

AATF (Apoptosis Antagonizing Transcription Factor)

Identity

Other names	DED CHE1 CHE-1
Hugo	AATF
Location	17q12
Note	AATF affects cell growth by interfering with the recruitment of HDAC1 by retinoblastoma protein. Its over-expression activates DNA synthesis in quiescent NIH-3T3 cells through HDAC1 displacement. Also, it is considered as a general HDAC1 competitor and its down-regulation is involved in colon carcinoma cell proliferation. It is also found to bind to TSG101 in a process that enhances androgen receptor-mediated transcription by promoting its mono-ubiquitination. It has been observed lately that AATF 12th exon truncation by HIV-1 specific encoded miRNA leads to HIV-1 disease progression. On other side its over-expression has been observed in various leukemic cell lines and is considered to be important for maintaining leukemic state.

DNA/RNA

Note	Protein AATF (Apoptosis-antagonizing transcription factor) (Rb-binding protein Che-1). Total gene size being 107.996 kb and having transcribed region of 2.141 kb it codes for 561 amino acids.
Description	Spans on 107.996 kb on genomic fragment and contains 12 exons.
Transcription	2023 bp mRNA
Pseudogene	No pseudogenes for AATF are known.

Protein

Note	561 amino acids long protein contains POLR2J binding site at 273-315 amino acids, RB1 binding site at 316-372 amino acids, RB1 and SP1 binding site at 373-472 amino acids and Glu-rich region at 96-195 amino acids.
Description	AATF was identified as an interacting partner with MAP3K12/DLK which happens to be a protein kinase known to be involved in the induction of cell apoptosis. Its protein contains a leucine zipper, which is a characteristic motif of transcription factors, and was shown to exhibit strong transactivation activity when fused to Gal4 DNA binding domain. Overexpression of this gene interfered with MAP3K12 induced apoptosis.
Expression	Ubiquitously expressed. Expressed at high levels in brain, heart, kidney, placenta, thymus and moderate levels in blood mononuclear cells.
Localisation	Nucleus; nucleolus.
Function	It functions as a general inhibitor of the histone deacetylase HDAC1. Binding to the pocket region of RB1 may displace HDAC1 from RB1/E2F complexes, leading to activation of E2F target genes and cell cycle progression. Conversely, displacement of HDAC1 from SP1 bound to the CDKN1A promoter leads to increased expression of this CDK inhibitor and blocks cell cycle progression. Also antagonizes PAWR mediated induction of aberrant amyloid peptide production in Alzheimer disease (presenile and senile dementia), although the molecular basis for this phenomenon has not been described to date.

Mutations

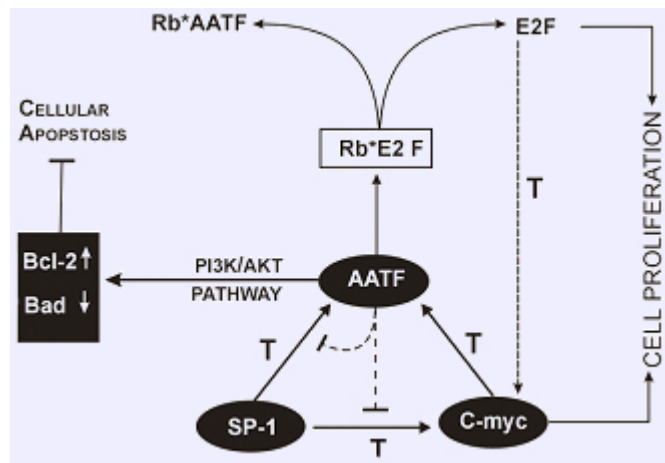
Note Several polymorphisms have been identified and but none of them has shown any association with any disease.

Implicated in

Entity Leukemia

Note AATF plays a major role in immortalization of leukemic cells through up-regulation of [Bcl2](#) gene expression.

