

Gene Section

Mini Review

ATF2 (activating transcription factor 2)

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Identity

Hugo: ATF2

Other names: CREB1; CRE-BP1; CREB2; CREBP1; HB16; MGC111558; TREB7; Cyclic AMP-dependent transcription factor ATF-2; cAMP response elementbinding protein CRE- BP1 **Location:** 2q31.1

T(2;12)(q31;q13)					T(2;11)(q31;p15)		
Mb 175,40	175,60	175,80	176,00	176,20	176,40	176,60	176,80 T - I
genes CHN1 ATF2 ATP53G					KIAA17	15 Hox	I el

DNA/RNA

Description

Gene size: 115.93Kb.



ATF2 gene structure based on data available in the Ensembl release 44. Upstream non-coding exons (green). Coding exons (pink), 3' untranslated sequence (red). The size of the exons in nucleotides is indicated below each exon. Exon number is indicated within the exon.

Transcription

Initiation codon located in exon 4. Normal message is 2109 nucleotides. Some alternatively spliced RNA messages have been detected; but they are likely to represent splicing intermediates since no protein has been detected/expressed from these alternative messages in humans.

Protein

Note: Protein of 505 aminoacids and a size of 52.27 kDa. Functions as a dimer, either homodimer or heterodimer with proteins of the jun family (e.g.: c-Jun, c-Fos).



Localisation

Nuclear protein.

Function

Transcription factor which binds to the cAMPresponsive element (CRE) (consensus: 5'-GTGACGT[AC][AG]-3'). ATF2 binds DNA as a dimer. The specificity of the DNA target sequence that is recognized by dimers containing ATF2 is different depending on whether it is a homodimer or it forms a heterodimer with another JUN protein.

Mutations

Note: Lung cancer.

Somatic

G to A transition in exon 10. Val258Ile Substitution.

Implicated in

Clear cell sarcoma

Cytogenetics t(2;12)(q31.1;q13)



The arrow indicates the location of the breakpoint in chromosome 2. The ATF2 gene breaks within intron 6. In the translocation partner EWS the breakpoint occurs in intron 7. The transcript resulting from the hybrid gene fuses exon7 of EWS to exon 7 of ATF2.

Hybrid/Mutated Gene

EWS -ATF2 fusion transcript.

Abnormal Protein

The EWS-ATF2 fusion protein retains the ATF2 Cterminal region that contains the bZIP dimerization domain. But the fusion protein has lost the N-terminal domain of ATF2 that is kinase inducible. The Nterminal region of EWS is retained in the fusion protein but has lost both its RNA binding domain and its Zincfinger Ran binding domain.



Structure of the EWS-ATF2 fusion protein.

Oncogenesis

EWS-ATF2 may define a novel subset of clear cell sarcoma that occurs preferentially in the gastrointestinal tract and presents little or no melanocytic differentiation.

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