

LCK (lymphocyte-specific protein tyrosine kinase)

Identity

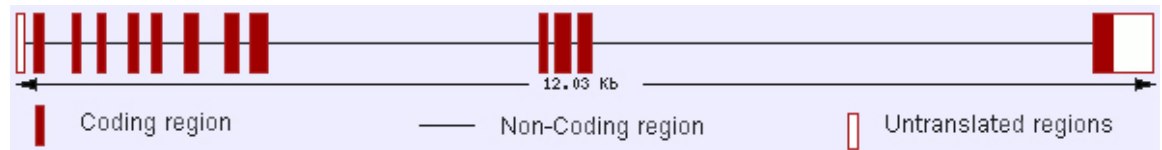
Other names **P56-LCK LSK (T cell-specific protein-tyrosine kinase)**

lck tyrosine kinase (AA 1-142)
membrane associated protein tyrosine kinase
proto-oncogene LCK
protein-tyrosine kinase
put. ptk (135aa); tyrosine kinase

Hugo [LCK](#)

Location 1p34.3

DNA/RNA

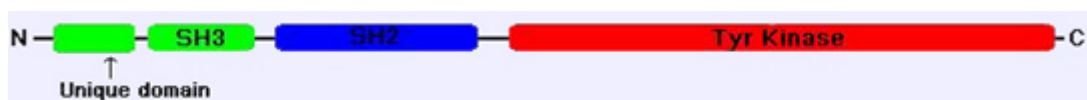


Description DNA sequence is located on chromosome no.1 on the arm 1(p).

Transcription Consists of 13 exons and 12 introns spanning 12.3 kb.

Pseudogene Unknown

Protein



Description The kinase p56lck (509 aa) is a T-lymphocyte-specific member of the Src family of non-receptor protein tyrosine kinase. Lck is a 56 kDa phosphoprotein expressed in variety of lymphoid and non-lymphoid cell lineages. Lck contain myristylation sequence, unique amino-terminal regions, followed by Src homology domains SH3 and SH2, a tyrosine kinase catalytic domain, and C-terminal regulatory domain. Lck associates with the inner face of the plasma membrane through its amino-terminus. This interaction is mediated by both myristic acid and palmitic acid that are bound to the amino terminal glycine and Cys-3 and/or Cys-5. The Unique region of Lck represents the domain possessing the greatest sequence diversity within this group of enzymes. This domain is thought to be involved in the interaction of the Lck with specific cellular proteins including Lck substrate. In T-cells it is

known, to mediate association with the cytoplasmic tail of T-cell coreceptors CD4 and CD8a. SH3 (Src homology 3) domain is mainly implicated in the regulation of protein-protein interactions, recognizing proline-rich region found in guanine nucleotide exchange factors and GTPase activating proteins. SH2 (Src homology 2) domain of Lck recognizes phosphorylated tyrosine residues on other proteins thereby facilitating the formation of tyrosine phosphorylation-induced multimeric complexes. The tyrosine kinase domain is the catalytic domain of Lck catalyzing the transfer of the gamma-phosphate from ATP to tyrosine residues on proteins. The catalytic domain contains a site of autophosphorylation (Tyr-394), which plays an important role in regulating the protein kinase activity. A C-terminal regulatory domain is also seen containing the major site of tyrosine phosphorylation in vivo (Tyr-505). Phosphorylation of Csk (C-terminal Src kinase) at Tyr-505 leads to inactivation of Lck. Lck is also activated by oxidative stress. Reoxygenation after hypoxia induces Lck kinase activity.

Expression	Expressed in variety of lymphoid and non-lymphoid cell lineages (Breast cancer tissues and other cancers too).
Localisation	Cell membrane
Function	T-cell development, T-cell activation.
Homology	Shares sequence homology with other Src family kinases (Src, Hck, Fyn, Blk, Lyn, Fgr, Yes, and Yrk).

Mutations

Note	Not reported yet
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Implicated in

Entity [Breast cancer](#), T-cell Leukemia, [Colon carcinoma](#).

