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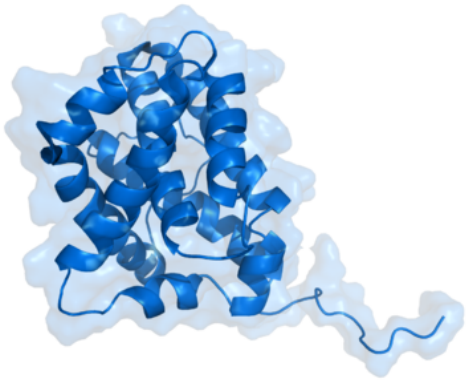
Bcl-2-associated X protein

Apoptosis regulator BAX, also known as **bcl-2-like protein 4**, is a protein that in humans is encoded by the *BAX* gene. *BAX* is a member of the Bcl-2 gene family. BCL2 family members form hetero- or homodimers and act as anti- or pro-apoptotic regulators that are involved in a wide variety of cellular activities. This protein forms a heterodimer with BCL2, and functions as an apoptotic activator. This protein is reported to interact with, and increase the opening of, the mitochondrial voltage-dependent anion channel (VDAC), which leads to the loss in membrane potential and the release of cytochrome c. The expression of this gene is regulated by the tumor suppressor P53 and has been shown to be involved in P53-mediated apoptosis.[5]

Structure

The *BAX* gene was the first identified pro-apoptotic member of the Bcl-2 protein family.[6] Bcl-2 family members share one or more of the four characteristic domains of homology entitled the Bcl-2 homology (BH) domains (named BH1, BH2, BH3 and BH4), and can form hetero- or homodimers.[6][7] These domains are composed of nine α-helices, with a hydrophobic α-helix core surrounded by amphipathic helices and a transmembrane C-terminal α-helix anchored to the mitochondrial outer membrane (MOM). A hydrophobic

BAX



Available structures

PDB Ortholog search: PDBe (https://www.ebi.ac.uk/pdbe/searchResults.html?display=both&term=Q07813%20or%20Q07812%20or%20Q5ZPJ0%20or%20H0YA56) RCSB (https://www.rcsb.org/search?q=rcsb_polymer_entity_container_identifiers.reference_sequence_identifiers.database_name:UniProt%20AND%20rcsb_polymer_entity_container_identifiers.reference_sequence_identifiers.database_accession:Q07813,Q07812,Q5ZPJ0,H0YA56)

List of PDB id codes

4BDU (https://www.rcsb.org/structure/4BDU), 1F16 (https://www.rcsb.org/structure/1F16), 2G5B (https://www.rcsb.org/structure/2G5B), 2K7W (https://www.rcsb.org/structure/2K7W), 2LR1 (https://www.rcsb.org/structure/2LR1), 3PK1 (https://www.rcsb.org/structure/3PK1), 3PL7 (https://www.rcsb.org/structure/3PL7), 4BD2 (https://www.rcsb.org/structure/4BD2), 4BD6 (https://www.rcsb.org/structure/4BD6), 4BD7 (https://www.rcsb.org/structure/4BD7), 4BD8 (https://www.rcsb.org/structure/4BD8), 4UF2 (https://www.rcsb.org/structure/4UF2), 4ZIE (https://www.rcsb.org/structure/4ZIE), 4ZIF (https://www.rcsb.org/structure/4ZIF), 4ZIG (https://www.rcsb.org/structure/4ZIG), 4ZIH (https://www.rcsb.org/structure/4ZIH), 4ZII (https://www.rcsb.org/structure/4ZII), 4S0O (https://www.rcsb.org/structure/4S0O)

groove formed along the C-terminal of α2 to the N-terminal of α5, and some residues from α8, binds the BH3 domain of other BAX or BCL-2 proteins in its active form. In the protein's inactive form, the groove binds its transmembrane domain, transitioning it from a membrane-bound to a cytosolic protein. A smaller hydrophobic groove formed by the α1 and α6 helices is located on the opposite side of the protein from the major groove, and may serve as a BAX activation site.[8]

Orthologs of the *BAX* gene have been identified in most mammals for which complete genome data are available.[9]

