

Q15116 · PDCD1\_HUMAN

Protein<sup>i</sup>

Programmed cell death protein 1

Amino acids

288

Gene<sup>i</sup>

PDCD1

Protein existence<sup>i</sup>

Evidence at protein level

SPARQL UniProtKB

Advanced | List

Search

Help

- Function
- Names & Taxonomy
- Subcellular Location
- Disease & Variants
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- Interaction
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Homo sapiens (Human)

Entry Feature viewer Publications External links History

Download Add a publication Entry feedback

Function<sup>i</sup>

Inhibitory receptor on antigen activated T-cells that plays a critical role in induction and maintenance of immune tolerance to self (PubMed:21276005).  
Delivers inhibitory signals upon binding to ligands CD274/PDCD1L1 and CD273/PDCD1LG2 (PubMed:21276005).  
Following T-cell receptor (TCR) engagement, PDCD1 associates with CD3-TCR in the immunological synapse and directly inhibits T-cell activation (By similarity).  
Suppresses T-cell activation through the recruitment of PTPN11/SHP-2: following ligand-binding, PDCD1 is phosphorylated within the ITSM motif, leading to the recruitment of the protein tyrosine phosphatase PTPN11/SHP-2 that mediates dephosphorylation of key TCR proximal signaling molecules, such as ZAP70, PRKCQ/PKCtheta and CD247/CD3zeta (By similarity).

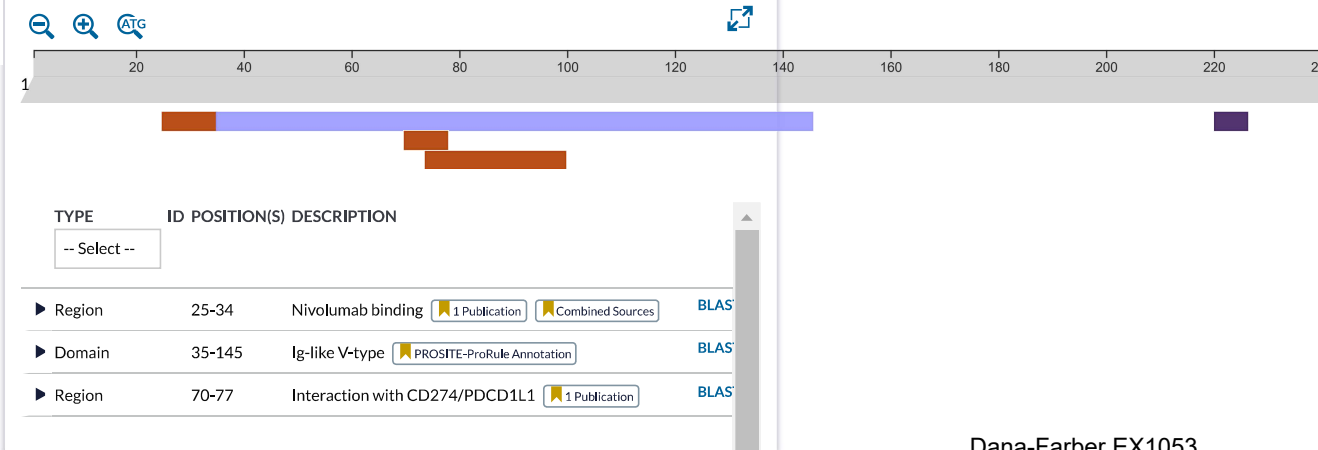
The PDCD1-mediated inhibitory pathway is exploited by tumors to attenuate anti-tumor immunity and escape destruction by the immune system, thereby facilitating tumor survival (PubMed:28951311).  
The interaction with CD274/PDCD1L1 inhibits cytotoxic T lymphocytes (CTLs) effector function (PubMed:28951311).  
The blockage of the PDCD1-mediated pathway results in the reversal of the exhausted T-cell phenotype and the normalization of the anti-tumor response, providing a rationale for cancer immunotherapy (PubMed:22658127, PubMed:25034862, PubMed:25399552).

