

ABL2 (Abelson homolog 2)

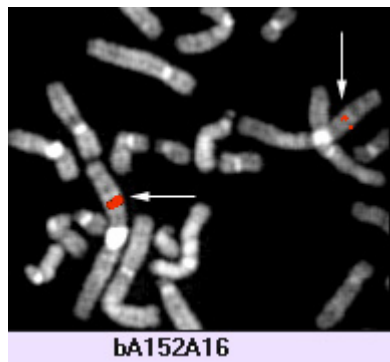
Identity

Other names **ARG (Abelson related gene)**

ABLL

Hugo **ABL2**

Location 1q25



[ABL2](#) (1q25) - Courtesy Mariano Rocchi, [Resources for Molecular Cytogenetics](#). Laboratories willing to validate the probes are welcome : contact rocchi@biologia.uniba.it

DNA/RNA

Transcription alternate splicing in 5 prime; 3.8 kb mRNA; ORF: 3548 bp

Protein

Description 1182 amino acids; 128 kDa; comprises SH3 and SH2 domains, a protein tyrosine kinase domain, a nuclear localization domain

Function cytoplasmic tyrosine kinase

Homology SRC homology; closely related to [ABL1](#)

Implicated in

Entity [t\(1;12\)\(q25;p13\)](#) --> ABL2-[ETV6](#)

Disease acute non lymphocytic leukemia

Abnormal Protein the fusion protein is composed of the HLH oligomerization domain of ETV6 and the SH2, SH3, and protein tyrosine kinase domains of ABL2

External links

Nomenclature

Hugo	ABL2
GDB	ABL2
Entrez_Gene	ABL2 27 v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)

Cards

Atlas	ABL2ID226
GeneCards	ABL2
Ensembl	ABL2
Genatlas	ABL2
GeneLynx	ABL2
eGenome	ABL2
euGene	27

Genomic and cartography

GoldenPath	ABL2 - 1q25 chr1:177343380-177378808 - 1q25.2 (hg18-Mar_2006)
Ensembl	ABL2 - 1q25.2 [CytoView]
NCBI	Genes Cyto Gene Seq [Map View - NCBI]
OMIM	Disease map [OMIM]
HomoloGene	

[ABL2](#)

Gene and transcription

Genbank	BC065912 [ENTREZ]
Genbank	BX538317 [ENTREZ]
RefSeq	M35296 [ENTREZ]
RefSeq	NM_005158 [SRS] NM_005158 [ENTREZ]
AceView	NM_007314 [SRS] NM_007314 [ENTREZ]
TRASER	ABL2 AceView - NCBI
Unigene	ABL2 Traser - Stanford
	Hs.159472 [SRS] Hs.159472 [NCBI] HS159472 [spliceNest]

Protein : pattern, domain, 3D structure

Prosit	P42684 [SRS] P42684 [EXPASY] P42684 [INTERPRO]
Prosit	PS00107 PROTEIN KINASE ATP [SRS] PS00107 PROTEIN KINASE ATP [Expasy]
Prosit	PS50011 PROTEIN KINASE DOM [SRS] PS50011 PROTEIN KINASE DOM [Expasy]
Prosit	PS00109 PROTEIN KINASE TYR [SRS] PS00109 PROTEIN KINASE TYR [Expasy]
Prosit	PS50001 SH2 [SRS] PS50001 SH2 [Expasy]