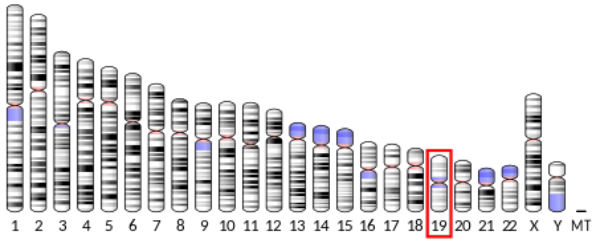
Function

In healthy mammalian cells, the majority of BAX is found in the cytosol, but upon initiation of apoptotic signaling, Bax undergoes a conformational shift. Upon induction of apoptosis, BAX becomes organelle membrane-associated, and in particular, mitochondrial membrane associated.[10][11][12][13][14]

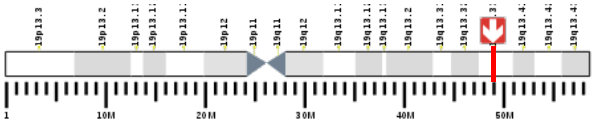
BAX is believed to interact with, and induce the opening of the mitochondrial voltage-dependent anion channel, VDAC.[15] Alternatively, growing evidence also suggests that activated BAX and/or Bak form an oligomeric pore, MAC in the MOM (mitochondrial outer membrane).[16][17] This results in the release of cytochrome c and other pro-apoptotic factors from the mitochondria, often referred to as mitochondrial outer membrane permeabilization, leading to activation of caspases.[18] This defines a direct role for BAX in

Identifiers	
Aliases	BAX (https://www.genenames.org/data/gene-symbol-report/#!/hgnc_id/959), BCL2L4, BCL2 associated X protein, BCL2 associated X, apoptosis regulator
External IDs	OMIM: 600040 (https://omim.org/entry/600040) MGI: 99702 (http://www.informatics.jax.org/marker/MGI:99702) HomoloGene: 7242 (https://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=homologene&dopt=HomoloGene&list_uids=7242) GeneCards: BAX (https://www.genecards.org/cgi-bin/carddisp.pl?gene=BAX)

Gene location (Human)

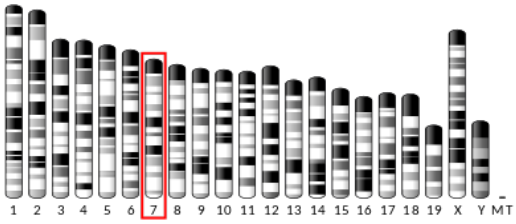


Chr. Chromosome 19 (human)[1]

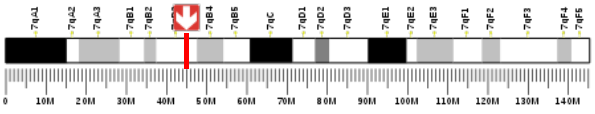


Band 19q13.33 **Start** 48,954,815 bp[1]
End 48,961,798 bp[1]

Gene location (Mouse)



Chr. Chromosome 7 (mouse)[2]



Band 7 B3|7 29.32 cM **Start** 45,111,121 bp[2]
End 45,116,322 bp[2]

RNA expression pattern

Bgee (https://bgee.org/)	Human	Mouse (ortholog)
	Top expressed in (https://bgee.org/gene/ENSG00000087088)	Top expressed in (https://bgee.org/gene/ENSMUSG00000003873)

mitochondrial outer membrane permeabilization. BAX activation is stimulated by various abiotic factors, including heat, hydrogen peroxide, low or high pH, and mitochondrial membrane remodeling. In addition, it can become activated by binding BCL-2, as well as non-BCL-2 proteins such as p53 and Bif-1. Conversely, BAX can become inactivated by interacting with VDAC2, Pin1, and IBRDC2.[8]

