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# INS insulin [ Homo sapiens (human) ]

**Download Datasets** 

Gene ID: 3630, updated on 28-Aug-2022

#### Summary

Official Symbol INS provided by HGNC
Official Full Name insulin provided by HGNC
Primary source HGNC:HGNC:6081

See related Ensembl:ENSG00000254647 MIM:176730; AllianceGenome:HGNC:6081

Gene type protein coding
RefSeq status REVIEWED
Organism Homo sapiens

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria;

Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

Also known as IDDM; ILPR; IRDN; IDDM1; IDDM2; PNDM4; MODY10

**Summary** This gene encodes insulin, a peptide hormone that plays a vital role in the regulation of

carbohydrate and lipid metabolism. After removal of the precursor signal peptide, proinsulin is post-translationally cleaved into three peptides: the B chain and A chain peptides, which are covalently linked via two disulfide bonds to form insulin, and C-peptide. Binding of insulin to the insulin receptor (INSR) stimulates glucose uptake. A multitude of mutant alleles with phenotypic effects have been identified, including insulin-dependent diabetes mellitus, permanent neonatal diabetes diabetes mellitus, maturity-onset diabetes of the young type 10 and hyperproinsulinemia. There is a read-through gene, INS-IGF2, which overlaps with this gene at the 5' region and with the IGF2 gene at the 3' region. [provided by RefSeq, May

2020]

**Expression** Restricted expression toward pancreas (RPKM 671.7) See more

Orthologs mouse all

**NEW** Try the new Gene table

Try the new **Transcript table** 

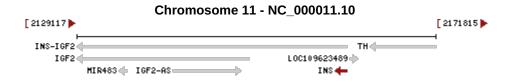
#### **Genomic context**

**Location:** 11p15.5

See INS in Genome Data Viewer

Exon count: 3

Annotation release	Status	Assembly	Chr	Location
110	current	GRCh38.p14 (GCF_000001405.40)	11	NC_000011.10 (21597792161209, complement)
110	current	T2T-CHM13v2.0 (GCF_009914755.1)	11	NC_060935.1 (22474272248857, complement)
105.20220307	previous assembly	GRCh37.p13 (GCF_000001405.25)	11	NC_000011.9 (21810092182439, complement)



### Genomic regions, transcripts, and products

Genes, Ensembl release 107

ENSG00000254647 [...

Go to reference sequence details

Genomic Sequence: NC\_000011.10 Chromosome 11 Reference GRCh38.p14 Primary Assembly > Go to nucleotide: Graphics FASTA <u>GenBank</u> Find: NC\_000011.10 To 2,161,200 2,160,800 2,160,600 2,160,400 2,160,200 2,161,400 2,161 K Genes, MANE Project (release v1.0) H H INS NM\_000207.3 ----Genes, NCBI Homo sapiens Annotation Release 110, 2022-04-08 114 [M] NR\_003512.4 ->> NM\_001042376.3 INS NM\_000207.3 NM\_001185097.2 -> NM\_001291897.2 NM\_001185098.2 D Biological regions, aggregate, NCBI NCBI Homo sapiens Annotat… 🔣 lity\_r...

2 of 15 10/24/22, 15:30

114

100

See details

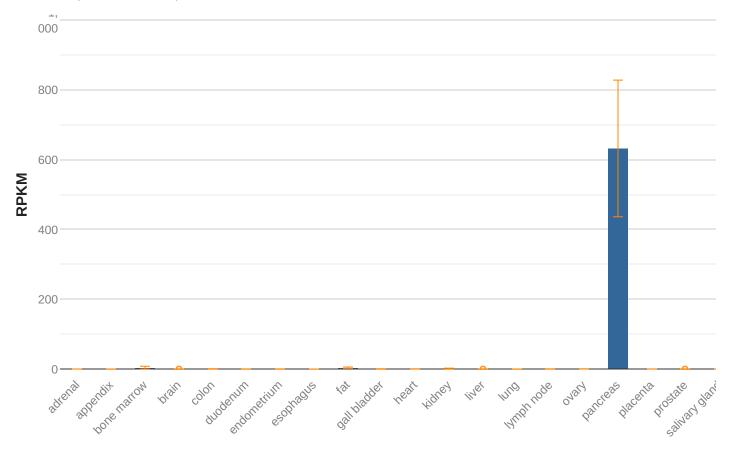
HPA RNA-seq normal tissues

- Project title: HPA RNA-seq normal tissues
- Description: RNA-seq was performed of tissue samples from 95 human individuals representing 27 different tissues

~

in order to determine tissue-specificity of all protein-coding genes

- BioProject: PRJEB4337
- Publication: PMID 24309898
- Analysis date: Wed Apr 4 07:08:55 2018



#### **Samples**

#### **Bibliography**

#### Related articles in PubMed

1. <u>Insulin Directs Dichotomous Translational Regulation to Control Human Pluripotent Stem Cell Survival</u>, Proliferation and Pluripotency.