Activity regulation

Inhibited by pembrolizumab (also named MK-3475 or lambrolizumab), a monoclonal antibody that prevents the interaction with CD274/PDCD1L1 (PubMed:27734966, PubMed:27325296).  
Inhibited by nivolumab (also named ONO-4538, BMS-936558 or Opdivo), a monoclonal antibody that prevents the interaction with CD274/PDCD1L1 (PubMed:28165004).  
The interaction with nivolumab is not dependent on glycosylation and depends on a loop at the N-terminus (N-terminal loop, corresponding to residues 25-34) (PubMed:28165004).  
Targeting the interaction between PDCD1 and CD274/PDCD1L1 with pembrolizumab and nivolumab antibodies has demonstrated great promise as a strategy for controlling and eradicating cancer (PubMed:22658127, PubMed:25034862, PubMed:25399552).  
Pembrolizumab and nivolumab are used for treatment of patients with advanced melanoma (PubMed:25034862, PubMed:25399552).  
These antibodies are also effective against other cancers, such as non-small cell lung cancer, renal cell carcinoma, bladder cancer and Hodgkin's lymphoma (PubMed:25034862).

Features

Showing features for region<sup>i</sup>, domain<sup>i</sup>, motif<sup>i</sup>.



TYPEID POSITION(S) DESCRIPTION

► Region

74-99

Pembrolizumab binding

2 Publications

Combined Sources

BLAST

GO Annotations<sup>i</sup>

Slimming set:

generic

Expand table

all annotations

all molecular function

virus receptor activity

rna binding

cytoskeletal motor activity

catalytic activity

space activity

structural molecule activity

transporter activity

cytoskeletal protein binding

lipid binding

cydase activity

antioxidant activity

oxidoreductase activity

hydrolase activity

transferase activity

isomerase activity

ligase activity

protein tag

cargo receptor activity

histone binding

protein folding chaperone

nutrient receptor activity

receptor ligand activity

molecular r

mole

Cell color indicative of number of GO terms

ASPECT

TERM

Cellular Component

external side of plasma membrane

Source:GO\_Central

1 Publication

Cellular Component

plasma membrane

Source:Reactome

Biological Process

adaptive immune response

Source:UniProtKB-KW

Biological Process

apoptotic process

Source:ProtInc

1 Publication

Biological Process

B cell apoptotic process

Source:Ensembl

Biological Process

humoral immune response

Source:ProtInc

1 Publication

Biological Process

negative regulation of B cell apoptotic process

Source:Ensembl

Biological Process

negative regulation of immune response

Source:UniProtKB

Biological Process

negative regulation of tolerance induction

Source:Ensembl

Biological Process

positive regulation of T cell apoptotic process

Source:UniProtKB

Expand table

Complete GO annotation on QuickGO

Keywords<sup>i</sup>

Biological process

#Adaptive immunity

#Apoptosis

#Immunity

Enzyme and pathway databases

PathwayCommons

Q15116

Reactome

R-HSA-389948

PD-1 signaling

R-HSA-9679191

Potential therapeutics for SARS

SIGNOR

Q15116

Signalink

Q15116

Protein family/group databases

TCDB

8.A.17.4.1

the na<sup>+</sup> channel auxiliary subunit

Beta1-Beta4 (sca-Beta) family

Names & Taxonomy<sup>i</sup>

Protein names<sup>i</sup>

Recommended name

Programmed cell death protein 1

1 Publication

Short names

Protein PD-1

1 Publication

hPD-1

2 Publications

CD Antigen Name

CD279

Gene names<sup>i</sup>

Help

Name

PDCD1 

1 Publication

Imported

Synonyms

PD1 

1 Publication

Organism names

Organism<sup>i</sup>

Homo sapiens (Human)

Taxonomic identifier<sup>i</sup>

9606 NCBI [↗](#)

Taxonomic lineage<sup>i</sup>

Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria > Euarchontoglires > Primates > Haplorrhini > Catarrhini > Hominidae > Homo

Accessions

Primary accession

Q15116

Secondary accessions

O00517

Q8IX89

Proteomes<sup>i</sup>

Identifier

UP000005640

Component<sup>i</sup>

Chromosome 2

Organism-specific databases

HGNC

HGNC:8760 [↗](#) PDCD1

MIM

600244 [↗](#) gene

605218 [↗](#) phenotype

VEuPathDB

HostDB:ENSG00000188389 [↗](#)

neXtProt

NX\_Q15116 [↗](#)

