions. The TSC2 product - tuberin - is also novel, but shows homology to the GTPase-activating protein (GAP) for Rap1 protein, a Ras superfamily member. Rap1's cellular function is not known, however, many Ras-related proteins help to pass stimulatory signals - from the plasma membrane to the nucleus - that tell a cell when to divide. The GTP-dependent proteins within these signaling cascades can only transmit a signal when in a GTP-bound state. The role of the GAP is to inactivate the signaling protein by hydrolyzing itts bound GTP to GDP. GAPs are therefore critical negative regulators of the Ras-like proteins and thus prevent cells from dividing unchecked.

The discovery last year of *TSC1* and *TSC2* homologs in *Drosophila* strengthens the idea that they are fundamental to cell division control. Mutant flies lacking tuberin possess enlarged cells that contain on average ten times the normal amount of DNA, indicating that the cells repeatedly replicated their DNA without going through intervening cell divisions. A similar process may explain the giant, multinucleated cells seen in certain neuronal tumors of TSC patients. In addition, experiments in human cells have shown that

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when tuberin protein levels are reduced, the cells prematurely enter the cell division cycle.

What about hamartin? It may be telling that TSC1 patients are clinically indistinguishable from TSC2 patients. One idea is that tuberin and hamartin bind to each other in cells, facilitated by hamartin's coiled-coil domain. Perhaps hamartin is there to keep tuberin fully active, or the tuberin-hamartin complex itself is the functional tumor suppressor. While the precise cellular actions of tuberin and hamartin remain to be discovered, the strong homologous proteins found in *Drosophila* offer the potential for further experimental investigation.

Comments?
Questions?
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Figure Coffee Break

Tuberous Sclerosis Complex in flies too?

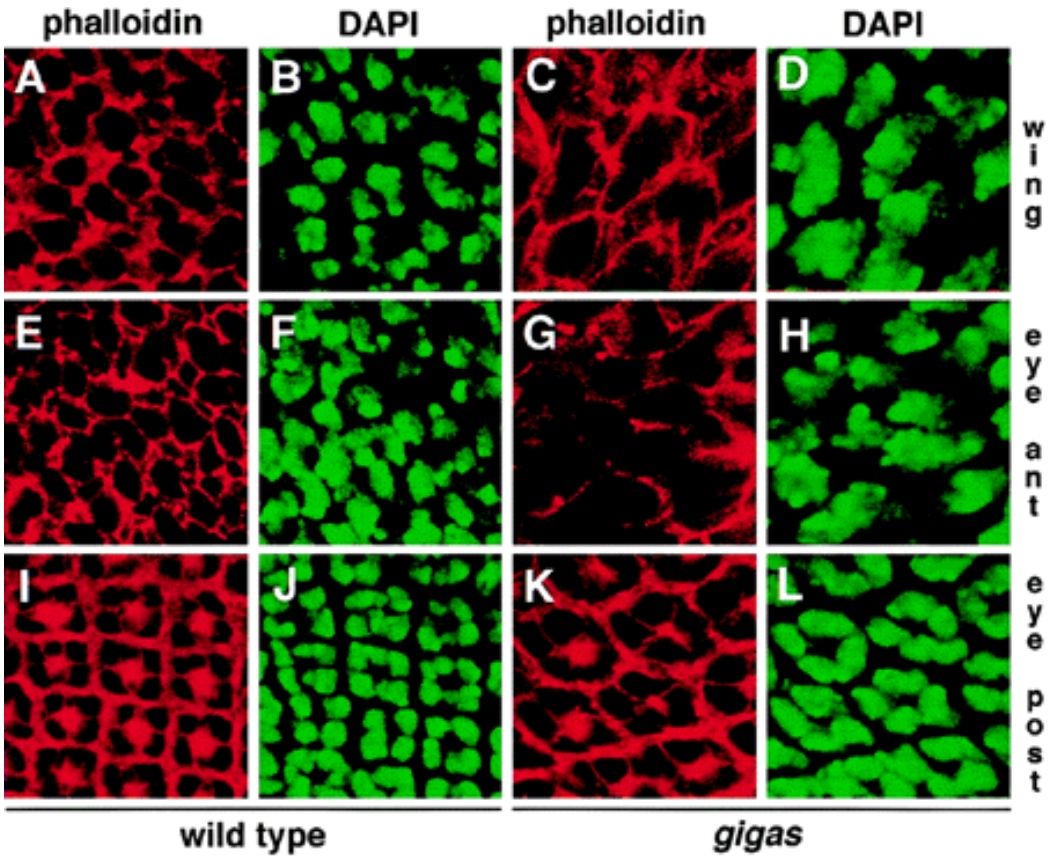

Figure 1. In *Drosophila*, the *gigas* gene codes for a protein homologous to human *TSC2*. Fly cells from the wing and eye imaginal discs that contain mutant *gigas* are enlarged, suggesting that the cells failed to undergo cell division at the appropriate time. The figure shows confocal images of DNA-stained (green; DAPI) and phalloidin-stained (red - phalloidin is a toxin that tightly binds actin) wild-type (left-most two columns) and mutant (right-most two columns) cells. **(A-D)** are wing disc cells, **(E-H)** are cells from the eye disc anterior to the morphogenetic furrow (MF), while **(I—L)** are from the eye disc posterior to the MF. The red actin stain shows that the size of the whole cell increases in mutant cells, while the green DNA stain shows that the size of the nucleus also increases in mutant cells.

Figure reproduced with kind permission from: Ito, N. and Rubin, G.M. (1999) *gigas*, a *Drosophila* homolog of tuberous sclerosis gene product-2, regulates the cell cycle. *Cell* 19, 29-39

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PubMed is the National Library of Medicine's search service that provides access to over 10 million citations in MEDLINE, PreMEDLINE, and other related databases, with links to participating online journals.

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At times, search terms do not match specific controlled vocabulary terms in the database and a search turns up **no** article citations.

One way around this problem is to **click on MeSH Browser** on the left sidebar to see how the National Library of Medicine's controlled vocabulary specifically words your concept(s).

MeSH or the **Me**dical **S**ubject **H**eadings list contains the National Library of Medicine's list of terms used to describe the subjects of articles indexed in MEDLINE.

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No exact match for your term was found. Please select from the following possibilities:

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Research, Outcomes
Pregnancy Outcomes
Treatment Outcome
Outcome Scale, Glasgow
Outcome Measurement Error
Outcome and Process Assessment
Outpatient
Acting Out
Outtakes
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Browse this term

The controlled vocabulary does not exactly match your term, so highlight the term nearest to your meaning as shown and click on 'Browse this term.'

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Treatment Outcome [Detailed display]

Evaluation undertaken to assess the results or consequences of management and procedures used in combating disease in order to determine the efficacy, effectiveness, safety, practicability, etc., of these interventions in individual cases or series.

Add this term to the Search using operator: AND

Click on 'Add' to incorporate the term 'Treatment Outcome' into your search (after reading its definition and verifying that it is indeed the best MeSH term for your search).

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    - Prognosis
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        - Treatment Failure

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    - Quality of Health Care
      - Outcome and Process Assessment (Health Care)
        - Outcome Assessment (Health Care)
          - **Treatment Outcome**
            - Medical Futility
            - Treatment Failure

All MeSH Categories
- Health Care Category
  - Health Care Quality, Access, and Evaluation
    - Quality of Health Care
      - Health Care Evaluation Mechanisms
        - Outcome and Process Assessment (Health Care)
          - Outcome Assessment (Health Care)
            - **Treatment Outcome**
              - Medical Futility
              - Treatment Failure

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```
"Treatment Outcome"[MESH]
for surgery in TSC
```

PubMed Search

The MeSH term **Treatment Outcome** now appears in the Search Box. Type in additional appropriate search terms as shown and click on **PubMed Search** to run your search again.

If you like, try coming back to this page to combine **Treatment Outcome** with other search terms or returnto PubMed Tutorial.

Treatment Outcome [Detailed display]

Evaluation undertaken to assess the results or consequences of management and procedures used in combating disease in order to determine the efficacy, effectiveness, safety, practicability, etc., of these interventions in individual cases or series.

Add this term to the Search using operator: AND

Term **Treatment Outcome** appears in more than one place in the MeSH tree.

All MeSH Categories
- Analytical, Diagnostic and Therapeutic Techniques and Equipment Category
  - Diagnosis
    - Prognosis
      - **Treatment Outcome**
        - Medical Futility
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All MeSH Categories
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All MeSH Categories
- Health Care Category
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    - Quality of Health Care
      - Health Care Evaluation Mechanisms
        - Outcome and Process Assessment (Health Care)
          - Outcome Assessment (Health Care)
            - **Treatment Outcome**
              - Medical Futility
              - Treatment Failure

1 : Guerreiro MM, Andermann F, Andermann E, Palmini A, Hwang P, Hoffman HJ, Otsubo H, Bastos A, Dubeau F, Snipes GJ, Olivier A, Rasmussen T. Related Articles
Surgical treatment of epilepsy in tuberous sclerosis: strategies and results in 18 patients.
Neurology. 1998 Nov;51(5):1263-9.
PMID: 9818843; UI: 99034152

2 : Baumgartner JE, Wheless JW, Kulkarni S, Northrup H, Au KS, Smith A, Brookshire B. Related Articles
On the surgical treatment of refractory epilepsy in tuberous sclerosis complex.
Pediatr Neurosurg. 1997 Dec;27(6):311-8.
PMID: 9655146; UI: 98317852

3 : Liptak GS. Related Articles
Tethered spinal cord: update of an analysis of published articles.
Eur J Pediatr Surg. 1995 Dec;5 Suppl 1:21-3.
PMID: 8770573; UI: 96366396

NCBI

Tutorial **Coffee Break**

This is the query page for a BLAST search. The sequence of the human tuberin protein, TSC2, 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 [nr]

The amino acid query sequence is filtered for low complexity regions by default.

Enter here your **amino acid sequence** as [Sequence in FASTA format]

```
NLVSLQCR
KDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTD
IYPSKWIARLRHIKRL
RQRICEEAAYSNPSLPLVHPPSHSKAPAQTPAEPTPGYEVGQRKRL
ISSVEDFTEFV
```

[Submit Query] [Reset]

Please read about FASTA format description

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

Advanced options for the BLAST server:

Expect [10] Filter [default] ☐ NCBI-gi ☑ Graphical Overview

Descriptions [50] Alignments [50]

Expect value for inclusion in PSI-BLAST iteration 1 [0.001]

Other advanced options: [ ]

[Submit Query] [Reset]

Query = gi|1717799 TSC2_human tuberin protein (1807 letters)
Database: Non-redundant GenBank CDS translations+PDB+ SwissProt+PIR+PRF; 494,850 sequences; 155,136,466 total letters

Below are the results from a PSI-BLAST (see Altschul et al., 1997) search of the non-redundant database using human tuberin protein 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.

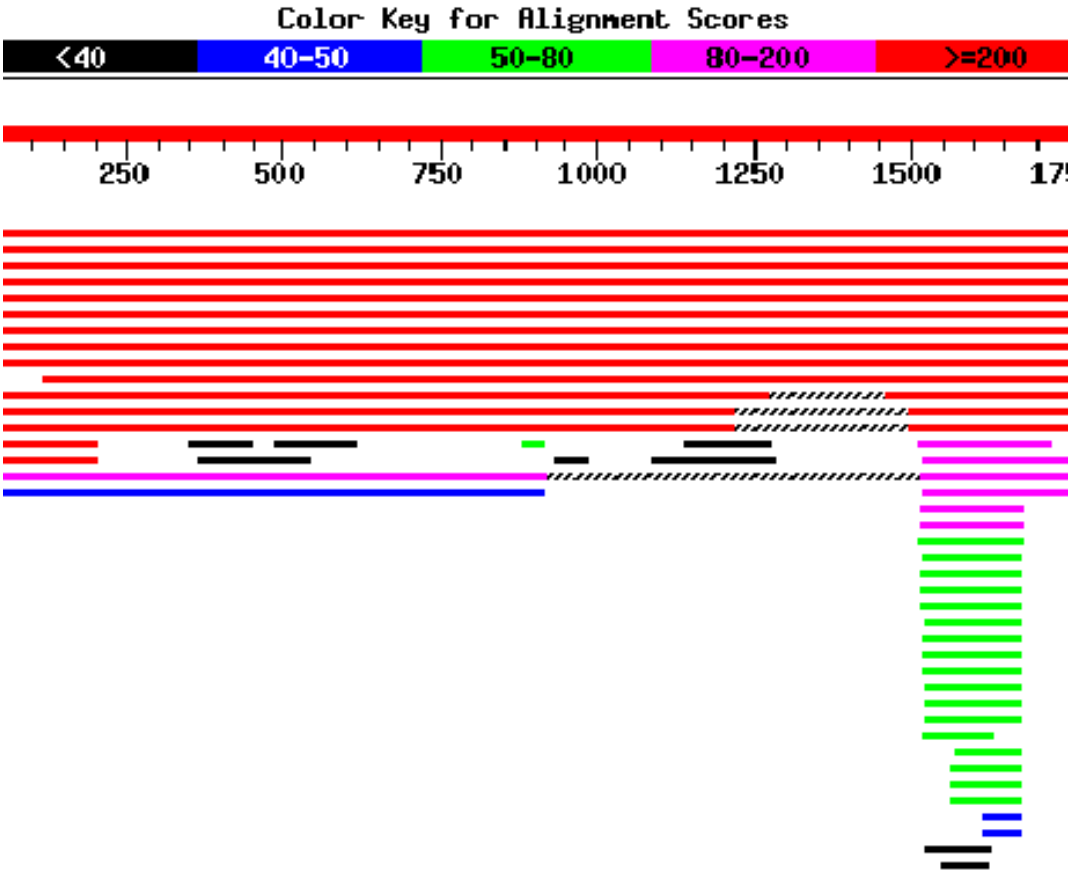
E-value threshold for inclusion in PSI-Blast iteration 1: 0.001
E-value threshold for inclusion in PSI-Blast iteration 2: 0.001

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 54 Blast Hits on the Query Sequence

Mouse-over to show defline and

Color Key for Alignment Scores



BLAST Alignments

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About the alignments

The top hits to tuberin found in the database are to other human TSC2 proteins, plus tuberin homologs in the rat, mouse and zebra fish. After this comes gigas from *Drosophila*, followed by hits to Rap GTPase-activating domains.

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.

Back to BLAST result

or
Click here to see the analysis of this BLAST search.

Sequences with E-value BETTER than threshold

Sequences producing significant alignments:	Score (bits)	E Value
ref|NP_000539.1|| tuberous sclerosis 2 >gi|1717799|sp|P49815|...	3329	0.0
emb|CAA53287.1| (X75621) tuberin [Homo sapiens]	3322	0.0
pir||A49420 tuberous sclerosis protein 2 - human	3269	0.0
gb|AAC34210.1| (AC005600) tuberin [Homo sapiens]	3260	0.0
ref|NP_036812.1|| tuberous sclerosis 2, (renal carcinoma) >gi...	3028	0.0
sp|P49816|TSC2_RAT TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROT...	3021	0.0
gb|AAA86902.1| (U37775) tuberin [Mus musculus]	2963	0.0
ref|NP_035777.1|| tuberous sclerosis 2 >gi|1236402|gb|AAB1875...	2923	0.0
gb|AAA86901.1| (U37775) tuberin [Mus musculus]	2863	0.0
gb|AAD27867.1|AF132986_1 (AF132986) tuberous sclerosis 2 prot...	2696	0.0
gb|AAB86682.1| (AF013614) TSC2 gene product [Fugu rubripes]	1590	0.0
gb|AAF49066.1| (AE003514) gig gene product [Drosophila melano...	521	e-146
gb|AAD48498.1|AF172995_1 (AF172995) gigas protein [Drosophila...	517	e-145
dbj|BAA32694.1| (AB014460) tuberin [Homo sapiens]	378	e-103
dbj|BAA28845.1| (AB009371) tuberin [Mus musculus]	354	3e-96
pir||T38991 conserved hypothetical protein SPAC630.13c - fiss...	164	9e-39
dbj|BAA86586.1| (AB033098) KIAA1272 protein [Homo sapiens]	102	4e-20
pir||T08722 hypothetical protein DKFZp566D133.1 - human (frag...	97	1e-18
gb|AAB97076.1| (AF041107) tulip 2 [Rattus norvegicus]	96	2e-18
gb|AAB87873.1| (AF023478) GTPase activating protein for Rap1 ...	80	1e-13
gb|AAF52526.1| (AE003617) Rapgap1 gene product [Drosophila me...	80	1e-13
gb|AAC71116.2| (U80838) strong similarity to human GTPase-act...	79	3e-13
gb|AAD38161.1|AF152608_1 (AF152608) tuberin [Canis familiaris...	78	7e-13
pir||T21738 hypothetical protein T27F2.2 - Caenorhabditis ele...	77	2e-12
pir||B39897 GTPase-activating protein rap1GAP long form - hum...	74	1e-11
ref|NP_002876.1|| RAP1, GTPase activating protein 1 >gi|13505...	74	1e-11
gb|AAD45946.1|AF151966_1 (AF151966) GTPase activating protein...	73	2e-11
dbj|BAA92627.1| (AB037810) KIAA1389 protein [Homo sapiens]	67	1e-09
gb|AAD12543.1| (AF090989) high-risk human papilloma viruses E...	65	5e-09
gb|AAC32547.1| (AF029789) GTPase-activating protein [Homo sap...	65	5e-09
ref|NP_006738.1|| signal-induced proliferation-associated gen...	65	5e-09
gb|AAD12544.1| (AF090990) high-risk human papilloma viruses E...	65	5e-09
dbj|BAA22197.1| (AB005666) GTPase-activating protein [Homo sa...	65	5e-09
pir||T14106 probable GTPase-activating protein SPA-1 - rat >g...	65	5e-09
gb|AAB97075.1| (AF041106) tulip 1 [Rattus norvegicus]	61	1e-07
dbj|BAA82991.1| (AB028962) KIAA1039 protein [Homo sapiens]	57	1e-06
ref|NP_035509.1|| signal-induced proliferation associated gen...	55	8e-06
sp|P46062|SPA1_MOUSE GTPASE-ACTIVATING PROTEIN SPA-1 >gi|7513...	55	8e-06
pir||S27869 GTPase-activating protein - mouse	55	8e-06

Sequences with E-value WORSE than threshold

dbj|BAA23712.1|	(AB007900) HH0452 cDNA clone for KIAA0440 has...	47	0.001
dbj|BAA25471.1|	(AB011117) KIAA0545 protein [Homo sapiens]	45	0.009
sp|Q09716|YA3B_SCHPO	HYPOTHETICAL 149.2 KD PROTEIN C18B11.11 ...	41	0.098
emb|CAB11382.1|	(Z98741) dihydrolipoamide succinyltransferase...	38	1.1
emb|CAB82690.1|	(AL162295) guanine nucleotide exchange factor...	37	1.5
sp|Q10038|VHP1_CAEEL	PROTEIN-TYROSINE PHOSPHATASE VHP-1 >gi|7...	36	2.5
gb|AAC83179.1|	(AC004974) spa-1-like; similar to AF026504 (PI...	36	2.5
gb|AAF21208.1|AC013483_32	(AC013483) putative MAP3K epsilon p...	35	5.6
gb|AAD49971.1|AC008075_4	(AC008075) Contains similarity to gi...	35	5.6
pir||T41006	ubiquitin carboxyl-terminal hydrolase - fission y...	35	7.3

Alignments

```
ref|NP_000539.1|| tuberous sclerosis 2 >gi|1717799|sp|P49815|TSC2_HUMAN TUBERIN
           (TUBEROUS SCLEROSIS 2 PROTEIN) >gi|1063586|gb|AAB41564.1|
           (L48546) tuberin [Homo sapiens]
           Length = 1807

 Score = 3329 bits (8535), Expect = 0.0
 Identities = 1681/1807 (93%), Positives = 1681/1807 (93%)

Query: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
            MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM
Sbjct: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60

Query: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
            IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR
Sbjct: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120

Query: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
            ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEF
Sbjct: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFLLVL 180

Query: 181  XXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240
                KFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI
Sbjct: 181  VNLVKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240

Query: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300
            VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG
Sbjct: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300

Query: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360
            MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI
Sbjct: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360

Query: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420
            LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE
Sbjct: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420

Query: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480
            SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY
Sbjct: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480

Query: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540
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Sbjct: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540

Query: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600
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Sbjct: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600

Query: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKXX 660
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Sbjct: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKTS 660

Query: 661  XXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720
                              VRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK
Sbjct: 661  GPLSPPTGPPGPAPAGPAVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720

Query: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780
```

```
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            DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA
Sbjct: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840

Query: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900
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Sbjct: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900

Query: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960
            RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS
Sbjct: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960

Query: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020
            PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL
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Query: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXXXXX 1080
            ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNK
Sbjct: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGTGTRSL 1080

Query: 1081 XXXDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140
               DSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG
Sbjct: 1081 LGLDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140

Query: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200
            ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR
Sbjct: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200

Query: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260
            RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST
Sbjct: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260

Query: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMXXXXXXXXXXXXXXXXXXX 1320
            AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVM
Sbjct: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMEEGSPGEVPVLVEPPGLEDV 1320

Query: 1321 XAALGMDRRTDAYXXXXXXXXQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDXXXXXXX 1380
             AALGMDRRTDAY        QEEKSLHAEELVGRGIPIERVVSSEGGRPSVD
Sbjct: 1321 EAALGMDRRTDAYSRSSSVSSQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDLSFQPSQ 1380

Query: 1381 XXXXXXXXXXXXTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ 1440
                        TLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ
Sbjct: 1381 PLSKSSSSPELQTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ 1440

Query: 1441 PEXXXXXXXXXXXXXXXXXXYTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV 1500
            PE                  YTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV
Sbjct: 1441 PEGPLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV 1500

Query: 1501 FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA 1560
            FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA
Sbjct: 1501 FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA 1560

Query: 1561 ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH 1620
            ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH
Sbjct: 1561 ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH 1620

Query: 1621 IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC 1680
            IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC
Sbjct: 1621 IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC 1680

Query: 1681 NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW 1740
            NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW
Sbjct: 1681 NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW 1740

Query: 1741 IARLRHIKRLRQRICEEAAYXXXXXXXXXXXXXXKAPAQTPAEPTPGYEVGQRKRLISSV 1800
            IARLRHIKRLRQRICEEAAY              KAPAQTPAEPTPGYEVGQRKRLISSV
Sbjct: 1741 IARLRHIKRLRQRICEEAAYSNPSLPLVHPPSHSKAPAQTPAEPTPGYEVGQRKRLISSV 1800