Clinical significance

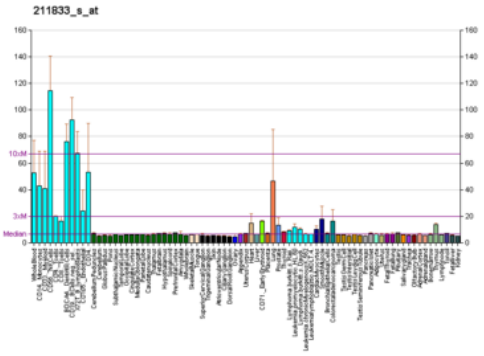
The expression of *BAX* is upregulated by the tumor suppressor protein p53, and BAX has been shown to be involved in p53-mediated apoptosis. The p53 protein is a transcription factor that, when activated as part of the cell's response to stress, regulates many downstream target genes, including *BAX*. Wild-type p53 has been demonstrated to upregulate the transcription of a chimeric reporter plasmid utilizing the consensus promoter sequence of *BAX* approximately 50-fold over mutant p53. Thus it is likely that p53 promotes *BAX's* apoptotic faculties *in vivo* as a primary transcription factor. However, p53 also has a transcription-independent role in apoptosis. In particular, p53 interacts with BAX, promoting its activation as well as its insertion into the mitochondrial membrane.[19][20][21]

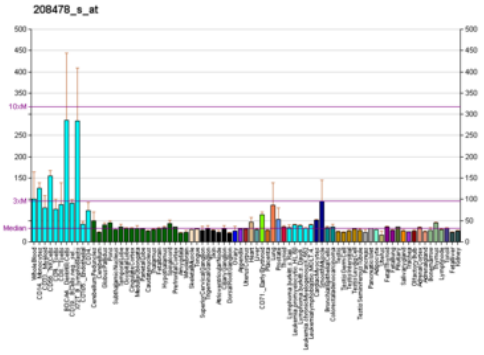
Drugs that activate BAX, such as ABT-737, a BH3 mimetic, hold promise as anticancer treatments by inducing apoptosis in cancer cells.[8] For instance, binding of HA-BAD to BCL-xL and concomitant disruption of

- stromal cell of endometrium
- monocyte
- gallbladder
- right lung
- rectum
- upper lobe of left lung
- spleen
- ascending aorta
- right coronary artery
- canal of the cervix
- yolk sac
- neural tube
- calvaria
- ganglionic eminence
- medial ganglionic eminence
- lip
- somite
- mirror
- abdominal wall
- thymus

More reference expression data (https://bgee.org/gene/ENSG00000087088)

BioGPS (http://biogps.org/)





More reference expression data (http://biogps.org/gene/581/)

Gene ontology

Molecular function

- protein homodimerization activity (http://amigo.geneontology.org/amigo/term/GO:0042803)
- channel activity (http://amigo.geneontology.org/amigo/term/GO:0015267)
- protein binding (http://amigo.geneontology.org/a

BAX:BCL-xL interaction was found to partly reverse paclitaxel resistance in human ovarian cancer cells.[22] Meanwhile, excessive apoptosis in such conditions as ischemia reperfusion injury and amyotrophic lateral sclerosis may benefit from drug inhibitors of BAX.[8]

Interactions

Bcl-2-associated X protein has been shown to interact with:

- Bcl-2,[6][7][23][24][25]
- BCL2L1,[7][22][26][27]
- BCL2A1[7][28]
- SH3GLB1,[13][29]
- SLC25A4,[30]
- VDAC1,[15][18]
- TCTP,[31]
- YWHAQ,[32]
- Bid,[8]
- Bim,[8]
- Puma,[8]
- Noxa,[8]
- Mfn2,[33]
- cholesterol,[34] and
- cardiolipin.[34]

See also

- Apoptosis
- Apoptosome
- Bcl-2
- BH3 interacting domain death agonist (BID)
- Caspases
- Cytochrome c
- Noxa
- Mitochondrion
- p53 upregulated modulator of