Subcellular Location<sup>i</sup>

UniProt Annotation

GO Annotation

Cell membrane

1 Publication

 : Single-pass type I membrane protein

Features

Showing features for topological domain<sup>i</sup>, transmembrane<sup>i</sup>.

| TYPE                    | ID | POSITION(S) | DESCRIPTION                                                      |
|-------------------------|----|-------------|------------------------------------------------------------------|
| <div>-- Select --</div> |    |             |                                                                  |
| ▶ Topological domain    |    | 24-170      | Extracellular <div>Sequence Analysis</div> <a href="#">BLAST</a> |
| ▶ Transmembrane         |    | 171-191     | Helical <div>Sequence Analysis</div> <a href="#">BLAST</a>       |
| ▶ Topological domain    |    | 192-288     | Cytoplasmic <div>Sequence Analysis</div> <a href="#">BLAST</a>   |

Expand table

Keywords<sup>i</sup>

Cellular component

#Cell membrane

#Membrane

Disease & Variants<sup>i</sup>

Involvement in disease<sup>i</sup>

Systemic lupus erythematosus 2 (SLEB2)

1 Publication

Note

Disease susceptibility is associated with variants affecting the gene represented in this entry

Help

Description

A chronic, relapsing, inflammatory, and often febrile multisystemic disorder of connective tissue, characterized principally by involvement of the skin, joints, kidneys and serosal membranes. It is of unknown etiology, but is thought to represent a failure of the regulatory mechanisms of the autoimmune system. The disease is marked by a wide range of system dysfunctions, an elevated erythrocyte sedimentation rate, and the formation of LE cells in the blood or bone marrow.

See also

MIM:605218

Features

Showing features for mutagenesis<sup>i</sup>.

| TYPE          | ID  | POSITION(S) | DESCRIPTION                                                                                                     |
|---------------|-----|-------------|-----------------------------------------------------------------------------------------------------------------|
| -- Select --  |     |             |                                                                                                                 |
| ▶ Mutagenesis | 49  |             | Decreased N-glycosylation without affecting binding to binding to nivolumab drug. <a href="#">1 Publication</a> |
| ▶ Mutagenesis | 58  |             | Decreased N-glycosylation without affecting binding to binding to nivolumab drug. <a href="#">1 Publication</a> |
| ▶ Mutagenesis | 74  |             | Decreased N-glycosylation without affecting binding to binding to nivolumab drug. <a href="#">1 Publication</a> |
| ▶ Mutagenesis | 116 |             | Decreased N-glycosylation without affecting binding to binding to nivolumab drug. <a href="#">1 Publication</a> |
| ▶ Mutagenesis | 210 |             | Does not affect ubiquitination by the SCF(FBXO38) complex. <a href="#">1 Publication</a>                        |
| ▶ Mutagenesis | 233 |             | Abolishes ubiquitination by the SCF(FBXO38) complex. <a href="#">1 Publication</a>                              |

Expand table

Variants

Keywords<sup>i</sup>

Disease

#Systemic lupus erythematosus

Organism-specific databases

DisGeNET

5133

MIM

600244 gene

605218 phenotype

MalaCards

PDCD1

OpenTargets

ENSG00000188389

Orphanet

802 NON RARE IN EUROPE: Multiple sclerosis

536 Systemic lupus erythematosus

PharmGKB

PA33110

Chemistry

ChEMBL

CHEMBL3307223

DrugCentral

Q15116

DrugBank

DB15767 AMP-224

DB14776 Camrelizumab

DB14707 Cemiplimab

DB05916 CT-011

DB15627 Dostarlimab

More DrugBank links

GuidetoPHARMACOLOGY

2760

Genetic variation databases

BioMuta

PDCD1

ClinGen

HGNC:8760

DMDM

145559515

GenCC

HGNC:8760

PTM/Processing<sup>i</sup>

Features

Showing features for signal<sup>i</sup>, chain<sup>i</sup>, glycosylation<sup>i</sup>, disulfide bond<sup>i</sup>, modified residue<sup>i</sup>, cross-link<sup>i</sup>.

| TYPE         | ID | POSITION(S) | DESCRIPTION                                             |
|--------------|----|-------------|---------------------------------------------------------|
| -- Select -- |    |             |                                                         |
| ▶ Signal     |    | 1-23        | <a href="#">Sequence Analysis</a> <a href="#">BLAST</a> |

TYPEIDPOSITION(S)DESCRIPTION

ChainPRO\_000001489224-288Programmed cell death protein 1BLAST

Glycosylation49N-linked (GlcNAc...) asparagine1 Publication

Disulfide bond54-123PROSITE-ProRule Annotation4 PublicationsCombined SourcesBLAST

Post-translational modification<sup>i</sup>

Ubiquitinated at Lys-233 by the SCF(FBXO38) complex, leading to its proteasomal degradation (PubMed:30487606).