Query: 1801 EDFTEFV 1807
            EDFTEFV
Sbjct: 1801 EDFTEFV 1807
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 emb|CAA53287.1| (X75621) tuberin [Homo sapiens]
            Length = 1807

 Score = 3322 bits (8517), Expect = 0.0
 Identities = 1678/1807 (92%), Positives = 1678/1807 (92%)

Query: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
            MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM
Sbjct: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60

Query: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
            IGQICEVAKTKKFEEHAVEALWKAVADLLQPER LEARHAVLALLKAIVQGQGERLGVLR
Sbjct: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERPLEARHAVLALLKAIVQGQGERLGVLR 120

Query: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
            ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEF
Sbjct: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFLLVL 180

Query: 181  XXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240
                KFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI
Sbjct: 181  VNLVKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240

Query: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300
            VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG
Sbjct: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300

Query: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360
            MALWGAHRLYSLRNSPTSV PSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI
Sbjct: 301  MALWGAHRLYSLRNSPTSVLPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360

Query: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420
            LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE
Sbjct: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420

Query: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480
            SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY
Sbjct: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480

Query: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540
            EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS
Sbjct: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540

Query: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600
            PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH
Sbjct: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600

Query: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKXX 660
            SYTLPIASSIRLQAFDFL LLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKK
Sbjct: 601  SYTLPIASSIRLQAFDFLLLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKTS 660

Query: 661  XXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720
                              VRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK
Sbjct: 661  GPLSPPTGPPGPAPAGPAVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720

Query: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780
            VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL
Sbjct: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780

Query: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840
            DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA
Sbjct: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840

Query: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900
            VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC
Sbjct: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900

Query: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960
            RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS
Sbjct: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960

Query: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020
            PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL
Sbjct: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020
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Query: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXXXXX 1080
            ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNK
Sbjct: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGTGTRSL 1080

Query: 1081 XXXDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140
               DSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG
Sbjct: 1081 LGLDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140

Query: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200
            ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR
Sbjct: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200

Query: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260
            RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST
Sbjct: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260

Query: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMXXXXXXXXXXXXXXXXXXXX 1320
            AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVM
Sbjct: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMEEGSPGEVPVLVEPPGLEDV 1320

Query: 1321 XAALGMDRRTDAYXXXXXXXXQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDXXXXXXX 1380
             AALGMDRRTDAY        QEEKSLHAEELVGRGIPIERVVSSEGGRPSVD
Sbjct: 1321 EAALGMDRRTDAYSRSSSVSSQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDLSFQPSQ 1380

Query: 1381 XXXXXXXXXXXXTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ 1440
                        TLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ
Sbjct: 1381 PLSKSSSSPELQTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ 1440

Query: 1441 PEXXXXXXXXXXXXXXXXXXYTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV 1500
            PE                  YTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV
Sbjct: 1441 PEGPLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV 1500

Query: 1501 FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA 1560
            FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA
Sbjct: 1501 FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA 1560

Query: 1561 ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH 1620
            ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH
Sbjct: 1561 ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH 1620

Query: 1621 IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC 1680
            IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC
Sbjct: 1621 IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC 1680

Query: 1681 NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW 1740
            NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW
Sbjct: 1681 NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW 1740

Query: 1741 IARLRHIKRLRQRICEEAAYXXXXXXXXXXXXXXKAPAQTPAEPTPGYEVGQRKRLISSV 1800
            IARLRHIKRLRQRICEEAAY              KAPAQTPAEPTPGYEVGQRKRLISSV
Sbjct: 1741 IARLRHIKRLRQRICEEAAYSNPSLPLVHPPSHSKAPAQTPAEPTPGYEVGQRKRLISSV 1800

Query: 1801 EDFTEFV 1807
            EDFTEFV
Sbjct: 1801 EDFTEFV 1807

 pir||A49420 tuberous sclerosis protein 2 - human
            Length = 1784

 Score = 3269 bits (8382), Expect = 0.0
 Identities = 1658/1807 (91%), Positives = 1658/1807 (91%), Gaps = 23/1807 (1%)

Query: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
            MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM
Sbjct: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60

Query: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
            IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR
Sbjct: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120

Query: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
            ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEF
Sbjct: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFLLVL 180
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Query: 181  XXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240
                KFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI
Sbjct: 181  VNLVKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240

Query: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300
            VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG
Sbjct: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300

Query: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360
            MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI
Sbjct: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360

Query: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420
            LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE
Sbjct: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420

Query: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480
            SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY
Sbjct: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480

Query: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540
            EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS
Sbjct: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540

Query: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600
            PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH
Sbjct: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600

Query: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKXX 660
            SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKK
Sbjct: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKTS 660

Query: 661  XXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720
                              VRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK
Sbjct: 661  GPLSPPTGPPGPAPAGPAVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720

Query: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780
            VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL
Sbjct: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780

Query: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840
            DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA
Sbjct: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840

Query: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900
            VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC
Sbjct: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900

Query: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960
            RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS
Sbjct: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960

Query: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020
            PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL
Sbjct: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020

Query: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXXXXX 1080
            ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNK
Sbjct: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGTGTRSL 1080

Query: 1081 XXXDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140
               DSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG
Sbjct: 1081 LGLDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140

Query: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200
            ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR
Sbjct: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200

Query: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260
            RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST
Sbjct: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260

Query: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMXXXXXXXXXXXXXXXXXXX 1320
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            AKPPPLPRSNT                       DSAVVM
Sbjct: 1261 AKPPPLPRSNT-----------------------DSAVVMEEGSPGEVPVLVEPPGLEDV 1297

Query: 1321 XAALGMDRRTDAYXXXXXXXXQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDXXXXXXX 1380
             AALGMDRRTDAY        QEEKSLHAEELVGRGIPIERVVSSEGGRPSVD
Sbjct: 1298 EAALGMDRRTDAYSRSSSVSSQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDLSFQPSQ 1357

Query: 1381 XXXXXXXXXXXXTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ 1440
                        TLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ
Sbjct: 1358 PLSKSSSSPELQTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ 1417

Query: 1441 PEXXXXXXXXXXXXXXXXXXYTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV 1500
            PE                  YTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV
Sbjct: 1418 PEGPLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV 1477

Query: 1501 FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA 1560
            FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA
Sbjct: 1478 FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA 1537

Query: 1561 ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH 1620
            ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH
Sbjct: 1538 ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH 1597

Query: 1621 IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC 1680
            IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC
Sbjct: 1598 IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC 1657

Query: 1681 NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW 1740
            NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW
Sbjct: 1658 NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW 1717

Query: 1741 IARLRHIKRLRQRICEEAAYXXXXXXXXXXXXXXKAPAQTPAEPTPGYEVGQRKRLISSV 1800
            IARLRHIKRLRQRICEEAAY              KAPAQTPAEPTPGYEVGQRKRLISSV
Sbjct: 1718 IARLRHIKRLRQRICEEAAYSNPSLPLVHPPSHSKAPAQTPAEPTPGYEVGQRKRLISSV 1777

Query: 1801 EDFTEFV 1807
            EDFTEFV
Sbjct: 1778 EDFTEFV 1784
```

gb|AAC34210.1| (AC005600) tuberin [Homo sapiens]
Length = 1784

Score = 3260 bits (8358), Expect = 0.0
Identities = 1654/1807 (91%), Positives = 1654/1807 (91%), Gaps = 23/1807 (1%)

```
Query: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
            MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM
Sbjct: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60

Query: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
            IGQICEVAKTKKFEEHAVEALWKAVADLLQPER LEARHAVLALLKAIVQGQGERLGVLR
Sbjct: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERPLEARHAVLALLKAIVQGQGERLGVLR 120

Query: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
            ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEF
Sbjct: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFLLVL 180

Query: 181  XXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240
                KFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI
Sbjct: 181  VNLVKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240

Query: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300
            VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG
Sbjct: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300

Query: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360
            MALWGAHRLYSLRNSPTSV PSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI
Sbjct: 301  MALWGAHRLYSLRNSPTSVLPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360

Query: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420
            LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE
Sbjct: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420

Query: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480
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            SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY
Sbjct: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480

Query: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540
            EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS
Sbjct: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540

Query: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600
            PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH
Sbjct: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600

Query: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKXX 660
            SYTLPIASSIRLQAFDFL LLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKK
Sbjct: 601  SYTLPIASSIRLQAFDFLLLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKTS 660

Query: 661  XXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720
                               VRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK
Sbjct: 661  GPLSPPTGPPGPAPAGPAVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720

Query: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780
            VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL
Sbjct: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780

Query: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840
            DKTKQREMVYCLEQGLIHRCA QCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA
Sbjct: 781  DKTKQREMVYCLEQGLIHRCASQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840

Query: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900
            VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC
Sbjct: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900

Query: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960
            RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS
Sbjct: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960

Query: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020
            PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL
Sbjct: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020

Query: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXXXXX 1080
            ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNK
Sbjct: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGTGTRSL 1080

Query: 1081 XXXDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140
               DSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG
Sbjct: 1081 LGLDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140

Query: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200
            ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR
Sbjct: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200

Query: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260
            RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST
Sbjct: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260

Query: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMXXXXXXXXXXXXXXXXXXX 1320
            AKPPPLPRSNT                        DSAVVM
Sbjct: 1261 AKPPPLPRSNT-----------------------DSAVVMEEGSPGEVPVLVEPPGLEDV 1297

Query: 1321 XAALGMDRRTDAYXXXXXXXXQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDXXXXXXX 1380
             AALGMDRRTDAY        QEEKSLHAEELVGRGIPIERVVSSEGGRPSVD
Sbjct: 1298 EAALGMDRRTDAYSRSSSVSSQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDLSFQPSQ 1357

Query: 1381 XXXXXXXXXXXXTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ 1440
                        TLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ
Sbjct: 1358 PLSKSSSSPELQTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDSRGQ 1417

Query: 1441 PEXXXXXXXXXXXXXXXXXXYTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV 1500
            PE                  YTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV
Sbjct: 1418 PEGPLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFV 1477

Query: 1501 FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA 1560
            FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA
Sbjct: 1478 FLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELA 1537
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Query: 1561 ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH 1620
            ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH
Sbjct: 1538 ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFH 1597

Query: 1621 IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC 1680
            IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC
Sbjct: 1598 IATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYEC 1657

Query: 1681 NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW 1740
            NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW
Sbjct: 1658 NLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKW 1717

Query: 1741 IARLRHIKRLRQRICEEAAYXXXXXXXXXXXXXXKAPAQTPAEPTPGYEVGQRKRLISSV 1800
            IARLRHIKRLRQRICEEAAY              KAPAQTPAEPTPGYEVGQRKRLISSV
Sbjct: 1718 IARLRHIKRLRQRICEEAAYSNPSLPLVHPPSHSKAPAQTPAEPTPGYEVGQRKRLISSV 1777

Query: 1801 EDFTEFV 1807
            EDFTEFV
Sbjct: 1778 EDFTEFV 1784
```

ref|NP_036812.1|| tuberous sclerosis 2, (renal carcinoma) >gi|1363334|pir||S57329
tuberous sclerosis 2 homolog - rat
>gi|994784|dbj|BAA08914.1| (D50413) tuberin [Rattus
norvegicus]
Length = 1809

```
 Score = 3028 bits (7763), Expect = 0.0
 Identities = 1533/1812 (84%), Positives = 1583/1812 (86%), Gaps = 8/1812 (0%)

Query: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
            MAKPTSKDSGLKEKFKILLGLGT RPNPR AEGKQTEFIITAEILRELS ECGLNNRIRM
Sbjct: 1    MAKPTSKDSGLKEKFKILLGLGTSRPNPRCAEGKQTEFIITAEILRELSGECGLNNRIRM 60

Query: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
            IGQIC+VAKTKK EEHAVEALWKAV+DLLQPER  EARHAVLALLKAIVQGQG+RLGVLR
Sbjct: 61   IGQICDVAKTKKLEEHAVEALWKAVSDLLQPERPPEARHAVLALLKAIVQGQGDRLGVLR 120

Query: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
            ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELA+FVLQWMDVGLSSEF
Sbjct: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELAEFVLQWMDVGLSSEFLLVL 180

Query: 181  XXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240
                KFNSCYLDEYIA MV MICLLC+RT SSVDIEVSLQVLDAVVCYNCLPAESLPLFI
Sbjct: 181  VNLVKFNSCYLDEYIAPMVHMICLLCIRTVSSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240

Query: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300
            +TLCRT+NVKELCEPCWKLMRNLLGTHLGHSAIYNMC +ME+R+YMEDAPLLRGAVFFVG
Sbjct: 241  ITLCRTVNVKELCEPCWKLMRNLLGTHLGHSAIYNMCRIMENRSYMEDAPLLRGAVFFVG 300

Query: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360
            MALWGAHRLYSL+NSPTSV PSFY+AM CPNEVVSYEIVLSITRLIKKYRKELQ V WDI
Sbjct: 301  MALWGAHRLYSLKNSPTSVLPSFYEAMTCPNEVVSYEIVLSITRLIKKYRKELQAVTWDI 360

Query: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420
            LL+IIERLLQQLQ LDSPELRTIVHDLLTTVEELCDQNEFHGSQERY+ELVE  ADQRPE
Sbjct: 361  LLDIIERLLQQLQNLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYYELVESYADQRPE 420

Query: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480
            SSLLNLI+YRAQSIHPAKDGWIQNLQ LMERFFR+E R AVRIKVLDVLSFVLLINRQFY
Sbjct: 421  SSLLNLITYRAQSIHPAKDGWIQNLQLLMERFFRNECRSAVRIKVLDVLSFVLLINRQFY 480

Query: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540
            EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS
Sbjct: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540

Query: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600
            PP ELEERD+A YSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYE L+SHIQLHYKH
Sbjct: 541  PPLELEERDLAVYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYETLISHIQLHYKH 600

Query: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKXX 660
             Y+LPIASSIRLQAFDFL LLRADSLHRLGLPNKDGVVRFSPYC+CD  E +R SEKK
Sbjct: 601  GYSLPIASSIRLQAFDFLLLLRADSLHRLGLPNKDGVVRFSPYCLCDCAELDRASEKKAS 660
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Query: 661  XXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720
                              VRLG +PYSLLFRVLLQCLKQE+DWKVLKLVL +LPESLRYK
Sbjct: 661  GPLSPPTGPPSPVPTGPAVRLGHLPYSLLFRVLLQCLKQETDWKVLKLVLSKLPESLRYK 720

Query: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780
            VLIFTSPCSVDQL SALCSMLS PKTLERLRG PEGFSRTDLHLAVVPVLTALISYHNYL
Sbjct: 721  VLIFTSPCSVDQLSSALCSMLSAPKTLERLRGTPEGFSRTDLHLAVVPVLTALISYHNYL 780

Query: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840
            DKT+QREMVYCLEQGLI+RCA QCVVAL+ICSVEMPDIIIKALPVLVVKLTHISATASMA
Sbjct: 781  DKTRQREMVYCLEQGLIYRCASQCVVALAICSVEMPDIIIKALPVLVVKLTHISATASMA 840

Query: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900
            +PLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC
Sbjct: 841  IPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900

Query: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960
            RLPFRKDFVP+ITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIAR PKQGLNNS
Sbjct: 901  RLPFRKDFVPYITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARAPKQGLNNS 960

Query: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020
            PPVKEFKES AAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENS+AQADD+LKNLHL
Sbjct: 961  PPVKEFKESCAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSMAQADDNLKNLHL 1020

Query: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXXXXX 1080
            ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNK
Sbjct: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGTGTRSL 1080

Query: 1081 XXXDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140
               DSG+LQ G  SSS PG HVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG
Sbjct: 1081 LGLDSGDLQGGSASSSDPGTHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140

Query: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200
             LD  A    G   S G + APAA+PEK  AG ++P  EK NLAAYVPLLTQGWAEILVR
Sbjct: 1141 VLDTSAPYTPGGPASLGAQAAPAARPEKPCAGAQLPAAEKANLAAYVPLLTQGWAEILVR 1200

Query: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260
            RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAA T
Sbjct: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAGT 1260

Query: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMXXXXXXXXXXXXXXXXXXX 1320
            AKPP LPRSNTVASFSSLYQ SCQGQLHRSVSWADSAVV+
Sbjct: 1261 AKPPTLPRSNTVASFSSLYQPSCQGQLHRSVSWADSAVVLEEGSPGEAHVPVEPPELEDF 1320

Query: 1321 XAALGMDR---RTDAYXXXXXXXXQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDXXXX 1377
             AALG DR   R DAY        QEEKS H EEL   GIPIER +SSEG RP+VD
Sbjct: 1321 EAALGTDRHCQRPDAYSRSSSASSQEEKS-HLEELAAGGIPIERAISSEGARPTVDLSFQ 1379

Query: 1378 XXXXXXXXXXXXXXXTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDS 1437
                            TLQDILGD GDK D+GRLSPE K RSQSG LDGE+A WSA GE+S
Sbjct: 1380 PSQPLSKSSSSPELQTLQDILGDLGDKTDIGRLSPEAKVRSQSGILDGEAATWSAPGEES 1439

Query: 1438 R--GQPEXXXXXXXXXXXXXXXXXXYTISDSAPSRRGKRVERDALKSRATASNAEKVPGI 1495
            R    PE                   YTISDSAPSRRGKRVERD  KSR  AS+AEKVPGI
Sbjct: 1440 RITVPPEGPLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDNFKSRTAASSAEKVPGI 1499

Query: 1496 NPSFVFLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQS 1555
            NPSFVFLQLYHSPFFGDESNKPILLPNE  SFERSVQLLDQIPSYDTHKIAVLYVGEGQS
Sbjct: 1500 NPSFVFLQLYHSPFFGDESNKPILLPNE--SFERSVQLLDQIPSYDTHKIAVLYVGEGQS 1557

Query: 1556 NSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM 1615
            +SELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM
Sbjct: 1558 SSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM 1617

Query: 1616 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTP 1675
            QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSI+YNDSGEDFKLGTIKGQFNFVHVI+TP
Sbjct: 1618 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIIYNDSGEDFKLGTIKGQFNFVHVIITP 1677

Query: 1676 LDYECNLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDI 1735
            LDY+CNL++LQCRKDMEGLVDTSVAKIVSDRNL FVARQMALHANMASQVHHSRSNPTDI
Sbjct: 1678 LDYKCNLLTLQCRKDMEGLVDTSVAKIVSDRNLSFVARQMALHANMASQVHHSRSNPTDI 1737

Query: 1736 YPSKWIARLRHIKRLRQRICEEAAYXXXXXXXXXXXXXXKAPAQTPAEPTPGYEVGQRKR 1795
            YPSKWIARLRHIKRLRQRI EE  Y              K PAQ P E TP YE GQRKR
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Sbjct: 1738 YPSKWIARLRHIKRLRQRIREEVHYSNPSLPLMHPPAHTKVPAQAPTEATPTYETGQRKR 1797

Query: 1796 LISSVEDFTEFV 1807
            LISSV+DFTEFV
Sbjct: 1798 LISSVDDFTEFV 1809
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sp|P49816|TSC2_RAT TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN)
>gi|1061325|gb|AAC52289.1| (U24150) tuberous sclerosis 2 homolog [Rattus norvegicus]
Length = 1809

Score = 3021 bits (7746), Expect = 0.0
Identities = 1530/1812 (84%), Positives = 1580/1812 (86%), Gaps = 8/1812 (0%)

```
Query: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
            MAKPTSKDSGLKEKFKILLGLGT RPNPR AEGKQTEFIITAEILRELS ECGLNNRIRM
Sbjct: 1    MAKPTSKDSGLKEKFKILLGLGTSRPNPRCAEGKQTEFIITAEILRELSGECGLNNRIRM 60

Query: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
            IGQIC+VAKTKK EEHAVEALWKAV+DLLQPER  EARHAVLALLKAIVQGQG+RLGVLR
Sbjct: 61   IGQICDVAKTKKLEEHAVEALWKAVSDLLQPERPPEARHAVLALLKAIVQGQGDRLGVLR 120

Query: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
            ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELA+FVLQWMDVGLSSEF
Sbjct: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELAEFVLQWMDVGLSSEFLLVL 180

Query: 181  XXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240
                KFNSCYLDEYIA MV MICLLC+RT SSVDIEVSLQVLDAVVCYNCLPAESLPLFI
Sbjct: 181  VNLVKFNSCYLDEYIAPMVHMICLLCIRTVSSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240

Query: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300
            +TLCRT+NVKELCEPCWKLMRNLLGTHLGHSAIYNMC +ME+R+YMEDAPLLRGAVFFVG
Sbjct: 241  ITLCRTVNVKELCEPCWKLMRNLLGTHLGHSAIYNMCRIMENRSYMEDAPLLRGAVFFVG 300

Query: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360
            MALWGAHRLYSL+NSPTSV PSFY+AM CPNEVVSYEIVLSITRLIKKYRKELQ V WDI
Sbjct: 301  MALWGAHRLYSLKNSPTSVLPSFYEAMTCPNEVVSYEIVLSITRLIKKYRKELQAVTWDI 360

Query: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420
            LL+IIERLLQQLQ LDSPELRTIVHDLLTTVEELCDQNEFHGSQERY+ELVE  ADQRPE
Sbjct: 361  LLDIIERLLQQLQNLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYYELVESYADQRPE 420

Query: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480
            SSLLNLI+YRAQSIHPAKDGWIQNLQ LMERFFR+E R AVRIKVLDVLSFVLLINRQFY
Sbjct: 421  SSLLNLITYRAQSIHPAKDGWIQNLQLLMERFFRNECRSAVRIKVLDVLSFVLLINRQFY 480

Query: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540
            EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS
Sbjct: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540

Query: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600
            PP ELEERD+A YSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYE L+SHIQLHYKH
Sbjct: 541  PPLELEERDLAVYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYETLISHIQLHYKH 600

Query: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKXX 660
             Y+LPIASSIRLQAFDFL LLRADSLHRLGLPNKDGVVRFSPYC+CD  E +R SEKK
Sbjct: 601  GYSLPIASSIRLQAFDFLLLLRADSLHRLGLPNKDGVVRFSPYCLCDCAELDRASEKKAS 660

Query: 661  XXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720
                                VRLG +PYSLLFRVLLQCLKQE+DWKVLKLVL +LPESLRYK
Sbjct: 661  GPLSPPTGPPSPVPTGPAVRLGHLPYSLLFRVLLQCLKQETDWKVLKLVLSKLPESLRYK 720

Query: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780
            VLIFTSPCSVDQL SALCSMLS PKTLERLRG PEGFSRTDLHLAVVPVLTALISYHNYL
Sbjct: 721  VLIFTSPCSVDQLSSALCSMLSAPKTLERLRGTPEGFSRTDLHLAVVPVLTALISYHNYL 780

Query: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840
            DKT+QREMVYCLEQGLI+RCA QCVVAL+ICSVEMPDIIIKALPVLVVKLTHISATASMA
Sbjct: 781  DKTRQREMVYCLEQGLIYRCASQCVVALAICSVEMPDIIIKALPVLVVKLTHISATASMA 840

Query: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900
            +PLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC
Sbjct: 841  IPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900
```