	migo/term/GO:0005515)
	▪ BH3 domain binding (http://amigo.geneontology.org/amigo/term/GO:0051434)
	▪ chaperone binding (http://amigo.geneontology.org/amigo/term/GO:0051087)
	▪ protein heterodimerization activity (http://amigo.geneontology.org/amigo/term/GO:0046982)
	▪ identical protein binding (http://amigo.geneontology.org/amigo/term/GO:0042802)
	▪ lipid binding (http://amigo.geneontology.org/amigo/term/GO:0008289)
	▪ Hsp70 protein binding (http://amigo.geneontology.org/amigo/term/GO:0030544)
Cellular component	▪ cytosol (http://amigo.geneontology.org/amigo/term/GO:0005829)
	▪ nuclear envelope (http://amigo.geneontology.org/amigo/term/GO:0005635)
	▪ membrane (http://amigo.geneontology.org/amigo/term/GO:0016020)
	▪ Bcl-2 family protein complex (http://amigo.geneontology.org/amigo/term/GO:0097136)
	▪ mitochondrion (http://amigo.geneontology.org/amigo/term/GO:0005739)
	▪ nucleus (http://amigo.geneontology.org/amigo/term/GO:0005634)
	▪ mitochondrial permeability transition pore complex (http://amigo.geneontology.org/amigo/term/GO:0005757)
	▪ mitochondrial membrane (http://amigo.geneontology.org/amigo/term/GO:0031966)
	▪ BAX complex (http://amigo.geneontology.org/amigo/term/GO:0097144)
	▪ endoplasmic reticulum (http://amigo.geneontology.org/amigo/term/GO:0005783)
	▪ extracellular exosome (http://amigo.geneontology.org/amigo/term/GO:0070062)
	▪ pore complex (http://amigo.geneontology.org/amigo/term/GO:0046930)
	▪ integral component of membrane (http://amigo.geneontology.org/amigo/term/GO:0016021)

apoptosis (PUMA)	▪ intracellular anatomical structure (http://amigo.geneontology.org/amigo/term/GO:0005622) ▪ endoplasmic reticulum membrane (http://amigo.geneontology.org/amigo/term/GO:0005789) ▪ cytoplasm (http://amigo.geneontology.org/amigo/term/GO:0005737) ▪ mitochondrial outer membrane (http://amigo.geneontology.org/amigo/term/GO:0005741) ▪ cell periphery (http://amigo.geneontology.org/amigo/term/GO:0071944)
Biological process	▪ negative regulation of neuron apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0043524) ▪ response to ionizing radiation (http://amigo.geneontology.org/amigo/term/GO:0010212) ▪ germ cell development (http://amigo.geneontology.org/amigo/term/GO:0007281) ▪ positive regulation of calcium ion transport into cytosol (http://amigo.geneontology.org/amigo/term/GO:0010524) ▪ glycosphingolipid metabolic process (http://amigo.geneontology.org/amigo/term/GO:0006687) ▪ B cell apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0001783) ▪ response to salt stress (http://amigo.geneontology.org/amigo/term/GO:0009651) ▪ Sertoli cell proliferation (http://amigo.geneontology.org/amigo/term/GO:0060011) ▪ thymocyte apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0070242) ▪ T cell homeostatic proliferation (http://amigo.geneontology.org/amigo/term/GO:0001777) ▪ post-embryonic development (http://amigo.geneontology.org/amigo/term/GO:0009791) ▪ regulation of mitochondrial membrane permeability involved in apoptotic process (http://amigo.geneontology.org/amigo/term/GO:1902108) ▪ negative regulation of protein binding (http://amigo.geneontology.org/amigo/term/GO:0032091)

- cellular response to DNA damage stimulus (http://amigo.geneontology.org/amigo/term/GO:0006974)
- regulation of mitochondrial membrane permeability involved in programmed necrotic cell death (http://amigo.geneontology.org/amigo/term/GO:1902445)
- odontogenesis of dentin-containing tooth (http://amigo.geneontology.org/amigo/term/GO:0042475)
- positive regulation of extrinsic apoptotic signaling pathway in absence of ligand (http://amigo.geneontology.org/amigo/term/GO:2001241)
- positive regulation of IRE1-mediated unfolded protein response (http://amigo.geneontology.org/amigo/term/GO:1903896)
- blood vessel remodeling (http://amigo.geneontology.org/amigo/term/GO:0001974)
- positive regulation of neuron apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0043525)
- apoptotic process involved in blood vessel morphogenesis (http://amigo.geneontology.org/amigo/term/GO:1902262)
- activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c (http://amigo.geneontology.org/amigo/term/GO:0008635)
- spermatogenesis (http://amigo.geneontology.org/amigo/term/GO:0007283)
- apoptotic signaling pathway (http://amigo.geneontology.org/amigo/term/GO:0097190)
- cell population proliferation (http://amigo.geneontology.org/amigo/term/GO:0008283)
- mitochondrion morphogenesis (http://amigo.geneontology.org/amigo/term/GO:0070584)
- activation of cysteine-type endopeptidase activity involved in apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0006919)
- negative regulation of cell population

proliferation (http://amigo.geneontology.org/amigo/term/GO:0008285)

