

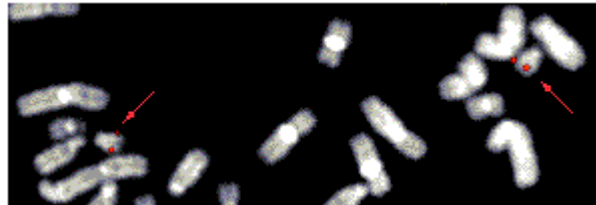
AML1 (acute myeloid leukemia 1) (updated: old version not available)

RUNX1 (runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene))

CBFA2 (core binding factor A2)

Identity

Other names **PEBP α B** (polyomavirus enhancer binding protein α B)
 Hugo **RUNX1**
 Location 21q22.3



[AML1](#) (21q22.3) in normal cells: clone dJ1107L6 - Courtesy Mariano Rocchi, [Resources for Molecular Cytogenetics](#). Laboratories willing to validate the probes are welcome: contact [M Rocchi](#)

DNA/RNA

AML1 Runt transactiv.

DNA Diagram

Description the gene spans a region of more than 120 kb
 Transcription transcription is from telomere to centromere --> the fusion gene is located on the 'other' chromosome (eg the der(8) of the t(8;21), the der(3) of the t(3;21)...); alternate splicing --> transcripts of 2, 3.3, ->7.5 and 8 kb

Protein



CBF β and CBF α association to bind on the DNA core site : Py-G-Py-G-G-T-Py

Protein Diagram

Description 250, 453 amino acids and other forms; forms heterodimers with [CBFB](#)
 Expression widely expressed, including hematopoietic cells at various stages of differentiation: role in haematopoiesis
 Localisation nuclear
 Function transcription factor (activator) for various hematopoietic-specific genes:

binds to the core site 5' PyGPyGGTPy 3' of a number of promoters and enhancers, as in GM-CSF (granulocyte-macrophage colony stimulating factor, CSF1R (colony stimulating factor 1 receptor), TCRb sites (T cell antigen receptors), and myeloid myeloperoxidase

Homology 1- Runt (drosophila): nuclear DNA binding protein; role in segmentation (embryology); 2- AML2 (also called: CBFA3, CBFa3, PEBPaC), located in 1p35-36, expressed in B lineage (3 and 5 kb RNA); AML3: (also called: CBFA1, CBFa1, PEBPaA) in 6p21; 3- cbfa family (mouse)

Implicated in

Entity Familial platelet disorder with predisposition to acute non lymphocytic leukemia

Entity [t\(1;21\)\(p36;q22\)](#) treatment related acute non lymphocytic leukemia (ANLL) --> ?/ AML1

Entity [t\(2;21\)\(p11;q22\)](#) ANLL --> ?/ AML1

Entity [t\(3;21\)\(q26;q22\)](#)/ myelodysplastic syndrome (MDS) or ANLL --> [-EVI1](#) or EAP/ MDS1 - AML1

Disease CML-BC of myeloid type; ANLL and MDS, often therapy related (secondary to antitopoisomerase II)

Hybrid/Mutated Gene 5' AML1 - 3' EAP or MDS1 or EVI1

Entity [t\(4;21\)\(q31;q22\)](#) T-cell acute lymphoblastic leukemia (T-ALL) --> ?/ AML1

Entity [t\(5;21\)\(q13;q22\)](#) myelodysplastic syndrome (MDS) and ANLL --> ?/ AML1

Entity [t\(8;21\)\(q22;q22\)](#)/ANLL. --> [ETO](#) - AML1

Disease ANLL, M2 mostly

Prognosis CR is obtained; median survival (1.5-2 yrs) is the range with other ANLL or relatively better

Cytogenetics additional anomalies are frequent: loss of Y or X chromosome, del(7q)/-7, +8, del (9q); complex t(8;21;Var) are known and have revealed that the crucial event lies on der(8); in agreement with the fact that both genes are transcribed from telomere to centromere