Disease Haematopoitic malignancies

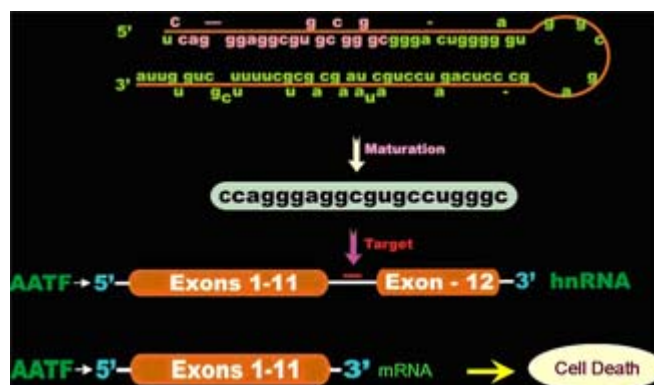


AATF dependent cross talk between cellular apoptosis and proliferation.

Entity AIDS

Note HIV-1 encodes a specific miRNA that has the inherent capacity to cleave 12th exon of AATF gene resulting in truncated AATF gene product which is destined to undergo degradation. Down-regulation of AATF gene expression is always accompanied by significant reduction in cell viability and down-regulation of gene coding for dicer which plays a crucial role in providing immunity at the nucleic acid level.

Disease Immunodeficiency, Lymphadenopathy, Kaposi's sarcoma, AIDS dementia



HIV-1 encoded miRNA dependent AATF gene down-regulation and subsequent cell death.

External links

Nomenclature

[Hugo](#) [AATF](#)
[GDB](#) [AATF](#)
[Entrez_Gene](#) [AATF 26574](#) apoptosis antagonizing transcription factor

Cards

[Atlas](#) [AATFID534ch17q11](#)
[GeneCards](#) [AATF](#)
[Ensembl](#) [AATF](#)
[GenAtlas](#) [AATF](#)
[GeneLynx](#) [AATF](#)
[eGenome](#) [AATF](#)
[euGene](#) [26574](#)

Genomic and cartography

[GoldenPath](#) [AATF - 17q12 chr17:32380288-32488283 + 17q11.2-q12](#) (hg18-Mar_2006)
[Ensembl](#) [AATF - 17q11.2-q12 \[CytoView\]](#)
[NCBI](#) [Genes Cyto](#) [Gene Seq](#) [Map View - NCBI]
[OMIM](#) [Disease map \[OMIM\]](#)
[HomoloGene](#) [AATF](#)

Gene and transcription

[Genbank](#) [AF083208](#) [ENTREZ]
[Genbank](#) [AF161395](#) [ENTREZ]
[Genbank](#) [AJ249940](#) [ENTREZ]
[Genbank](#) [AK026173](#) [ENTREZ]
[Genbank](#) [AK057229](#) [ENTREZ]
[RefSeq](#) [NM_012138](#) [SRS] [NM_012138](#) [ENTREZ]
[RefSeq](#) [AC_000060](#) [SRS] [AC_000060](#) [ENTREZ]
[RefSeq](#) [NC_000017](#) [SRS] [NC_000017](#) [ENTREZ]
[RefSeq](#) [NT_078100](#) [SRS] [NT_078100](#) [ENTREZ]
[RefSeq](#) [NW_926817](#) [SRS] [NW_926817](#) [ENTREZ]
[AceView](#) [AATF](#) AceView - NCBI
[Unigene](#) [Hs.195740](#) [SRS] [Hs.195740](#) [NCBI] [HS195740](#) [spliceNest]

Protein : pattern, domain, 3D structure

[SwissProt](#) [Q4L235](#) [SRS] [Q4L235](#) [EXPASY] [Q4L235](#) [INTERPRO]
[Prosite](#) [PS50075 ACP_DOMAIN](#) [SRS] [PS50075 ACP_DOMAIN](#) [Expasy]
[Prosite](#) [PS00455 AMP_BINDING](#) [SRS] [PS00455 AMP_BINDING](#) [Expasy]
[Interpro](#) [IPR009081 ACP_like](#) [SRS] [IPR009081 ACP_like](#) [EBI]
[Interpro](#) [IPR000873 AMP-bind](#) [SRS] [IPR000873 AMP-bind](#) [EBI]
[Interpro](#) [IPR006163 Phosphopanteth_bd](#) [SRS] [IPR006163 Phosphopanteth_bd](#) [EBI]
[Interpro](#) [IPR011047 Quino_alc_DH](#) [SRS] [IPR011047 Quino_alc_DH](#) [EBI]
[CluSTr](#) [Q4L235](#)
[Pfam](#) [PF00501 AMP-binding](#) [SRS] [PF00501 AMP-binding](#) [Sanger] [pfam00501](#) [NCBI-CDD]
[Pfam](#) [PF00550 PP-binding](#) [SRS] [PF00550 PP-binding](#) [Sanger] [pfam00550](#) [NCBI-CDD]

