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DorMatcher EMBOSS

Human
Vs
Vs House/Mouse/Drosophila

Database: UniProt

UniProtKB results

UniProtKB consists of two sections:

- Reviewed (Swiss-Prot) - Manually annotated**
Records with information extracted from literature and curator-evaluated computational analysis.
- Unreviewed (TrEMBL) - Computationally analyzed**
Records that await full manual annotation.

The UniProt Knowledgebase (UniProtKB) is the central hub for the collection of functional information on proteins, with accurate, consistent and rich annotation. In addition to capturing the core data mandatory for each UniProtKB entry (namely, the amino acid sequence, protein name or description, taxonomic data and citation information), as much annotation information as possible is added.

Filter by:

Entry	Entry name	Protein name	Other names	Organism	Length
Q9V3H1	FLNA_DROME	Filamin-A	other (chick, skin), CG22023	Drosophila melanogaster (fruit fly)	2,210
Q9BT68	FLNA_MOUSE	Filamin-A	Flna F5, Fln1	Mus musculus (Mouse)	2,847
P21333	FLNA_HUMAN	Filamin-A	FLNA FLN, FLN1	Homo sapiens (Human)	2,847
B7FA09	B7FA09_MOUSE	Filamin, alpha	Flna RP23-KIN3 1.002	Mus musculus (Mouse)	2,839
F70C40	F70C40_MACMU	Filamin A	FLNA	Macaca mulatta (Rhesus macaque)	2,847

UniProtKB - P21333 (FLNA_HUMAN)

Display

Links: Protein **Filamin-A**, Gene **FLNA**, Organism **Homo sapiens (Human)**, Status **Reviewed**, Annotation score ********* - Experimental evidence at protein level!

Function:

Promotes orthogonal branching of actin filaments and links actin filaments to membrane glycoproteins. Anchors various transmembrane proteins to the actin cytoskeleton and serves as a scaffold for a wide range of cytoplasmic signaling proteins. Interaction with F-actin may allow recruitment of proteins from the ventricular zone into the cortical plate. Tethers cell surface-localized fure, modulates its rate of internalization and directs its intracellular trafficking (By similarity). Involved in oligodendrocyte. Plays a role in cell-cell contacts and adherens junctions during the development of blood vessels, heart and brain regions. Plays a role in platelet recognition through interaction with SYC that regulates Flna, and Flna then contains receptor signaling, resulting in by platelet activation (epigenetic) maintenance (By similarity). **By similarity** **1 Publication**

PTM / Processing

Molecule processing

Feature name	Position(s)	Evidence	Action	Original view	Length
Initiator					
Start-transfer	2	16 annotations	0 Combined sources	16 Publications	1
End-transfer					
Modification					
Modified residue	11	Phosphoserine	0 Combined sources	16 Publications	1
Cross-link	42	Oxy-Lysine (see O6)	Interacts with G-Cter in ubiquitin	16 Publications	1
Phospho					
Oxy-Lysine	43	Oxy-Lysine (see O6)	Interacts with G-Cter in ubiquitin	16 Publications	1
Oxidation	130	Oxy-Lysine (see O6)	Interacts with G-Cter in ubiquitin	16 Publications	1
Phospho					
Oxidation	209	Oxy-Lysine (see O6)	Interacts with G-Cter in SUMO1	16 Publications	1
Cross-link	209	Oxy-Lysine (see O6)	Interacts with G-Cter in SUMO1	16 Publications	1
Phospho					
Modified residue	110	N6-acetyllysine	16 Publications		1
Modified residue	108	N6-acetyllysine	0 Combined sources	16 Publications	1

Sequences (2+)

Sequence status: Complete
Sequence processing: The displayed sequence is further processed into a mature form.
This entry includes 2 isoforms produced by alternative splicing. [Align](#) [Add to basket](#)

This entry has 2 described isoforms and 6 potential isoforms that are computationally mapped. [Show all](#) [Align all](#)

Position	10	20	30	40	50
ISOFORM 1	ISSSSQSSQ	SAAKAAAGGG	YVYVYQKDAK	YVYVYQKDAK	YVYVYQKDAK
ISOFORM 2	ISQ	ISQ	ISQ	ISQ	ISQ
ISOFORM 3	IKRQRSLKQY	IKRQRSLKQY	LKQSLKQY	LVYLVKQY	RKRQRSLKQY
ISOFORM 4	110	120	130	140	150
ISOFORM 5	IKRQRSLKQY	LVYLVKQY	LKQSLKQY	LVYLVKQY	LVYLVKQY
ISOFORM 6	140	170	180	190	200
ISOFORM 7	IKRQRSLKQY	IKRQRSLKQY	IKRQRSLKQY	IKRQRSLKQY	IKRQRSLKQY

