

EBAG9 (Estrogen receptor-binding fragment-associated antigen 9)

Identity

Other names	EB9 PDAF RCAS1
Hugo	<u>EBAG9</u>
Location	8q23.2

DNA/RNA

Description	The EBAG9 gene contains 7 exons and 6 introns. It was predicted to span over approximately 24.6 kb of the genomic DNA with mRNA size approximately 1182 bp. The exon 3 was the smallest at 79 bp; the other exons ranged from 92-720 bp. The EBAG9 was isolated from MCF-7, human breast cancer cell library and it has been reported identical with RCAS1 (receptor-binding cancer antigen expressed on SiSo cells) gene from human uterine adenocarcinoma cell line.
Transcription	The EBAG9 mRNA is up-regulated by estrogen in MCF-7 cells and its promoter responds to estrogen through the complete palindromic estrogen responsive element (ERE) that was located in the 5'-up stream region of the gene.
Pseudogene	One pseudogene located in chromosome 10 associated with RCAS1/EBAG9.

Protein

Description	The EBAG9/RCAS1 consists of 213 amino acids (aa) corresponding to a molecular weight of 24.4 kDa. The EBAG9/RCAS1 has an N-terminal trans-membrane segment (8-27 aa) and a coiled-coil structure in the C-terminal portion (179-206 aa), indicating that the EBAG9/RCAS1 is a type II membrane protein able to form oligomers through the coiled-coil structure, which is expressed on the surfaces of human cancer cells.
Expression	The EBAG9/RCAS1 mRNA is expressed in ovary, testis, prostate, thymus, muscle, and heart. At the protein level the EBAG9/RCAS1 not detected in normal ovary tissues or any of the other above. Neither mRNA nor protein was detected in small intestine, colon, lymph node or peripheral blood lymphocytes.
Localisation	Mainly in the golgi, membrane and cytoplasm of cancer tissues, but its expression is very low or hardly detected in normal tissues.
Function	The biological functions of the EBAG9/RCAS1 secreted by non-cancerous tissues remain unknown. In cancer cells, the EBAG9/RCAS1 is a ligand for a putative receptor present on various human cell lines and normal peripheral lymphocytes such as T-, B- and natural killer (NK)-cells. The expression of this receptor is enhanced by activation of these lymphocytes. The EBAG9/RCAS1 acts to inhibit the growth of receptor-binding cells and induced apoptotic cell death. Over-expression of the EBAG9/RCAS1 is known to inhibit the growth and induced apoptosis of immune cells. As the results, cancer cells might evade immune surveillance by expressing the EBAG9/RCAS1 and inducing the apoptosis of the EBAG9/RCAS1 receptor-positive immune cells.
Homology	Mouse and human EBAG9/RCAS1 shows a high degree of homology at the amino acid level (98%). Mouse (<i>Mus musculus</i>) ebag9 gene spans about 30 kb in genomic DNA and consists of 7 exons. Dog (<i>Canis familiaris</i>) EBAG9/RCAS1 also shows highly homologues to human (96,2%) and to mouse (96,7%). For chimpanzee- (<i>Pan troglodytes</i>) 100%, rat- (<i>Rattus norvegicus</i>) 94% and chicken-ebag9 (<i>Gallus gallus</i>) 91%.

Mutations

Germinal Not known in *Homo sapiens*.
Somatic Not known in *Homo sapiens*.

Implicated in

Entity Immunity

Note During pregnancy, EBAG9/RCAS1 may play a role in the down-regulation of the maternal immune response and may participate in the initiation of the labor. In the healthy women, higher EBAG9/RCAS1 expression was observed in the periovulatory and the secretory menstrual cycle phases than in the proliferation phase. The changes in EBAG9/RCAS1 expression were combined with significant differences in the number of immune cells and their activity. It suggested that EBAG9/RCAS1 endometrial expression may favor the coexistence of active lymphocytes and endometrial cells.

Disease The elevated serum level of EBAG9/RCAS1 reported to be associated with a poor immunological prognosis in HIV-1-infected patients, and also associated with the apoptosis of CD4+ T cells in HIV infection. In addition, the induction and secretion of EBAG9/RCAS1 in HIV-Trans-acting transcriptional activator-stimulated CD4+ T cells and monocytes suggested that EBAG9/RCAS1 may involved in the CD4+ T cell apoptosis observed in HIV-1 infection along with FasL and TRAIL.

Entity Malignancy.