Zhou X, et al. Int J Biol Sci, 2022. PMID 35813470, Free PMC Article

2. <u>Comparison of Quality of Carbohydrate Metrics Related to Fasting Insulin, Glycosylated Hemoglobin and HOMA-IR in Brazilian Adolescents.</u>

da Rocha CMM, et al. Nutrients, 2022 Jun 19. PMID 35745274, Free PMC Article

- 3. <u>Participation of Magnesium in the Secretion and Signaling Pathways of Insulin: an Updated Review.</u>
  de Sousa Melo SR, *et al.* Biol Trace Elem Res, 2022 Aug. PMID 35666386
- 4. <u>Association between single nucleotide polymorphisms in non-coding regions of the insulin (INS) gene and schizophrenia.</u>

Melkersson K, et al. Neuro Endocrinol Lett, 2022 Apr. PMID 35490421

5. <u>A Novel Nonsense INS Mutation Causes Inefficient Preproinsulin Translocation Into the Endoplasmic Reticulum.</u>

Yang Y, et al. Front Endocrinol (Lausanne), 2021. PMID 35069438, Free PMC Article

See all (970) citations in PubMed

See citations in PubMed for homologs of this gene provided by HomoloGene

#### GeneRIFs: Gene References Into Functions

#### What's a GeneRIF?

- Aberrant crosstalk between insulin signaling and mTOR in young Down syndrome individuals revealed by neuronal-derived extracellular vesicles.
- 2. <u>Association between single nucleotide polymorphisms in non-coding regions of the insulin (INS) gene and schizophrenia.</u>
- 3. <u>Insulin Directs Dichotomous Translational Regulation to Control Human Pluripotent Stem Cell Survival, Proliferation and Pluripotency.</u>
- 4. Comparison of Quality of Carbohydrate Metrics Related to Fasting Insulin, Glycosylated Hemoglobin and HOMA-IR in Brazilian Adolescents.
- 5. Participation of Magnesium in the Secretion and Signaling Pathways of Insulin: an Updated Review.
- Progressive endoplasmic reticulum stress over time due to human insulin gene mutation contributes to pancreatic beta cell dysfunction.
- 7. In celebration of a century with insulin Update of insulin gene mutations in diabetes.
- 8. <u>Nicotinamide mononucleotide: a potential effective natural compound against insulin resistance.</u>
- 9. A Novel Nonsense INS Mutation Causes Inefficient Preproinsulin Translocation Into the Endoplasmic Reticulum.
- Evaluation of serum insulin-like growth factor-1, insulin, glucose levels in patients with adolescent and postadolescent acne.

Submit: New GeneRIF Correction See all GeneRIFs (734)

#### **Phenotypes**

BioGRID CRISPR Screen Phenotypes (382 hits/1121 screens)

Find tests for this gene in the NIH Genetic Testing Registry (GTR)

Review eQTL and phenotype association data in this region using PheGenI

#### Associated conditions

Description	Tests
<u>Diabetes mellitus, permanent neonatal 4</u> MedGen: <u>C5394307</u> , OMIM: <u>618858</u> , GeneReviews: Not available	Compare labs
Hyperproinsulinemia  MedGen: C0342283, OMIM: 616214, GeneReviews: Not available	Compare labs

Description	Tests
Maturity-onset diabetes of the young type 10  MedGen: C3150617, OMIM: 613370, GeneReviews: Maturity-Onset Diabetes of the Young Overview	Compare labs
Permanent neonatal diabetes mellitus  MedGen: C1833104, GeneReviews: Permanent Neonatal Diabetes Mellitus	Compare labs
Type 1 diabetes mellitus 2  MedGen: C1852092, OMIM: 125852, GeneReviews: Not available	Compare labs

### Copy number response

#### Description

Copy number response

Haploinsufficency

No evidence available (Last evaluated 2012-03-22)

ClinGen Genome Curation Page

Triplosensitivity

No evidence available (Last evaluated 2012-03-22)

ClinGen Genome Curation Page

#### **EBI GWAS Catalog**

#### Description

A genome-wide association study identifies KIAA0350 as a type 1 diabetes gene.