Ubiquitinated via 'Lys-48'-linked polyubiquitin chains (PubMed:30487606).1 Publication

Tyrosine phosphorylated at Tyr-223 (within ITIM motif) and Tyr-248 (ITSM motif) upon ligand binding. Phosphorylation at Tyr-248 promotes the recruitment of the protein tyrosine phosphatase PTPN11/SHP-2 that mediates dephosphorylation of key TCR proximal signaling molecules, such as ZAP70, PRKCQ/PKCtheta and CD247/CD3zeta. By Similarity

N-glycosylation at Asn-58 contains at least two N-acetylglucosamine units and one fucose (PubMed:28165004).

N-glycosylation does not affect binding to nivolumab drug (PubMed:28165004).1 Publication

Expand table

Keywords<sup>i</sup>

PTM

#Disulfide bond

#Glycoprotein

#Isopeptide bond

#Phosphoprotein

#Ubl conjugation

Proteomic databases

MassIVEQ15116

PeptideAtlasQ15116

PaxDbQ15116

ProteomicsDB60443

PTM databases

GlyGenQ151164 sites

iPTMnetQ15116

PhosphoSitePlusQ15116

Expression<sup>i</sup>

Developmental stage<sup>i</sup>

Induced at programmed cell death.1 Publication

Gene expression databases

BgeeENSG00000188389Expressed in lymph node and 85 other tissues

ExpressionAtlasQ15116baseline and differential

GenevisibleQ15116HS

Organism-specific databases

HPAENSG00000188389Tissue enhanced (heart muscle, lymphoid tissue)

Interaction<sup>i</sup>

Subunit<sup>i</sup>

Monomer (PubMed:26602187).

Interacts with CD274/PDCD1L1 (PubMed:26602187).

Interacts with CD273/PDCD1LG2 (By similarity).

Interacts with FBXO38; leading to ubiquitination and degradation of PDCD1 by the proteasome (PubMed:30487606).By Similarity2 Publications

Binary interactions<sup>i</sup>



| TYPE   | ENTRY 1                | ENTRY 2                         | NUMBER OF EXPERIMENTS | INTACT                                    |
|--------|------------------------|---------------------------------|-----------------------|-------------------------------------------|
| BINARY | <a href="#">Q15116</a> | <a href="#">CD274 Q9NZQ7</a>    | 17                    | <a href="#">EBI-4314328, EBI-4314282</a>  |
| BINARY | <a href="#">Q15116</a> | <a href="#">CD274 Q9NZQ7-1</a>  | 2                     | <a href="#">EBI-4314328, EBI-15686469</a> |
| BINARY | <a href="#">Q15116</a> | <a href="#">PDCD1LG2 Q9BQ51</a> | 14                    | <a href="#">EBI-4314328, EBI-16427978</a> |
| BINARY | <a href="#">Q15116</a> | <a href="#">PTPN11 Q06124</a>   | 3                     | <a href="#">EBI-4314328, EBI-297779</a>   |

Expand table

### Protein-protein interaction databases

BioGRID

[111160](#)

117 interactors

DIP

[DIP-44126N](#)

IntAct

[Q15116](#)

54 interactors

MINT

[Q15116](#)

STRING

[9606.ENSP00000335062](#)

### Chemistry

BindingDB

[Q15116](#)

## Structure<sup>i</sup>



### Features

Showing features for beta strand<sup>i</sup>, helix<sup>i</sup>.