Hybrid/Mutated Gene 5' AML1 - 3' ETO

Abnormal Protein N-term AML1 with the Runt domain fused to the nearly entire ETO

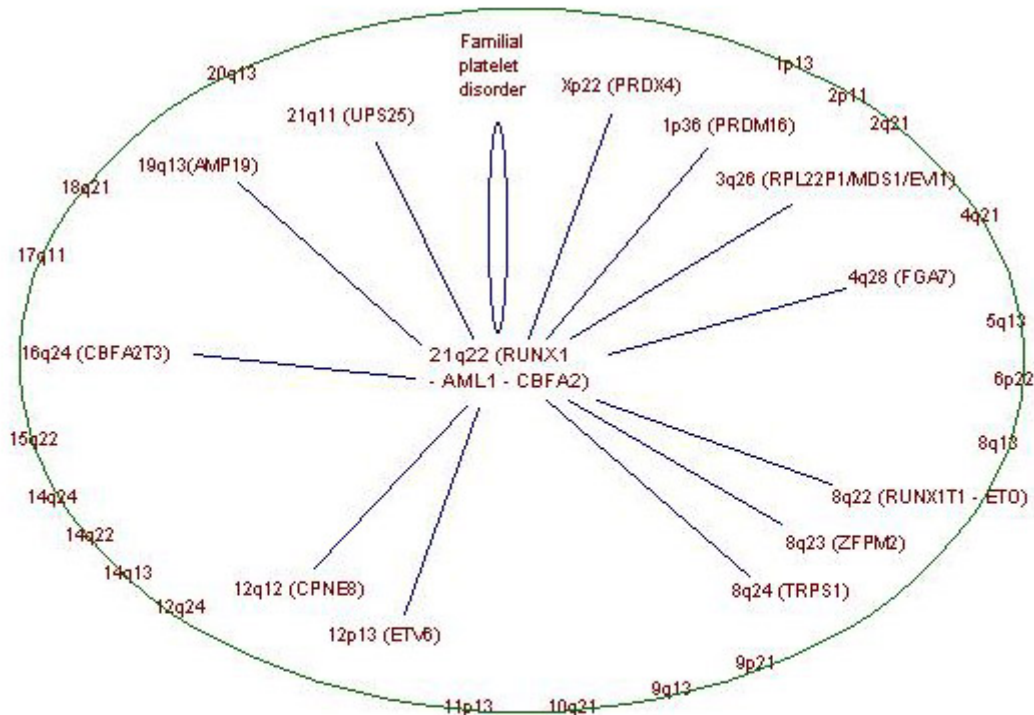
Oncogenesis the fusion protein retain the ability to recognize the AML1 concensus binding site (--> negative dominant competitor with the normal AML1) and to dimerize with the cbtb/CBTB subunit --> probable altered transcriptional regulation of normal AML1 target genes

Entity t(8;21)(q23;q22) MDS --> FOG2 / AML1

Entity [t\(8;21\)\(q24;q22\)](#) ALL and ANLL --> TRPS1 / AML1

- Entity** [t\(12;21\)\(p13;q22\)/ALL](#) --> [ETV6-AML1](#)
Disease B cell ALL (CD10+)
Prognosis CR in all cases; prognosis seems good
Cytogenetics often undetectable without FISH; additional anomalies: frequent del(12)(p12) on the other allele
Hybrid/Mutated Gene 5' ETV6 - 3' AML1 on the der(21)
Abnormal Protein Helix loop helix of TEL fused to the nearly entire AML1 protein; the other TEL allele is often deleted
- Entity** [t\(12;21\)\(q24;q22\)](#) ANLL --> ?/ AML1
- Entity** [t\(16;21\)\(q24;q22\)](#) ANLL --> MTG16-AML1
Disease ANLL and therapy related ANLL; mainly with preceding MDS
Prognosis very poor
- Entity** [t\(17;21\)\(q11;q22\)](#) ANLL
- Entity** [t\(19;21\)\(q13;q22\)](#) treatment related ANLL --> [AMP19](#) / AML1
- Entity** [t\(20;21\)\(q1;3q22\)](#) treatment related ANL --> ? / AML1
- Entity** t(21;21)(q11;q22) MDS --> UPS25 / AML1

Breakpoints



AML1 and 32 partners - recurrent translocations. Editor 02/2003; last update 08/2005.

Note: cases of AML1 translocations with either 4q21, 4q27, 8q24 (not the TRPS1 one), 11q24, 14q11, 16p13 have been proved to be cryptic t(12;21) with ETV6/AML1 involvement, and we have therefore to be cautious with breakpoints without a partner described.