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Query: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960
            RLPFRKDFVP+ITKGLRSNVLLSFDDTPEKD FRARSTSLNERPKSLRIAR PKQGLNNS
Sbjct: 901  RLPFRKDFVPYITKGLRSNVLLSFDDTPEKDKFRARSTSLNERPKSLRIARAPKQGLNNS 960

Query: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020
            PPVKEFKES AAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENS+AQADD+LKNLHL
Sbjct: 961  PPVKEFKESCAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSMAQADDNLKNLHL 1020

Query: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXXXXX 1080
            ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNK
Sbjct: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGTGTRSL 1080

Query: 1081 XXXDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140
               DSG+LQ G  SSS PG HVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG
Sbjct: 1081 LGLDSGDLQGGSASSSDPGTHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140

Query: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200
             LD  A    G   S G + APAA+PEK  AG ++P  EK NLAAYVPLLTQGWAEILVR
Sbjct: 1141 VLDTSAPYTPGGPASLGAQAAPAARPEKPCAGAQLPAAEKANLAAYVPLLTQGWAEILVR 1200

Query: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260
            RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAA T
Sbjct: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAGT 1260

Query: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMXXXXXXXXXXXXXXXXXXX 1320
            AKPP LPRSNTVASFSSLYQ SCQGQLHRSVSWADSAVV+
Sbjct: 1261 AKPPTLPRSNTVASFSSLYQPSCQGQLHRSVSWADSAVVLEEGSPGEAHVPVEPPELEDF 1320

Query: 1321 XAALGMDR---RTDAYXXXXXXXXQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDXXXX 1377
             AALG DR   R DAY        QEEKS H EEL   GIPIER +SSEG RP+VD
Sbjct: 1321 EAALGTDRHCQRPDAYSRSSSASSQEEKS-HLEELAAGGIPIERAISSEGARPTVDLSFQ 1379

Query: 1378 XXXXXXXXXXXXXXXTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDS 1437
                            TLQDILGD GDK D+GRLSPE K RSQSG LDGE+A WSA GE+S
Sbjct: 1380 PSQPLSKSSSSPELQTLQDILGDLGDKTDIGRLSPEAKVRSQSGILDGEAATWSAPGEES 1439

Query: 1438 R--GQPEXXXXXXXXXXXXXXXXXXYTISDSAPSRRGKRVERDALKSRATASNAEKVPGI 1495
            R    PE                   YTISDSAPSRRGKRVERD  KSR  AS+AEKVPGI
Sbjct: 1440 RITVPPEGPLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDNFKSRTAASSAEKVPGI 1499

Query: 1496 NPSFVFLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQS 1555
            NPSFVFLQLYHSPF GDESNKPILLPNE  SFERSVQLLDQIPSYDTHKIAVLYVGEGQS
Sbjct: 1500 NPSFVFLQLYHSPFCGDESNKPILLPNE--SFERSVQLLDQIPSYDTHKIAVLYVGEGQS 1557

Query: 1556 NSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM 1615
            +SELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM
Sbjct: 1558 SSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM 1617

Query: 1616 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTP 1675
            QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSI+YNDSGEDFKLGTIKGQFNFVHVI+TP
Sbjct: 1618 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIIYNDSGEDFKLGTIKGQFNFVHVIITP 1677

Query: 1676 LDYECNLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDI 1735
            LDY+CNL++LQCRKDMEGLVDTSVAKIVSDRNL FVARQMALHANMASQVHH RSNPTDI
Sbjct: 1678 LDYKCNLLTLQCRKDMEGLVDTSVAKIVSDRNLSFVARQMALHANMASQVHHRRSNPTDI 1737

Query: 1736 YPSKWIARLRHIKRLRQRICEEAAYXXXXXXXXXXXXXXKAPAQTPAEPTPGYEVGQRKR 1795
            YPSKWIARLRHIKRLRQRI EE  Y              K PAQ P E TP YE GQRKR
Sbjct: 1738 YPSKWIARLRHIKRLRQRIREEVHYSNPSLPLMHPPAHTKVPAQAPTEATPTYETGQRKR 1797

Query: 1796 LISSVEDFTEFV 1807
            LISSV+DFTEFV
Sbjct: 1798 LISSVDDFTEFV 1809

 gb|AAA86902.1| (U37775) tuberin [Mus musculus]
            Length = 1784

 Score = 2963 bits (7597), Expect = 0.0
 Identities = 1512/1812 (83%), Positives = 1564/1812 (85%), Gaps = 33/1812 (1%)

Query: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
            MAKPTSKDSGLKEKFKILLGLGT RPNPR AEGKQTEFIIT+EILRELS ECGLNNRIRM
Sbjct: 1    MAKPTSKDSGLKEKFKILLGLGTSRPNPRCAEGKQTEFIITSEILRELSGECGLNNRIRM 60
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Query: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
            IGQIC+VAKTKK EEHAVEALWKAV+DLLQPER  EARHAVL LLKAIVQGQG+RLGVLR
Sbjct: 61   IGQICDVAKTKKLEEHAVEALWKAVSDLLQPERPPEARHAVLTLLKAIVQGQGDRLGVLR 120

Query: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
            ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEEL +FVLQWMDVGLSSEF
Sbjct: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEEL-EFVLQWMDVGLSSEFLLVL 179

Query: 181  XXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240
                KFNSCYLDEYIA MV MICLLC+RT SSVDIEVSLQVLDAVVCYNCLPAESLPLFI
Sbjct: 180  VNLVKFNSCYLDEYIASMVHMICLLCIRTVSSVDIEVSLQVLDAVVCYNCLPAESLPLFI 239

Query: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300
            +TLCRTINVKELCEPCWKLMRNLLGTHL HSAIYNMC +MEDR+YMEDAPLLRGAVFFVG
Sbjct: 240  ITLCRTINVKELCEPCWKLMRNLLGTHLSHSAIYNMCRIMEDRSYMEDAPLLRGAVFFVG 299

Query: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360
            MALWGAHRLYSL+NSPTSV PSFY+AM CPNEVVSYEIVLSITRLIKKYRKELQ V WDI
Sbjct: 300  MALWGAHRLYSLKNSPTSVLPSFYEAMTCPNEVVSYEIVLSITRLIKKYRKELQAVTWDI 359

Query: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420
            LL+IIERLLQQLQ LDSPEL+TIVHDLLTTVEELCDQNEFHGSQERY+ELVE  ADQRPE
Sbjct: 360  LLDIIERLLQQLQNLDSPELKTIVHDLLTTVEELCDQNEFHGSQERYYELVESYADQRPE 419

Query: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480
            SSLLNLISYRAQSIHPAKDGWIQNLQ LMERFFR+E R AVRIKVLDVLSFVLLINRQFY
Sbjct: 420  SSLLNLISYRAQSIHPAKDGWIQNLQLLMERFFRNECRSAVRIKVLDVLSFVLLINRQFY 479

Query: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540
            EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS
Sbjct: 480  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 539

Query: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600
            PPPELEER++A +SASLEDVKTAVLGLLVILQTKLYTLPASHATRVYE L+SHIQLHYKH
Sbjct: 540  PPPELEERNLAVHSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYESLISHIQLHYKH 599

Query: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKXX 660
             Y+LPIASSIRLQAFDFL LLRADSLHRLGLPNKDGVVRFSPYC+CD ME +R SEKK
Sbjct: 600  GYSLPIASSIRLQAFDFLLLLRADSLHRLGLPNKDGVVRFSPYCLCDCMELDRASEKKAS 659

Query: 661  XXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720
                               VRLG +PYSLLFRVLLQCLKQESDWKVLKLVL RLPESLRYK
Sbjct: 660  GPLSPPTGPPSPVPMGPAVRLGYLPYSLLFRVLLQCLKQESDWKVLKLVLSRLPESLRYK 719

Query: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780
            VLIFTSPCSVDQL SALCSMLS PKTLERLRG PEGFSRTDLHLAVVPVLTALISYHNYL
Sbjct: 720  VLIFTSPCSVDQLSSALCSMLSAPKTLERLRGTPEGFSRTDLHLAVVPVLTALISYHNYL 779

Query: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840
            DKT+QREMVYCLEQGLI+RCA QCVVAL+ICSVEMPDIIIKALPVLVVKLTHISATASMA
Sbjct: 780  DKTRQREMVYCLEQGLIYRCASQCVVALAICSVEMPDIIIKALPVLVVKLTHISATASMA 839

Query: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900
            +PLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC
Sbjct: 840  IPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 899

Query: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960
            RLPFRKDFVP+ITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIAR PKQGLNNS
Sbjct: 900  RLPFRKDFVPYITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARAPKQGLNNS 959

Query: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020
            PPVKEFKES AAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENS+AQADD+LKNLHL
Sbjct: 960  PPVKEFKESCAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSMAQADDNLKNLHL 1019

Query: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXXXXX 1080
            ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNK
Sbjct: 1020 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGTGTRSL 1079

Query: 1081 XXXDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140
               DSG+LQ G +SSS P  HVRQTKEAPAKLESQAGQQVSRGARD VRSMSGGHGLRVG
Sbjct: 1080 LGLDSGDLQGGSDSSSDPSTHVRQTKEAPAKLESQAGQQVSRGARDPVRSMSGGHGLRVG 1139

Query: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200
             LD  A    G + S GP+TA AAKPEK  AG ++P  EKTNLAAYVPLLTQGWAEILVR
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Sbjct: 1140 VLDTSAPYSPGGSASLGPQTAVAAKPEKPPAGAQLPTAEKTNLAAYVPLLTQGWAEILVR 1199

Query: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260
            RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAA T
Sbjct: 1200 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAGT 1259

Query: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMXXXXXXXXXXXXXXXXXXXX 1320
            AKPP LPRSNT                        DSA+V+
Sbjct: 1260 AKPPTLPRSNT----------------------DSAMVLEEGSPGETQVPVEPPELEDF 1296

Query: 1321 XAALGMDR---RTDAYXXXXXXXXQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDXXXX 1377
             AALG DR   R D Y        QEEKS H EEL   GIPIER +SSEG RP+VD
Sbjct: 1297 EAALGTDRHCQRPDTYSRSSSASSQEEKS-HLEELAAGGIPIERAISSEGARPAVDLSFQ 1355

Query: 1378 XXXXXXXXXXXXXXXTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDS 1437
                            TLQDILGD GDK D+GRLSPE K RSQSG LDGE+A WSA+GE+S
Sbjct: 1356 PSQPLSKSSSSPELQTLQDILGDLGDKIDIGRLSPEAKVRSQSGILDGEAATWSATGEES 1415

Query: 1438 R--GQPEXXXXXXXXXXXXXXXXXXYTISDSAPSRRGKRVERDALKSRATASNAEKVPGI 1495
            R    PE                   YTISDSAPSRRGKRVERD  KSRA AS+AEKVPGI
Sbjct: 1416 RITVPPEGPLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDNFKSRAAASSAEKVPGI 1475

Query: 1496 NPSFVFLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQS 1555
            NPSFVFLQLYHSPFFGDESNKPILLPNE  SFERSVQLLDQIPSYDTHKIAVLYVGEGQS
Sbjct: 1476 NPSFVFLQLYHSPFFGDESNKPILLPNE--SFERSVQLLDQIPSYDTHKIAVLYVGEGQS 1533

Query: 1556 NSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM 1615
            +SELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM
Sbjct: 1534 SSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM 1593

Query: 1616 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTP 1675
            QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSI+YNDSGEDFKLGTIKGQFNFVHVI+TP
Sbjct: 1594 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIIYNDSGEDFKLGTIKGQFNFVHVIITP 1653

Query: 1676 LDYECNLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDI 1735
            LDY+CNL++LQCRKDMEGLVDTSVAKIVSDRNL FVARQMALHANMASQVHHSRSNPTDI
Sbjct: 1654 LDYKCNLLTLQCRKDMEGLVDTSVAKIVSDRNLSFVARQMALHANMASQVHHSRSNPTDI 1713

Query: 1736 YPSKWIARLRHIKRLRQRICEEAAYXXXXXXXXXXXXXXKAPAQTPAEPTPGYEVGQRKR 1795
            YPSKWIARLRHIKRLRQRI EE  Y               KAPAQ P E TP YE GQRKR
Sbjct: 1714 YPSKWIARLRHIKRLRQRIREEVHYSNPSLPLMHPPAHTKAPAQAP-EATPTYETGQRKR 1772

Query: 1796 LISSVEDFTEFV 1807
            LISSV+DFTEFV
Sbjct: 1773 LISSVDDFTEFV 1784
```

ref|NP_035777.1|| tuberous sclerosis 2 >gi|1236402|gb|AAB18754.1| (U39818) tuberin [Mus musculus]
Length = 1814

Score = 2923 bits (7495), Expect = 0.0
Identities = 1495/1823 (82%), Positives = 1553/1823 (85%), Gaps = 25/1823 (1%)

```
Query: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
            MAKPTSKDSGLKEKFKILLGLGT RPNPR AEGKQTEFIIT+EILRELS ECGLNNRIRM
Sbjct: 1    MAKPTSKDSGLKEKFKILLGLGTSRPNPRCAEGKQTEFIITSEILRELSGECGLNNRIRM 60

Query: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
            IGQIC+VAKTKK EEHAVEALWKAV+DLLQPER  EARHAVL LLKAIVQGQG+RLGVLR
Sbjct: 61   IGQICDVAKTKKLEEHAVEALWKAVSDLLQPERPPEARHAVLTLLKAIVQGQGDRLGVLR 120

Query: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
            ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELA+FVLQWMDVGLSSEF
Sbjct: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELAEFVLQWMDVGLSSEFLLVL 180

Query: 181  XXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240
                KFNSCYLDEYIA MV MICLLC+RT SSVDIEVSLQVLDAVVCYNCLPAESLPLFI
Sbjct: 181  VNLVKFNSCYLDEYIASMVHMICLLCIRTVSSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240

Query: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300
            +TLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMC +MEDR+YMEDAPLLRGAVFFVG
Sbjct: 241  ITLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCRIMEDRSYMEDAPLLRGAVFFVG 300

Query: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360
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            MALWGAHRLYSL+NSPTSV PSFY+AM CPNEVVSYEIVLSITRLIKKYRKELQ V WDI
Sbjct: 301  MALWGAHRLYSLKNSPTSVLPSFYEAMTCPNEVVSYEIVLSITRLIKKYRKELQAVTWDI 360

Query: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420
            LL+IIERLLQQLQ LDSPEL+TIVHDLLTTVEELCDQNEFHGSQERY+ELVE  ADQRPE
Sbjct: 361  LLDIIERLLQQLQNLDSPELKTIVHDLLTTVEELCDQNEFHGSQERYYELVESYADQRPE 420

Query: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480
            SSLLNLISYRAQSIHPAKDGWIQNLQ LMERFFR+E R AV IKVLDVLSFVLLI RQFY
Sbjct: 421  SSLLNLISYRAQSIHPAKDGWIQNLQLLMERFFRNECRSAVAIKVLDVLSFVLLIIRQFY 480

Query: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540
            EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS
Sbjct: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540

Query: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600
            PPPELEERD+A +SASLEDVKTAVLGLLVILQTKLYTLPASHATRVYE L+SHIQLHYKH
Sbjct: 541  PPPELEERDLAVHSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYESLISHIQLHYKH 600

Query: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKXX 660
             Y+LPIASSIRLQAFDFL LLRADSLHRLGLPNKDGVVRFSPYC+CD ME +R SEKK
Sbjct: 601  GYSLPIASSIRLQAFDFLLLLRADSLHRLGLPNKDGVVRFSPYCLCDCMELDRASEKKAS 660

Query: 661  XXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720
                               VRLG +PYSLLFRVLLQCLKQESDWKVLKLVL RLPESLRYK
Sbjct: 661  GPLSPPTGPPSPVPMGPAVRLGYLPYSLLFRVLLQCLKQESDWKVLKLVLSRLPESLRYK 720

Query: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780
            VLIFTSPCSVDQL SALCSMLS PKTLERLRG PEGFSRTDLHLAVVPVLTALISYHNYL
Sbjct: 721  VLIFTSPCSVDQLSSALCSMLSAPKTLERLRGTPEGFSRTDLHLAVVPVLTALISYHNYL 780

Query: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840
            DKT+QREMVYCLEQGLI+RCA QCVVAL+ICSVEMPDIIIKALPVLVVKLTHISATASMA
Sbjct: 781  DKTRQREMVYCLEQGLIYRCASQCVVALAICSVEMPDIIIKALPVLVVKLTHISATASMA 840

Query: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900
            +PLLEFLSTLARLPHLYRNF  EQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC
Sbjct: 841  IPLLEFLSTLARLPHLYRNFVPEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900

Query: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960
            RLPFRKDFVP+ITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIAR PKQGLNNS
Sbjct: 901  RLPFRKDFVPYITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARAPKQGLNNS 960

Query: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020
            PPVKEFKES AAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENS+AQADD+LKNLHL
Sbjct: 961  PPVKEFKESCAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSMAQADDNLKNLHL 1020

Query: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXXXXX 1080
            ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNK
Sbjct: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGTGTRSL 1080

Query: 1081 XXXDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140
               DSG+LQ G +SSS P  HVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG
Sbjct: 1081 LGLDSGDLQGGSDSSSDPSTHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140

Query: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200
             LD  A    G + S GP+TA AAKPEK  AG ++P  EKTNLAAYVPLLTQGWAEILVR
Sbjct: 1141 VLDTSAPYSPGGSASLGPQTAVAAKPEKPPAGAQLPTAEKTNLAAYVPLLTQGWAEILVR 1200

Query: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260
            RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEH    +   +S     T
Sbjct: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHGHAPVQVIVSA-TGCT 1259

Query: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMXXXXXXXXXXXXXXXXXXXX 1320
            AKPP LPRSNTVASFSSLYQ SCQGQLHRSVSWADSA+V+
Sbjct: 1260 AKPPTLPRSNTVASFSSLYQPSCQGQLHRSVSWADSAMVLEEGSPGETQVPVEPPELEDF 1319

Query: 1321 XAALGMDR---RTDAYXXXXXXXXQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDXXXX 1377
             AALG DR   R D Y        QEEKS H EEL   GIPIER +SSEG RP+VD
Sbjct: 1320 EAALGTDRHCQRPDTYSRSSSASSQEEKS-HLEELAAGGIPIERAISSEGARPAVDLSFQ 1378

Query: 1378 XXXXXXXXXXXXXXXTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDS 1437
                            TLQDILGD GDK D+GRLSPE K RSQSG LDGE+A WSA+GE+S
Sbjct: 1379 PSQPLSKSSSSPELQTLQDILGDLGDKIDIGRLSPEAKVRSQSGILDGEAATWSATGEES 1438
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Query: 1438 R--GQPEXXXXXXXXXXXXXXXXXXYTISDSAPSRRGKRVERDALKSRATASNAEKVPGI 1495
            R    PE                  YTISDSAPSRRGKRVERD  KSRA AS+AEKVPGI
Sbjct: 1439 RITVPPEGPLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDNFKSRAAASSAEKVPGI 1498

Query: 1496 NPSFVFLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQS 1555
            NPSFVFLQLYHSPFFGDESNKPILLPNE  SFERSVQLLDQIPSYDTHKIAVLYVGEGQS
Sbjct: 1499 NPSFVFLQLYHSPFFGDESNKPILLPNE--SFERSVQLLDQIPSYDTHKIAVLYVGEGQS 1556

Query: 1556 NSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM 1615
            +SELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM
Sbjct: 1557 SSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM 1616

Query: 1616 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIK-GQFNFVHVIVT 1674
            QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSI+YNDSGEDFKLGTIK GQFNFVHVI+T
Sbjct: 1617 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIIYNDSGEDFKLGTIKQGQFNFVHVIIT 1676

Query: 1675 PLDYECNLVSLQCRKD----------MEGLVDTSVAKIVSDRNLPFVARQMALHANMASQ 1724
            PLDY+CNL++LQCRKD            G +      +V +  +      +  H  MASQ
Sbjct: 1677 PLDYKCNLLTLQCRKDGPACKCEWWRQPGEIVVWALPVVMELTVTI----LLCHLQMASQ 1732

Query: 1725 VHHSRSNPTDIYPSKWIARLRHIKRLRQRICEEAAYXXXXXXXXXXXXXXKAPAQTPAEP 1784
            VHHSRSNPTDIYPSKWIARLRHIKRLRQRI EE  Y              KAPAQ P E
Sbjct: 1733 VHHSRSNPTDIYPSKWIARLRHIKRLRQRIREEVHYSNPSLPLMHPPAHTKAPAQAP-EA 1791