Disease The EBAG9/RCAS1 reported to be over-expressed in many human cancers. Among them: breast, female-genital, gastrointestinal, blood, [lung](#), pancreas, liver, [renal](#), biliary-tract, hepatic, prostate, thyroid, gall bladder, and brain cancer.

Prognosis The EBAG9/RCAS1 over-expression could be used as a predictor of poor prognosis in malignant diseases.

Oncogenesis The EBAG9/RCAS1 plays a role in the immune escape of cancer cells. The EBAG9/RCAS1 could help cancer cells to survive and avoid immunosurveillance. This gene over-expression might cause progression, invasion and metastasis. The EBAG9 acts as one of the estrogen responsive genes in estrogen receptor-positive tumors and mediate estrogen function. Overall, the EBAG9/RCAS1 has an etiological role in the development and progression of cancer cells.

External links

Nomenclature

[Hugo](#) [EBAG9](#)

[GDB](#) [EBAG9](#)

[Entrez_Gene](#) [EBAG9_9166](#) estrogen receptor binding site associated, antigen, 9

Cards

[Atlas](#) [EBAG9ID40393ch8q23](#)

[GeneCards](#) [EBAG9](#)

[Ensembl](#) [EBAG9](#)

[Genatlas](#) [EBAG9](#)

[GeneLynx](#) [EBAG9](#)

[eGenome](#) [EBAG9](#)

[euGene](#) [9166](#)

Genomic and cartography

[GoldenPath](#) [EBAG9 - 8q23.2 chr8:110621486-110646565 + 8q23](#) (hg18-Mar_2006)

[Ensembl](#) [EBAG9 - 8q23 \[CytoView\]](#)

[NCBI](#) [Mapview](#)

OMIM	Disease map [OMIM]
HomoloGene	EBAG9
Gene and transcription	
Genbank	AB007619 [ENTREZ]
Genbank	AF006265 [ENTREZ]
Genbank	AK290651 [ENTREZ]
Genbank	AL515533 [ENTREZ]
Genbank	AY515724 [ENTREZ]
RefSeq	NM_004215 [SRS] NM_004215 [ENTREZ]
RefSeq	NM_198120 [SRS] NM_198120 [ENTREZ]
RefSeq	AC_000051 [SRS] AC_000051 [ENTREZ]
RefSeq	NC_000008 [SRS] NC_000008 [ENTREZ]
RefSeq	NT_008046 [SRS] NT_008046 [ENTREZ]
RefSeq	NW_923984 [SRS] NW_923984 [ENTREZ]
AceView	EBAG9 AceView - NCBI
Unigene	Hs.409368 [SRS] Hs.409368 [NCBI] HS409368 [spliceNest]
Fast-db	7832
Protein : pattern, domain, 3D structure	
SwissProt	O00559 [SRS] O00559 [EXPASY] O00559 [INTERPRO]
CluSTr	O00559
Blocks	O00559
HPRD	05775
Protein Interaction databases	
DIP	O00559
IntAct	O00559
Polymorphism : SNP, mutations, diseases	
OMIM	605772 [map]
GENECLINICS	605772
SNP	EBAG9 [dbSNP-NCBI]
SNP	NM_004215 [SNP-NCI]
SNP	NM_198120 [SNP-NCI]
SNP	EBAG9 [GeneSNPs - Utah] EBAG9 [HGBASE - SRS]
HAPMAP	EBAG9 [HAPMAP]
COSMIC	EBAG9 [Somatic mutation (COSMIC-CGP-Sanger)]
HGMD	EBAG9
General knowledge	
Family Browser	EBAG9 [UCSC Family Browser]
SOURCE	NM_004215
SOURCE	NM_198120
SMD	Hs.409368
SAGE	Hs.409368
GO	regulation of cell growth [Amigo] regulation of cell growth
GO	soluble fraction [Amigo] soluble fraction

[GO](#) [Golgi apparatus](#) [Amigo] [Golgi apparatus](#)
[GO](#) [apoptosis](#) [Amigo] [apoptosis](#)
[GO](#) [membrane](#) [Amigo] [membrane](#)
[GO](#) [integral to membrane](#) [Amigo] [integral to membrane](#)
[GO](#) [apoptotic protease activator activity](#) [Amigo] [apoptotic protease activator activity](#)
[PubGene](#) [EBAG9](#)

Other databases

Probes

[Probe](#) [EBAG9 Related clones \(RZPD - Berlin\)](#)

PubMed

[PubMed](#) [43 Pubmed reference\(s\) in LocusLink](#)

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Medline [17159823](#)

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