[Blocks](#) [Q4L235](#)

[HPRD](#) [Q4L235](#)

Protein Interaction databases

[DIP](#) [Q4L235](#)

[IntAct](#) [Q4L235](#)

Polymorphism : SNP, mutations, diseases

[OMIM](#) [608463](#) [[map](#)]

[GENECLINICS](#) [608463](#)

[SNP](#) [AATF](#) [dbSNP-NCBI]

[SNP](#) [NM_012138](#) [SNP-NCI]

[SNP](#) [AATF](#) [GeneSNPs - Utah] [AATF](#) [HGBASE - SRS]

[HAPMAP](#) [AATF](#) [HAPMAP]

General knowledge

[Family Browser](#) [AATF](#) [UCSC Family Browser]

[SOURCE](#) [NM_012138](#)

[SMD](#) [Hs.195740](#)

[SAGE](#) [Hs.195740](#)

[GO](#) [transcription factor activity](#) [Amigo] [transcription factor activity](#)

[GO](#) [protein binding](#) [Amigo] [protein binding](#)

[GO](#) [nucleus](#) [Amigo] [nucleus](#)

[GO](#) [anti-apoptosis](#) [Amigo] [anti-apoptosis](#)

[PubGene](#) [AATF](#)

Other databases

Probes

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

PubMed

[PubMed](#) [16 Pubmed reference\(s\) in LocusLink](#)

Bibliography

Che-1 affects cell growth by interfering with the recruitment of HDAC1 by Rb.

Bruno T, De Angelis R, De Nicola F, Barbato C, Di Padova M, Corbi N, Libri V, Benassi B, Mattei E, Chersi A, Soddu S, Floridi A, Passananti C, Fanciulli M.

Cancer Cell. 2002; 2(5): 387-99.

Medline [12450794](#)

Che-1 arrests human colon carcinoma cell proliferation by displacing HDAC1 from the p21WAF1/CIP1 promoter.

Di Padova M, Bruno T, De Nicola F, Iezzi S, D'Angelo C, Gallo R, Nicosia D, Corbi N, Biroccio A, Floridi A, Passananti C, Fanciulli M.

J Biol Chem. 2003; 278(38): 36496-504.

Medline [12847090](#)

TSG101 interacts with apoptosis-antagonizing transcription factor and enhances androgen receptor-mediated transcription by promoting its monoubiquitination.

Burgdorf S, Leister P, Scheidtmann KH.

J Biol Chem. 2004; 279(17): 17524-34.

Medline [14761944](#)

Evidence and Nature of a novel miRNA Encoded by HIV-1.

Kaul D, Khanna A, Suman

Proc Indian Natn Sci Acad 72 No.2 pp91-95 2006

Functional characterization of AATF transcriptome in human leukemic cells.

Kaul D, Mehrotra A.

Mol Cell Biochem. 2006 Sep 28

Medline [17006618](#)

[REVIEW articles](#) *automatic search in PubMed*

[Last year publications](#) *automatic search in PubMed*

[BiblioGene - INIST](#)

[Search in all EBI](#)

Contributor(s)

Written 12-2006 Deepak Kaul, Amit Khanna

Citation

This paper should be referenced as such :

Kaul D, Khanna A . AATF (Apoptosis Antagonizing Transcription Factor). Atlas Genet Cytogenet Oncol Haematol. December 2006 .

URL : <http://AtlasGeneticsOncology.org/Genes/AATFID534ch17q11.html>

© *Atlas of Genetics and Cytogenetics in Oncology and Haematology*