**EBI GWAS Catalog** 

EBI GWAS Catalog, PubMed

A possible mechanism behind autoimmune disorders discovered by genome-wide linkage and association analysis in celiac disease.

**EBI GWAS Catalog** 

EBI GWAS Catalog, PubMed

Genome-wide association analysis of autoantibody positivity in type 1 diabetes cases.

**EBI GWAS Catalog** 

EBI GWAS Catalog, PubMed

Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes.

**EBI GWAS Catalog** 

EBI GWAS Catalog, PubMed

Identification of seven new prostate cancer susceptibility loci through a genome-wide association study.

**EBI GWAS Catalog** 

EBI GWAS Catalog, PubMed

### Description

Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes.

**EBI GWAS Catalog** 

EBI GWAS Catalog, PubMed

#### **Variation**

See variants in ClinVar

See studies and variants in dbVar

See Variation Viewer (GRCh37.p13)

See Variation Viewer (GRCh38)

#### Genotypes

<u>See SNP Geneview Report</u> <u>See 1000 Genomes Browser (GRCh37.p13)</u>

#### **HIV-1** interactions

#### Protein interactions

Protein	Gene	Interaction	Pubs
<u>Vpr</u>	<u>vpr</u>	HIV-1 Vpr antagonizes insulin's effect on the expression of glucose 6-phosphatase, manganese superoxide dismutase, and sterol carrier protein 2 genes in HepG2 cells	<u>PubMed</u>
	<u>vpr</u>	HIV-1 Vpr inhibits insulin-induced association of 14-3-3 and Foxo3a in HeLa cells	PubMed
	<u>vpr</u>	HIV-1 Vpr inhibits insulin-induced cytoplasmic translocation of Foxo3a, a subtype of the forkhead transcription factors	<u>PubMed</u>

Go to the HIV-1, Human Interaction Database

# **Pathways from PubChem**

# 61 items View More Rows & Details

	9	SORT BY <b>Taxonon</b>	ny
Pathway	Source	External ID	Taxonomy
Developmental Biology	Reactome	R-HSA-1266738	Homo sapiens (human)
Regulation of beta-cell development	Reactome	R-HSA-186712	Homo sapiens (human)
Regulation of gene expression in beta cells	Reactome	R-HSA-210745	Homo sapiens (human)
Metabolism	Reactome	R-HSA-1430728	Homo sapiens (human)
Integration of energy metabolism	Reactome	R-HSA-163685	Homo sapiens (human)
Regulation of insulin secretion	Reactome	R-HSA-422356	Homo sapiens (human)
Signaling Pathways	Reactome	R-HSA-162582	Homo sapiens (human)
Signaling by Receptor Tyrosine Kinases	Reactome	R-HSA-9006934	Homo sapiens (human)
Signaling by Insulin receptor	Reactome	R-HSA-74752	Homo sapiens (human)
Insulin receptor signalling cascade	Reactome	R-HSA-74751	Homo sapiens (human)
IRS activation	Reactome	R-HSA-74713	Homo sapiens (human)
Signal attenuation	Reactome	R-HSA-74749	Homo sapiens (human)
Insulin receptor recycling	Reactome	R-HSA-77387	Homo sapiens (human)
Metabolism of proteins	Reactome	R-HSA-392499	Homo sapiens (human)
Peptide hormone metabolism	Reactome	R-HSA-2980736	Homo sapiens (human)
Insulin processing	Reactome	R-HSA-264876	Homo sapiens (human)
Synthesis, secretion, and deacylation of Ghrelin	Reactome	R-HSA-422085	Homo sapiens (human)
Gene expression (Transcription)	Reactome	R-HSA-74160	Homo sapiens (human)
RNA Polymerase II Transcription	Reactome	R-HSA-73857	Homo sapiens (human)
Generic Transcription Pathway	Reactome	R-HSA-212436	Homo sapiens (human)
Cori cycle	WikiPathways	WP1946	Homo sapiens (human)
Sterol regulatory element-binding proteins (SREBP) signaling	WikiPathways	WP1982	Homo sapiens (human)
Alzheimer's disease and miRNA effects	WikiPathways	WP2059	Homo sapiens (human)
Adipogenesis	WikiPathways	WP236	Homo sapiens (human)
Cardiac progenitor differentiation	WikiPathways	WP2406	Homo sapiens (human)