Query: 1785 TPGYEVGQRKRLISSVEDFTEFV 1807
            TP YE GQRKRLISSV+DFTEFV
Sbjct: 1792 TPTYETGQRKRLISSVDDFTEFV 1814
```

gb|AAA86901.1| (U37775) tuberin [Mus musculus]
Length = 1741

Score = 2863 bits (7340), Expect = 0.0
Identities = 1471/1812 (81%), Positives = 1523/1812 (83%), Gaps = 76/1812 (4%)

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Query: 1    MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
            MAKPTSKDSGLKEKFKILLGLGT RPNPR AEGKQTEFIIT+EILRELS ECGLNNRIRM
Sbjct: 1    MAKPTSKDSGLKEKFKILLGLGTSRPNPRCAEGKQTEFIITSEILRELSGECGLNNRIRM 60

Query: 61   IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
            IGQIC+VAKTKK EEHAVEALWKAV+DLLQPER  EARHAVL LLKAIVQGQG+RLGVLR
Sbjct: 61   IGQICDVAKTKKLEEHAVEALWKAVSDLLQPERPPEARHAVLTLLKAIVQGQGDRLGVLR 120

Query: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
            ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEEL +FVLQWMDVGLSSEF
Sbjct: 121  ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEEL-EFVLQWMDVGLSSEFLLVL 179

Query: 181  XXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFI 240
                KFNSCYLDEYIA MV MICLLC+RT SSVDIEVSLQVLDAVVCYNCLPAESLPLFI
Sbjct: 180  VNLVKFNSCYLDEYIASMVHMICLLCIRTVSSVDIEVSLQVLDAVVCYNCLPAESLPLFI 239

Query: 241  VTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVG 300
            +TLCRTINVKELCEPCWKLMRNLLGTHL HSAIYNMC +MEDR+YMEDAPLLRGAVFFVG
Sbjct: 240  ITLCRTINVKELCEPCWKLMRNLLGTHLSHSAIYNMCRIMEDRSYMEDAPLLRGAVFFVG 299

Query: 301  MALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAWDI 360
            MALWGAHRLYSL+NSPTSV PSFY+AM CPNEVVSYEIVLSITRLIKKYRKELQ V WDI
Sbjct: 300  MALWGAHRLYSLKNSPTSVLPSFYEAMTCPNEVVSYEIVLSITRLIKKYRKELQAVTWDI 359

Query: 361  LLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPE 420
            LL+IIERLLQQLQ LDSPEL+TIVHDLLTTVEELCDQNEFHGSQERY+ELVE  ADQRPE
Sbjct: 360  LLDIIERLLQQLQNLDSPELKTIVHDLLTTVEELCDQNEFHGSQERYYELVESYADQRPE 419

Query: 421  SSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQFY 480
            SSLLNLISYRAQSIHPAKDGWIQNLQ LMERFFR+E R AVRIKVLDVLSFVLLINRQFY
Sbjct: 420  SSLLNLISYRAQSIHPAKDGWIQNLQLLMERFFRNECRSAVRIKVLDVLSFVLLINRQFY 479

Query: 481  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540
            EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS
Sbjct: 480  EEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 539

Query: 541  PPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHYKH 600
            PPPELEER++A +SASLEDVKTAVLGLLVILQTKLYTLPASHATRVYE L+SHIQLHYKH
Sbjct: 540  PPPELEERNLAVHSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYESLISHIQLHYKH 599
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Query: 601  SYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKKXX 660
             Y+LPIASSIRLQAFDFL LLRADSLHRLGLPNKDGVVRFSPYC+CD ME +R SEKK
Sbjct: 600  GYSLPIASSIRLQAFDFLLLLRADSLHRLGLPNKDGVVRFSPYCLCDCMELDRASEKKAS 659

Query: 661  XXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLRYK 720
                               VRLG +PYSLLFRVLLQCLKQESDWKVLKLVL RLPESLRYK
Sbjct: 660  GPLSPPTGPPSPVPMGPAVRLGYLPYSLLFRVLLQCLKQESDWKVLKLVLSRLPESLRYK 719

Query: 721  VLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHNYL 780
            VLIFTSPCSVDQL SALCSMLS PKTLERLRG PEGFSRTDLHLAVVPVLTALISYHNYL
Sbjct: 720  VLIFTSPCSVDQLSSALCSMLSAPKTLERLRGTPEGFSRTDLHLAVVPVLTALISYHNYL 779

Query: 781  DKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATASMA 840
            DKT+QREMVYCLEQGLI+RCA QCVVAL+ICSVEMPDIIIKALPVLVVKLTHISATASMA
Sbjct: 780  DKTRQREMVYCLEQGLIYRCASQCVVALAICSVEMPDIIIKALPVLVVKLTHISATASMA 839

Query: 841  VPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 900
            +PLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC
Sbjct: 840  IPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFIRC 899

Query: 901  RLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNS 960
            RLPFRKDFVP+ITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPK
Sbjct: 900  RLPFRKDFVPYITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPK--------------- 944

Query: 961  PPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHL 1020
                                          SRIQTSLTSASLGSADENS+AQADD+LKNLHL
Sbjct: 945  ----------------------------SRIQTSLTSASLGSADENSMAQADDNLKNLHL 976

Query: 1021 ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXXXXX 1080
            ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNK
Sbjct: 977  ELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGTGTRSL 1036

Query: 1081 XXXDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLRVG 1140
               DSG+LQ G +SSS P  HVRQTKEAPAKLESQAGQQVSRGARD VRSMSGGHGLRVG
Sbjct: 1037 LGLDSGDLQGGSDSSSDPSTHVRQTKEAPAKLESQAGQQVSRGARDPVRSMSGGHGLRVG 1096

Query: 1141 ALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEILVR 1200
             LD  A    G + S GP+TA AAKPEK  AG ++P  EKTNLAAYVPLLTQGWAEILVR
Sbjct: 1097 VLDTSAPYSPGGSASLGPQTAVAAKPEKPPAGAQLPTAEKTNLAAYVPLLTQGWAEILVR 1156

Query: 1201 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAST 1260
            RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAA T
Sbjct: 1157 RPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAAGT 1216

Query: 1261 AKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMXXXXXXXXXXXXXXXXXXX 1320
            AKPP LPRSNT                       DSA+V+
Sbjct: 1217 AKPPTLPRSNT----------------------DSAMVLEEGSPGETQVPVEPPELEDF 1253

Query: 1321 XAALGMDR---RTDAYXXXXXXXXQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDXXXX 1377
             AALG DR   R D Y        QEEKS H EEL   GIPIER +SSEG RP+VD
Sbjct: 1254 EAALGTDRHCQRPDTYSRSSSASSQEEKS-HLEELAAGGIPIERAISSEGARPAVDLSFQ 1312

Query: 1378 XXXXXXXXXXXXXXXTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGEDS 1437
                           TLQDILGD GDK D+GRLSPE K RSQSG LDGE+A WSA+GE+S
Sbjct: 1313 PSQPLSKSSSSPELQTLQDILGDLGDKIDIGRLSPEAKVRSQSGILDGEAATWSATGEES 1372

Query: 1438 R--GQPEXXXXXXXXXXXXXXXXXXYTISDSAPSRRGKRVERDALKSRATASNAEKVPGI 1495
            R    PE                   YTISDSAPSRRGKRVERD  KSRA AS+AEKVPGI
Sbjct: 1373 RITVPPEGPLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDNFKSRAAASSAEKVPGI 1432

Query: 1496 NPSFVFLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQS 1555
            NPSFVFLQLYHSPFFGDESNKPILLPNE  SFERSVQLLDQIPSYDTHKIAVLYVGEGQS
Sbjct: 1433 NPSFVFLQLYHSPFFGDESNKPILLPNE--SFERSVQLLDQIPSYDTHKIAVLYVGEGQS 1490

Query: 1556 NSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM 1615
            +SELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM
Sbjct: 1491 SSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIM 1550

Query: 1616 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTP 1675
            QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSI+YNDSGEDFKLGTIKGQFNFVHVI+TP
Sbjct: 1551 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIIYNDSGEDFKLGTIKGQFNFVHVIITP 1610

Query: 1676 LDYECNLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDI 1735
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            LDY+CNL++LQCRKDMEGLVDTSVAKIVSDRNL FVARQMALHANMASQVHHSRSNPTDI
Sbjct: 1611 LDYKCNLLTLQCRKDMEGLVDTSVAKIVSDRNLSFVARQMALHANMASQVHHSRSNPTDI 1670

Query: 1736 YPSKWIARLRHIKRLRQRICEEAAYXXXXXXXXXXXXXXKAPAQTPAEPTPGYEVGQRKR 1795
            YPSKWIARLRHIKRLRQRI EE  Y              KAPAQ P E TP YE GQRKR
Sbjct: 1671 YPSKWIARLRHIKRLRQRIREEVHYSNPSLPLMHPPAHTKAPAQAP-EATPTYETGQRKR 1729

Query: 1796 LISSVEDFTEFV 1807
            LISSV+DFTEFV
Sbjct: 1730 LISSVDDFTEFV 1741
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gb|AAD27867.1|AF132986_1 (AF132986) tuberous sclerosis 2 protein [Mus musculus domesticus]

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            Length = 1687

 Score = 2696 bits (6912), Expect = 0.0
 Identities = 1379/1696 (81%), Positives = 1432/1696 (84%), Gaps = 25/1696 (1%)

Query: 119  LRALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXX 178
            LRALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELA+FVLQWMDVGLSSEF
Sbjct: 1    LRALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELAEFVLQWMDVGLSSEFLL 60

Query: 179  XXXXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPL 238
                  KFNSCYLDEYIA MV MICLLC+RT SSVDIEVSLQVLDAVVCYNCLPAESLPL
Sbjct: 61   VLVNLVKFNSCYLDEYIASMVHMICLLCIRTVSSVDIEVSLQVLDAVVCYNCLPAESLPL 120

Query: 239  FIVTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFF 298
            FI+TLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMC +MEDR+YMEDAPLLRGAVFF
Sbjct: 121  FIITLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCRIMEDRSYMEDAPLLRGAVFF 180

Query: 299  VGMALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVVAW 358
            VGMALWGAHRLYSL+NSPTSV PSFY+AM CPNEVVSYEIVLSITRLIKKYRKELQ V W
Sbjct: 181  VGMALWGAHRLYSLKNSPTSVLPSFYEAMTCPNEVVSYEIVLSITRLIKKYRKELQAVTW 240

Query: 359  DILLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQR 418
            DILL+IIERLLQQLQ LDSPEL+TIVHDLLTTVEELCDQNEFHGSQERY+ELVE  ADQR
Sbjct: 241  DILLDIIERLLQQLQNLDSPELKTIVHDLLTTVEELCDQNEFHGSQERYYELVESYADQR 300

Query: 419  PESSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVLDVLSFVLLINRQ 478
            PESSLLNLISYRAQSIHPAKDGWIQNLQ LMERFFR+E R AV IKVLDVLSFVLLI RQ
Sbjct: 301  PESSLLNLISYRAQSIHPAKDGWIQNLQLLMERFFRNECRSAVAIKVLDVLSFVLLIIRQ 360

Query: 479  FYEEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARS 538
            FYEEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARS
Sbjct: 361  FYEEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARS 420

Query: 539  LSPPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEMLVSHIQLHY 598
            LSPPPELEERD+A +SASLEDVKTAVLGLLVILQTKLYTLPASHATRVYE L+SHIQLHY
Sbjct: 421  LSPPPELEERDLAVHSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYESLISHIQLHY 480

Query: 599  KHSYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFSPYCVCDYMEPERGSEKK 658
            KH Y+LPIASSIRLQAFDFL LLRADSLHRLGLPNKDGVVRFSPYC+CD ME +R SEKK
Sbjct: 481  KHGYSLPIASSIRLQAFDFLLLLRADSLHRLGLPNKDGVVRFSPYCLCDCMELDRASEKK 540

Query: 659  XXXXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDWKVLKLVLGRLPESLR 718
                                VRLG +PYSLLFRVLLQCLKQESDWKVL LVL RLPESLR
Sbjct: 541  ASGPLSPPTGPPSPVPMGPAVRLGYLPYSLLFRVLLQCLKQESDWKVLNLVLSRLPESLR 600

Query: 719  YKVLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLHLAVVPVLTALISYHN 778
            YKVLIFTSPCSVDQL SALCSMLS PKTLERLRG PEGFSRTDLHLAVVPVLTALISYHN
Sbjct: 601  YKVLIFTSPCSVDQLSSALCSMLSAPKTLERLRGTPEGFSRTDLHLAVVPVLTALISYHN 660

Query: 779  YLDKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPDIIIKALPVLVVKLTHISATAS 838
            YLDKT+QREMVYCLEQGLI+RCA QCVVAL+ICSVEMPDIIIKALPVLVVKLTHISATAS
Sbjct: 661  YLDKTRQREMVYCLEQGLIYRCASQCVVALAICSVEMPDIIIKALPVLVVKLTHISATAS 720

Query: 839  MAVPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFI 898
            MA+PLLEFLSTLARLPHLYRNF  EQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFI
Sbjct: 721  MAIPLLEFLSTLARLPHLYRNFVPEQYASVFAISLPYTNPSKFNQYIVCLAHHVIAMWFI 780

Query: 899  RCRLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLN 958
            RCRLPFRKDFVP+ITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIAR PKQGLN
Sbjct: 781  RCRLPFRKDFVPYITKGLRSNVLLSFDDTPEKDSFRARSTSLNERPKSLRIARAPKQGLN 840

Query: 959  NSPPVKEFKESSAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSVAQADDSLKNL 1018
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            NSPPVKEFKES AAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENS+AQADD+LKNL
Sbjct: 841  NSPPVKEFKESCAAEAFRCRSISVSEHVVRSRIQTSLTSASLGSADENSMAQADDNLKNL 900

Query: 1019 HLELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXXX 1078
            HLELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNK
Sbjct: 901  HLELTETCLDMMARYVFSNFTAVPKRSPVGEFLLAGGRTKTWLVGNKLVTVTTSVGTGTR 960

Query: 1079 XXXXXDSGELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLR 1138
                 DSG+LQ G +SSS P  HVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLR
Sbjct: 961  SLLGLDSGDLQGGSDSSSDPSTHVRQTKEAPAKLESQAGQQVSRGARDRVRSMSGGHGLR 1020

Query: 1139 VGALDVPASQFLGSATSPGPRTAPAAKPEKASAGTRVPVQEKTNLAAYVPLLTQGWAEIL 1198
            VG LD  A    G + S GP+TA AAKPEK  AG ++P  EKTNLAAYVPLLTQGWAEIL
Sbjct: 1021 VGVLDTSAPYSPGGSASLGPQTAVAAKPEKPPAGAQLPTAEKTNLAAYVPLLTQGWAEIL 1080

Query: 1199 VRRPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPAA 1258
            VRRPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEH    +   +S
Sbjct: 1081 VRRPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHGHAPVQVIVSA-TG 1139

Query: 1259 STAKPPPLPRSNTVASFSSLYQSSCQGQLHRSVSWADSAVVMXXXXXXXXXXXXXXXXX 1318
             TAKPP LPRSNTVASFSSLYQ SCQGQLHRSVSWADSA+V+
Sbjct: 1140 CTAKPPTLPRSNTVASFSSLYQPSCQGQLHRSVSWADSAMVLEEGSPGETQVPVEPPELE 1199

Query: 1319 XXXAALGMDR---RTDAYXXXXXXXXQEEKSLHAEELVGRGIPIERVVSSEGGRPSVDXX 1375
               AALG DR   R D Y        QEEKS H EEL   GIPIER +SSEG RP+VD
Sbjct: 1200 DFEAALGTDRHCQRPDTYSRSSSASSQEEKS-HLEELAAGGIPIERAISSEGARPAVDLS 1258

Query: 1376 XXXXXXXXXXXXXXXXXTLQDILGDPGDKADVGRLSPEVKARSQSGTLDGESAAWSASGE 1435
                             TLQDILGD GDK D+GRLSPE K RSQSG LDGE+A WSA+GE
Sbjct: 1259 FQPSQPLSKSSSSPELQTLQDILGDLGDKIDIGRLSPEAKVRSQSGILDGEAATWSATGE 1318

Query: 1436 DSR--GQPEXXXXXXXXXXXXXXXXXXYTISDSAPSRRGKRVERDALKSRATASNAEKVP 1493
            +SR    PE                   YTISDSAPSRRGKRVERD  KSRA AS+AEKVP
Sbjct: 1319 ESRITVPPEGPLPSSSPRSPSGLRPRGYTISDSAPSRRGKRVERDNFKSRAAASSAEKVP 1378

Query: 1494 GINPSFVFLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEG 1553
            GINPSFVFLQLYHSPFFGDESNKPILLPNE  SFERSVQLLDQIPSYDTHKIAVLYVGEG
Sbjct: 1379 GINPSFVFLQLYHSPFFGDESNKPILLPNE--SFERSVQLLDQIPSYDTHKIAVLYVGEG 1436

Query: 1554 QSNSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDD 1613
            QS+SELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDD
Sbjct: 1437 QSSSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDD 1496

Query: 1614 IMQAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIK-GQFNFVHVI 1672
            IMQAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSI+YNDSGEDFKLGTIK GQFNFVHVI
Sbjct: 1497 IMQAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIIYNDSGEDFKLGTIKQGQFNFVHVI 1556

Query: 1673 VTPLDYECNLVSLQCRKD----------MEGLVDTSVAKIVSDRNLPFVARQMALHANMA 1722
            +TPLDY+CNL++LQCRKD            G +      +V +  +      +  H  MA
Sbjct: 1557 ITPLDYKCNLLTLQCRKDGPACKCEWWRQPGEIVVWALPVVMELTVTI----LLCHLQMA 1612

Query: 1723 SQVHHSRSNPTDIYPSKWIARLRHIKRLRQRICEEAAYXXXXXXXXXXXXXXKAPAQTPA 1782
            SQVHHSRSNPTDIYPSKWIARLRHIKRLRQRI EE  Y              KAPAQ P
Sbjct: 1613 SQVHHSRSNPTDIYPSKWIARLRHIKRLRQRIREEVHYSNPSLPLMHPPAHTKAPAQAP- 1671

Query: 1783 EPTPGYEVGQRKRLIS 1798
            E TP YE GQRKRLIS
Sbjct: 1672 EATPTYETGQRKRLIS 1687

 gb|AAB86682.1| (AF013614) TSC2 gene product [Fugu rubripes]
            Length = 1782

 Score = 1590 bits (4072), Expect = 0.0
 Identities = 818/1253 (65%), Positives = 966/1253 (76%), Gaps = 27/1253 (2%)

Query: 45   LRELSMECGLNNRIRMIGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLAL 104
            L+EL  +CGL+NR+RM+ Q+C++AKTKKFEEHAVEA+WK+V D+L PE+  EARHAVL L
Sbjct: 4    LQELHPDCGLSNRVRMLNQVCDLAKTKKFEEHAVEAVWKSVEDMLSPEQPPEARHAVLQL 63

Query: 105  LKAIVQGQGERLGVLRALFFKVIKDY-PSNEDLHERLEVFKALTDNGRHITYLEEELADF 163
            L+A++QGQGE LG LRA FFKVI+DY P NEDL +RLEVFKALT+NG+ ITYLEE++A F
Sbjct: 64   LRAVIQGQGEWLGPLRAYFFKVIRDYQPCNEDLSDRLEVFKALTENGKDITYLEEDIARF 123

Query: 164  VLQWMDVGLSSEFXXXXXXXXKFNSCYLDEYIARMVQMICLLCVRTASSVDIEVSLQVLD 223
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            VL WMD+GL+S+F        KFNSCYLD+ ++ MVQ ICLLC RT SS DIEV+LQVLD
Sbjct: 124  VLLWMDIGLTSDFLHVLVNLVKFNSCYLDQNVSSMVQNICLLCNRTTSSTDIEVALQVLD 183

Query: 224  AVVCYNCLPAESLPLFIVTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDR 283
            AVVCYNCLP++SL +FI+TLCRT+NVKE CE CWKLMR +LGTHLGHSAIY MC +ME+R
Sbjct: 184  AVVCYNCLPSDSLTIFIITLCRTVNVKEFCEACWKLMRKVLGTHLGHSAIYTMCRIMEER 243

Query: 284  AYMEDAPLLRGAVFFVGMALWGAHRLYSLRNSPTSVFPSFYQAMACPNEVVSYEIVLSIT 343
             Y EDAPLLRGAVFFVGMALWGAHRL +L+N+PT V PSFY+AM+  NEVVSYEIVLSIT
Sbjct: 244  VYTEDAPLLRGAVFFVGMALWGAHRLPALKNTPTLVLPSFYKAMSSANEVVSYEIVLSIT 303

Query: 344  RLIKKYRKELQVVAWDILLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGS 403
            RLIKKY KELQVV WDILL IIERLLQQ+QT+ S EL+ IV++LLTTVEEL +QN +HGS
Sbjct: 304  RLIKKYGKELQVVTWDILLGIIERLLQQIQTIGSAELKAIVYELLTTVEELYEQNSYHGS 363

Query: 404  QERYFELVERCADQRPESSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRI 463
             E++F LVE+CAD+RP++S+L LISYRAQSI PAKDGWIQ+L  LM++FFR+ESR  +RI
Sbjct: 364  MEKFFNLVEKCADKRPDASVLTLISYRAQSIQPAKDGWIQSLHRLMDKFFRNESRTVIRI 423

Query: 464  KVLDVLSFVLLINRQFYEEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHH 523
            KVL +LSFVL  NRQ YE+ELI +VVI QLS I ED+D  VRK ATQLLVDLAEGC THH
Sbjct: 424  KVLHILSFVLSTNRQLYEDELIETVVIPQLSGIAEDRDLAVRKQATQLLVDLAEGCSTHH 483

Query: 524  FNSLLDIIEKVMARSL--SPPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPAS 581
            F SLLDIIE+V +RSL  S   E+ ERD  A SA +EDV+TAVLGLL ILQ+KLY+LPA
Sbjct: 484  FTSLLDIIERVASRSLVCSGSLEMPERDPTAESA-MEDVRTAVLGLLEILQSKLYSLPAV 542

Query: 582  HATRVYEMLVSHIQLHYKHSYTLPIASSIRLQAFDFLFLLRADSLHRLGLPNKDGVVRFS 641
            HA+RVYE+L+SH+QLHYK+ Y+  IASSIRLQ FDF  ++RADSLHR+G+PNKD  +RFS
Sbjct: 543  HASRVYELLISHLQLHYKNKYSSAIASSIRLQVFDFFLMMRADSLHRIGVPNKDRAMRFS 602

Query: 642  PYCVCDYMEPE-RGSEKKXXXXXXXXXXXXX---XXXXXXXVRLGSVPYSLLFRVLLQCL 697
            PYC CD  EPE RG EKK                       VR   +PY+  F VLLQCL
Sbjct: 603  PYCYCDNGEPEKRGGEKKPTGSTSPPVGSPAPPPAPSSSGSVRSAFLPYAPAFNVLLQCL 662

Query: 698  KQESDWKVLKLVLGRLPESLRYKVLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGF 757
            K E+DWKVLKLVL +LP  L+YKVL+ TSPCS+D LCS LC M++     ERL+  PEGF
Sbjct: 663  KMETDWKVLKLVLDKLPWMLQYKVLLLTSPCSLDHLCSTLCCMVTDRLISERLKKTPEGF 722

Query: 758  SRTDLHLAVVPVLTALISYHNYLDKTKQREMVYCLEQGLIHRCARQCVVALSICSVEMPD 817
            SRTD+ LAVVPVLTA+ SYHNYL++++QRE+V CLE GLIHRCA+QCVVAL++C+VEMPD
Sbjct: 723  SRTDVQLAVVPVLTAITSYHNYLEQSRQRELVQCLETGLIHRCAKQCVVALTMCTVEMPD 782

Query: 818  IIIKALPVLVVKLTHISATASMAVPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPYTN 877
            I+IK LP L+VKLTHISAT +MA P+LEFLSTL RLPHLY NF AEQY SVFAISLPYTN
Sbjct: 783  IMIKLLPSLMVKLTHISATVAMASPMLEFLSTLVRLPHLYANFVAEQYVSVFAISLPYTN 842

Query: 878  PSKFNQYIVCLAHHVIAMWFIRCRLPFRKDFVPFITKGLRSNVLLSFDDTPEKDSFRARS 937
            PSKFNQYIV LAHHVIAMWFIRCRLPFRKDFV +ITKGLRSN LL FDD+ E+ SFRARS
Sbjct: 843  PSKFNQYIVSLAHHVIAMWFIRCRLPFRKDFVQYITKGLRSNALLPFDDSHEQSSFRARS 902

Query: 938  TSLNERPKSLRIARPPKQGL----NNSPPVKEFKESSAAEAFRCRSISVSEHVVRSRIQT 993
            TSLNERPKSLR A+  K       N+S PVKE ++ SA +AFR RSISVSEH VR R+ T
Sbjct: 903  TSLNERPKSLRAAKVVKATAAVTNNSSSPVKELRDLSAMDAFRSRSISVSEHAVR-RMHT 961

Query: 994  SLTSASLGSADENSVAQADDSLKNLHLELTETCLDMMARYVFSNFTAVPKRSPVGEFLLA 1053
            S T+ SLGSADEN+V QAD+ LK +HLELTETCLDMMARYVFSNF+A+PKRSP+ EFLLA
Sbjct: 962  STTTCSLGSADENAVTQADEGLKTVHLELTETCLDMMARYVFSNFSALPKRSPIAEFLLA 1021

Query: 1054 GGRTKTWLVGNKXXXXXXXXXXXXXXXXXXDSGE-LQSGPE-SSSSPGVHVRQTKEAPAK 1111
            GGR+ TWLVGNK                  D  E L  G E + S P +H R TKEAPAK
Sbjct: 1022 GGRSMTWLVGNKLVTITTSGGVRTQALLGLDVVERLGGGGEMTRSDPSLHTRLTKEAPAK 1081

Query: 1112 LESQAGQQVSRGARDRVRSMSGGHGLR------VGALDVPASQFLGS--ATSPGPRTAPA 1163
            LESQ+ QQ SR  R RVRSMSGGH LR      +  L  P+   L +  + S GP
Sbjct: 1082 LESQSSQQQSRATRTRVRSMSGGHALRSLPTQNLSPLVSPSEGELAAPLSASTGPSLDGL 1141

Query: 1164 AKPEKA--SAGTRVPVQEKTNLAAYVPLLTQGWAEILVRRPTGNTSWLMSLENPLSPFSS 1221
              P  +  +     P+++  +LA +VP+LTQGWAEI +RRP+GNTSWLM LENP SPFSS
Sbjct: 1142 GPPSSSCPTPNAPPPLKDNPSLAEFVPMLTQGWAEIFIRRPSGNTSWLMCLENPPSPFSS 1201

Query: 1222 DINNMPLQELSNALMAAERFKE--HRDTALYKSLSVPAASTAKPPPLPRSNTV 1272
            ++ NMPLQELS+ LMA E  KE      +   S + PA +    PP  R N +
Sbjct: 1202 ELGNMPLQELSSVLMAMEGVKEPPTETASAPASTAAPAPTLVSEPPNQRPNVI 1254
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 Score =  469 bits (1193), Expect = e-130
 Identities = 223/348 (64%), Positives = 277/348 (79%), Gaps = 2/348 (0%)

Query: 1461 YTISDSAPSRRGKRVERDALKSRATASNAEKVPGINPSFVFLQLYHSPFFGDESNKPILL 1520
            +TIS SAPSRR +R +RD+  SR+   N EK+ G++PSFVFLQLYHSPFFG+E+NKP+LL
Sbjct: 1436 HTISVSAPSRRERRTDRDSYHSRSGPGNTEKIAGLSPSFVFLQLYHSPFFGNEANKPLLL 1495

Query: 1521 PNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLGR 1580
            P ++Q  +R+V++LDQ+P YDTHKI V++VG GQ N+E+AILSNE+GS RY  FLTGLG+
Sbjct: 1496 P-KTQVIDRAVKVLDQMPPYDTHKIGVVFVGAGQVNNEVAILSNEYGSNRYAAFLTGLGK 1554

Query: 1581 LIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKKRH 1640
            LI LKDC PD+++LGGLD  G+DG+FTYCWHDDIMQA+FHIATLMP ++ DK  C+KKRH
Sbjct: 1555 LIHLKDCDPDQIFLGGLDQYGDDGEFTYCWHDDIMQAIFHIATLMPNRESDKGCCNKKRH 1614

Query: 1641 LGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYECNLVSLQCRKDMEGLVDTSVA 1700
            +GNDFV +VYNDSGE++KLGTIKGQFNFV VI+ PLDYECNLV+LQCRKD+EGLVDT+V
Sbjct: 1615 IGNDFVIVVYNDSGEEYKLGTIKGQFNFVEVIIKPLDYECNLVTLQCRKDLEGLVDTTVT 1674

Query: 1701 KIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKWIARLRHIKRLRQRICEEAAY 1760
            KIVSDRNLP + RQMALHANMAS VH  R+NP+D Y SKW+ARLRHIKR+R R  E+
Sbjct: 1675 KIVSDRNLPLLVRQMALHANMASLVHQFRANPSDAYASKWLARLRHIKRIRTRALEDIQS 1734

Query: 1761 XXXXXXXXXXXXXXKAPAQTPAEPTPGYEV-GQRKRLISSVEDFTEFV 1807
                           +  +   +      EV GQRKRL+S+V+DFT+FV
Sbjct: 1735 RPTPGISVTQGHSQQNKSMQQSTSAGNPEVTGQRKRLVSTVDDFTDFV 1782

 gb|AAF49066.1| (AE003514) gig gene product [Drosophila melanogaster]
            Length = 1847

 Score =  521 bits (1328), Expect = e-146
 Identities = 373/1286 (29%), Positives = 630/1286 (48%), Gaps = 179/1286 (13%)

Query: 6    SKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRMIGQIC 65
            SKD   K KFK+ L     +  P    G++T   +  E  REL  E  +  R RM+ ++
Sbjct: 3    SKD---KSKFKLFL-----KSLPAGYVGERT---LRPEFERELRPEQPVAQRCRMLKELG 51

Query: 66   EVAKTK-KFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLRALFF 124
            +        +E A+  L+    DL+ P +  E R   L+  K ++  Q + L ++R  FF
Sbjct: 52   DTQLHNFNLDESAITILFNLTNDLIVPNKPAETRQIALSFYKRLIHTQYKNLTIMREKFF 111

Query: 125  KVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWM----DVGLSSEFXXXX 180
             VI+++ + EDL   LE+   LTDNG+ IT  EE++  F+L W+    +  L + +
Sbjct: 112  LVIQNHEAREDLRHLLELLDTLTDNGKDITNFEEKIGKFMLLWIPAITEANLLTPYLDIL 171

Query: 181  XXXXKFNSCYLD-EYIARMVQMIC-LLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPL 238
                KFN+ +LD + +  +VQ  C L C  T + + ++  L +L+ V+ Y   P+E LP
Sbjct: 172  VNLIKFNAAHLDKDILVGIVQNACDLSCSVTVNEIGLQC-LTILEMVIGYTIFPSEPLPQ 230

Query: 239  FIVTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFF 298
             I TLCRT+N    C   +K+M+NLLGT LG+ ++  MC ++ DRA  +DA LLRGAVF
Sbjct: 231  CITTLCRTVNHAPYCPSSFKIMKNLLGTQLGYHSMKMMCSILNDRALYDDAHLLRGAVFH 290

Query: 299  VGMALWGAHRLYSLR--NSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVV 356
            + M ++G++ ++ +      T+V  +F +A+     +V++E++LS+  +I K  ++L  +
Sbjct: 291  LNMNIFGSNIIFQVSPMTYATNVLTAFLRALDSRQVIVTFEVILSVRMVITK--RQLSEI 348

Query: 357  AWDILLNIIERLLQQLQTLDSPE--------LRTIVHDLLTTVEELC--DQNEFHGSQER 406
             WD++ +I+  ++  ++  +           L+   H+ +  +E+L   D+++  G+ ER
Sbjct: 349  IWDLICDIMSSIVSNIEYYEEVNINKDRLHHLQINFHENIDCIEKLLQQDRSQILGNVER 408

Query: 407  YFELVERCADQRPESSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVL 466
             ++L+ER AD+RPE+S+L LI YR++ +   +  W+Q L   + R++R  S   VRIK +
Sbjct: 409  IYDLIERVADRRPEASVLALIEYRSRRVTATRPDWLQVLAQFVRRYYRM-SNVNVRIKTI 467

Query: 467  DVLSFVLLINRQFYEEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNS 526
            + L  ++  NR  YEEE+++ VV+  LSHI  +   QVR    + L + A  C T
Sbjct: 468  EALVQIMDQNRACYEEEILSRVVLVHLSHIHLESSVQVRVAVARALSNFATHCDTKRCMD 527

Query: 527  LLDIIEKVMAR--------SLSPPPELEERDVAAYS--ASLEDVKTAVLGLLVILQTKLY 576
            LLDI+E ++ R        S S    L E      +  + + D+  AV GL+ +   KL+
Sbjct: 528  LLDILEALINRPFEHTRHGSSSGEGTLAEVTFGLVNNESEISDIIAAVDGLVKVFAIKLH 587
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Query: 577  TLPASHATRVYEMLVSHIQLHYKHSYTLPIASSIRLQAFDFLFLLRADSLHRLGLPN-KD 635
             LP  HA +++ +L+ H++LHY+        S +R + F +L   RA+  + +G P
Sbjct: 588  RLPGIHALKIFNILMDHLELHYERPKIFEHISVVRYKIFAWLLKARANGSYHIGYPEGST 647

Query: 636  GVVRFSPYCVCDY-MEPERGSEKKXXXXXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLL 694
             VV+FSPY   D  + P+                             ++    + ++++
Sbjct: 648  EVVKFSPYLGIDSPLLPQAHPT-------------------------AISIRRVCKLIV 681

Query: 695  QCLKQESDWKVLKLVLGRLPESLRYKVLIFTSPCSVDQLCSALC--SMLSGPKTLERLRG 752
            +CL+ ++D++V +LV+  LP+ L+ K L+  +   +++L + L   +++S  K
Sbjct: 682  RCLEHDTDYQVFQLVIRELPKVLQNKALVQGN--DIEELANTLLKINLVSNNK------- 732

Query: 753  APEGFSRT--DLHLAVVPVLTALISYHNYLDKTKQREMVYCLEQGLIHRCARQCVVALSI 810
                F R   + H  V+P + +L+ YH  L   +   ++  L   ++   A  C+  ++I
Sbjct: 733  ----FKRPTDEFHALVLPAIASLVIYHESLQPQQHYGIITALNSRVLTGIASVCINTMTI 788

Query: 811  CSVEMPDIIIKALPVLVVKLTHISATASMAVPLLEFLSTLARLP-HLYRNFAAEQYASVF 869
              +EMP+ +++ LP ++++++ +S T ++A P+LEFLS L  L  HL+ NF +     VF
Sbjct: 789  LILEMPEALMRKLPDVLLQMSKMSDTNALATPVLEFLSLLIHLSKHLFANFTSMHNMYVF 848

Query: 870  AISLPYTNPSKFNQYIVCLAHHVIAMWFIRCRLPFRKDFVPFITKGLRSNV------LLS 923
            AI+LPYT P +++ Y V LAHHVIA WF++C+L  R++ V +I   ++SN       +++
Sbjct: 849  AITLPYTKPHRYDHYTVSLAHHVIAGWFLKCKLELRRNCVNYIKSSIQSNAKMLSSDIVN 908

Query: 924  FDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNSPPVKEFKESSAAEAFRCRSISVS 983
             +   E  S R RSTSL E            +G  N+           A A+
Sbjct: 909  LNSLNEDSSNRKRSTSLTE------------RGSRNN-----------ANAWN------- 938

Query: 984  EHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHLELTETCLDMMARYVFSNFTAVPK 1043
                                D     Q ++ L+N H EL ETC D +AR+ +S   ++PK
Sbjct: 939  --------------------DLEMRPQMNNGLRNFHAELAETCFDFLARHTYSPCPSMPK 978

Query: 1044 RSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXX----------XXXXXXDSGELQSGPE 1093
            R P  EFLL  G ++TWLVGN                              S  L S
Sbjct: 979  RLPAAEFLLKDGVSQTWLVGNNLVTITTSGCPSAPARSGLCERCAQLGKAPSISLNSKSL 1038

Query: 1094 SSSSPGVH-VRQTKEAPAKLESQAGQQVSRGARDRVRSMS------GGHGLRVGALDVPA 1146
            S ++P +   R+ +     L+  +G + S G+ +   S S      GGH  R  +    A
Sbjct: 1039 SDAAPPLSPERERRYTKVSLQHSSGNE-SAGSTELTSSSSSNSAAAGGHPHRQISNSSTA 1097

Query: 1147 SQFLGSATSPGPRTAPAAKPEKASAGTR------------VPVQEKTNLAAYVPLLTQ-- 1192
            S    S     P    +A  E A  G+             V +   +      P+  +
Sbjct: 1098 SLDALSRRGSNPEALGSALGEGAHTGSNTSLLGNSLSQSSVSMSPSSGSVVQQPVCVRAC 1157

Query: 1193 -GWAEILVRRPTGNTSWLMSLENPLS 1217
             GWAE+LVRRPTGN SW+  ++NP++
Sbjct: 1158 TGWAEVLVRRPTGNVSWITRIQNPIT 1183

 Score =  248 bits (627), Expect = 3e-64
 Identities = 128/265 (48%), Positives = 180/265 (67%), Gaps = 11/265 (4%)

Query: 1495 INPSFVFLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQ 1554
            +NPSF+F+QLY +   G  +++P+ +  E+ S   +V L+D +P ++THKI VLYVG+GQ
Sbjct: 1554 MNPSFIFMQLYTTGQLG-VTDEPLKVGPENSS---AVSLIDLVPPFETHKIGVLYVGQGQ 1609

Query: 1555 SNSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDI 1614
             N+E+ IL N HGS RY EFL  +G L+ LK+ + + +++  LD  G DG+F Y W DDI
Sbjct: 1610 CNNEVEILRNSHGSARYVEFLRNIGTLVSLKEAEQNNLFIM-LDRNGADGKFAYIWKDDI 1668

Query: 1615 MQAVFHIATLMPTKDVDKHRC-DKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIV 1673
            +Q  FH+ATLMPT   D   C +KK H+GNDFV I+YN+SGE++ L TI GQFN+  VIV
Sbjct: 1669 LQVTFHVATLMPTNLQDDPNCNEKKSHIGNDFVKIIYNESGEEYNLNTISGQFNYACVIV 1728

Query: 1674 TPLDYECNLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHS--RSN 1731
             PLD   N V ++ R ++   V  +  +IVSDR+ P +ARQMALHAN+AS V+ S  + +
Sbjct: 1729 EPLDLNSNRVYVKARSEISKFVCHAEYRIVSDRSAPLLARQMALHANLASLVYQSVQKKH 1788

Query: 1732 PTDIYPSKWIARLRHIKRLRQRICE 1756
            P   Y S W+ RLR +KRLR ++ E
Sbjct: 1789 P---YASNWLERLRKLKRLRSKLIE 1810
```