- cellular response to organic substance (http://amigo.geneontology.org/amigo/term/GO:0071310)
- B cell homeostatic proliferation (http://amigo.geneontology.org/amigo/term/GO:0002358)
- limb morphogenesis (http://amigo.geneontology.org/amigo/term/GO:0035108)
- release of matrix enzymes from mitochondria (http://amigo.geneontology.org/amigo/term/GO:0032976)
- extrinsic apoptotic signaling pathway (http://amigo.geneontology.org/amigo/term/GO:0097191)
- kidney development (http://amigo.geneontology.org/amigo/term/GO:0001822)
- activation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway (http://amigo.geneontology.org/amigo/term/GO:0097296)
- negative regulation of apoptotic signaling pathway (http://amigo.geneontology.org/amigo/term/GO:2001234)
- myeloid cell homeostasis (http://amigo.geneontology.org/amigo/term/GO:0002262)
- regulation of neuron apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0043523)
- regulation of cysteine-type endopeptidase activity involved in apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0043281)
- endoplasmic reticulum calcium ion homeostasis (http://amigo.geneontology.org/amigo/term/GO:0032469)
- response to wounding (http://amigo.geneontology.org/amigo/term/GO:0009611)
- intrinsic apoptotic signaling pathway by p53 class mediator (http://amigo.geneontology.org/amigo/term/GO:0072332)
- hypothalamus development (http://amigo.geneontology.org/amigo/term/GO:0021854)
- viral process (http://amigo.geneontology.org/amigo/term/GO:0016032)

- protein homooligomerization (http://amigo.geneontology.org/amigo/term/GO:0051260)
- response to gamma radiation (http://amigo.geneontology.org/amigo/term/GO:0010332)
- negative regulation of fibroblast proliferation (http://amigo.geneontology.org/amigo/term/GO:0048147)
- positive regulation of intrinsic apoptotic signaling pathway (http://amigo.geneontology.org/amigo/term/GO:2001244)
- response to toxic substance (http://amigo.geneontology.org/amigo/term/GO:0009636)
- B cell negative selection (http://amigo.geneontology.org/amigo/term/GO:0002352)
- mitochondrial fusion (http://amigo.geneontology.org/amigo/term/GO:0008053)
- neuron apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0051402)
- male gonad development (http://amigo.geneontology.org/amigo/term/GO:0008584)
- positive regulation of B cell apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0002904)
- regulation of protein heterodimerization activity (http://amigo.geneontology.org/amigo/term/GO:0043497)
- positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway (http://amigo.geneontology.org/amigo/term/GO:1901030)
- cellular response to UV (http://amigo.geneontology.org/amigo/term/GO:0034644)
- sex differentiation (http://amigo.geneontology.org/amigo/term/GO:0007548)
- neuron migration (http://amigo.geneontology.org/amigo/term/GO:0001764)
- B cell homeostasis (http://amigo.geneontology.org/amigo/term/GO:0001782)
- positive regulation of release of sequestered calcium ion into cytosol (http://amigo.geneontology.org/amigo/term/GO:0051281)