PubChem

# **Interactions**

		Items 1 - 25 of 5	525 << Firs	st < Prev	Page 1	of 21 Next >	Last >>
Products	Interactant	Other Gene	Complex	Source	Pubs	Description	
P01308	P48745	CCN3	_	<u>HPRD</u>	PubMed		
P01308	P16870	CPE	-	<u>HPRD</u>	PubMed		
P01308	P07858	CTSB	-	<u>HPRD</u>	PubMed		
P01308	P07339	CTSD	-	<u>HPRD</u>	PubMed		
P01308	P14091	CTSE	_	<u>HPRD</u>	PubMed		
P01308	P35557	<u>GCK</u>	-	<u>HPRD</u>	PubMed		
P01308	P01906	HLA-DQA2	-	<u>HPRD</u>	PubMed		
P01308	P01918	HLA-DQB1	-	<u>HPRD</u>	PubMed		
P01308	P14735	<u>IDE</u>	-	<u>HPRD</u>	PubMed		
P01308	P08069	IGF1R	-	<u>HPRD</u>	<u>PubMed</u>		
P01308	Q16270	IGFBP7	-	<u>HPRD</u>	PubMed		
P01308	P01308	<u>INS</u>	-	<u>HPRD</u>	PubMed		
P01308	P06213	<u>INSR</u>	-	<u>HPRD</u>	<u>PubMed</u>		
P01308	P98164	LRP2	_	<u>HPRD</u>	PubMed		
P01308	P06400	RB1	-	<u>HPRD</u>	PubMed		
P01308	Q96C24	SYTL4	-	<u>HPRD</u>	<u>PubMed</u>		
P01308	Q9BRA2	TXNDC17	_	<u>HPRD</u>	PubMed		
BioGRID:109842	BioGRID:119004	A1CF	-	<u>BioGRID</u>	PubMed	Affinity Captur	e-MS
BioGRID:109842	BioGRID:116520	AAK1	-	<u>BioGRID</u>	PubMed	Affinity Captur	e-MS
BioGRID:109842	BioGRID:106540	ABCB7	-	BioGRID	PubMed	Affinity Captur	e-MS
BioGRID:109842	BioGRID:112700	ABCC8	_	<u>BioGRID</u>	PubMed	Affinity Captur	e-MS
BioGRID:109842	BioGRID:111783	ABCD3	-	<u>BioGRID</u>	PubMed	Affinity Captur	e-MS
BioGRID:109842	BioGRID:106541	ABCF1	_	<u>BioGRID</u>	PubMed	Affinity Captur	e-MS
BioGRID:109842	BioGRID:115372	ABCF2	_	<u>BioGRID</u>	PubMed	Affinity Captur	e-MS
BioGRID:109842	BioGRID:117541	ABHD12	_	<u>BioGRID</u>	PubMed	Affinity Captur	e-MS
		Items 1 - 25 of 5	525 << Firs	st < Prev	Page 1	of 21 Next >	Last >>

# **General gene information**

Markers

Readthrough INS-IGF2

Readthrough gene: <u>INS-IGF2</u>, Included gene: <u>IGF2</u>

#### Homology

<u>Homologs of the INS gene</u>: The INS gene is conserved in chimpanzee, dog, mouse, rat, chicken, zebrafish, and frog. <u>Orthologs from Annotation Pipeline</u>: 269 organisms have orthologs with human gene INS <u>Orthologs</u>

# Gene Ontology Provided by GOA

Function	Evidence Code	Pubs
enables hormone activity.	IC	PubMed
enables hormone activity	<u>IMP</u>	<u>PubMed</u>
enables hormone activity	<u>NAS</u>	PubMed
enables identical protein binding	<u>IPI</u>	PubMed
enables insulin receptor binding	<u>IDA</u>	<u>PubMed</u>
enables insulin receptor binding	<u>IPI</u>	PubMed
enables insulin-like growth factor receptor binding	<u>IPI</u>	PubMed
enables protease binding	<u>IPI</u>	PubMed
enables protein binding	<u>IPI</u>	<u>PubMed</u>