Interpro	PS50002 SH3 [SRS] PS50002 SH3 [Expasy]
Interpro	IPR001720 PI3kinase_P85 [SRS] IPR001720 PI3kinase_P85 [EBI]
Interpro	IPR000719 Prot_kinase [SRS] IPR000719 Prot_kinase [EBI]
Interpro	IPR000980 SH2 [SRS] IPR000980 SH2 [EBI]
Interpro	IPR001452 SH3 [SRS] IPR001452 SH3 [EBI]
Interpro	IPR001245 Tyr_pkinase [SRS] IPR001245 Tyr_pkinase [EBI]
CluSTr	IPR008266 Tyr_pkinase_AS [SRS] IPR008266 Tyr_pkinase_AS [EBI]
Pfam	P42684
Pfam	PF00017 SH2 [SRS] PF00017 SH2 [Sanger] pfam00017 [NCBI-CDD]
Smart	PF00018 SH3_1 [SRS] PF00018 SH3_1 [Sanger] pfam00018 [NCBI-CDD]
	SM00252 SH2 [EMBL]
Smart	
	SM00326 SH3 [EMBL]
Smart	
	SM00219 TyrKc [EMBL]
Prodom	
	PD000001 Prot_kinase [INRA-Toulouse]
Prodom	
Prodom	P42684 ABL2_HUMAN [Domain structure] P42684 ABL2_HUMAN [sequences sharing at least 1 domain]
	PD000001 [INRA-Toulouse]
Prodom	
Prodom	P42684 ABL2_HUMAN [Domain structure] P42684 ABL2_HUMAN [sequences sharing at least 1 domain]
	PD000001 [INRA-Toulouse]
Prodom	
Blocks	P42684 ABL2_HUMAN [Domain structure] P42684 ABL2_HUMAN [sequences sharing at least 1 domain]
	P42684
DIP	Protein Interaction databases
IntAct	P42684
	P42684
OMIM	Polymorphism : SNP, mutations, diseases
	164690 [map]
GENECLINICS	
	164690
SNP	
	ABL2 [dbSNP-NCBI]
SNP	

[SNP](#) [NM_005158](#) [SNP-NCI]
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[ABL2](#) [GeneSNPs - Utah] [ABL2](#) [HGBASE - SRS] [ABL2](#) [SNP - HAPMAP]

[Family](#)
[Browser](#)

General knowledge

[SOURCE](#) [ABL2](#) [UCSC Family Browser]
[SOURCE](#)

[NM_005158](#)

[SMD](#)

[SAGE](#) [NM_007314](#)

[Enzyme](#)

[Amigo](#) [Hs.159472](#)

[Hs.159472](#)

[Amigo](#) [2.7.1.112](#) [Enzyme-SRS] [2.7.1.112](#) [Brenda-SRS] [2.7.1.112](#) [KEGG]
[2.7.1.112](#) [WIT]

[nucleotide binding](#)

[Amigo](#)

[protein-tyrosine kinase activity](#)

[Amigo](#)

[ATP binding](#)

[Amigo](#)

[cytoplasm](#)

[Amigo](#)

[phosphoinositide 3-kinase complex](#)

[Amigo](#)

[protein amino acid phosphorylation](#)

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[intracellular signaling cascade](#)

[Amigo](#)

[transferase activity](#)

[BIOCARTA](#)

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[Probe](#)

Other databases

Probes

[Cancer Cytogenetics \(Bari\)](#)

[PubMed](#)

[ABL2 Related clones \(RZPD - Berlin\)](#)

PubMed

[20 Pubmed reference\(s\) in LocusLink](#)

Bibliography

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Kruh GD, King CR, Kraus MH, Popescu NC, Amsbaugh SC, McBride WO, Aaronson SA.

Science 1986; 234: 1545-1548.

Medline [87069952](#)

Mapping of Abl within a conserved linkage group on distal mouse chromosome 1 syntenic with human chromosome 1 using an interspecific cross.

Seldin MF, Kruh GD.

Genomics 1989; 4: 221-223.

Medline [89290853](#)

The complete coding sequence of arg defines the Abelson subfamily of cytoplasmic tyrosine kinases.

Kruh GD, Perego R, Miki T, Aaronson SA.

Proc Natl Acad Sci USA 1990; 87: 5802-5806.

Medline [90332670](#)

The tyrosine kinase ABL-related gene "ARG" is fused to ETV6 in an AML-M4Eo patient with a t(1;12)(q25;p13): molecular cloning of both reciprocal transcripts.

Cazzaniga G, Tosi S, Aloisi A, Giudici G, Pioltelli P, Kearney L, Biondi A.

Blood 1999; 94 Suppl 1: Abst 233.

The tyrosine kinase abl-related gene ARG is fused to ETV6 in an AML-M4Eo patient with a t(1;12)(q25;p13): molecular cloning of both reciprocal transcripts.

Cazzaniga G, Tosi S, Aloisi A, Giudici G, Daniotti M, Pioltelli P, Kearney L, Biondi A.

Blood 1999; 94: 4370-4373.

Medline [20057691](#)

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Written 02-
2000 Jean-Loup Huret

Citation

This paper should be referenced as such :

Huret JL . ABL2 (Abelson homolog 2). Atlas Genet Cytogenet Oncol Haematol.
February 2000 .

URL : <http://AtlasGeneticsOncology.org/Genes/ABL2ID226.html>

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