| TYPE        | ID | POSITION(S) | DESCRIPTION                                            |
|-------------|----|-------------|--------------------------------------------------------|
| Beta strand |    | 27-29       | <a href="#">Combined Sources</a> <a href="#">BLAST</a> |
| Beta strand |    | 36-38       | <a href="#">Combined Sources</a> <a href="#">BLAST</a> |
| Beta strand |    | 40-45       | <a href="#">Combined Sources</a> <a href="#">BLAST</a> |
| Beta strand |    | 50-55       | <a href="#">Combined Sources</a> <a href="#">BLAST</a> |
| Beta strand |    | 59-61       | <a href="#">Combined Sources</a> <a href="#">BLAST</a> |
| Beta strand |    | 63-70       | <a href="#">Combined Sources</a> <a href="#">BLAST</a> |
| Beta strand |    | 72-74       | <a href="#">Combined Sources</a> <a href="#">BLAST</a> |

Expand table

### 3D structure databases

AlphaFoldDB

[Q15116](#)

BMRB

[Q15116](#)

SMR

[Q15116](#)

ModBase

[Search...](#)

PDBe-KB

[Search...](#)

## Family & Domains<sup>i</sup>

### Features

Showing features for region<sup>i</sup>, domain<sup>i</sup>, motif<sup>i</sup>.

TYPE

ID POSITION(S) DESCRIPTION

-- Select --

|          |         |                                                                                                   |
|----------|---------|---------------------------------------------------------------------------------------------------|
| ▶ Region | 25-34   | Nivolumab binding <div>1 Publication</div> <div>Combined Sources</div> <a href="#">BLAST</a>      |
| ▶ Domain | 35-145  | Ig-like V-type <div>PROSITE-ProRule Annotation</div> <a href="#">BLAST</a>                        |
| ▶ Region | 70-77   | Interaction with CD274/PDCD1L1 <div>1 Publication</div> <a href="#">BLAST</a>                     |
| ▶ Region | 74-99   | Pembrolizumab binding <div>2 Publications</div> <div>Combined Sources</div> <a href="#">BLAST</a> |
| ▶ Motif  | 221-226 | ITIM motif <div>By Similarity</div> <a href="#">BLAST</a>                                         |
| ▶ Motif  | 247-251 | ITSM motif <div>By Similarity</div> <a href="#">BLAST</a>                                         |
| ▶ Region | 254-288 | Disordered <div>Automatic Annotation</div> <a href="#">BLAST</a>                                  |

Expand table

Keywords<sup>i</sup>

Domain

#Immunoglobulin domain

#Signal

#Transmembrane

#Transmembrane helix

Phylogenomic databases

GeneTree

ENSGT00390000013662 [↗](#)

OrthoDB

1437063at2759 [↗](#)

HOGENOM

CLU\_1075828\_0\_0\_1 [↗](#)

PhylomeDB

Q15116 [↗](#)

InParanoid

Q15116 [↗](#)

TreeFam

TF336181 [↗](#)

OMA

HTEYATI [↗](#)

eggNOG

ENOG502SUIW [↗](#) Eukaryota

Family and domain databases

Gene3D

2.60.40.10 [↗](#) 1 hit

Pfam

[View protein in Pfam](#) [↗](#)

PF07686 [↗](#) V-set 1 hit

InterPro

[View protein in InterPro](#) [↗](#)

IPR007110 [↗](#) Ig-like\_dom

IPR036179 [↗](#) Ig-like\_dom\_sf

IPR013783 [↗](#) Ig-like\_fold

IPR003599 [↗](#) Ig\_sub

[More InterPro links](#)

SMART

[View protein in SMART](#) [↗](#)

SM00409 [↗](#) IG 1 hit

SM00406 [↗](#) IGv 1 hit

SUPFAM

SSF48726 [↗](#) Immunoglobulin 1 hit

PANTHER

[PTHR15264](#) [↗](#) PROGRAMMED CELL DEATH

PROTEIN 1 1 hit

MobiDB

[Search...](#) [↗](#)

PROSITE

[View protein in PROSITE](#) [↗](#)

P550835 [↗](#) IG\_LIKE 1 hit

ProtoNet

[Search...](#) [↗](#)

Sequence<sup>i</sup>

Sequence status<sup>i</sup>

Complete

Sequence processing<sup>i</sup>

The displayed sequence is further processed into a mature form.