gb|AAD48498.1|AF172995_1 (AF172995) gigas protein [Drosophila melanogaster]
Length = 1847

```
 Score =  517 bits (1318), Expect = e-145
 Identities = 372/1286 (28%), Positives = 628/1286 (47%), Gaps = 179/1286 (13%)

Query: 6    SKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRMIGQIC 65
            SKD   K KFK+ L     +  P    G++T   +  E  REL  E  +  R RM+ ++
Sbjct: 3    SKD---KSKFKLFL-----KSLPAGYVGERT---LRPEFERELRPEQPVAQRCRMLKELG 51

Query: 66   EVAKTK-KFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLRALFF 124
            +        +E A+  L     DL+ P +  E R   L+  K ++  Q + L ++R  FF
Sbjct: 52   DTQLHNFNLDESAITILLNLTNDLIVPNKPAETRQIALSFYKRLIHTQYKNLTIMREKFF 111

Query: 125  KVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWM----DVGLSSEFXXXX 180
             VI+++ + EDL   LE+   LTDNG+ IT  EE++  F+L W+    +  L + +
Sbjct: 112  LVIQNHEAREDLRHLLELLDTLTDNGKDITNFEEKIGKFMLLWIPAITEANLLTPYLDIL 171

Query: 181  XXXXKFNSCYLD-EYIARMVQMIC-LLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPL 238
                KFN+ +LD + +  +VQ  C L C  T + + ++  L +L+ V+ Y   P+E LP
Sbjct: 172  VNLIKFNAAHLDKDILVGIVQNACDLSCSVTVNEIGLQC-LTILEMVIGYTIFPSEPLPQ 230

Query: 239  FIVTLCRTINVKELCEPCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFF 298
             I TLCRT+N    C   +K+M+NLLGT LG+ ++  MC ++ DRA  +DA LLRGAVF
Sbjct: 231  CITTLCRTVNHAPYCPSSFKIMKNLLGTQLGYHSMKMMCSILNDRALYDDAHLLRGAVFH 290

Query: 299  VGMALWGAHRLYSLR--NSPTSVFPSFYQAMACPNEVVSYEIVLSITRLIKKYRKELQVV 356
            + M ++G++ ++ +      T+V  +F +A+     +V++E++LS+  +I K  ++L  +
Sbjct: 291  LNMNIFGSNIIFQVSPMTYATNVLTAFLRALDSRQVIVTFEVILSVRMVITK--RQLSEI 348

Query: 357  AWDILLNIIERLLQQLQTLDSPE--------LRTIVHDLLTTVEELC--DQNEFHGSQER 406
             WD++ +I+  ++  ++  +           L+   H+ +  +E+L   D+++  G+ ER
Sbjct: 349  IWDLICDIMSSIVSNIEYYEEVNINKDRLHHLQINFHENIDCIEKLLQQDRSQILGNVER 408

Query: 407  YFELVERCADQRPESSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIKVL 466
             ++L+ER AD+RPE+S+L LI YR++ +   +  W+Q L   + R++R  S   VRIK +
Sbjct: 409  IYDLIERVADRRPEASVLALIEYRSRRVTATRPDWLQVLAQFVRRYYRM-SNVNVRIKTI 467

Query: 467  DVLSFVLLINRQFYEEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFNS 526
            + L  ++  NR  YEEE+++ VV+  LSHI  +   QVR    + L + A  C T
Sbjct: 468  EALVQIMDQNRACYEEEILSRVVLVHLSHIHLESSVQVRVAVARALSNFATHCDTKRCMD 527

Query: 527  LLDIIEKVMAR--------SLSPPPELEERDVAAYS--ASLEDVKTAVLGLLVILQTKLY 576
            LLDI+E ++ R        S S    L E      +  + + D+  AV GL+ +   KL+
Sbjct: 528  LLDILEALINRPFEHTRHGSSSGEGTLAEVTFGLVNNESEISDIIAAVDGLVKVFAIKLH 587

Query: 577  TLPASHATRVYEMLVSHIQLHYKHSYTLPIASSIRLQAFDFLFLLRADSLHRLGLPN-KD 635
             LP  HA +++ +L+ H++LHY+        S +R + F +L   RA+  + +G P
Sbjct: 588  RLPGIHALKIFNILMDHLELHYERPKIFEHISVVRYKIFAWLLKARANGSYHIGYPEGST 647

Query: 636  GVVRFSPYCVCDY-MEPERGSEKKXXXXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLL 694
             VV+FSPY   D  + P+                              ++    + ++++
Sbjct: 648  EVVKFSPYLGIDSPLLPQAHPT--------------------------AISIRRVCKLIV 681

Query: 695  QCLKQESDWKVLKLVLGRLPESLRYKVLIFTSPCSVDQLCSALC--SMLSGPKTLERLRG 752
            +CL+ ++D++V +LV+  LP+ L+ K L+  +   +++L + L   +++S  K
Sbjct: 682  RCLEHDTDYQVFQLVIRELPKVLQNKALVQGN--DIEELANTLLKINLVSNNK------- 732

Query: 753  APEGFSRT--DLHLAVVPVLTALISYHNYLDKTKQREMVYCLEQGLIHRCARQCVVALSI 810
                F R   + H  V+P + +L+ YH  L   +   ++  L   ++   A  C+  ++I
Sbjct: 733  ----FKRPTDEFHALVLPAIASLVIYHESLQPQQHYGIITALNSRVLTGIASVCINTMTI 788

Query: 811  CSVEMPDIIIKALPVLVVKLTHISATASMAVPLLEFLSTLARLP-HLYRNFAAEQYASVF 869
              +EMP+ +++ LP ++++++ +S T ++A P+LEFLS L  L  HL+ NF +     VF
Sbjct: 789  LILEMPEALMRKLPDVLLQMSKMSDTNALATPVLEFLSLLIHLSKHLFANFTSMHNMYVF 848

Query: 870  AISLPYTNPSKFNQYIVCLAHHVIAMWFIRCRLPFRKDFVPFITKGLRSNV------LLS 923
            AI+LPYT P +++ Y V LAHHVIA WF++C+L  R++ V +I   ++SN       +++
Sbjct: 849  AITLPYTKPHRYDHYTVSLAHHVIAGWFLKCKLELRRNCVNYIKSSIQSNAKMLSSDIVN 908

Query: 924  FDDTPEKDSFRARSTSLNERPKSLRIARPPKQGLNNSPPVKEFKESSAAEAFRCRSISVS 983
             +   E  S R RSTSL E            +G  N+           A A+
Sbjct: 909  LNSLNEDSSNRKRSTSLTE------------RGSRNN-----------ANAWN------- 938

Query: 984  EHVVRSRIQTSLTSASLGSADENSVAQADDSLKNLHLELTETCLDMMARYVFSNFTAVPK 1043
                                 D     Q ++ L+N H EL ETC D +AR+ +S   ++PK
Sbjct: 939  --------------------DLEMRPQMNNGLRNFHAELAETCFDFLARHTYSPCPSMPK 978
```

```
Query: 1044 RSPVGEFLLAGGRTKTWLVGNKXXXXXXXXXXXX----------XXXXXXDSGELQSGPE 1093
            R P  EFLL  G ++TWLVGN                             S  L S
Sbjct: 979  RLPAAEFLLKDGVSQTWLVGNNLVTITTSGCPSAPARSGLCERCAQLGKAPSISLNSKSL 1038

Query: 1094 SSSSPGVH-VRQTKEAPAKLESQAGQQVSRGARDRVRSMS------GGHGLRVGALDVPA 1146
            S ++P +   R+ +     L+  +G + S G+ +   S S      GGH  R  +    A
Sbjct: 1039 SDAAPPLSPERERRYTKVSLQHSSGNE-SAGSTELTSSSSSNSAAAGGHPHRQISNSSTA 1097

Query: 1147 SQFLGSATSPGPRTAPAAKPEKASAGTR------------VPVQEKTNLAAYVPLLTQ-- 1192
            S    S     P    +A  E A  G+             V +   +      P+  +
Sbjct: 1098 SLDALSRRGSNPEALGSALGEGAHTGSNTSLLGNSLSQSSVSMSPSSGSVVQQPVCVRAC 1157

Query: 1193 -GWAEILVRRPTGNTSWLMSLENPLS 1217
             GWAE+LVR PTGN SW+  ++NP++
Sbjct: 1158 TGWAEVLVRPPTGNVSWITRIQNPIT 1183

 Score =  248 bits (627), Expect = 3e-64
 Identities = 128/265 (48%), Positives = 180/265 (67%), Gaps = 11/265 (4%)

Query: 1495 INPSFVFLQLYHSPFFGDESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQ 1554
            +NPSF+F+QLY +   G  +++P+ +  E+ S   +V L+D +P ++THKI VLYVG+GQ
Sbjct: 1554 MNPSFIFMQLYTTGQLG-VTDEPLKVGPENSS---AVSLIDLVPPFETHKIGVLYVGQGQ 1609

Query: 1555 SNSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQFTYCWHDDI 1614
             N+E+ IL N HGS RY EFL  +G L+ LK+ + + +++  LD  G DG+F Y W DDI
Sbjct: 1610 CNNEVEILRNSHGSARYVEFLRNIGTLVSLKEAEQNNLFIM-LDRNGADGKFAYIWKDDI 1668

Query: 1615 MQAVFHIATLMPTKDVDKHRC-DKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIV 1673
            +Q  FH+ATLMPT   D   C +KK H+GNDFV I+YN+SGE++ L TI GQFN+  VIV
Sbjct: 1669 LQVTFHVATLMPTNLQDDPNCNEKKSHIGNDFVKIIYNESGEEYNLNTISGQFNYACVIV 1728

Query: 1674 TPLDYECNLVSLQCRKDMEGLVDTSVAKIVSDRNLPFVARQMALHANMASQVHHS--RSN 1731
             PLD   N V ++ R ++   V  +  +IVSDR+ P +ARQMALHAN+AS V+ S  + +
Sbjct: 1729 EPLDLNSNRVYVKARSEISKFVCHAEYRIVSDRSAPLLARQMALHANLASLVYQSVQKKH 1788

Query: 1732 PTDIYPSKWIARLRHIKRLRQRICE 1756
            P   Y S W+ RLR +KRLR ++ E
Sbjct: 1789 P---YASNWLERLRKLKRLRSKLIE 1810

 dbj|BAA32694.1| (AB014460) tuberin [Homo sapiens]
           Length = 199

 Score =  378 bits (960), Expect = e-103
 Identities = 190/199 (95%), Positives = 190/199 (95%)

Query: 1   MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
           MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM
Sbjct: 1   MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60

Query: 61  IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
           IGQICEVAKTKKFEEHAVEALWKAVADLLQPER LEARHAVLALLKAIVQGQGERLGVLR
Sbjct: 61  IGQICEVAKTKKFEEHAVEALWKAVADLLQPERPLEARHAVLALLKAIVQGQGERLGVLR 120

Query: 121 ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
           ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEF
Sbjct: 121 ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFLLVL 180

Query: 181 XXXXKFNSCYLDEYIARMV 199
               KFNSCYLDEYIARMV
Sbjct: 181 VNLVKFNSCYLDEYIARMV 199

 dbj|BAA28845.1| (AB009371) tuberin [Mus musculus]
           Length = 199

 Score =  354 bits (900), Expect = 3e-96
 Identities = 178/199 (89%), Positives = 183/199 (91%)

Query: 1   MAKPTSKDSGLKEKFKILLGLGTPRPNPRSAEGKQTEFIITAEILRELSMECGLNNRIRM 60
           MAKPTSKDSGLKEKFKILLGLGT RPNPR AEGKQTEFIIT+EILRELS ECGLNNRIRM
Sbjct: 1   MAKPTSKDSGLKEKFKILLGLGTSRPNPRCAEGKQTEFIITSEILRELSGECGLNNRIRM 60

Query: 61  IGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEARHAVLALLKAIVQGQGERLGVLR 120
           IGQIC+VAKTKK EEHAVEALWKAV+DLLQPER  EARHAVL LLKAIVQGQG+RLGVLR
```

```
Sbjct: 61  IGQICDVAKTKKLEEHAVEALWKAVSDLLQPERPPEARHAVLTLLKAIVQGQGDRLGVLR 120

Query: 121 ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELADFVLQWMDVGLSSEFXXXX 180
           ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELA+FVLQWMDVGLSSEF
Sbjct: 121 ALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELAEFVLQWMDVGLSSEFLLVL 180

Query: 181 XXXXKFNSCYLDEYIARMV 199
               KFNSCYLDEYIA MV
Sbjct: 181 VNLVKFNSCYLDEYIASMV 199
```