Oncogenesis Upregulation of Lck is seen in many cases of Breast cancer. It is also overexpressed in lymphoma, colon cancer. Rearrangement of LCK gene is also reported in murine lymphoma cell line. Oncogenic activation of Lck due translocation of the LCK gene is reported in the human HSB2 T-cell leukemia with [t\(1;7\)\(p34;q34\)](#) with LCK/ [TCRB](#) involvement. Lck regulates cell motility through NF-KB mediated uPA secretion following hypoxia and reoxygenation in Breast cancer.

Disease Type 1 Diabetes

Prognosis T-cell mediated Type diabetes (Autoimmune disease) shows defect in TCR/CD3-mediated T-cell activation due to the abnormal expression of LCK.

External links

Nomenclature

[Hugo](#)

[LCK](#)

[GDB](#) [LCK](#)
[Entrez Gene](#) [LCK 3932](#) lymphocyte-specific protein tyrosine kinase

Cards

[Atlas](#) [LCKID14ch1p34](#)

[GeneCards](#) [LCK](#)

[Ensembl](#) [LCK](#)

[CancerGene](#) [LCK](#)

[Genatlas](#) [LCK](#)

[GeneLynx](#) [LCK](#)

[eGenome](#) [LCK](#)

[euGene](#) [3932](#)

Genomic and cartography

[GoldenPath](#) [LCK - 1p34.3](#) [chr1:32386025-32420854 + 1p35.1](#) (hg17-May_2004)

[Ensembl](#) [LCK - 1p35.1 \[CytoView\]](#)

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

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

[HomoloGene](#) [LCK](#)

Gene and transcription

[Genbank](#) [BN000073](#) [SRS] [BN000073](#) [ENTREZ]

[Genbank](#) [M21510](#) [SRS] [M21510](#) [ENTREZ]

[Genbank](#) [M26692](#) [SRS] [M26692](#) [ENTREZ]

[Genbank](#) [M26693](#) [SRS] [M26693](#) [ENTREZ]

[Genbank](#) [X14055](#) [SRS] [X14055](#) [ENTREZ]

[RefSeq](#) [NM_005356](#) [SRS] [NM_005356](#) [ENTREZ]

[RefSeq](#) [NT_086582](#) [SRS] [NT_086582](#) [ENTREZ]

[AceView](#) [LCK](#) AceView - NCBI

[TRASER](#) [LCK](#) Traser - Stanford

[Unigene](#) [Hs.470627](#) [SRS] [Hs.470627](#) [NCBI] [HS470627](#) [spliceNest]

Protein : pattern, domain, 3D structure

[SwissProt](#) [P06239](#) [SRS] [P06239](#) [EXPASY] [P06239](#) [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]

[Prosit](#) [PS50002](#) SH3 [SRS] [PS50002](#) SH3 [Expasy]

