

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

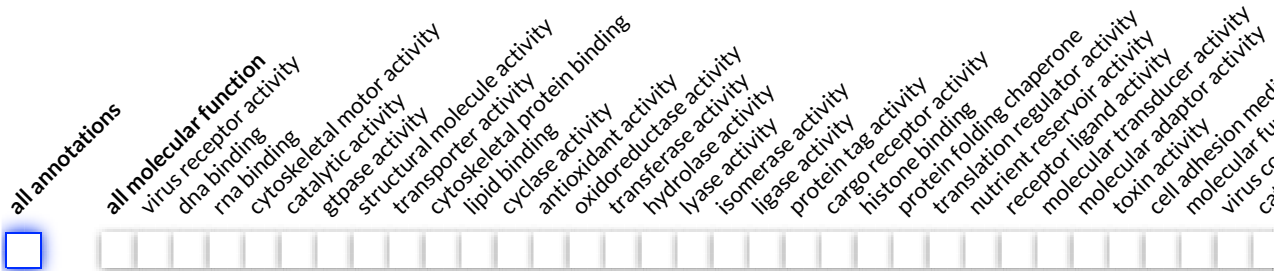
BLAST Download Add Add a publication Entry feedback

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.

that 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	
<div>-- Select --</div>				
▶ Chain	PRO_0000072342	1-548	Protein swallow	BLAST Add
▶ Modified residue		362	Phosphoserine <div>1 Publication</div>	
▶ Modified residue		368	Phosphoserine <div>1 Publication</div>	
▶ Modified residue		463	Phosphoserine <div>1 Publication</div>	
▶ Modified residue		471	Phosphoserine <div>1 Publication</div>	
▶ 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

DIP

DIP-17669N

ELM

P40688

IntAct

P40688 6 interactors

STRING

7227.FBpp0070884

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	OrthoDB
CLU_042201_0_0_1	3618153at2759
InParanoid	PhylomeDB
P40688	P40688
OMA	eggNOG
HQPAAFE	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

MSLQDESFP TDELFDQLNNLSSSGARNTWFAEHHKPAVFERDTAPFLEICYADPDFDADGDVANKSAKTC
VSDPVGRDQEDEDYDEDVDGDDHKLGC EKAPLGSGRSSKAVSYQDIHSAYTKRRFQHVT SKVGQYIAEI
QAQDQKRRNVKFAGFQRVNSMPESLTPTLQQVYVHDGDFKVDKNCQTHSNSDSNYNSNSNNSSSFDR
LLAENESLQQKINSLRVEAKRLQGFNEYVQERLDRKTDDFVKMKCNFETLRTELSECQQKLRRQQDNSQH
HFMYHIRSATS AKATQTDFLVD TIPASGNVLVTPHPLGDLTYNSSKGSIELALLSVAPSARVAQNPVQVQRAI
HPQSLDFSSVSTEADGSGSGEHRVETSSRALVR RTPAPNNSETSQPSSNDSAIEVEAHEEERPSSRRQWEQ
QGELISPRQWGQHEGMYFFDKRNNRVIEVMGFNISQGRNQSHDTIHNQSINDSQTRLLVHSMMSHLEA
HDHFRSKRTTLGSRMLRFLGPCVRCRNGDPLNRSNV TYKDGLPAMPEEEFVDQRNQ R

Features

Showing features for compositional biasⁱ.

TYPE	ID	POSITION(S)	DESCRIPTION
------	----	-------------	-------------

-- Select --

► Compositional bias	186-206	Polar residues	Automatic Annotation	BLAST Add
► Compositional bias	383-403	Polar residues	Automatic Annotation	BLAST Add
► Compositional bias	404-419	Basic and acidic residues	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	
AY069487	EMBL	· GenBank	· DDBJ	AAL39632.1	EMBL	· GenBank	· DDBJ	mRNA

Genome annotation databases

EnsemblMetazoa

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

KEGG

[dme:Dmel_CG3429](#)

UCSC

GenelD

[31580](#)

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



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

Similar Proteinsⁱ



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