- positive regulation of apoptotic process involved in mammary gland involution (http://amigo.geneontology.org/amigo/term/GO:0060058)
- nervous system development (http://amigo.geneontology.org/amigo/term/GO:0007399)
- spermatid differentiation (http://amigo.geneontology.org/amigo/term/GO:0048515)
- development of secondary sexual characteristics (http://amigo.geneontology.org/amigo/term/GO:0045136)
- positive regulation of developmental pigmentation (http://amigo.geneontology.org/amigo/term/GO:0048087)
- retina development in camera-type eye (http://amigo.geneontology.org/amigo/term/GO:0060041)
- response to axon injury (http://amigo.geneontology.org/amigo/term/GO:0048678)
- positive regulation of mitochondrial membrane permeability involved in apoptotic process (http://amigo.geneontology.org/amigo/term/GO:1902110)
- cerebral cortex development (http://amigo.geneontology.org/amigo/term/GO:0021987)
- ovarian follicle development (http://amigo.geneontology.org/amigo/term/GO:0001541)
- fertilization (http://amigo.geneontology.org/amigo/term/GO:0009566)
- ectopic germ cell programmed cell death (http://amigo.geneontology.org/amigo/term/GO:0035234)
- homeostasis of number of cells within a tissue (http://amigo.geneontology.org/amigo/term/GO:0048873)
- positive regulation of release of cytochrome c from mitochondria (http://amigo.geneontology.org/amigo/term/GO:0090200)
- B cell receptor apoptotic signaling pathway (http://amigo.geneontology.org/amigo/term/GO:1990117)
- negative regulation of endoplasmic reticulum

calcium ion concentration (http://amigo.geneontology.org/amigo/term/GO:0032471)

- regulation of protein homodimerization activity (http://amigo.geneontology.org/amigo/term/GO:0043496)
- apoptotic process involved in embryonic digit morphogenesis (http://amigo.geneontology.org/amigo/term/GO:1902263)
- leukocyte homeostasis (http://amigo.geneontology.org/amigo/term/GO:0001776)
- positive regulation of apoptotic DNA fragmentation (http://amigo.geneontology.org/amigo/term/GO:1902512)
- mitochondrial fragmentation involved in apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0043653)
- positive regulation of endoplasmic reticulum unfolded protein response (http://amigo.geneontology.org/amigo/term/GO:1900103)
- establishment or maintenance of transmembrane electrochemical gradient (http://amigo.geneontology.org/amigo/term/GO:0010248)
- homeostasis of number of cells (http://amigo.geneontology.org/amigo/term/GO:0048872)
- vagina development (http://amigo.geneontology.org/amigo/term/GO:0060068)
- post-embryonic camera-type eye morphogenesis (http://amigo.geneontology.org/amigo/term/GO:0048597)
- regulation of mammary gland epithelial cell proliferation (http://amigo.geneontology.org/amigo/term/GO:0033599)
- retinal cell programmed cell death (http://amigo.geneontology.org/amigo/term/GO:0046666)
- regulation of cell cycle (http://amigo.geneontology.org/amigo/term/GO:0051726)
- regulation of mitochondrial membrane potential (http://amigo.geneontology.org/amigo/term/GO:0051881)
- intrinsic apoptotic signaling pathway in response

to endoplasmic reticulum stress (http://amigo.geneontology.org/amigo/term/GO:0070059)

- apoptotic mitochondrial changes (http://amigo.geneontology.org/amigo/term/GO:0008637)
- protein complex oligomerization (http://amigo.geneontology.org/amigo/term/GO:0051259)
- regulation of nitrogen utilization (http://amigo.geneontology.org/amigo/term/GO:0006808)
- negative regulation of peptidyl-serine phosphorylation (http://amigo.geneontology.org/amigo/term/GO:0033137)
- positive regulation of apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0043065)
- positive regulation of protein oligomerization (http://amigo.geneontology.org/amigo/term/GO:0032461)
- extrinsic apoptotic signaling pathway via death domain receptors (http://amigo.geneontology.org/amigo/term/GO:0008625)
- release of cytochrome c from mitochondria (http://amigo.geneontology.org/amigo/term/GO:0001836)
- apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0006915)
- protein insertion into mitochondrial membrane involved in apoptotic signaling pathway (http://amigo.geneontology.org/amigo/term/GO:0001844)
- intrinsic apoptotic signaling pathway (http://amigo.geneontology.org/amigo/term/GO:0097193)
- regulation of apoptotic process (http://amigo.geneontology.org/amigo/term/GO:0042981)
- DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (http://amigo.geneontology.org/amigo/term/GO:0006977)
- intrinsic apoptotic signaling pathway in response to DNA damage (http://amigo.geneontology.org/amigo/term/GO:0008630)
- extrinsic apoptotic signaling pathway in absence

of ligand (http://amigo.geneontology.org/amigo/term/GO:0097192)