1 MMSVYQKDAKISSSSQSSQSAAKAAAGGGYVYVYQKDAK... 200

UniProtKB - Q8BTM8 (FLNA_MOUSE)

Display: [FASTA](#) [Align](#) [Format](#) [Add to basket](#) [History](#) [Feedback](#) [Help](#) [Other formats](#)

Links: [Protein](#) [Flamin A](#)

Publications: [Gene](#) [Flna](#)

Feature view: [Mus musculus \(Mus\)](#)

Feature table: [Status](#) [Review](#) [Annotation score: 5*****](#) - Experimental evidence at protein level

Function

Actin binding protein that promotes orthogonal branching of actin filaments and links actin filaments to membrane glycoprotein. Anchors various transmembrane proteins to the actin cytoskeleton and serves as a scaffold for a wide range of cytoplasmic signaling proteins (By similarity). Interaction with F-actin may allow recruited migration from the ventricular zone into the cortical plate. Tethers cell surface calibrated form, modulates its site of internalization and directs its intracellular trafficking. Involved in oligodendrocyte. Plays a role in cell-cell contacts and adherens junctions during the development of limb, viscera, heart and brain organs (PubMed:1712451). Plays a role in placental morphogenesis through interaction with CD9, but requires CD41 and HMM. Associates with neoplasia, resulting in by placental cytoskeleton organization maintenance (PubMed:2071993). [By similarity](#) [4 Publications](#)

Sequences (2+)
 Sequence status: Complete
 This entry describes 2 isoforms produced by **alternative splicing**.
 This entry has 2 described isoforms and 0 potential isoforms that are computationally mapped.

isoform 1 (identifier Q9B7M8-1) [pI=4.7] [FASTA] [Add to basket]
 Length: 2447
 Mass (Da): 28,320
 Last modified: Jul 27, 2011
 Checksum: 21E32F848F8E

Position	10	20	30	40	50
Sequence	MSKSRKIQG	AMNKAQGG	ISDQKAPRA	YKQKLSKAP	WPKQIQYTY
Position	60	70	80	90	100
Sequence	IKPKSLEKTY	SRKALQKQ	LDKGLKLL	LYKLSKQK	SRKQKPKPT
Position	110	120	130	140	150
Sequence	IQKQKQKTY	LEPKLQKQ	LVKLSKQK	DKKGLKLL	LVKLSKQK
Position	160	170	180	190	200

Sequences (2+)
 Sequence status: Complete
 This entry describes 2 isoforms produced by **alternative splicing**.

isoform 1 (identifier Q9B7M8-1) [pI=4.7] [FASTA] [Add to basket]
 Length: 2447
 Mass (Da): 28,320
 Last modified: Jul 27, 2011
 Checksum: 21E32F848F8E

```

MSKSRKIQGAMNKAQGGISDQKAPRAYKQKLSKAPWPKQIQYTYIKPKSLEKTYSRKALQKQLDKGLKLLYKLSKQKSRKQKPKPTIQKQKTYLEPKLQKQLVKLSKQKDKKGLKLLVKLSKQK
    
```

UniProtKB - Q9VEN1 (FLNA_DROME)
 BLAST Align RefSeq ID mapping Peptide search

Display | BLAST | Align | FASTA | Add to basket | History

Entry
 Protein: **Filamin A**
 Gene: **cher**
 Organism: *Drosophila melanogaster* (Ful 9)
 Status: Reviewed | Annotation score: 4.00 | Experimental evidence at protein level

Function
 Involved in the germline ring canal formation. May tether actin microfilaments within the ovarian ring canal to the cell membrane. Contributes to actin microfilaments organization. [MGI:104105]

GO - Molecular function
 • actin binding [Source: Protocols]

Sequences (2+)
 Sequence status: Complete
 This entry describes 2 isoforms produced by **alternative splicing**.
 This entry has 2 described isoforms and 7 potential isoforms that are computationally mapped.

isoform 1 (identifier Q9VEN1-1) [pI=4.7] [FASTA] [Add to basket]
 Length: 229
 Mass (Da): 23891
 Last modified: April 26, 2005
 Checksum: 600051078A5F08

