

Ikaros

Identity

Other names **IK1**
LYF1
ZNFN1A1 (zinc finger protein, subfamily 1A, 1)

Hugo [ZNFN1A1](#)

Location 7p12

DNA/RNA

Transcription 3629 bp mRNA; coding sequence: 1559 bp; 6 different splicings (--> 6 isoform proteins: ik1-ik6)

Protein

Description 519 amino acids; 58 kDa; possesses 2 Zinc-finger (C2H2-type) domains: one with 4 ZnF, the second with 2 ZnF; DNA binding

Expression specificity for hematopoietic organs in the foetus and in the adult as well

Localisation nuclear

Function transcription regulator; can repress transcription through the recruitment of histone deacetylase complexes; role in conjunction with Aiolos; hemopoietic-specific zinc finger protein regulator of B and T-cell differentiation

Implicated in

Entity [t\(3;7\)\(q27;p12\)](#) diffuse large B-cell lymphoma (DLCL) --> [BCL6](#) / Ikaros

Note only 2 cases to date

Hybrid/Mutated Gene 5' Ikaros - 3' BCL6 fusion transcript; it is supposed that substitution of the promoter of BCL6 may be responsible for BCL6 deregulation

External links

	Nomenclature
Hugo	ZNFN1A1
GDB	ZNFN1A1
Entrez_Gene	ZNFN1A1_10320 zinc finger protein, subfamily 1A, 1 (Ikaros)

Cards

Atlas **IkarosID258**

GeneCards ZNFN1A1

Ensembl ZNFN1A1

Genatlas ZNFN1A1

GeneLynx ZNFN1A1

eGenome ZNFN1A1

euGene 10320

Genomic and cartography

GoldenPath ZNFN1A1 - 7p12 chr7:50314924-50438053 + 7p12.2 (hg18-Mar_2006)

Ensembl ZNFN1A1 - 7p12.2 [CytoView]

NCBI Genes Cyto Gene Seg [Map View - NCBI]

OMIM Disease map [OMIM]

HomoloGene ZNFN1A1

Gene and transcription

Genbank AF116605 [ENTREZ]

Genbank AF432219 [ENTREZ]

Genbank AM085310 [ENTREZ]

Genbank AY377974 [ENTREZ]

Genbank BC018349 [ENTREZ]

RefSeq NM_006060 [SRS] NM_006060 [ENTREZ]

AceView ZNFN1A1 AceView - NCBI

TRASER ZNFN1A1 Traser - Stanford

Unigene Hs.488251 [SRS] Hs.488251 [NCBI] HS488251 [spliceNest]

Protein : pattern, domain, 3D structure

SwissProt Q13422 [SRS] Q13422 [EXPASY] Q13422 [INTERPRO]

Prosite PS00028 ZINC FINGER C2H2 1 [SRS] PS00028 ZINC FINGER C2H2 1 [Expasy]

Prosite PS50157 ZINC FINGER C2H2 2 [SRS] PS50157 ZINC FINGER C2H2 2 [Expasy]

Interpro IPR007087 Znf_C2H2 [SRS] IPR007087 Znf_C2H2 [EBI]

CluSTr Q13422

Pfam PF00096 zf-C2H2 [SRS] PF00096 zf-C2H2 [Sanger] pfam00096 [NCBI-CDD]

Smart SM00355 ZnF_C2H2 [EMBL]

Prodom PD000003 Znf_C2H2 [INRA-Toulouse]

Prodom Q13422 IKAR_HUMAN [Domain structure] Q13422 IKAR_HUMAN [sequences sharing at least 1 domain]

Blocks Q13422

Protein Interaction databases

[DIP](#) [Q13422](#)

[IntAct](#) [Q13422](#)

Polymorphism : SNP, mutations, diseases

[OMIM](#) [603023](#) [[map](#)]

[GENECLINICS](#) [603023](#)

[SNP](#) [ZNFN1A1](#) [dbSNP-NCBI]

[SNP](#) [NM_006060](#) [SNP-NCI]

[SNP](#) [ZNFN1A1](#) [GeneSNPs - Utah] [ZNFN1A1](#) [HGBASE - SRS] [ZNFN1A1](#) [SNP - HAPMAP]

General knowledge

[Family Browser](#) [ZNFN1A1](#) [UCSC Family Browser]

[SOURCE](#) [NM_006060](#)

[SMD](#) [Hs.488251](#)

[SAGE](#) [Hs.488251](#)

[Amigo](#) [DNA binding](#)

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

[Amigo](#) [transcription](#)

[Amigo](#) [regulation of transcription, DNA-dependent](#)

[Amigo](#) [mesoderm development](#)

[Amigo](#) [zinc ion binding](#)

[Amigo](#) [metal ion binding](#)

[PubGene](#) [ZNFN1A1](#)

Other databases

Probes

[Probe](#) [ZNFN1A1 Related clones \(RZPD - Berlin\)](#)

PubMed

[PubMed](#) [33 Pubmed reference\(s\) in LocusLink](#)

Bibliography

Association of transcriptionally silent genes with Ikaros complexes at centromeric heterochromatin.

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Cell 1997; 91: 845-854.

Medline [98074804](#)

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Georgopoulos K, Winandy S, Avitahl N.

Annu Rev Immunol 1997; 15: 155- 176.

Medline [97288734](#)

Ikaros in hemopoietic lineage determination and homeostasis.

Nichogiannopoulou A, Trevisan M, Friedrich C, Georgopoulos K.
Semin Immunol 1998; 10: 119-125.

Medline [98282479](#)

Pre-T cell receptor (TCR) and TCR-controlled checkpoints in T cell differentiation are set by Ikaros.

Winandy S, Wu L, Wang JH, Georgopoulos K.
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Medline [20105774](#)

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Hosokawa Y, Maeda Y, Ichinohasama R, Miura I, Taniwaki M, Seto M.
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Medline [20218760](#)

Ikaros interactions with CtBP reveal a repression mechanism that is independent of histone deacetylase activity.

Koipally J, Georgopoulos K.
J Biol Chem 2000; 275: 19594-19602..

Medline [20347860](#)

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Written 08-2000 Jean-Loup Huret

Citation

This paper should be referenced as such :

Huret JL . Ikaros. Atlas Genet Cytogenet Oncol Haematol. August 2000 .

URL : <http://AtlasGeneticsOncology.org/Genes/IkarosID258.html>

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