pir||T38991 conserved hypothetical protein SPAC630.13c - fission yeast (Schizosaccharomyces pombe) >gi|5734474|emb|CAB52735.1| (AL109832) conserved hypothetical protein [Schizosaccharomyces pombe] Length = 1339

Score = 164 bits (410), Expect = 9e-39
Identities = 98/249 (39%), Positives = 142/249 (56%), Gaps = 16/249 (6%)

```
Query: 1515 NKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEF 1574
            N+P+LLP+   S  R++ + D+IP  ++ K  ++YVG  Q   E  IL+N + S  +  F
Sbjct: 1064 NQPLLLPSNDDSVRRAISVFDRIPVIESLKAGLVYVGY-QQRREADILANTNPSEDFLTF 1122

Query: 1575 LTGLGRLIELKDCQPDKVYLGGLDVCGE-DGQFTYCWHDDIMQAVFHIATLMPTKDVDKH 1633
            L GLG L ELK  Q  KV+ GGLD   + DG F YCW D + Q VFH  T+MPT
Sbjct: 1123 LNGLGTLFELKTDQ--KVFAGGLDRENDIDGAFAYCWKDKVTQMVFHCTTMMPTNIEHDP 1180

Query: 1634 RCD-KKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYECNLVSLQCR-KDM 1691
             C  KKRH+GNDFV+I++N+SG ++   TI  QFNFV++++TP          Q +   +
Sbjct: 1181 GCTLKKRHIGNDFVTIIFNESGLEYDFDTIPSQFNFVNIVITPESESIRRTGRQIKFYKV 1240

Query: 1692 EGL----VDTSV---AKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKWIARL 1744
            + L    +D S+    KIVS   LP + R + L+A + S ++H  +     Y   W  RL
Sbjct: 1241 KALTKYDIDFSLFRRYKIVSSDALPAIVRDVTLNAAVFSHIYHRSAGD---YVHIWAERL 1297

Query: 1745 RHIKRLRQR 1753
            R +KRLR++
Sbjct: 1298 RQLKRLREK 1306
```

Score = 124 bits (308), Expect = 8e-27
Identities = 193/954 (20%), Positives = 359/954 (37%), Gaps = 112/954 (11%)

```
Query: 43  EILRELSMECGLNNRIRMIGQICEVAKTKKFEEHAVEALWKAVADLLQPERTLEA-RHAV 101
           +IL           R +++  I    K   +   ++  +W+ + D +  +    A R  V
Sbjct: 19  DILSYFDANLPFKKRHQIVRSIYHGLKYYIYSSTSIIQVWQNIQDFISTKNDNAAFRELV 78

Query: 102 LALLKAIVQGQGERLGVLRALFFKVIKDYPSNE--DLHERLEVFKALTDNGRHITYLEEE 159
             L+   V  Q     + R  FF+ I+  P  +  +L  RL+    LTD G  I+ +E
Sbjct: 79  YNLMMRYVSTQKHLSIIERHTFFQTIEKDPFQDIAELQLRLKSLSVLTDEGHKISGIENR 138

Query: 160 LADFVLQWMDVGLS-----------------------SEFXXXXXXXXKFNSCYLDE-YI 195
           +   +  W +  L                                KF    + E  +
Sbjct: 139 VGPLLSAWFNQYLQWQSQATELQGKDADSKLVHLLFFKSLFKFSTNLVKFQWFLVPEPQM 198

Query: 196 ARMVQMICLLCVRTASSVDIEVSLQVLDAVVCYNCLPAESLPLFIVTLCRT-INVKELCE 254
            ++V  +  +C        +   L   D+++ Y+ +P  SL   ++ LC T I+     +
Sbjct: 199 LQLVNSVVQICNHARLEDVVTEVLMFFDSMIRYSVIPKASLYDTVLILCSTYISTYSYSK 258

Query: 255 PCWKLMRNLLGTHLGHSAIYNMCHLMEDRAYMEDAPLLRGAVFFVGMALWGAHRLYSLRN 314
               ++ NL+ + + + A  N+ ++++      +A  +RGAV  +   +    +  ++ +
Sbjct: 259 LAQSVIFNLISSPVSNLAFENVFNILQYNRSNVNA--VRGAVRLMRFLMLQEVKNDAIAS 316

Query: 315 SPTSVFPSFYQAMACPNEVVSYEIVLSITRLIK--KYRKELQVVAWDILLNIIERLLQQL 372
              S    F +     NE V +EI+ ++   ++       L  + W  +LNI+    Q L
Sbjct: 317 ITLSSSIEFTEFPLGFNENVDFEILGTVYLFLRTPSILNRLNFLDWHRILNILMYCSQYL 376

Query: 373 --QTLDSPELRTIVHDLLTTVEELCDQNEFHGS----QERYFELVERCADQRP------E 420
            +   S E  +         + + D  +F       Q+   +LV    D  P
Sbjct: 377 PLKASTSKEAFSKTAAFANIYDRVLDFLDFEALIPLLQQFQVKLVFFLKDVLPVLKPKIR 436

Query: 421 SSLLNLISYRAQSIHPAKDGWIQNLQALMERF----FRSESRGAVRIKVLDVLSFVLLIN 476
            LL L       I P    W+ NL+ L+  +    F  E R  +   V D  S    +
Sbjct: 437 KKLLRLFE-TYNLIFPCNQYWVFNLEFLLGIYQCKTFDLEDRALLFKLVEDACS----VA 491
```

```
Query: 477 RQFYEEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLA--------EGCHTHHFNSLL 528
           +     L +  +   +    ++ D  V      +L  L+        + C  H F  L+
Sbjct: 492 DENSAPILCSKFLFPVIESFSKESDDCVVSPVYNMLFFLSVNFQNPGLKDCIDHIFQQLI 551

Query: 529 DIIEKVMARSLSPPPELEERDVAAYSASLED---VKTAVLGLLVILQTKLYTLPASHATR 585
                V  R L+    +    +  Y   L D   ++  +  +L IL+T  +
Sbjct: 552 SDTSSVTVRRLATSTLIR---LFYYYYDLRDAVPIQETLAKMLEILETPSFPF------- 601

Query: 586 VYEMLVSHIQLHYKHSYT-LPIASSIRL-QAFDFLFLLRADSLHRLGLPNKDGVVRFSPY 643
           V  ML     L ++ + T + I  +I L + F  L              N D  +  + Y
Sbjct: 602 VSRMLCLQFFLRFRANGTSIYICENIDLNEPFKVL--------------NVDSELIPAVY 647

Query: 644 CVCDYMEPERGSEKKXXXXXXXXXXXXXXXXXXXXVRLGSVPYSLLFRVLLQCLKQESDW 703
           + D        EK                         + P S L R   + +  ES+W
Sbjct: 648 PISDSFVNSATVEKHIWERKENDLIKISNHSTEYGKDFVTFPTSSLLRFYRKSMATESNW 707

Query: 704 KVLKLVLGRLPESLRYKVLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEGFSRTDLH 763
           +L  ++  L + +  + +   +   +  L   +C ++    ++      P    + ++
Sbjct: 708 TILMFMITHLADQISNRSMFIGALEEIYNLLDFMCDIVFERVSISA--EIPSNIRKANIM 765

Query: 764 LAVVPVLTALISYHNYLDKTKQREMVYCLEQGLI--HRCARQCVVALSICSVEMPDIIIK 821
           + ++  +  L  YH+   + ++ E+V     GL   +      + +L +C  E+P  I K
Sbjct: 766 IPILQNVQMLFVYHDQFSRAQEDELVSVFFAGLQKWNEACHVSIHSLMLCCYELPVSIRK 825

Query: 822 ALPVLVVKLTHISATASMAVPLLEFLSTLARLPHLYRNFAAEQYASVFAISLPY------ 875
           LP ++V L+ +     ++V +LEFL +LARLP L  NF    Y  +FAI+L Y
Sbjct: 826 QLPAILVTLSRLITKPDLSVHILEFLCSLARLPDLIANFTDADYRQIFAIALKYIQHRDF 885

Query: 876 TNPSK------------FNQYIVCLAHHVIAMWFIRCRLPFRKDFVPFITKGLR 917
           T  SK            ++ Y++ LA+ V+ +WF+  RL  RK FVP+I +GL+
Sbjct: 886 TKESKDSNDTESILKNSYSSYVLALAYSVLQIWFLSLRLTERKKFVPWILRGLK 939
```

dbj|BAA86586.1| (AB033098) KIAA1272 protein [Homo sapiens]
Length = 1023

Score = 102 bits (251), Expect = 4e-20
Identities = 66/211 (31%), Positives = 108/211 (50%), Gaps = 7/211 (3%)

```
Query: 1513 ESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYT 1572
            +  K   L  ++    R ++ LD     +THKIAV Y+ EGQ + + +ILSNE GS  Y
Sbjct: 805  DRRKNFHLLKKNSKLLRELKNLDSRQCRETHKIAVFYIAEGQED-KCSILSNERGSQAYE 863

Query: 1573 EFLTGLGRLIELKD-CQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVD 1631
            +F+ GLG  ++L   C     ++GGL   G  GQ    +    ++ +FH++T MP+ D D
Sbjct: 864  DFVAGLGWEVDLSTHCG----FMGGLQRNGSTGQTAPYYATSTVEVIFHVSTRMPS-DSD 918

Query: 1632 KHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYECNLVSLQCRKDM 1691
                 K RHLGND V IV+++   D++ G I   F  V +I+ P+      +++  + ++
Sbjct: 919  DSLTKKLRHLGNDEVHIVWSEHSRDYRRGIIPTAFGDVSIIIYPMKNHMFFIAITKKPEV 978

Query: 1692 EGLVDTSVAKIVSDRNLPFVARQMALHANMA 1722
                       IVS + LP +     ++A+ A
Sbjct: 979  PFFGPLFDGAIVSGKLLPSLVCATCINASRA 1009
```

pir||T08722 hypothetical protein DKFZp566D133.1 - human (fragment)
>gi|4884288|emb|CAB43250.1| (AL050050) hypothetical
protein [Homo sapiens]
Length = 381

Score = 97.1 bits (238), Expect = 1e-18
Identities = 68/242 (28%), Positives = 121/242 (49%), Gaps = 13/242 (5%)

```
Query: 1520 LPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLG 1579
            L  +++   R ++ LD     +THKIAV YV EGQ +   +IL+N  GS  Y +F+ GLG
Sbjct: 130  LLKKNEKLLRELRNLDSRQCRETHKIAVFYVAEGQEDKH-SILTNTGGSQAYEDFVAGLG 188

Query: 1580 RLIELKD-CQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKK 1638
              + L + C     ++GGL      G  T  +    ++ +FH++T MP+ D D     K
Sbjct: 189  WEVNLTNHCG----FMGGLQKNKSTGLTTPYFATSTVEVIFHMSTRMPS-DSDDSLTKKL 243

Query: 1639 RHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYECNLVSLQCRKDMEGLVDTS 1698
            RHLGND V IV+++   D++ G I  +F  V +++ P+      + +  + ++
Sbjct: 244  RHLGNDEVHIVWSEHTRDYRRGIIPTEFGDVLIVIYPMKNHMFSIQIMRKPEVPFFGPLF 303
```

```
Query: 1699 VAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKWIARLRHIKRLRQRICEEA 1758
               IV+ + LP + R  A++A+ A +      +   +Y + +  R R+++ + Q   E
Sbjct: 304  DGAIVNGKVLPIMVRATAINASRALK------SLIPLYQNFYEERARYLQTIVQHHLEPT 357

Query: 1759 AY 1760
             +
Sbjct: 358  TF 359
```

gb|AAB97076.1| (AF041107) tulip 2 [Rattus norvegicus]
Length = 866

Score = 96.3 bits (236), Expect = 2e-18
Identities = 67/242 (27%), Positives = 122/242 (49%), Gaps = 13/242 (5%)

```
Query: 1520 LPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLG 1579
            L  +++   R ++ LD     +THKIAV YV EGQ + + +IL+N  GS  Y +F+ GLG
Sbjct: 610  LLKKNEKLLRELRNLDSRQCRETHKIAVFYVAEGQED-KYSILTNIGGSQAYEDFVAGLG 668

Query: 1580 RLIELKD-CQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKK 1638
              + L + C     ++GGL      G  T  +    ++ +FH++T MP++  D     K
Sbjct: 669  WEVNLTNHCG----FMGGLQKNKSTGLTTPYFATSTVEVIFHVSTRMPSES-DDSLTKKL 723

Query: 1639 RHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLDYECNLVSLQCRKDMEGLVDTS 1698
            RHLGND V IV+++   D++ G I  +F  V +++ P+      + +  + ++
Sbjct: 724  RHLGNDEVHIVWSEHTRDYRRGIIPTEFGDVLIVIYPMKNHMFSIQIMKKPEVPFFGPLF 783

Query: 1699 VAKIVSDRNLPFVARQMALHANMASQVHHSRSNPTDIYPSKWIARLRHIKRLRQRICEEA 1758
               IV+ + LP + R  A++A+ A +      +   +Y + +  R R+++ + Q   E
Sbjct: 784  DGAIVNGKVLPIMVRSTAINASRALK------SLIPLYQNFYEERARYLQTIVQHHLEPT 837

Query: 1759 AY 1760
             +
Sbjct: 838  TF 839
```

gb|AAB87873.1| (AF023478) GTPase activating protein for Rap1 [Drosophila melanogaster]
Length = 850

Score = 80.4 bits (195), Expect = 1e-13
Identities = 54/165 (32%), Positives = 81/165 (48%), Gaps = 15/165 (9%)

```
Query: 1517 PILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLT 1576
            PIL P  SQ     + + D+       K  VLY   GQ+  E  +  N+  S  + EFL
Sbjct: 311  PILCPKASQL----ISVYDEHVLVSHFKFGVLYQRYGQTTEE-ELFGNQQTSPAFDEFLD 365

Query: 1577 GLGRLIELKDCQPDKVYLGGLDV----CGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDK 1632
             LG+ I LKD    K Y GGLD+     G+   +      +IM   FH++TL+P  + D
Sbjct: 366  VLGQRIRLKD---HKGYRGGLDIQNGHTGDTAVYEVFKEREIM---FHVSTLLPHTEGDP 419

Query: 1633 HRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLD 1677
             +  +KRH+GND V+IV+ ++   F    I   F    ++V P++
Sbjct: 420  QQLQRKRHIGNDIVAIVFQETNTPFSPDMIASHFLHAFIVVQPIE 464
```

gb|AAF52526.1| (AE003617) Rapgap1 gene product [Drosophila melanogaster]
Length = 850

