

BAD (BCL2-antagonist of cell death)

Identity

Other names **BAD (BCLXL/BCL2 associated death promoter homolog**

BBC2

BCL2L8 (Bcl-2-like 8 protein)

Location 11q13.1

DNA/RNA

Description The gene spans 14,9 kb, on reverse strand

Transcription alternate splicing encoding for the same protein

Protein

Description 168 amino acids, 18,4 kDa.; 'BH3 only' Bcl2 family member (do not possess BH1, 2 and 4 domains). The BH3 domain is essential for proapoptotic function. There is structural similarities between the Bcl2 family proteins and bacterial toxins which form membrane pores after oligomerisation. Do not possess a transmembrane domain in COOH term, in contrast with a number of other BCL2 family members; may be phosphorylated on serine residues (see below).

Expression wide

Localisation cytoplasm vs membrane of the mitochondria (see below)

Function Proapoptotic protein:

In its inactive form, Bad is phosphorylated. Proteins which phosphorylate BAD are: RAF1, ribosomal S6 kinase 1 (p90/RSK1), AKT/PKB (PI3K-AKT pathway) at Serine 136 (in murine BAD), PKA at Ser 155, PIM1 and PIM2 at Ser 112 (Ser 75, 99, and 118 in human BAD correspond to Ser 112, 136, and 155 in murine BAD respectively). Phosphorylated BAD interacts with 14-3-3 scaffold proteins in the cytoplasm (14-3-3 is a protein which can interact with a hundred other proteins).

Cleavage of the 14-3-3 protein by caspase-3 allows the release of BAD from its association with the 14-3-3 protein and facilitates BAD translocation from the cytosol to the mitochondria. Under apoptotic stimuli also, calcineurin (Ca⁺⁺ activated protein phosphatase) dephosphorylates BAD, also allowing its dissociation from 14-3-3.

Once BAD is dephosphorylated (posttranslational modification), it is active; it translocates to the outer membrane of the mitochondria (like other proapoptotic members of the Bcl2 family), and forms heterodimers with BCL-XL (and, to a lesser extent, heterodimers with BCL2 or BCL2L2) to block BCL-XL antiapoptotic function. Dimers BCL-XL /BAD are similar to dimers BCL-XL /BAK

Homology Bcl2 family members:

The antiapoptotic members with BH 1 to 4 domains: [BCL2](#) (18q21), BCL1L1/BCLX-L ID: n129> (20q11), BCL2L2/BCL-W (14q11), BCL1L10/BCL-B/BOO/DIVA (15q21), BCL2A1/BFL1/A1 (15q24), BNIP1/EIB-19K (5q33), MCL1 (1q21) HOMOLOG

The proapoptotic members with BH 1 to 3 domains: BAK1/BCL2L7 (6p21), BAX (19q13), (22q11),

The only-BH3 apoptotic members: [BBC3/PUMA](#) (19q13), BCL2L11/BIM/BOD (2q13), BID (22q11), BIK/NBK/BBC1 (22q13), BLK (8p23), BMF (15q14), BNIP3/NIP3 (10q26), BMIP3L/NIX (8p21), HRK/DP5/BID3 (12q24), PMAIP1/NOXA (18q21)

External links

	Nomenclature
GDB	BAD
Entrez Gene	BAD_572 BCL2-antagonist of cell death
	Cards
Atlas	BADID130ch11q13
GeneCards	BAD
Ensembl	BAD
CancerGene	BAD
Genatlas	BAD
GeneLynx	BAD
eGenome	BAD
euGene	572
	Genomic and cartography
GoldenPath	BAD - 11q13.1 chr11:63793878-63808657 - 11q13.1 (hg17-May_2004)
Ensembl	BAD - 11q13.1 [CytoView]
NCBI	Genes Cyto Gene Seq [Map View - NCBI]
OMIM	Disease map [OMIM]
HomoloGene	BAD
	Gene and transcription
Genbank	AF021792 [SRS] AF021792 [ENTREZ]
Genbank	AF031523 [SRS] AF031523 [ENTREZ]
Genbank	AK023420 [SRS] AK023420 [ENTREZ]
Genbank	BC001901 [SRS] BC001901 [ENTREZ]
Genbank	BE255791 [SRS] BE255791 [ENTREZ]
RefSeq	NM_004322 [SRS] NM_004322 [ENTREZ]
RefSeq	NM_032989 [SRS] NM_032989 [ENTREZ]
RefSeq	NT_086784 [SRS] NT_086784 [ENTREZ]
AceView	BAD AceView - NCBI
TRASER	BAD Traser - Stanford
Unigene	Hs.370254 [SRS] Hs.370254 [NCBI] HS370254 [spliceNest]
	Protein : pattern, domain, 3D structure
SwissProt	Q92934 [SRS] Q92934 [EXPASY] Q92934 [INTERPRO]
Prosite	PS01259 BH3 [SRS] PS01259 BH3 [Expasy]
Interpro	IPR000712 Bcl2_BH [SRS] IPR000712 Bcl2_BH [EBI]
CluSTr	Q92934
Blocks	Q92934
PDB	1G5J [SRS] 1G5J [PdbSum], 1G5J [IMB]
	Polymorphism : SNP, mutations, diseases
OMIM	603167 [map]
GENECLINICS	603167
SNP	BAD [dbSNP-NCBI]
SNP	NM_004322 [SNP-NCI]

[SNP](#) [NM_032989](#) [SNP-NCI]
[SNP](#) [BAD](#) [GeneSNPs - Utah] [BAD](#) [SNP - CSHL] [BAD](#) [HGBASE - SRS]

General knowledge

[Family Browser](#) [BAD](#) [UCSC Family Browser]
[SOURCE](#) [NM_004322](#)
[SOURCE](#) [NM_032989](#)
[SMD](#) [Hs.370254](#)
[SAGE](#) [Hs.370254](#)
[Amigo](#) [process|apoptotic program](#)
[Amigo](#) [component|cytoplasm](#)
[Amigo](#) [process|induction of apoptosis](#)
[Amigo](#) [component|mitochondrial outer membrane](#)
[Amigo](#) [function|protein binding](#)
[BIOCARTA](#) [Role of nicotinic acetylcholine receptors in the regulation of apoptosis](#)
[BIOCARTA](#) [AKT Signaling Pathway](#)
[BIOCARTA](#) [Regulation of BAD phosphorylation](#)
[BIOCARTA](#) [Ceramide Signaling Pathway](#)
[BIOCARTA](#) [Apoptotic Signaling in Response to DNA Damage](#)
[BIOCARTA](#) [Inhibition of Cellular Proliferation by Gleevec](#)
[BIOCARTA](#) [Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation](#)
[BIOCARTA](#) [IL-2 Receptor Beta Chain in T cell Activation](#)
[BIOCARTA](#) [Phosphoinositides and their downstream targets.](#)
[BIOCARTA](#) [Ras Signaling Pathway](#)
[BIOCARTA](#) [Trefoil Factors Initiate Mucosal Healing](#)
[PubGene](#) [BAD](#)

Other databases

[Probes](#)

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Contributor(s)

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