Items 1 - 25 of 69 << First < Prev Page 1	of 3 Next >	Last >>
Process	Evidence Code	Pubs
involved_in G protein-coupled receptor signaling pathway	<u>IDA</u>	<u>PubMed</u>
involved_in activation of protein kinase B activity	<u>IDA</u>	<u>PubMed</u>
involved_in acute-phase response	<u>IDA</u>	PubMed
involved_in alpha-beta T cell activation	<u>IDA</u>	PubMed
involved_in cell-cell signaling	<u>IC</u>	<u>PubMed</u>
involved_in cognition	<u>TAS</u>	PubMed
involved_in fatty acid homeostasis	<u>IMP</u>	<u>PubMed</u>
involved_in_glucose homeostasis	<u>IBA</u>	PubMed
involved_in_glucose homeostasis	<u>IMP</u>	PubMed
involved_in_glucose metabolic process	<u>IEA</u>	
involved_in insulin receptor signaling_pathway	IDA	PubMed
involved_in negative regulation of NAD(P)H oxidase activity	<u>IDA</u>	PubMed
involved_in negative regulation of acute inflammatory response	<u>IDA</u>	PubMed
involved_in negative regulation of fatty acid metabolic process	<u>IMP</u>	<u>PubMed</u>

Process	Evidence Code	Pubs
involved_in negative regulation of feeding behavior	<u>IDA</u>	<u>PubMed</u>
acts_upstream_of negative regulation of gene expression	<u>IDA</u>	<u>PubMed</u>
involved_in negative regulation of gluconeogenesis	NAS	<u>PubMed</u>
involved_in negative regulation of glycogen catabolic process	<u>IMP</u>	<u>PubMed</u>
involved_in negative regulation of lipid catabolic process	<u>IMP</u>	<u>PubMed</u>
involved_in negative regulation of lipid catabolic process	<u>NAS</u>	<u>PubMed</u>
involved_in negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	NAS	PubMed
involved_in negative regulation of protein catabolic process	<u>IDA</u>	<u>PubMed</u>
involved_in negative regulation of protein secretion	<u>IDA</u>	<u>PubMed</u>
involved_in negative regulation of proteolysis	<u>IMP</u>	<u>PubMed</u>
involved_in negative regulation of reactive oxygen species biosynthetic process	<u>IGI</u>	<u>PubMed</u>
Items 1 - 25 of 69 << First < Prev Page 1	of 3 Next >	Last >>

Component	Evidence Code	Pubs
located_in Golgi lumen	<u>TAS</u>	
located_in Golgi membrane	<u>TAS</u>	
located_in endoplasmic reticulum lumen	<u>TAS</u>	
located_in endoplasmic reticulum-Golgi intermediate compartment membrane	<u>TAS</u>	
located_in endosome lumen	<u>TAS</u>	
located_in extracellular region	<u>IC</u>	<u>PubMed</u>
located_in extracellular region	<u>TAS</u>	
is_active_in extracellular space	<u>IBA</u>	<u>PubMed</u>
located_in extracellular space	<u>IDA</u>	<u>PubMed</u>
located_in secretory granule lumen	<u>TAS</u>	
located_in transport vesicle	<u>TAS</u>	

# **General protein information**

Preferred Names insulin

Names

preproinsulin proinsulin

# NCBI Reference Sequences (RefSeq)

### **NEW Try the new <u>Transcript table</u>**

#### **RefSeqs maintained independently of Annotated Genomes**

These reference sequences exist independently of genome builds. Explain

#### Genomic

#### 1. NG\_007114.1 RefSeqGene

Range	49866416
Download	GenBank, FASTA, Sequence Viewer (Graphics)

### mRNA and Protein(s)

### 1. NM 000207.3 → NP 000198.1 insulin preproprotein

See identical proteins and their annotated locations for NP 000198.1

### Status: REVIEWED

Description	Transcript Variant: This variant (1) represents the shortest variant. All variants encode the same protein.			
Source sequence(s)	BC005255, BM510748			
Consensus CDS	CCDS7729.1			
UniProtKB/Swiss-Prot	P01308, Q5EEX2			
UniProtKB/TrEMBL	I3WAC9			
Related	ENSP00000370731.5, ENST00000381330.5			
Conserved Domains (1) <u>su</u>	<u>summary</u>			
	<u>cd04367</u> Location:26 → 110	IIGF_insulin_like; IIGF_like family, insulin_like subgroup, specific to vertebrates. Members include a number of peptides including insulin and insulin-like growth factors I and II, which play a variety of roles in controlling processes such as metabolism, growth and		