Score = 80.4 bits (195), Expect = 1e-13
Identities = 54/165 (32%), Positives = 81/165 (48%), Gaps = 15/165 (9%)

```
Query: 1517 PILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLT 1576
            PIL P  SQ     + + D+       K  VLY   GQ+  E  +  N+  S  + EFL
Sbjct: 311  PILCPKASQL----ISVYDEHVLVSHFKFGVLYQRYGQTTEE-ELFGNQQTSPAFDEFLD 365

Query: 1577 GLGRLIELKDCQPDKVYLGGLDV----CGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDK 1632
             LG+ I LKD    K Y GGLD+     G+   +      +IM   FH++TL+P  + D
Sbjct: 366  VLGQRIRLKD---HKGYRGGLDIQNGHTGDTAVYEVFKEREIM---FHVSTLLPHTEGDP 419

Query: 1633 HRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLD 1677
             +  +KRH+GND V+IV+ ++   F    I   F    ++V P++
Sbjct: 420  QQLQRKRHIGNDIVAIVFQETNTPFSPDMIASHFLHAFIVVQPIE 464
```

gb|AAC71116.2| (U80838) strong similarity to human GTPase-activating protein rap1GAP (GI:190856) [Caenorhabditis elegans]
Length = 586

```
 Score = 79.2 bits (192), Expect = 3e-13
 Identities = 51/169 (30%), Positives = 83/169 (48%), Gaps = 15/169 (8%)

Query: 1513 ESNKPILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYT 1572
            E   P+  P  S+   +     D+    +T+K  V+Y   GQ+  E  +  N HGS  +
Sbjct: 113  EQFSPVAFPGGSELIVQ----YDEHVLTNTYKFGVIYQKGGQTTEE-QLFGNPHGSPAFD 167

Query: 1573 EFLTGLGRLIELKDCQPDKVYLGGLDVC----GEDGQFTYCWHDDIMQAVFHIATLMPTK 1628
            EFL+ +G  ++L   Q    Y GGLD      G    F+   + +IM   FH++T++P
Sbjct: 168  EFLSMIGDSVQLNGFQK---YRGGLDTAHNQTGHQSVFSEFKNREIM---FHVSTMLPYT 221

Query: 1629 DVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLD 1677
              D  +  +KRH+GND V+I++ ++   F    I   F   +V+V P+D
Sbjct: 222  IGDAQQLQRKRHIGNDIVAIIFQEANTPFAPDMIASNFLHAYVVVQPID 270

 gb|AAD38161.1|AF152608_1 (AF152608) tuberin [Canis familiaris]
          >gi|5031502|gb|AAD38193.1|AF155145_1 (AF155145) tuberin
          [Mesocricetus auratus]
          Length = 34

 Score = 78.0 bits (189), Expect = 7e-13
 Identities = 33/34 (97%), Positives = 34/34 (99%)

Query: 881 FNQYIVCLAHHVIAMWFIRCRLPFRKDFVPFITK 914
           FNQYIVCLAHHVIAMWFIRCRLPFRKDFVP+ITK
Sbjct: 1   FNQYIVCLAHHVIAMWFIRCRLPFRKDFVPYITK 34

 pir||T21738 hypothetical protein T27F2.2 - Caenorhabditis elegans
           >gi|5832751|emb|CAA98469.2| (Z74032) Similarity to Mouse
           GTPase-activating protein SPA-1 (SW:SPA1_MOUSE); cDNA EST
           EMBL:C12678 comes from this gene; cDNA EST EMBL:C13605
           comes from this gene; cDNA EST yk248e9.5 comes from this
           gene; cDNA EST yk249e3.5 comes from this gene; cDNA E>
           >gi|5832754|emb|CAA98554.2| (Z74045) Similarity to Mouse
           GTPase-activating protein SPA-1 (SW:SPA1_MOUSE); cDNA EST
           EMBL:C12678 comes from this gene; cDNA EST EMBL:C13605
           comes from this gene; cDNA EST yk248e9.5 comes from this
           gene; cDNA EST yk249e3.5 comes from this gene; cDNA E>
           Length = 924

 Score = 76.9 bits (186), Expect = 2e-12
 Identities = 49/159 (30%), Positives = 83/159 (51%), Gaps = 7/159 (4%)

Query: 1518 ILLPN-ESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLT 1576
            IL P+ +S   E  +  +D+ P Y  +K+ ++     QS  E  + +NE  +  + EFL
Sbjct: 278  ILRPSIQSPRVEELIMKIDEQPIYTRYKVGIMLCKNEQSTEE-QMYNNEFSTPSFDEFLD 336

Query: 1577 GLGRLIELKDCQPDKVYLGGLDVCGED-GQFTYCWHDDIMQAVFHIATLMPTKDVDKHRC 1635
             LG+ + LK  +    Y GGLD  G+  G  +        + +FH++TL+P    ++ +
Sbjct: 337  FLGQRVTLKGFE---AYKGGLDTRGDTTGTHSIYSEYQAHEIMFHVSTLLPFTPSNRQQL 393

Query: 1636 DKKRHLGNDFVSIVYNDSGE-DFKLGTIKGQFNFVHVIV 1673
             +KRH+GND V+IV+ + G   F   T++  F  V +IV
Sbjct: 394  SRKRHIGNDMVTIVFQEPGALPFSPITVRSHFQHVFIIV 432

 pir||B39897 GTPase-activating protein rap1GAP long form - human (fragment)
           Length = 615

 Score = 73.7 bits (178), Expect = 1e-11
 Identities = 51/159 (32%), Positives = 82/159 (51%), Gaps = 11/159 (6%)

Query: 1517 PILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLT 1576
            P+L P  S    R +   D+    +  K  V+Y   GQ++ E    +NE  S  + EFL
Sbjct: 97   PVLYPKAS----RLIVTFDEHVISNNFKFGVIYQKLGQTSEEELFSTNEE-SPAFVEFLE 151

Query: 1577 GLGRLIELKDCQPDKVYLGGLDVC-GEDG-QFTYCWHDDIMQAVFHIATLMPTKDVDKHR 1634
             LG+ ++L+D    K + GGLDV  G+ G +  YC   +  + +FH++T +P  + D  +
Sbjct: 152  FLGQKVKLQDF---KGFRGGLDVTHGQTGTESVYCNFRN-KEIMFHVSTKLPYTEGDAQQ 207

Query: 1635 CDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIV 1673
              +KRH+GND V++V+ D    F    I   F   +V+V
Sbjct: 208  LQRKRHIGNDIVAVVFQDENTPFVPDMIASNFLHAYVVV 246
```

```
 ref|NP_002876.1|| RAP1, GTPase activating protein 1 >gi|1350590|sp|P47736|RGP2_HUMAN
            RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP)
            >gi|106199|pir||A39897 GTPase-activating protein rap1GAP
            short form - human >gi|190856|gb|AAA60252.1| (M64788)
            GTPase activating protein [Homo sapiens]
            Length = 663

 Score = 73.7 bits (178), Expect = 1e-11
 Identities = 51/159 (32%), Positives = 82/159 (51%), Gaps = 11/159 (6%)

Query: 1517 PILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLT 1576
            P+L P  S    R +   D+    +  K  V+Y   GQ++ E    +NE  S  + EFL
Sbjct: 171  PVLYPKAS----RLIVTFDEHVISNNFKFGVIYQKLGQTSEEELFSTNEE-SPAFVEFLE 225

Query: 1577 GLGRLIELKDCQPDKVYLGGLDVC-GEDG-QFTYCWHDDIMQAVFHIATLMPTKDVDKHR 1634
             LG+ ++L+D    K + GGLDV  G+ G +  YC   +  + +FH++T +P  + D  +
Sbjct: 226  FLGQKVKLQDF---KGFRGGLDVTHGQTGTESVYCNFRN-KEIMFHVSTKLPYTEGDAQQ 281

Query: 1635 CDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIV 1673
              +KRH+GND V++V+ D    F    I   F   +V+V
Sbjct: 282  LQRKRHIGNDIVAVVFQDENTPFVPDMIASNFLHAYVVV 320

 gb|AAD45946.1|AF151966_1 (AF151966) GTPase activating protein Rap1-GAP [Gallus gallus]
            Length = 556

 Score = 73.4 bits (177), Expect = 2e-11
 Identities = 49/158 (31%), Positives = 78/158 (49%), Gaps = 9/158 (5%)

Query: 1517 PILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLT 1576
            P+L P  SQ     +   D+    +  K  V+Y   GQ+  E  + SN   S  + EFL
Sbjct: 171  PVLYPKASQL----IVAFDEHVISNNFKFGVIYQKPGQTTEE-EVFSNTEESLGFLEFLD 225

Query: 1577 GLGRLIELKDCQPDKVYLGGLDVC-GEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRC 1635
             LG  I+L+D +    + GGLDV  G+ G  +   +    + +FH++T +P  + D  +
Sbjct: 226  FLGDKIQLQDFRG---FRGGLDVIRGQTGTESVYTNFRGKEIMFHVSTKLPFAEGDSQQL 282

Query: 1636 DKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIV 1673
             +KRH+GND V+I++ D    F    I   F   +V+V
Sbjct: 283  QRKRHIGNDIVAIIFQDESTPFVPDMIASNFLHAYVVV 320

 dbj|BAA92627.1| (AB037810) KIAA1389 protein [Homo sapiens]
            Length = 1514

 Score = 67.1 bits (161), Expect = 1e-09
 Identities = 50/154 (32%), Positives = 79/154 (50%), Gaps = 7/154 (4%)

Query: 1522 NESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLGRL 1581
            N  +  E+ ++L +Q  S+  HKI +LY   GQS  E  + +NE     + EFL  LG+
Sbjct: 379  NSPKVSEQLLKLDEQGLSFQ-HKIGILYCKAGQSTEE-EMYNNETAGPAFEEFLDLLGQR 436

Query: 1582 IELKDCQPDKVYLGG-LDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKKRH 1640
            + LK     +  L    D  G    +T     ++M   FH++TL+P    ++ +  +KRH
Sbjct: 437  VRLKGFSKYRAQLDNKTDSTGTHSLYTTYKDYELM---FHVSTLLPYMPNNRQQLLRKRH 493

Query: 1641 LGNDFVSIVYNDSGE-DFKLGTIKGQFNFVHVIV 1673
            +GND V+IV+ + G   F   +I+  F  V VIV
Sbjct: 494  IGNDIVTIVFQEPGALPFTPKSIRSHFQHVFVIV 527

 gb|AAD12543.1| (AF090989) high-risk human papilloma viruses E6 oncoproteins targeted
            protein E6TP1 alpha; putative GAP protein alpha [Homo
            sapiens]
            Length = 1783

 Score = 65.2 bits (156), Expect = 5e-09
 Identities = 48/154 (31%), Positives = 78/154 (50%), Gaps = 7/154 (4%)

Query: 1522 NESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLGRL 1581
            N  +  E+ ++L +Q  +Y   K+ ++Y   GQS  E  + +NE     + EFL  LG
Sbjct: 591  NTPKVTEQLMKLDEQGLNYQ-QKVGIMYCKAGQSTEE-EMYNNESAGPAFEEFLQLLGER 648

Query: 1582 IELKDCQPDKVYLGG-LDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKKRH 1640
            + LK  +  +  L    D  G    +T     +IM   FH++T++P    +K +  +KRH
Sbjct: 649  VRLKGFEKYRAQLDTKTDSTGTHSLYTTYKDYEIM---FHVSTMLPYTPNNKQQLLRKRH 705
```

```
Query: 1641 LGNDFVSIVYNDSG-EDFKLGTIKGQFNFVHVIV 1673
           +GND V+IV+ + G + F    I+  F  V VIV
Sbjct: 706  IGNDIVTIVFQEPGAQPFSPKNIRSHFQHVFVIV 739
```

gb|AAC32547.1| (AF029789) GTPase-activating protein [Homo sapiens]
Length = 1041

Score = 65.2 bits (156), Expect = 5e-09
Identities = 45/156 (28%), Positives = 79/156 (49%), Gaps = 6/156 (3%)

```
Query: 1520 LPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLG 1579
           L + S    R++  LD+       K+ +LY   GQ + E  + +N+     + +FLT LG
Sbjct: 310  LGSASPKVPRTLLTLDEQVLSFQRKVGILYCRAGQGSEE-EMYNNQEAGPAFMQFLTLLG 368

Query: 1580 RLIELKDCQPDKVYLGG-LDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKK 1638
            ++ LK  +  +  L    D  G    +T     +IM   FH++T++P    ++ +  +K
Sbjct: 369  DVVRLKGFESYRAQLDTKTDSTGTHSLYTTYQDHEIM---FHVSTMLPYTPNNQQQLLRK 425

Query: 1639 RHLGNDFVSIVYNDSG-EDFKLGTIKGQFNFVHVIV 1673
           RH+GND V+IV+ + G + F   TI+  F  V ++V
Sbjct: 426  RHIGNDIVTIVFQEPGSKPFCPTTIRSHFQHVFLVV 461
```

ref|NP_006738.1|| signal-induced proliferation-associated gene 1
>gi|3170450|gb|AAC32559.1| (AF052238) GTPase-activating
protein [Homo sapiens]
Length = 1041

Score = 65.2 bits (156), Expect = 5e-09
Identities = 45/156 (28%), Positives = 79/156 (49%), Gaps = 6/156 (3%)

```
Query: 1520 LPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLG 1579
           L + S    R++  LD+       K+ +LY   GQ + E  + +N+     + +FLT LG
Sbjct: 310  LGSASPKVPRTLLTLDEQVLSFQRKVGILYCRAGQGSEE-EMYNNQEAGPAFMQFLTLLG 368

Query: 1580 RLIELKDCQPDKVYLGG-LDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKK 1638
            ++ LK  +  +  L    D  G    +T     +IM   FH++T++P    ++ +  +K
Sbjct: 369  DVVRLKGFESYRAQLDTKTDSTGTHSLYTTYQDHEIM---FHVSTMLPYTPNNQQQLLRK 425

Query: 1639 RHLGNDFVSIVYNDSG-EDFKLGTIKGQFNFVHVIV 1673
           RH+GND V+IV+ + G + F   TI+  F  V ++V
Sbjct: 426  RHIGNDIVTIVFQEPGSKPFCPTTIRSHFQHVFLVV 461
```

gb|AAD12544.1| (AF090990) high-risk human papilloma viruses E6 oncoproteins targeted
protein E6TP1 beta; putative GAP protein beta [Homo
sapiens]
Length = 1804

Score = 65.2 bits (156), Expect = 5e-09
Identities = 48/154 (31%), Positives = 78/154 (50%), Gaps = 7/154 (4%)

```
Query: 1522 NESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLGRL 1581
           N  +  E+ ++L +Q  +Y   K+ ++Y   GQS  E  + +NE     + EFL  LG
Sbjct: 591  NTPKVTEQLMKLDEQGLNYQ-QKVGIMYCKAGQSTEE-EMYNNESAGPAFEEFLQLLGER 648

Query: 1582 IELKDCQPDKVYLGG-LDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKKRH 1640
           + LK  +  +  L    D  G    +T     +IM   FH++T++P    +K +  +KRH
Sbjct: 649  VRLKGFEKYRAQLDTKTDSTGTHSLYTTYKDYEIM---FHVSTMLPYTPNNKQQLLRKRH 705

Query: 1641 LGNDFVSIVYNDSG-EDFKLGTIKGQFNFVHVIV 1673
           +GND V+IV+ + G + F    I+  F  V VIV
Sbjct: 706  IGNDIVTIVFQEPGAQPFSPKNIRSHFQHVFVIV 739
```

dbj|BAA22197.1| (AB005666) GTPase-activating protein [Homo sapiens]
Length = 1042

Score = 65.2 bits (156), Expect = 5e-09
Identities = 45/156 (28%), Positives = 79/156 (49%), Gaps = 6/156 (3%)

```
Query: 1520 LPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLG 1579
           L + S    R++  LD+       K+ +LY   GQ + E  + +N+     + +FLT LG
Sbjct: 310  LGSASPKVPRTLLTLDEQVLSFQRKVGILYCRAGQGSEE-EMYNNQEAGPAFMQFLTLLG 368

Query: 1580 RLIELKDCQPDKVYLGG-LDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKK 1638
            ++ LK  +  +  L    D  G    +T     +IM   FH++T++P    ++ +  +K
```

```
Sbjct: 369  DVVRLKGFESYRAQLDTKTDSTGTHSLYTTYQDHEIM---FHVSTMLPYTPNNQQQLLRK 425

Query: 1639 RHLGNDFVSIVYNDSG-EDFKLGTIKGQFNFVHVIV 1673
            RH+GND V+IV+ + G + F   TI+  F  V ++V
Sbjct: 426  RHIGNDIVTIVFQEPGSKPFCPTTIRSHFQHVFLVV 461
```

pir||T14106 probable GTPase-activating protein SPA-1 - rat
>gi|2555183|gb|AAB81526.1| (AF026504) SPA-1 like protein p1294 [Rattus norvegicus]
Length = 1822

Score = 65.2 bits (156), Expect = 5e-09
Identities = 48/154 (31%), Positives = 78/154 (50%), Gaps = 7/154 (4%)

```
Query: 1522 NESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLGRL 1581
            N  +  E+ ++L +Q  +Y   K+ ++Y   GQS  E  + +NE     + EFL  LG
Sbjct: 630  NTPKVTEQFMKLDEQGLNYQ-QKVGIMYCKAGQSTEE-EMYNNESAGPAFEEFLQLLGER 687

Query: 1582 IELKDCQPDKVYLGG-LDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKKRH 1640
            + LK  +  +  L    D  G    +T     +IM   FH++T++P    +K +  +KRH
Sbjct: 688  VRLKGFEKYRAQLDTKTDSTGTHSLYTTYKDYEIM---FHVSTMLPYTPNNKQQLLRKRH 744

Query: 1641 LGNDFVSIVYNDSG-EDFKLGTIKGQFNFVHVIV 1673
            +GND V+IV+ + G + F    I+  F  V VIV
Sbjct: 745  IGNDIVTIVFQEPGAQPFSPKNIRSHFQHVFVIV 778
```

gb|AAB97075.1| (AF041106) tulip 1 [Rattus norvegicus]
Length = 747

Score = 60.5 bits (144), Expect = 1e-07
Identities = 38/113 (33%), Positives = 62/113 (54%), Gaps = 6/113 (5%)

```
Query: 1520 LPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLG 1579
            L  +++   R ++ LD     +THKIAV YV EGQ + + +IL+N  GS  Y +F+ GLG
Sbjct: 610  LLKKNEKLLRELRNLDSRQCRETHKIAVFYVAEGQED-KYSILTNIGGSQAYEDFVAGLG 668

Query: 1580 RLIELKD-CQPDKVYLGGLDVCGEDGQFTYCWHDDIMQAVFHIATLMPTKDVD 1631
              + L + C     ++GGL      G  T  +    ++ +FH++T MP++  D
Sbjct: 669  WEVNLTNHCG----FMGGLQKNKSTGLTTPYFATSTVEVIFHVSTRMPSESDD 717
```

dbj|BAA82991.1| (AB028962) KIAA1039 protein [Homo sapiens]
Length = 444

Score = 57.4 bits (136), Expect = 1e-06
Identities = 36/105 (34%), Positives = 56/105 (53%), Gaps = 6/105 (5%)

```
Query: 1571 YTEFLTGLGRLIELKDCQPDKVYLGGLDVC-GEDG-QFTYCWHDDIMQAVFHIATLMPTK 1628
            + EFL  LG  I L+D    K + GGLDV  G+ G +  Y    D  + +FH++T +P
Sbjct: 1    FKEFLDLLGDTITLQDF---KGFRGGLDVTHGQTGVESVYTTFRD-REIMFHVSTKLPFT 56

Query: 1629 DVDKHRCDKKRHLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIV 1673
            D D  +  +KRH+GND V+I++ +    F    I   F   +++V
Sbjct: 57   DGDAQQLQRKRHIGNDIVAIIFQEENTPFVPDMIASNFLHAYIVV 101
```

ref|NP_035509.1|| signal-induced proliferation associated gene 1
>gi|1565195|dbj|BAA13469.1| (D87849) GTPase-activating protein [Mus musculus]
Length = 693

Score = 54.7 bits (129), Expect = 8e-06
Identities = 34/113 (30%), Positives = 60/113 (53%), Gaps = 5/113 (4%)

```
Query: 1563 SNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGG-LDVCGEDGQFTYCWHDDIMQAVFHI 1621
            +N+     + +FLT LG ++ LK  +  +  L    D  G    +T     +IM   FH+
Sbjct: 3    NNQEAGAAFMQFLTLLGDVVRLKGFESYRAQLDTKTDSTGTHSLYTTYQDHEIM---FHV 59

Query: 1622 ATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSG-EDFKLGTIKGQFNFVHVIV 1673
            +T++P    ++ +  +KRH+GND V+IV+ + G + F   TI+  F  V ++V
Sbjct: 60   STMLPYTPNNQQQLLRKRHIGNDIVTIVFQEPGSKPFCPTTIRSHFQHVFLVV 112
```