- transcription initiation from RNA polymerase II promoter (http://amigo.geneontology.org/amigo/term/GO:0006367)
- cellular response to unfolded protein (http://amigo.geneontology.org/amigo/term/GO:0034620)
- negative regulation of mitochondrial membrane potential (http://amigo.geneontology.org/amigo/term/GO:0010917)

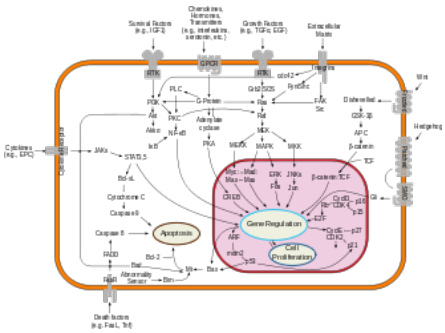
Sources: Amigo (http://amigo.geneontology.org/) / QuickGO (https://www.ebi.ac.uk/QuickGO/)

Orthologs

Species	Human	Mouse
Entrez	581 (https://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=retrieve&dopt=default&list_uids=581&rn=1)	12028 (https://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=retrieve&dopt=default&list_uids=12028&rn=1)
Ensembl	ENSG00000087088 (http://www.ensembl.org/Homo_sapiens/geneview?gene=ENSG00000087088;db=core)	ENSMUSG00000003873 (http://www.ensembl.org/Mus_musculus/geneview?gene=ENSMUSG00000003873;db=core)
UniProt	Q07812 (https://www.uniprot.org/uniprot/Q07812) Q5ZPJ0 (https://www.uniprot.org/uniprot/Q5ZPJ0)	Q07813 (https://www.uniprot.org/uniprot/Q07813)
RefSeq (mRNA)	**NM_001291428 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NM_001291428)** **NM_001291429 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=N**	NM_007527 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NM_007527)

	M_001291429) **NM_001291430 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NM_001291430)** **NM_001291431 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NM_001291431)** **NM_004324 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NM_004324)** NM_138761 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NM_138761) NM_138762 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NM_138762) NM_138763 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NM_138763) NM_138764 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NM_138764)	
RefSeq (protein)	**NP_001278357 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_001278357)** **NP_001278358 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_001278358)** **NP_001278359 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_001278359)** **NP_001278360 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=N**	NP_031553 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_031553)

	P_001278360) NP_004315 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_004315) NP_620116 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_620116) NP_620118 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_620118) NP_620119 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_620119) NP_001278358.1 (https://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=NP_001278358.1)	
Location (UCSC)	Chr 19: 48.95 – 48.96 Mb (https://genome.ucsc.edu/cgi-bin/hgTracks?org=Human&db=hg38&position=chr19:48954815-48961798)	Chr 7: 45.11 – 45.12 Mb (https://genome.ucsc.edu/cgi-bin/hgTracks?org=Mouse&db=mm0&position=chr7:45111121-45116322)
PubMed search	[3]	[4]
	Wikidata	
	View/Edit Human	View/Edit Mouse



Overview of signal transduction pathways involved with apoptosis.

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External links

- Human *BAX* (https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&singleSearch=knownCanonical&position=BAX) genome location and *BAX* (https://genome.ucsc.edu/cgi-bin/hgGene?db=hg38&hgg_type=knownGene&hgg_gene=BAX) gene details page in the UCSC Genome Browser.
- Overview of all the structural information available in the PDB for UniProt: *Q07812 (https://www.ebi.ac.uk/pdbe/pdbe-kb/proteins/Q07812)* (Human Apoptosis regulator BAX) at the PDBe-KB.
- Overview of all the structural information available in the PDB for UniProt: *Q07813 (https://www.ebi.ac.uk/pdbe/pdbe-kb/proteins/Q07813)* (Mouse Apoptosis regulator BAX) at the PDBe-KB.