### 2. <u>NM\_001185097.2</u> → <u>NP\_001172026.1</u> insulin preproprotein

See identical proteins and their annotated locations for NP 001172026.1

#### **Status: REVIEWED**

Description	Transcript Variant: This variant (2) differs in the 5' UTR, compared to variant 1. All variants encode the same protein.					
Source sequence(s)	AY899304, BM510347, BP322143					
Consensus CDS	CCDS7729.1					
UniProtKB/Swiss-Prot	P01308, Q5EEX2					
UniProtKB/TrEMBL	<u>I3WAC9</u>					
Related	ENSP00000250971.3, ENST00000250971.7					
Conserved Domains (1) <u>summary</u>						
	<u>cd04367</u> Location:26 → 110	IIGF_insulin_like; IIGF_like family, insulin_like subgroup, specific to vertebrates. Members include a number of peptides including insulin and insulin-like growth factors I and II, which play a variety of roles in controlling processes such as metabolism, growth and				

#### 3. NM\_001185098.2 → NP\_001172027.1 insulin preproprotein

See identical proteins and their annotated locations for NP 001172027.1

Status: REVIEWED

**Description** Transcript Variant: This variant (3) differs in the 5' UTR, compared to variant 1. All

variants encode the same protein.

Source sequence(s) <u>AC132217, BM510347, BP322143</u>

 Consensus CDS
 CCDS7729.1

 UniProtKB/Swiss-Prot
 P01308, Q5EEX2

UniProtKB/TrEMBL | 13WAC9

**Related** ENSP00000380432.1, ENST00000397262.5

Conserved Domains (1) summary

Location:26 → 110

Location:26

#### 4. NM\_001291897.2 → NP\_001278826.1 insulin preproprotein

See identical proteins and their annotated locations for NP\_001278826.1

**Status: REVIEWED** 

**Description** Transcript Variant: This variant (4) differs in the 5' UTR, compared to variant 1. All

variants encode the same protein.

Source sequence(s) AC132217, BM510347

 Consensus CDS
 CCDS7729.1

 UniProtKB/Swiss-Prot
 P01308, Q5EEX2

 UniProtKB/TrEMBL
 I3WAC9

Conserved Domains (1) <u>summary</u>

Location:26 → 110

| Coduction:26 → 110 | Location:26 → 110 | Loc

RefSeqs of Annotated Genomes: Homo sapiens Annotation Release 110 <u>details...</u> ₽

The following sections contain reference sequences that belong to a specific genome build. Explain

#### Reference GRCh38.p14 Primary Assembly

#### Genomic

1. NC\_000011.10 Reference GRCh38.p14 Primary Assembly

Range	21597792161209 complement	
Download	GenBank, FASTA, Sequence Viewer (Graphics)	

#### Alternate T2T-CHM13v2.0

# Genomic

# 1. NC\_060935.1 Alternate T2T-CHM13v2.0

Range	22474272248857 complement	
Download	GenBank, FASTA, Sequence Viewer (Graphics)	

# **Related sequences**

		Items 1 - 25 of 26 < Prev Page 1 of 2 Next >
Nucleotide		Protein
Heading	Accession and Version	FIOLEIII
genomic	AC132217.15 (8641987850)	None
genomic	AH002844.2	AAA59172.1
genomic	AJ009655.1	CAA08766.1
genomic	CH471158.1	EAX02488.1
		EAX02489.1
genomic	CP068267.2 (22474272248857)	None
genomic	L15440.1	AAA59179.1
genomic	M10039.1	AAA59173.1
genomic	<u>\$99616.1</u>	None
genomic	<u>V00565.1</u>	CAA23828.1
mRNA	AY899304.1	AAW83741.1
mRNA	BC005255.1	AAH05255.1
mRNA	BM510347.1	None
mRNA	BM510748.1	None
mRNA	BP322143.1	None
mRNA	BT006808.1	AAP35454.1
mRNA	DQ778082.1	<u>ABI63346.1</u>
mRNA	<u>JF909299.1</u>	AEG19452.1
mRNA	<u>JQ951950.1</u>	<u>AFK93533.1</u>
mRNA	MT335687.1	QMS45321.1
mRNA	MT335688.1	QMS45322.1
mRNA	MT335689.1	QMS45323.1
mRNA	MT335690.1	QMS45324.1
mRNA	MT335691.1	<u>QMS45325.1</u>
mRNA	MT335692.1	QMS45326.1

Nucleotide			Protein		
Heading	Accession a	nd Version	Protein		
mRNA	MT501209.1		None		
			Items 1 - 25 of 26	< Prev	Page 1 of 2 Next >
Protein Accession		Links			
Protein Accession		GenPept Link	UniProtKB Link		
P01308.1 <u>GenPept</u>			UniProtKB/Swiss-Prot:P01308		

# **Additional links**

Locus-specific Databases

INS database

Gene LinkOut