

📄 P40688 · SWA_DROME

Proteinⁱ

Protein swallow

Geneⁱ

swa

Statusⁱ

📄 UniProtKB reviewed (Swiss-Prot)

Organismⁱ

[Drosophila melanogaster \(Fruit fly\)](#)

Amino acids

548 ([go to sequence](#))

Protein existenceⁱ

Evidence at protein level

Annotation scoreⁱ

5/5

[Entry](#)

[Variant viewer](#)

[Feature viewer](#)

[Genomic coordinates](#)

[Publications](#)

[External link](#)

[BLAST](#) [↓ Download](#) [📄 Add](#) [Add a publication](#) [Entry feedback](#)

Functionⁱ

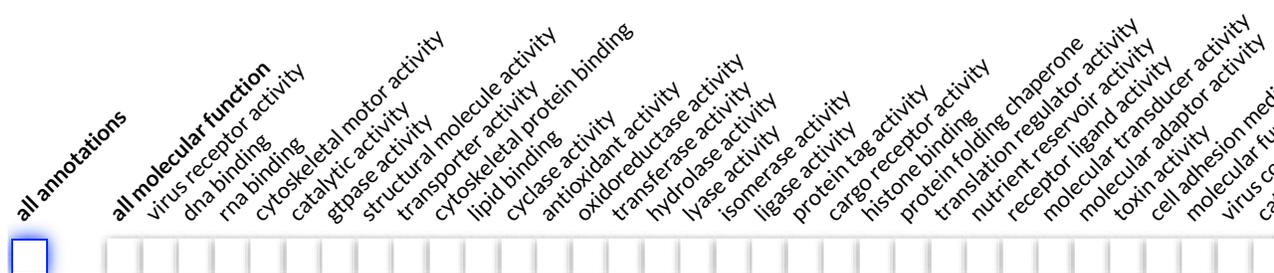
Has a role in localizing bicoid mRNA at the anterior margin of the oocyte during oogenesis, and a poorly characterized role in nuclear divisions in early embryogenesis. 📄 1 Publication

GO annotationsⁱ

[Access the complete set of GO annotations on QuickGO](#) [↗](#)

Slimming set:

generic



Cell color indicative of number of GO terms

ASPECT	TERM
Cellular	nucleus ↗

Component	nucleus	Source:UniProtKB-SubCell
Molecular Function	dynein complex binding	Source:FlyBase 1 Publication
Molecular Function	mRNA binding	Source:FlyBase By Similarity
Biological Process	actin filament organization	Source:FlyBase 1 Publication
Biological Process	anterior/posterior axis specification, embryo	Source:FlyBase 1 Publication
Biological Process	bicoid mRNA localization	Source:FlyBase 4 Publications
Biological Process	cell cycle	Source:UniProtKB-KW
Biological Process	cell division	Source:UniProtKB-KW
Biological Process	pole plasm mRNA localization	Source:FlyBase 1 Publication

Keywordsⁱ

Molecular function

#Developmental protein

Biological process

#Cell cycle

#Cell division

#Mitosis

Enzyme and pathway databases

Signalink

P40688

Names & Taxonomyⁱ

Protein namesⁱ

Recommended name

Protein swallow

Gene namesⁱ

Name

swa

ORF names

CG3429

Organism names

Organismⁱ

[Drosophila melanogaster \(Fruit fly\)](#)

Taxonomic identifierⁱ

[7227 NCBI](#)

Taxonomic lineageⁱ

Eukaryota > Metazoa > Ecdysozoa > Arthropoda > Hexapoda > Insecta > Pterygota > Neoptera > Endopterygota > Diptera > Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora

Accessions

Primary accession

P40688

Secondary accessions

Q9W400

Proteomesⁱ

Identifier

[UP000000803](#)

Componentⁱ

Chromosome X

Organism-specific databases

[AGR](#)

[FB:FBgn0003655](#)

[FlyBase](#)

[FBgn0003655](#) swa

[VEuPathDB](#)

[VectorBase:FBgn0003655](#)

Subcellular Locationⁱ

[UniProt Annotation](#)

[GO Annotation](#)

Nucleus

2 Publications

Note: Uniformly distributed in eggs, becomes localized to the nuclei during early mitotic divisions in early embryogenesis. Enters each nucleus at the beginning of mitosis, occupies a position complementary to that of condensed chromatin, and leaves each nucleus at the end of mitosis.

trial of condensed chromatin, and leaves each nucleus at the end of mitosis.

Keywordsⁱ

Cellular component

[#Nucleus](#)

PTM/Processingⁱ

Features

Showing features for chainⁱ, modified residueⁱ.