Length

288

Mass (Da)

31,647

Last updated

2007-04-17 v3

Checksum<sup>i</sup>

A5210FD40C304FB7

MQIQPAPWPVVWAVLQLGWRPGWFLDSPDRPWNPPTFSPALLVTEGDNATFTCSFSNTSESFVLNWYR

MSPSNQTDKLAAPFEDRSQPGQDCRFRVTQLPNGRDFHMSVVRARRNDSTYLCAISLAPKAQIKESLRA

ELRVTERAEVPTAHPSPSRPAGQFTLVVGVGGLLSLVLLVWVLAVICSRAARTGIGARRTGQPLKEDPS

AVPVFVSVDYGELDFQWREKTPEPPVPCVPEQTEYATIVFPSGMGTSSPARRGSADGPRSAQLRPEDGHCS  
WPL

Computationally mapped potential isoform sequences<sup>i</sup>

There are 2 potential isoforms mapped to this entry

View all

| <input type="checkbox"/> Entry                  | Entry name                                                                                     | Gene name | Length |
|-------------------------------------------------|------------------------------------------------------------------------------------------------|-----------|--------|
| <input type="checkbox"/> <a href="#">E7ER21</a> |  E7ER21_HUMAN | PDCD1     | 66     |
| <input type="checkbox"/> <a href="#">H0Y2W6</a> |  H0Y2W6_HUMAN | PDCD1     | 122    |

Features

Showing features for sequence conflict<sup>i</sup>.

| TYPE                    | ID  | POSITION(S)         | DESCRIPTION                                                                       |
|-------------------------|-----|---------------------|-----------------------------------------------------------------------------------|
| <div>-- Select --</div> |     |                     |                                                                                   |
| ▶ Sequence conflict     | 38  | in Ref. 2; AAC51773 |  |
| ▶ Sequence conflict     | 162 | in Ref. 1; AAC41700 |  |

Expand table

Keywords<sup>i</sup>

Technical term

#3D-structure

#Reference proteome

Sequence databases

|                                               |                                                         |
|-----------------------------------------------|---------------------------------------------------------|
| CCDS                                          | RefSeq                                                  |
| <a href="#">CCDS33428.1</a>                   | <a href="#">NP_005009.2</a> <a href="#">NM_005018.2</a> |
| PIR                                           |                                                         |
| <a href="#">A55737</a> <a href="#">A55737</a> |                                                         |

| SEQUENCE                                                                                       | PROTEIN                                                                                          | MOLECULE<br>TYPE | STATUS |
|------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------|------------------|--------|
| <a href="#">L27440</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> )   | <a href="#">AAC41700.1</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> ) | Genomic DNA      |        |
| <a href="#">U64863</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> )   | <a href="#">AAC51773.1</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> ) | mRNA             |        |
| <a href="#">AF363458</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> ) | <a href="#">AAN64003.1</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> ) | Genomic DNA      |        |
| <a href="#">AY238517</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> ) | <a href="#">AAO63583.1</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> ) | mRNA             |        |
| <a href="#">EF064716</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> ) | <a href="#">ABK41899.1</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> ) | Genomic DNA      |        |
| <a href="#">AK313848</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> ) | <a href="#">BAG36577.1</a> ( <a href="#">EMBL</a> <a href="#">GenBank</a> <a href="#">DDBJ</a> ) | mRNA             |        |

Expand table

Genome annotation databases

|                                                                      |                                                                      |
|----------------------------------------------------------------------|----------------------------------------------------------------------|
| Ensembl                                                              | KEGG                                                                 |
| <a href="#">ENST00000334409.10</a> <a href="#">ENSP00000335062.5</a> | <a href="#">hsa:5133</a>                                             |
| <a href="#">ENSG00000188389.11</a>                                   |                                                                      |
| <a href="#">ENST00000618185.3</a> <a href="#">ENSP00000480684.1</a>  | MANE-Select                                                          |
| <a href="#">ENSG00000276977.3</a>                                    | <a href="#">ENST00000334409.10</a> <a href="#">ENSP00000335062.5</a> |
|                                                                      | <a href="#">NM_005018.3</a> <a href="#">NP_005009.2</a>              |
| GeneID                                                               | UCSC                                                                 |
| <a href="#">5133</a>                                                 | <a href="#">uc002wcq.5</a> human                                     |

Similar Proteins<sup>i</sup>



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