sp|P46062|SPA1_MOUSE GTPASE-ACTIVATING PROTEIN SPA-1 >gi|7513670|pir||I49709 GTPase-activating protein - mouse
>gi|641939|dbj|BAA01973.1| (D11374) GTPase-activating protein [Mus musculus]

```
            Length = 693

 Score = 54.7 bits (129), Expect = 8e-06
 Identities = 34/113 (30%), Positives = 60/113 (53%), Gaps = 5/113 (4%)

Query: 1563 SNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGG-LDVCGEDGQFTYCWHDDIMQAVFHI 1621
            +N+     + +FLT LG ++ LK  +  +  L    D  G    +T     +IM   FH+
Sbjct: 3    NNQEAGAAFMQFLTLLGDVVRLKGFESYRAQLDTKTDSTGTHSLYTTYQDHEIM---FHV 59

Query: 1622 ATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSG-EDFKLGTIKGQFNFVHVIV 1673
            +T++P    ++ +  +KRH+GND V+IV+ + G + F   TI+  F  V ++V
Sbjct: 60   STMLPYTPNNQQQLLRKRHIGNDIVTIVFQEPGSKPFCPTTIRSHFQHVFLVV 112

 pir||S27869 GTPase-activating protein - mouse
            Length = 329

 Score = 54.7 bits (129), Expect = 8e-06
 Identities = 34/113 (30%), Positives = 60/113 (53%), Gaps = 5/113 (4%)

Query: 1563 SNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGG-LDVCGEDGQFTYCWHDDIMQAVFHI 1621
            +N+     + +FLT LG ++ LK  +  +  L    D  G    +T     +IM   FH+
Sbjct: 3    NNQEAGAAFMQFLTLLGDVVRLKGFESYRAQLDTKTDSTGTHSLYTTYQDHEIM---FHV 59

Query: 1622 ATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSG-EDFKLGTIKGQFNFVHVIV 1673
            +T++P    ++ +  +KRH+GND V+IV+ + G + F   TI+  F  V ++V
Sbjct: 60   STMLPYTPNNQQQLLRKRHIGNDIVTIVFQEPGSKPFCPTTIRSHFQHVFLVV 112

 dbj|BAA23712.1| (AB007900) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at
            position 1711 of the sequence of KIAA0440. [Homo sapiens]
            Length = 1138

 Score = 47.3 bits (110), Expect = 0.001
 Identities = 22/59 (37%), Positives = 37/59 (62%), Gaps = 1/59 (1%)

Query: 1616 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSG-EDFKLGTIKGQFNFVHVIV 1673
            + +FH++T++P    +K +  +KRH+GND V+IV+ + G + F    I+  F  V VIV
Sbjct: 15   EIMFHVSTMLPYTPNNKQQLLRKRHIGNDIVTIVFQEPGAQPFSPKNIRSHFQHVFVIV 73

 dbj|BAA25471.1| (AB011117) KIAA0545 protein [Homo sapiens]
            Length = 1129

 Score = 44.5 bits (103), Expect = 0.009
 Identities = 20/59 (33%), Positives = 36/59 (60%), Gaps = 1/59 (1%)

Query: 1616 QAVFHIATLMPTKDVDKHRCDKKRHLGNDFVSIVYNDSGE-DFKLGTIKGQFNFVHVIV 1673
            + +FH++TL+P    ++ +  +KRH+GND V+I++ + G   F    I+  F  V +IV
Sbjct: 41   EIMFHVSTLLPYTPNNRQQLLRKRHIGNDIVTIIFQEPGALPFTPKNIRSHFQHVFIIV 99

 sp|Q09716|YA3B_SCHPO HYPOTHETICAL 149.2 KD PROTEIN C18B11.11 IN CHROMOSOME I
           >gi|2130292|pir||S58307 hypothetical protein
           SPAC18B11.11 - fission yeast (Schizosaccharomyces pombe)
           >gi|7490657|pir||T37903 hypothetical 149.2 kd protein -
           fission yeast (Schizosaccharomyces pombe)
           >gi|929897|emb|CAA90595.1| (Z50728) hypothetical 149.2
           kd protein [Schizosaccharomyces pombe]
           Length = 1294

 Score = 41.0 bits (94), Expect = 0.098
 Identities = 160/958 (16%), Positives = 343/958 (35%), Gaps = 131/958 (13%)

Query: 44  ILRELSMECGLNNRIRMIGQICEVAKTKKFEEHAV-EALWKAVADLLQPERTLEARHAVL 102
           IL ++S +  L+ R + I ++      ++F ++ + + L  +  D+++ +       A +
Sbjct: 9   ILTQISNQQSLDKRYKRIKRLIN---NEQFCKNVILQKLVDSTKDIIENKVHGNILAATI 65

Query: 103 ALLKAIVQGQGERLGVLRALFFKVIKDYPSNEDLHERLEVFKALTDNGRHITYLEEELAD 162
           +L     +   E     RAL F  +   P++E     ++    +T  G        ++
Sbjct: 66  SLWTHAAEKHKEMSSDDRALLFNELSKVPNSEYYPATVDALIVITSQGERTESFSNDILK 125

Query: 163 FVLQWM-DVGLSSEFXXXXXXXXKFNSCYLDEYIARMVQMICLL---------------- 205
            + +W+ D+    +            S  L  Y     Q+I LL
Sbjct: 126 VLSEWLTDLFTIIDDMRAQSRKSFKGSAELRNYTRCFRQIILLLTNMFRVGFNLFDEMEV 185

Query: 206 ------CVRTASSV----DIEVSLQVLDAVVCYNCLPAESLPLFIVTLCRT-INVKELCE 254
                 CV  + S     DI +   +L+ ++ Y  + +  L   +  +CR    +    +
```

```
Sbjct: 186 SSMLANCVWVSKSTTDEEDIALVFSLLNCIISYGRISSAVLYSIVEVVCRAKFGLVASSQ 245

Query: 255 PCWKLMRNLLGTHLGHSAIYNMCHLMEDR----------------AYMEDAPLLRGAVFF 298
              +++  LL T   + A+ ++  +ME+                 A   D P  R
Sbjct: 246 SAQQIVEKLLKTATKYEALNSLKRIMEETDEGSYIAIMGGIQIVSALFTDIP--RSVYCT 303

Query: 299 VGMALWGAHRLYSLRNSPTSVF-------------PSFYQAMACPNEVVSYEIVLSITRL 345
            GM L    R  SL+N  + +               SF + +     +   ++++ I+
Sbjct: 304 RGMLLGFLQR--SLKNKSSRIALETTRSLYNALERRSFVEVLYADEWISLLDLLVEISSS 361

Query: 346 IKKYRKELQVVAWDILLNIIERLLQ-QLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQ 404
           + K           I  NIIE +   QLQ L       + +++L          +FH
Sbjct: 362 LPKSLNYRPGTWQHIEPNIIESIASYQLQHL------LLFNEILKPDSNHFVLEKFHEFL 415

Query: 405 ERYFELVERCADQRPESSLLNLISYRAQSIHPAKDGWIQNLQALMERFFRSESRGAVRIK 464
           +  F  +     Q+    L  ++  R+Q   P  +GW+++   L++ +F +       +
Sbjct: 416 KINFSYLTPTLSQK----LFTVLDLRSQL--PYSEGWLEDQTILLKSYFDTSFSLDFHVY 469

Query: 465 VLDVLSFVLLINRQFYEEELINSVVISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHF 524
           ++ +   VL         E+   ++   +  + +     +      L+ DL+    ++ F
Sbjct: 470 LIGLFRKVLFACPVELRPEVYARMLCPLVKSLDKSSSEVIIDEVISLVCDLSWIYPSNVF 529

Query: 525 NSLLDIIEKVMARSLSPPPELEERDVAAYSASLEDVKTAVLGLLVILQTKLYTLPASHAT 584
           + + D +                    A+++S  D++   +  +V L T  Y L     +
Sbjct: 530 HEVKDSL-----------------CFYAHNSSNGDLQLRSIQAIVSL-TFYYVLLPEFKS 571

Query: 585 RVYEMLVS-HIQLHYKHSYTLPIAS---SIRLQAFDFLFLLRADSLHRLGLPNKDGVVRF 640
            +Y+ LV        + ++ +P+      +R+   D+ F+  + +  +L L +
Sbjct: 572 VLYDGLVEISCDFKIRRTFRIPVLKLLLQLRINTNDYCFVNLSPA--QLELISVYSTQWH 629

Query: 641 SPYCVCDYMEPERGSEKKXXXXXXXXXXXXXXXXXXXXVRLG----SVPYSLLFRVLLQC 696
           +P+ + +  +  R ++ K                     L     S+P +   + ++
Sbjct: 630 NPF-ISEEAQRCRDNKVKDRDLSFSPVFQKFPLKVNTSATLSKDLMSLPINEWVKNVMYI 688

Query: 697 LKQESDWKVLKLVLGRLPESLRYKVLIFTSPCSVDQLCSALCSMLSGPKTLERLRGAPEG 756
           +  E+DWKV++ +L      LR   +   +  ++  L ++L  +++G ++L       +
Sbjct: 689 VTHETDWKVVQYILINFTNQLRNTKMFTKTVEALQLLLNSLRDIINGKQSLN--INFSDF 746

Query: 757 FSRTDLHLAVVPVLTALISYHNYLDKTKQREMVYCL----EQGLIHRCARQCVVALSICS 812
           F   DL +++  +L+ L+ Y + L  T   +    L    E+G   +    C+  L
Sbjct: 747 FRIEDLLVSLSKILSVLMVYKDVLPPTAHEQFFQLLNRFAEKG--DKTMESCIDTLITNC 804

Query: 813 VEMPDIIIKALPVLVVKLTHISATASMAVPLLEFLSTLARLPHLYRNFAAEQYASV--FA 870
             M    I  LP         + +    V  L  L  ++    L      E   S+  F
Sbjct: 805 CAMQSFSIMHLPKFFSITMSSNLSERSLVNFLRLLHVVSDNWELNEGLEKETIQSICLFC 864

Query: 871 ISLPYT--------------NPSKFNQYIVCLAHHVIAMWFIRCRLPFRKDFVPFITK 914
           + +  T              N   F  Y+V  ++ +I+  F+ C    R     F+ K
Sbjct: 865 LKVIRTKKEELDGHKKLVNPNTKVFCLYLVSFSYSIISNLFLGCETTERAQLASFLLK 922
```

emb|CAB11382.1| (Z98741) dihydrolipoamide succinyltransferase [Mycobacterium leprae]
Length = 530

Score = 37.5 bits (85), Expect = 1.1
Identities = 37/145 (25%), Positives = 58/145 (39%), Gaps = 12/145 (8%)

```
Query: 1140 GALDVPASQFLGSATSPGPRTAPAAKPE-KASAGTRVPVQEKTNLAAYVPLLTQGWAEIL 1198
            G L V  +    +A +P PR  P A+PE  AS+    P Q+ +  A   P+L     E +
Sbjct: 71   GELAVIGAPSEAAAAAPAPRPEPKAQPEPAASSQPAAPAQQPSGAATATPVLMPELGESV 130

Query: 1199 VRRPTGNTSWLMSL------ENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKS 1252
                   T WL  +      + PL   S+D  +  +      ++ +    E     +
Sbjct: 131  TEGTV--TRWLKKIGDSVQADEPLVEVSTDKVDTEIPSPVAGVLVSITTNEDTTVPVGGE 188

Query: 1253 LS---VPAASTAKPPPLPRSNTVAS 1274
            L+   V   S A P P PR+ +V S
Sbjct: 189  LARIGVTLDSIATPAPAPRAESVPS 213
```

emb|CAB82690.1| (AL162295) guanine nucleotide exchange factor-like protein
[Arabidopsis thaliana]
Length = 1793

Score = 37.1 bits (84), Expect = 1.5
Identities = 39/144 (27%), Positives = 63/144 (43%), Gaps = 19/144 (13%)

```
Query: 489  VISQLSHIPEDKDHQVRKLATQLLVDLAEGCHTHHFN---------SLLDIIEKVMARSL 539
            ++S LS +  D   ++RK A Q++ D     H H F+         S+L  I   +  S+
Sbjct: 1350 LLSGLSELSFDPRPEIRKSALQIMFDTLRN-HGHLFSLPLWEKVFESVLFPIFDYVRHSI 1408

Query: 540  SPPPELEERDVAA---------YSASLEDVKTAVLGLLVILQTKLYTLPASHATRVYEML 590
             P  E E  D  +         + A L +  T  L L+V L  K YT       +V  +L
Sbjct: 1409 DPSGEDESADQGSSGGEVDELDHDAWLYETCTLALQLVVDLFVKFYTTVNPLLEKVLMLL 1468

Query: 591  VSHIQLHYKHSYTLPIASSIRLQA 614
            VS I+  ++    + IA+ +RL +
Sbjct: 1469 VSFIKRPHQSLAGIGIAAFVRLMS 1492

 sp|Q10038|VHP1_CAEEL PROTEIN-TYROSINE PHOSPHATASE VHP-1 >gi|7498591|pir||T15969
            hypothetical protein F08B1.1 - Caenorhabditis elegans
            >gi|726422|gb|AAC46719.1| (U23178) similar to protein
            tyrosine phosphatase [Caenorhabditis elegans]
            Length = 619

 Score = 36.4 bits (82), Expect = 2.5
 Identities = 51/207 (24%), Positives = 81/207 (38%), Gaps = 21/207 (10%)

Query: 1086 GELQSGPESSSSPGVHVRQTKEAPAKLESQAGQQVSRGARD----RVRSMSGGHGLRVGA 1141
            G   S PE+SSS       T  AP  + S + Q  S G  +    R  +M  G   R  A
Sbjct: 337  GSAASEPETSSS-AASSSSTASAPPSMPSTSEQGTSSGTVNVNGKRNMTMDLGLPHRPKA 395

Query: 1142 LDVPASQFLGSATSPGPRTAPAAK----PEKASAGTRVPVQEKTNLAAYVPLLTQGWAEI 1197
            L +P+      A  P P T  +      PE  +  T  P+   TN     P++
Sbjct: 396  LGLPSRIGTSVAELPSPSTELSRLSFNGPEAIAPST--PILNFTNPCFNSPIIPVA---- 449

Query: 1198 LVRRPTGNTSWLMSLENPLSPFSSDINNMPLQELSNALMAAERFKEHRDTALYKSLSVPA 1257
                 + +   +++L  P +  SS  ++ P  + S+   ++       +   + S  VPA
Sbjct: 450  -----SSSREVILTLPTPAASSSSSTSSEPSFDFSS-FESSSSSSIVVENPFFASTEVPA 503

Query: 1258 ASTAKPPPLPRSNTVASFSSLYQSSCQ 1284
             S++   P    +T AS SS   S C+
Sbjct: 504  GSSSISTPSGSQSTPASASSSAASRCR 530

 gb|AAC83179.1| (AC004974) spa-1-like; similar to AF026504 (PID:g2555183) [Homo
            sapiens]
            Length = 699

 Score = 36.4 bits (82), Expect = 2.5
 Identities = 30/106 (28%), Positives = 51/106 (47%), Gaps = 6/106 (5%)

Query: 1522 NESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLGRL 1581
            N  +  E+ ++L +Q  +Y   K+ ++Y   GQS  E  + +NE     + EFL  LG
Sbjct: 591  NTPKVTEQLMKLDEQGLNYQ-QKVGIMYCKAGQSTEE-EMYNNESAGPAFEEFLQLLGER 648

Query: 1582 IELKDCQPDKVYLG-GLDVCGEDGQFTYCWHDDIMQAVFHIATLMP 1626
            + LK  +  +  L    D  G    +T     +IM   FH++T++P
Sbjct: 649  VRLKGFEKYRAQLDTKTDSTGTHSLYTTYKDYEIM---FHVSTMLP 691

 pir||T41230 hypothetical TPR domain-containing protein - fission yeast
           (Schizosaccharomyces pombe) >gi|4107308|emb|CAA22636.1|
           (AL035075) hypothetical TPR domain protein
           [Schizosaccharomyces pombe]
           Length = 1389

 Score = 36.0 bits (81), Expect = 3.3
 Identities = 27/97 (27%), Positives = 45/97 (45%), Gaps = 6/97 (6%)

Query: 352 ELQVVAWDILLNIIERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELV 411
           E  V+AW  L N+ E       T D  EL  I   L +   EL +QN+   +  +Y E+V
Sbjct: 67  EKAVLAWQGLWNLYE------STHDISELHKITPILASKFLELEEQNKCLNTVNKYMEVV 120

Query: 412 ERCADQRPESSLLNLISYRAQSIHPAKDGWIQNLQAL 448
           ++  ++  E   L L++     I+   +G +  LQ +
Sbjct: 121 KKYGNKADEFKALKLLTPEEGEIYEYLEGRVLPLQTV 157

 gb|AAF21208.1|AC013483_32 (AC013483) putative MAP3K epsilon protein kinase [Arabidopsis
            thaliana]
            Length = 1367
```

```
 Score = 35.2 bits (79), Expect = 5.6
 Identities = 36/179 (20%), Positives = 78/179 (43%), Gaps = 21/179 (11%)

Query: 365  IERLLQQLQTLDSPELRTIVHDLLTTVEELCDQNEFHGSQERYFELVERCADQRPESSLL 424
            I++L+  L+  + P +  I H++L+ +  LC  N+             R  +Q  E+ ++
Sbjct: 1115 IKQLIPNLELKEGPLVYQIHHEVLSALFNLCKINK------------RRQEQAAENGII 1161

Query: 425  NLISYRAQSIHPAKDGWIQNL--QALMERFFRSESRGAVRIKVLDVLSFVLLINRQFYEE 482
              +     S  P K   +  L   A   R  R + R    + V     ++ L++ +++
Sbjct: 1162 PHLMLFVMSDSPLKQYALPLLCDMAHASRNSREQLRAHGGLDV-----YLSLLDDEYWSV 1216

Query: 483  ELINSVVISQLSHIPEDKDHQ-VRKLATQLLVDLAEGCHTHHFNSLLDIIEKVMARSLS 540
              ++S+ +     + +  +   ++K A Q LV+  + C   HF  +L+   K++ +S S
Sbjct: 1217 IALDSIAVCLAQDVDQKVEQAFLKKDAIQKLVNFFQNCPERHFVHILEPFLKIITKSSS 1275

 gb|AAD49971.1|AC008075_4 (AC008075) Contains similarity to gi|3329316 cytosine deaminase from
            Chlamydia trachomatis genome gb|AE001357 and contains a
            PF|00383 cytidine deaminase zinc-binding region.  EST
            gb|W43306 comes from this gene. [Arabidopsis thaliana]
            >gi|6524188|gb|AAF15073.1|AC011914_15 (AC011914) unknown
            protein [Arabidopsis thaliana]
            Length = 1307

 Score = 35.2 bits (79), Expect = 5.6
 Identities = 21/52 (40%), Positives = 27/52 (51%), Gaps = 5/52 (9%)

Query: 933  FRARSTSLNERPKSLRIARPPKQGLNNSPPVKEFKESSAAEAFRCRSISVSE 984
            FR   T+L E P  L     P + L  SPP+KE  ESS  EA   ++ +V E
Sbjct: 961  FRLPETALTEVPMKL-----PSRNLIRSPPIKESSESSLTEASSDQNFTVGE 1007

 pir||T41006 ubiquitin carboxyl-terminal hydrolase - fission yeast
            (Schizosaccharomyces pombe) >gi|3184060|emb|CAA19303.1|
            (AL023776) putative ubiquitin carboxyl-terminal hydrolase
            [Schizosaccharomyces pombe]
            Length = 979

 Score = 34.8 bits (78), Expect = 7.3
 Identities = 26/77 (33%), Positives = 39/77 (49%), Gaps = 7/77 (9%)

Query: 1547 VLYVGEGQSNSELA-ILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGLDVCGEDGQ 1605
            V YV E    S+   IL  E    R+  FLT L + + ++  + D++YL  L+   EDG
Sbjct: 532  VKYVAEKSGCSDYRKILVTETYKGRFYRFLTQLSKSLLMEISEEDEIYLYELERPYEDGS 591

Query: 1606 FTYCWHDDIMQAVFHIA 1622
                  DDI+  V+HI+
Sbjct: 592  ------DDILVPVYHIS 602

CPU time:     0.55 user secs.       0.05 sys. secs          0.60 total secs.

  Database: nr
    Posted date:  Apr 23, 2000  9:58 PM
  Number of letters in database: 155,635,462
  Number of sequences in database:  496,378

Lambda     K      H
   0.320    0.135    0.394

Gapped
Lambda     K      H
   0.270   0.0470    0.230


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 503396004
Number of Sequences: 496378
Number of extensions: 19899466
Number of successful extensions: 48414
Number of sequences better than 10.0: 55
Number of HSP's better than 10.0 without gapping: 40
Number of HSP's successfully gapped in prelim test: 15
Number of HSP's that attempted gapping in prelim test: 48212
Number of HSP's gapped (non-prelim): 91
length of query: 1807
```

```
length of database: 155,635,462
effective HSP length: 61
effective length of query: 1746
effective length of database: 125,356,404
effective search space: 218872281384
effective search space used: 218872281384
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: 77 (34.4 bits)
```

Analysis Coffee Break

Tuberous Sclerosis Complex in flies too?

Tuberin proteins contain a GTPase-activating domain

```
Human       [1516] PILLPNESQSFERSVQLLDQIPSYDTHKIAVLYVGEGQSNSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGL
Rat         [1520] PILLPNES--FERSVQLLDQIPSYDTHKIAVLYVGEGQSSSELAILSNEHGSYRYTEFLTGLGRLIELKDCQPDKVYLGGL
Pufferfish  [1491] PLLLPKTQ-VIDRAVKVLDQMPPYDTHKIGVVFVGAGQVNNEVAILSNEYGSNRYAAFLTGLGKLIHLKDCDPDQIFLGGL
Fly gigas   [1574] PLKVGPENSS---AVSLIDLVPPFETHKIGVLYVGQGQCNNEVEILRNSHGSARYVEFLRNIGTLVSLKEAEQN-NLFIML
Rap1 GAP     [310] PILCPKASQ----LISVYDEHVLVSHFKFGVLYQRYGQT-TEEELFGNQQTSPAFDEFLDVLGQRIRLKDHKG---YRGGL
C. elegans   [276] GILRPSIQSPRVEELIMKIDEQPIYTRYKVGIMLCKNEQSTEEQMYNNEFSTPSFDEFLDFLGQRVTLKGFEA---YKGGL
                                                                        *

Human       DV-CGEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKKR-HLGNDFVSIVYNDSGEDFKLGTIKGQFNFVHVIVTPLD [130]
Rat         DVC-GEDGQFTYCWHDDIMQAVFHIATLMPTKDVDKHRCDKKR-HLGNDFVSIIYNDSGEDFKLGTIKGQFNFVHVIITPLD [132]
Pufferfish  DQY-GDDGEFTYCWHDDIMQAIFHIATLMPNRESDKGCCNKKR-HIGNDFVIVVYNDSGEEYKLGTIKGQFNFVEVIIKPLD [131]
Fly gigas   DRN-GADGKFAYIWKDDILQVTFHVATLMPTNLQDDPNCNEKKSHIGNDFVKIIYNESGEEYNLNTISGQFNYACVIVEPLD [115]
Rap1 GAP    DIQNGHTGDTAVYEVFKEREIMFHVSTLLPHTEGDPQQLQRKR-HIGNDIVAIVFQETNTPFSPDMIASHFLHAFIVVQPIE [386]
C. elegans  DTRGDTTGTHSIYSEYQAHEIMFHVSTLLPFTPSNRQQLSRKR-HIGNDMVTIVFQEPGALPFSPITVRSHFQHVFIIVRVH [489]
```

The figure shows the GTPase-activating domain, or GAP domain, from human tuberin (TSC2) aligned with three other tuberin proteins: one from rat, one from the pufferfish *Fugu rubripes,* and the recently discovered gigas from *Drosophila.* Also aligned is the GAP domain from a *Drosophila* Rap1GAP protein, and an as-yet uncharacterized protein from the worm *C. elegans* . Amino acid residues that are identical among the sequences are highlighted in green; numbers in parentheses at the beginning and end of the sequences represent the number of amino acids either side of this domain found in the complete protein. Clicking on the organism name will display the GenBank record for that sequence.

GAPs are responsible for down-regulating small GTP-binding proteins (small G proteins), by catalyzing the hydrolysis of bound GTP to GDP in order to switch the G protein off. There are now a number of GAPs that have been identified for several subfamilies of small G proteins, including Ras, Rho, Rap, Ran, Arf, and Ypt. While the mechanism of action remains to be demonstrated for all these families, there is strong evidence from crystal structures of Ras-GAP and Rho-GAP complexes that one or more conserved arginine (R) residues are critical [1].

The asterisk in the above alignment indicates a potential "arginine finger" R residue [2]. One of the criteria for an arginine finger is that it is invariant across all GAP subfamily members [1]. The crucial R residue stipulated as characteristic of RapGAPs is highlighted in red [1]. As the potential arginine finger residue for tuberins is not found in the same location, this suggests that they are not from the same GAP subfamily. Should an arginine finger catalytic role be demonstrated experimentally for the above site, then we may be looking at a new subclass of tuberin-specific GAPs.

Back to BLAST result

Human tuberin 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 GAP domain were selected from output from the first iteration. The multiple sequence alignment was constructed using ClustalW [4].

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