[Interpro](#) [IPR011009 Kinase like](#) [SRS] [IPR011009 Kinase like](#) [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]
[Interpro](#) [IPR008266 Tyr pkinase AS](#) [SRS] [IPR008266 Tyr pkinase AS](#) [EBI]
[CluSTr](#) [P06239](#)
[Pfam](#) [PF00069 Pkinase](#) [SRS] [PF00069 Pkinase](#) [Sanger] [pfam00069](#) [NCBI-CDD]
[Pfam](#) [PF00017 SH2](#) [SRS] [PF00017 SH2](#) [Sanger] [pfam00017](#) [NCBI-CDD]
[Pfam](#) [PF00018 SH3](#) [SRS] [PF00018 SH3](#) [Sanger] [pfam00018](#) [NCBI-CDD]
[Smart](#) [SM00252 SH2](#) [EMBL]
[Smart](#) [SM00326 SH3](#) [EMBL]
[Smart](#) [SM00219 TyrKc](#) [EMBL]
[Prodom](#) [PD000001 Prot kinase](#)[INRA-Toulouse]
[Prodom](#) [P06239 LCK HUMAN](#) [Domain structure] [P06239 LCK HUMAN](#) [sequences sharing at least 1 domain]
[Prodom](#) [PD000001](#)[INRA-Toulouse]
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[Blocks](#) [P06239](#)
[PDB](#) [1BHF](#) [SRS] [1BHF](#) [PdbSum], [1BHF](#) [IMB]
[PDB](#) [1BHH](#) [SRS] [1BHH](#) [PdbSum], [1BHH](#) [IMB]
[PDB](#) [1CWD](#) [SRS] [1CWD](#) [PdbSum], [1CWD](#) [IMB]
[PDB](#) [1CWE](#) [SRS] [1CWE](#) [PdbSum], [1CWE](#) [IMB]
[PDB](#) [1FBZ](#) [SRS] [1FBZ](#) [PdbSum], [1FBZ](#) [IMB]
[PDB](#) [1H92](#) [SRS] [1H92](#) [PdbSum], [1H92](#) [IMB]
[PDB](#) [1IJR](#) [SRS] [1IJR](#) [PdbSum], [1IJR](#) [IMB]
[PDB](#) [1KIK](#) [SRS] [1KIK](#) [PdbSum], [1KIK](#) [IMB]
[PDB](#) [1LCJ](#) [SRS] [1LCJ](#) [PdbSum], [1LCJ](#) [IMB]
[PDB](#) [1LCK](#) [SRS] [1LCK](#) [PdbSum], [1LCK](#) [IMB]
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[PDB](#) [1LKL](#) [SRS] [1LKL](#) [PdbSum], [1LKL](#) [IMB]
[PDB](#) [1Q68](#) [SRS] [1Q68](#) [PdbSum], [1Q68](#) [IMB]
[PDB](#) [1Q69](#) [SRS] [1Q69](#) [PdbSum], [1Q69](#) [IMB]
[PDB](#) [1QPC](#) [SRS] [1QPC](#) [PdbSum], [1QPC](#) [IMB]
[PDB](#) [1QPD](#) [SRS] [1QPD](#) [PdbSum], [1QPD](#) [IMB]

[PDB](#) [1QPE](#) [SRS] [1QPE](#) [PdbSum], [1QPE](#) [IMB]

[PDB](#) [1QPJ](#) [SRS] [1QPJ](#) [PdbSum], [1QPJ](#) [IMB]

[PDB](#) [3LCK](#) [SRS] [3LCK](#) [PdbSum], [3LCK](#) [IMB]

Polymorphism : SNP, mutations, diseases

[OMIM](#) [153390](#) [map]

[GENECLINICS](#) [153390](#)

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

[SNP](#) [NM_005356](#) [SNP-NCI]

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

General knowledge

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

[SOURCE](#) [NM_005356](#)

[SMD](#) [Hs.470627](#)

[SAGE](#) [Hs.470627](#)

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

[Amigo](#) [function|ATP binding](#)

[Amigo](#) [process|Ras protein signal transduction](#)

[Amigo](#) [process|intracellular signaling cascade](#)

[Amigo](#) [component|membrane fraction](#)

[Amigo](#) [process|protein amino acid phosphorylation](#)

[Amigo](#) [function|protein binding](#)

[Amigo](#) [function|protein-tyrosine kinase activity](#)

[Amigo](#) [process|regulation of cell cycle](#)

[Amigo](#) [function|transferase activity](#)

[BIOCARTA](#) [Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor](#)

[BIOCARTA](#) [The Co-Stimulatory Signal During T-cell Activation](#)

[BIOCARTA](#) [IL 2 signaling pathway](#)

[BIOCARTA](#) [IL-7 Signal Transduction](#)

[BIOCARTA](#) [T Cell Receptor Signaling Pathway](#)

[BIOCARTA](#) [Lck and Fyn tyrosine kinases in initiation of TCR Activation](#)

[PubGene](#) [LCK](#)

Other databases

Probes

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

PubMed

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Medline [15489910](#)

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Medline [15489916](#)

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Contributor(s)

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URL : <http://www.infobiogen.fr/services/chromcancer/Genes/LCKID14ch1p34.html>

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