

Tax_ID	GeneID	GO_ID	Evidence	Qualifier	GO_term
10090	59027	GO:0005634	ISO	-	nucleus
10116	297508	GO:0005737	ISO	-	cytoplasm
10116	297508	GO:0005886	IDA	-	plasma membrane
10116	297508	GO:0005737	IDA	-	cytoplasm
10116	297508	GO:0005634	IEA	-	nucleus
10116	297508	GO:0005634	IDA	-	nucleus
10116	297508	GO:0005615	IEA	-	extracellular space
9606	10135	GO:0070062	HDA	-	extracellular exosome
10090	59027	GO:0005576	IEA	-	extracellular region
10090	59027	GO:0005615	IEA	-	extracellular space
10116	297508	GO:0016607	IEA	-	nuclear speck
10116	297508	GO:0016607	ISO	-	nuclear speck
10116	297508	GO:0005737	IEA	-	cytoplasm
10116	297508	GO:0030054	ISO	-	cell junction
10090	59027	GO:0005737	IDA	-	cytoplasm
10090	59027	GO:0016607	ISO	-	nuclear speck
9606	10135	GO:0005829	TAS	-	cytosol
9606	10135	GO:0016607	IDA	-	nuclear speck
10090	59027	GO:0005737	ISO	-	cytoplasm
10090	59027	GO:0005886	ISO	-	plasma membrane
10090	59027	GO:0030054	ISO	-	cell junction
9606	10135	GO:0030054	IDA	-	cell junction
10116	297508	GO:0030054	IEA	-	cell junction
10090	59027	GO:0005829	TAS	-	cytosol
10090	59027	GO:0042802	IPI	-	identical protein binding
10090	59027	GO:0016740	IEA	-	transferase activity
10090	59027	GO:0016757	IEA	-	transferase activity, transferring glycosyl groups
10116	297508	GO:0005125	IEA	-	cytokine activity
10116	297508	GO:0004514	IEA	-	nicotinate-nucleotide diphosphorylase (carboxylating) activity
10116	297508	GO:0000166	IDA	-	nucleotide binding
10090	59027	GO:0042802	ISO	-	identical protein binding
10090	59027	GO:0047280	IDA	-	nicotinamide phosphoribosyltransferase activity
10090	59027	GO:0047280	ISO	-	nicotinamide phosphoribosyltransferase activity
10090	59027	GO:0003824	IEA	-	catalytic activity
9606	10135	GO:0004514	IEA	-	nicotinate-nucleotide diphosphorylase (carboxylating) activity
10116	297508	GO:0005125	IDA	-	cytokine activity
10116	297508	GO:0042802	IDA	-	identical protein binding
9606	10135	GO:0005125	IEA	-	cytokine activity
9606	10135	GO:0005515	IPI	-	protein binding
10116	297508	GO:0047280	ISO	-	nicotinamide phosphoribosyltransferase activity
10116	297508	GO:0047280	IEA	-	nicotinamide phosphoribosyltransferase activity
10090	59027	GO:0005125	ISO	-	cytokine activity
10116	297508	GO:0042802	ISO	-	identical protein binding

9606	10135	GO:0042802	IPI	-	identical protein binding
9606	10135	GO:0047280	TAS	-	nicotinamide phosphoribosyltransferase activity
10090	59027	GO:0004514	IEA	-	nicotinate-nucleotide diphosphorylase (carboxylating) activity
10090	59027	GO:0000166	ISO	-	nucleotide binding
10116	297508	GO:0047280	IDA	-	nicotinamide phosphoribosyltransferase activity
10090	59027	GO:0001774	ISO	-	microglial cell activation
10090	59027	GO:0007623	IEP	-	circadian rhythm
10090	59027	GO:0051770	ISO	-	positive regulation of nitric-oxide synthase biosynthetic process
9606	10135	GO:0007165	TAS	-	signal transduction
9606	10135	GO:0007267	TAS	-	cell-cell signaling
9606	10135	GO:0007623	TAS	-	circadian rhythm
9606	10135	GO:0008286	IDA	NOT	insulin receptor signaling pathway
9606	10135	GO:0045944	IDA	-	positive regulation of transcription by RNA polymerase II
9606	10135	GO:0060612	IDA	NOT	adipose tissue development
9606	10135	GO:0051770	IDA	-	positive regulation of nitric-oxide synthase biosynthetic process
10090	59027	GO:0009435	IDA	-	NAD biosynthetic process
9606	10135	GO:0032922	ISS	-	circadian regulation of gene expression
9606	10135	GO:0034356	TAS	-	NAD biosynthesis via nicotinamide riboside salvage pathway
9606	10135	GO:0008284	TAS	-	positive regulation of cell population
10116	297508	GO:0051770	ISO	-	positive regulation of nitric-oxide synthase biosynthetic process
10116	297508	GO:0014070	IEP	-	response to organic cyclic compound
10116	297508	GO:0014916	IMP	-	regulation of lung blood pressure
10116	297508	GO:0032922	IEA	-	circadian regulation of gene expression
10116	297508	GO:0032922	ISO	-	circadian regulation of gene expression
10116	297508	GO:0032922	ISS	-	circadian regulation of gene expression
10090	59027	GO:0048511	IEA	-	rhythmic process
10116	297508	GO:0048661	IMP	-	positive regulation of smooth muscle cell proliferation
10116	297508	GO:0009435	IEA	-	NAD biosynthetic process
10116	297508	GO:0060612	ISO	NOT	adipose tissue development
10116	297508	GO:0070997	IEP	-	neuron death
10116	297508	GO:0071479	IEP	-	cellular response to ionizing radiation
10116	297508	GO:0090650	IEP	-	cellular response to oxygen-glucose deprivation
10116	297508	GO:1904646	IEP	-	cellular response to amyloid-beta
10116	297508	GO:1905377	IEP	-	response to D-galactose
10116	297508	GO:0045944	ISO	-	positive regulation of transcription by RNA polymerase II
10116	297508	GO:0007165	IEA	-	signal transduction
10090	59027	GO:0014916	ISO	-	regulation of lung blood pressure
10090	59027	GO:0019363	IEA	-	pyridine nucleotide biosynthetic process
10090	59027	GO:0032922	IMP	-	circadian regulation of gene expression

10090	59027	GO:0045944	ISO	-	positive regulation of transcription by RNA polymerase II
10090	59027	GO:0048661	ISO	-	positive regulation of smooth muscle cell proliferation
10116	297508	GO:2000773	IDA	-	negative regulation of cellular senescence
10116	297508	GO:0010507	IMP	-	negative regulation of autophagy
10116	297508	GO:0001774	IMP	-	microglial cell activation
10116	297508	GO:0009435	ISO	-	NAD biosynthetic process
10116	297508	GO:0007565	IEP	-	female pregnancy
10116	297508	GO:0007568	IEP	-	aging
10116	297508	GO:0007623	IEP	-	circadian rhythm
10116	297508	GO:0007623	ISO	-	circadian rhythm
10116	297508	GO:0008286	ISO	NOT	insulin receptor signaling pathway
10090	59027	GO:0010507	ISO	-	negative regulation of autophagy
10090	59027	GO:2000773	ISO	-	negative regulation of cellular senescence