External links

[Hugo](#)

[GDB](#)

[Entrez Gene](#)

Nomenclature

[RUNX1](#)

[RUNX1](#)

[RUNX1 861](#) runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)

Cards

[Atlas](#)

[GeneCards](#)

[Ensembl](#)

[CancerGene](#)

[Genatlas](#)

[GeneLynx](#)

[eGenome](#)

[euGene](#)

[FGA7ID525](#)

[RUNX1](#)

[RUNX1](#)

[CBFA2](#)

[RUNX1](#)

[RUNX1](#)

[RUNX1](#)

[861](#)

Genomic and cartography

[GoldenPath](#)

[Ensembl](#)

[NCBI](#)

[OMIM](#)

[HomoloGene](#)

[RUNX1 - 21q22.3](#) [chr21:35081969-35182857 - 21q22.12](#) (hg17-May_2004)

[RUNX1 - 21q22.12 \[CytoView\]](#)

[Genes Cyto](#) [Gene Seq](#) [Map View - NCBI]

[Disease map \[OMIM\]](#)

[RUNX1](#)

Gene and transcription

[Genbank](#)

[Genbank](#)

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[Genbank](#)

[Genbank](#)

[RefSeq](#)

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[AF025841](#) [SRS] [AF025841](#) [ENTREZ]

[AJ229043](#) [SRS] [AJ229043](#) [ENTREZ]

[AA878154](#) [SRS] [AA878154](#) [ENTREZ]

[AK123035](#) [SRS] [AK123035](#) [ENTREZ]

[AL581043](#) [SRS] [AL581043](#) [ENTREZ]

[NM_001001890](#) [SRS] [NM_001001890](#) [ENTREZ]

[NM_001754](#) [SRS] [NM_001754](#) [ENTREZ]

[NT_086913](#) [SRS] [NT_086913](#) [ENTREZ]

[RUNX1](#) AceView - NCBI

[RUNX1](#) Traser - Stanford

[Hs.278446](#) [SRS] [Hs.278446](#) [NCBI] [HS278446](#) [spliceNest]

Protein : pattern, domain, 3D structure

[SwissProt](#)

[CluSTr](#)

[Blocks](#)

[Q01196](#) [SRS] [Q01196](#) [EXPASY] [Q01196](#) [INTERPRO]

[Q01196](#)

[Q01196](#)

Polymorphism : SNP, mutations, diseases

[OMIM](#)

[GENECLINICS](#)

[SNP](#)

[SNP](#)

[SNP](#)

[SNP](#)

[151385](#) [map]

[151385](#)

[RUNX1](#) [dbSNP-NCBI]

[NM_001001890](#) [SNP-NCI]

[NM_001754](#) [SNP-NCI]

[RUNX1](#) [GeneSNPs - Utah] [RUNX1](#) [SNP - CSHL] [RUNX1](#) [HGBASE - SRS]

General knowledge

[Family Browser](#)

[SOURCE](#)

[SOURCE](#)

[RUNX1](#) [UCSC Family Browser]

[NM_001001890](#)

[NM_001754](#)

[SMD](#) [Hs.278446](#)
[SAGE](#) [Hs.278446](#)
[Amigo](#) [function|ATP binding](#)
[Amigo](#) [process|development](#)
[Amigo](#) [component|nucleus](#)
[Amigo](#) [process|regulation of transcription, DNA-dependent](#)
[Amigo](#) [function|transcription factor activity](#)
[PubGene](#) [RUNX1](#)

Other databases

Probes

[Probe](#) [AML1 \(21q22.3\) in normal cells \(Bari\)](#)
[Probe](#) [RUNX1 Related clones \(RZPD - Berlin\)](#)

PubMed

[PubMed](#) [65 Pubmed reference\(s\) in LocusLink](#)

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Written 11-1997 Jean-Loup Huret

Updated 12-1997 Jean-Loup Huret

Updated 01-2003 Jean-Loup Huret and Sylvie Senon

Citation

This paper should be referenced as such :

Huret JL . AML1 (acute myeloid leukemia 1); RUNX1 (runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)); CBFA2 (core binding factor A2). Atlas Genet Cytogenet Oncol Haematol. November 1997 .

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