Position	10	20	30	40	50
Sequence	MSKSRKIQG	ADKQKIQG	YKPKKQKQ	YKLSKQKQ	YKLSKQKQ
Position	60 <td>70 <td>80 <td>90 <td>100 </td></td></td></td>	70 <td>80 <td>90 <td>100 </td></td></td>	80 <td>90 <td>100 </td></td>	90 <td>100 </td>	100
Sequence	ALPKLQKQ	IKPKSLEKTY	SRKALQKQ	LDKGLKLL	YKLSKQKQ
Position	110 <td>120 <td>130 <td>140 <td>150 </td></td></td></td>	120 <td>130 <td>140 <td>150 </td></td></td>	130 <td>140 <td>150 </td></td>	140 <td>150 </td>	150
Sequence	YKLSKQKQ	LDKGLKLL	YKLSKQKQ	LDKGLKLL	YKLSKQKQ
Position	160 <td>170 <td>180 <td>190 <td>200 </td></td></td></td>	170 <td>180 <td>190 <td>200 </td></td></td>	180 <td>190 <td>200 </td></td>	190 <td>200 </td>	200
Sequence	ADKQKIQG	YKPKKQKQ	YKLSKQKQ	YKLSKQKQ	YKLSKQKQ
Position	210 <td>220 <td>230 <td>240 <td>250 </td></td></td></td>	220 <td>230 <td>240 <td>250 </td></td></td>	230 <td>240 <td>250 </td></td>	240 <td>250 </td>	250

Sequences (2+)
 Sequence status: Complete
 This entry describes 2 isoforms produced by **alternative splicing**.

isoform 1 (identifier Q9VEN1-1) [pI=4.7] [FASTA] [Add to basket]
 Length: 229
 Mass (Da): 23891
 Last modified: April 26, 2005
 Checksum: 600051078A5F08

```

MSKSRKIQGADKQKIQGYKPKKQKYKLSKQKYKLSKQYALPKLQKQIKPKSLEKTYSRKALQKQLDKGLKLLYKLSKQKQYKLSKQQLDKGLKLLYKLSKQKADKQKIQGYKPKKQKYKLSKQKYKLSKQ
    
```

UniProtKB - F7BH02 (F7BH02_HORSE)

Display

Entry
 Protein: Submitted name: **Flamin A**
 Gene: **FLNA**
 Organism: **Equus caballus (Horse)**
 Status: **Unreviewed**, Annotation score: ********* - Protein predicted

Function
GO - Molecular function
 • actin filament binding **Source: Ensembl**
 • Fc gamma receptor 1 complex binding **Source: Ensembl**
 • G protein-coupled receptor binding **Source: Ensembl**
 • ion channel binding **Source: Ensembl**
 • protein binding **Source: Ensembl**

Function & Taxonomy
Protein Structure
Protein Family & Clusters
Protein Interactions

Display

PROSITE*
 View protein in PROSITE:
 P00009 ACTRIN_1.1.H
 P00009 ACTRIN_2.1.H
 P00021 DL2.H
 P00019 FLAMIN_REPEAT.24.H

Sequence (1+)
 Sequence status: Complete
 This entry has 1 described isoform and 1 potential isoform that is computationally mapped. [Show all](#) | [Align All](#)


F7BH02-1 (FLNA) [FASTA](#) [Add to basket](#)

Length: 2,648
 Mass (Da): 280,723
 Last modified: July 27, 2011 -v1
 Checksum: [GAGAGAGAG794CEF](#)


10	20	30	40	50
MERRSDVAG	RANGALAG	APFRRDRA	TREGLAETAP	WRGQQVFF
60	70	80	90	100
PKRCKEALCY	SKYKSLRQD	LKQGLLAL	LTVLQVQDR	IRKQKVVFR
110	120	130	140	150
QKLEKSTVA	LFLFLQKKE	LVFVSDKLV	DKLQKLLG	LVKLLEKSI
160	170	180	190	200
ENKRNQKDE	KEARAKTVD	KLGLQKQ	PLGPTTFR	ENKQKALGA
210	220	230	240	250

scientific name of drosophila

fruit fly | melanogaster | spotted wing | wing drosophila | species | biology



I. Fruit fly scientific name-
Drosophila melanogaster
 A. *Drosophila*-"dew lover" (dew-sugar)
 B. *Melanogaster*-"black belly"
 C. "Black bellied dew lover"



bioinformatics | dotmatcher

dotmatcher
 There is detailed help of two sequences ([read the manual](#))
 Unrelated files are ignored and are safely ignored. ([Click external file](#))

Input section

Select an input sequence. Use one of the following three fields:
 1. To access a sequence from a database, enter the ID here.
 2. To upload a sequence from your local computer, select a file: [Browse...](#) file to select.

3. To enter the sequence data manually, type here:

Select an input sequence. Use one of the following three fields:
 1. To access a sequence from a database, enter the ID here.
 2. To upload a sequence from your local computer, select a file: [Browse...](#) file to select.