TYPE	ID	POSITION(S)	DESCRIPTION	
<input type="text" value="-- Select --"/>				
▶ Chain	PRO_0000072342	1-548	Protein swallow	BLAST Add
▶ Modified residue		362	Phosphoserine 1 Publication	
▶ Modified residue		368	Phosphoserine 1 Publication	
▶ Modified residue		463	Phosphoserine 1 Publication	
▶ Modified residue		471	Phosphoserine 1 Publication	
▶ Modified residue		475	Phosphoserine	

Keywordsⁱ

PTM

[#Phosphoprotein](#)

Proteomic databases

PaxDb

[7227-FBpp0070884](#)

PTM databases

iPTMnet

[P40688](#)

Expressionⁱ

Developmental stageⁱ

Expressed both maternally and zygotically. 1 Publication

Gene expression databases

Bgee

FBgn0003655 Expressed in ovary and 8 other tissues

ExpressionAtlas

P40688 baseline and differential

Genevisible

P40688 DM

Interactionⁱ

Subunitⁱ

May be a homo- or heterodimer. 1 Publication

Protein-protein interaction databases

BioGRID

58067 6 interactors

IntAct

P40688 6 interactors

DIP

DIP-17669N

STRING

7227.FBpp0070884

ELM

P40688

Structureⁱ



Features

Showing features for helixⁱ, beta strandⁱ.

TYPE

-- Select --

ID POSITION(S)

DESCRIPTION

▶ Helix	207-269	Combined Sources	BLAST	Add
▶ Beta strand	288-294	Combined Sources	BLAST	Add

3D structure databases

AlphaFoldDB

P40688

BMRB

P40688

SMR

P40688

ModBase

Search...

PDBe-KB

Search...

Miscellaneous

EvolutionaryTrace

P40688

Family & Domainsⁱ

Features

Showing features for regionⁱ, compositional biasⁱ.

TYPE ID POSITION(S) DESCRIPTION

-- Select --

▶ Region	67-109	Disordered	Automatic Annotation	BLAST Add
▶ Region	184-206	Disordered	Automatic Annotation	BLAST Add
▶ Compositional bias	186-206	Polar residues	Automatic Annotation	BLAST Add
▶ Region	358-428	Disordered	Automatic Annotation	BLAST Add
▶ Compositional bias	383-403	Polar residues	Automatic Annotation	BLAST Add

Phylogenomic databases

HOGENOM

CLU_042201_0_0_1

InParanoid

P40688

OMA

HQPAAFE

OrthoDB

3618153at2759

PhylomeDB

P40688

eggNOG

ENOG502TB8W Eukaryota

Family and domain databases

MobiDB

Search...

Sequenceⁱ

See also

sequence in [UniParc](#) or sequence clusters in [UniRef](#)

Length

548

Mass (Da)

62,070

Last updated

1995-02-01 v1

Checksumⁱ

B8E0351C7B005159

MSLQDESFPTDELFDQLNNLSSSGARNTWFAEHHKPAVFERDTAPFLEICYADPDFDADGDVANKSAKTC
VSDPVGRDQEDEDYDEDVDGDDHKLKCEKAPLGSGRSSKAVSYQDIHSAYTKRRFQHVT SKVGQYIAEI
QAQDQKRRNVKFAGFQRVNSMPESLTPTLQQVYVHDGDFKVDKNCQTHSNSDSNYNSNSNNSSSSFDR
LLAENESLQQKINSLRVEAKRLQGFNEYVQERLDRKTDDFVKMKCNFETLRTELSECQQKLRRQQDNSQH
HFMYHIRSATSAKATQTDFLVD TIPASGNVLVTPHPLGLTYNSSKGSIELALLSVAPSARVAQNPVQVQRAI
HPQSLDFSSVSTEADGSGSGEHRVETSSRALVRRT PAPNNSSETS QPSSNDSAIEVEAHEEERPSSRRQWEQ
QGELISPRQWGQHEGMYFDKRNNRVIEVMGFNISQGRNQSHDTIHNSINDSQTRLLVHSMMSHLEA
HDHFRSKRTTLGSRMLRFLGPCVRCRNGDPLNRSNVTYKDGLPAMPEEEFVDQRNQR

Features

Showing features for compositional biasⁱ.

TYPE

ID POSITION(S) DESCRIPTION

-- Select --

▶ Compositional bias	186-206	Polar residues	<input type="button" value="Automatic Annotation"/>	BLAST Add
▶ Compositional bias	383-403	Polar residues	<input type="button" value="Automatic Annotation"/>	BLAST Add
▶ Compositional bias	404-419	Basic and acidic residues	<input type="button" value="Automatic Annotation"/>	BLAST Add

Keywordsⁱ

Technical term

[#3D-structure](#)

[#Reference proteome](#)

Sequence databases

PIR

[S20806](#) [S20806](#)

RefSeq

[NP_511060.2](#) [NM_078505.4](#)

NUCLEOTIDE SEQUENCE	PROTEIN SEQUENCE	MOLECULE TYPE	STATUS
X56023 EMBL · GenBank · DDBJ	CAA39500.1 EMBL · GenBank · DDBJ	Genomic DNA	
AE014298 EMBL · GenBank · DDBJ	AAF46160.3 EMBL · GenBank · DDBJ	Genomic DNA	
AY069487 EMBL · GenBank · DDBJ	AAL39632.1 EMBL · GenBank · DDBJ	mRNA	

Genome annotation databases

EnsemblMetazoa

[FBtr0070922](#) [FBpp0070884](#) [FBgn0003655](#)

KEGG

[dme:Dmel_CG3429](#)

UCSC

[CG3429-RA](#) [d.melanogaster](#)

GeneID

[31580](#)



Discover the new [Genomic coordinates](#) tab which has more genomic information about this entry

Similar Proteinsⁱ



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