

## NFKB2

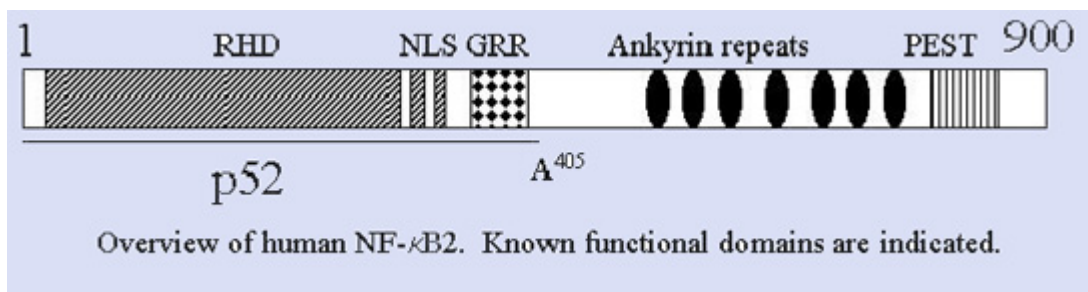
### Identity

Note	see also, in the Deep Insight section: <a href="#">Upstream Signal Transduction of NF-κB Activation</a>
Other names	<b>NF-κB p100</b> <b>NF-κB p52</b> <b>Lyt10</b>
Hugo	<a href="#">NFKB2</a>
Location	10q24

### DNA/RNA

**Description** The gene encoding human nfkb2 has 24 exons spanning 8 kb. The expression of nfkb2 can be regulated by two distinct promoters, P1 and P2, in which a number of consensus binding sites for transcription factors, including SP1, AP1 and putative NF-kappa B (kappa B sites), were identified.

### Protein



**Description** The human nfkb2 gene encodes a protein composed 900 amino acids with an approximately molecular weight of 100 kDa, which was considered as a precursor of p52 subunit of NF-κB complexes. The structural characteristics of NF-κB2 are much similar with that of NF-κB1: A N-terminal RHD; two nuclear localization sequences within the C-terminus of RHD, a putative GRR region that possibly contributes to the generation of NF-κB p52 from the precursor, NF-κB2. The C-terminal region of NF-κB2 also contains multiple copies of the so-called ankyrin repeats and one proline, glutamic acid, serine, and threonine (PEST) domain. Studies demonstrated that NF-κB2 was posttranslationally cleaved to produce the p52 molecule through the ubiquitin-proteasome dependent degradation of the C-terminal 406-900 portion of NF-κB2. However, other studies revealed that the mechanism

for the generation of NF-kB p52 is through cotranslational processing. Recent studies demonstrated that the processing of NF-kB p52 required IKKa- and/or NIK-dependent C-terminal phosphorylation of NF-kB2.

Expression nfkB2 is expressed mainly in lymphoid cells and mononuclear cells.

Localisation cytosol, nuclei after activation.

Function regulation of the genes involved in cell-to-cell interaction, intercellular communication, cell recruitment or transmigration, amplification or spreading of primary pathogenic signals, and initiation or acceleration of tumorigenesis. Similar with NF-kB1, the full length of NF-kB2 can serve as an endogenous inhibitor for the [NF-kB p50/ p65\(RelA\)](#) or NF-kB p52/p65 heterodimer. The homodimer of NF-kB p52 was transcriptionally inactive in the absence of Bcl3. Furthermore, the NF-kB p52 homodimer may function to competitively inhibit B binding by transactivating NF- B dimers. The Bcl3 protein can form a complex with this homodimer at B sites and act as a transactivator of NF-kB p52 homodimer. Interaction with : members of Ikb family and Rel family, Bcl3.

## Implicated in

Entity hematological malignancies (see below) and other diseases: autoimmune arthritis, glomerulonephritis, asthma, inflammatory bowel disease, septic shock, lung fibrosis, cancer, HTLV-1 infection, and AIDS.

Disease t(10;14)(q24;q11) or t(10;14)(q24;q32) in hematological malignancies

Cytogenetics poor.

Oncogenesis Unlike its relative nfkB1, rearrangement of nfkB2 gene locus has been found in many forms of lymphomas. The chromosomal translocations by t(10;14)(q24;q11) and t(10;14)(q24;q32) cause deletions of sequences encoding the ankyrin repeat motif of NF-kB2. Consequently, this carboxyl terminal truncated NF-kB2 is constitutively located in the nucleus of cells, which was found in small percentage of B-cell non-Hodgkin's lymphoma, [cutaneous lymphomas](#), T-cell acute lymphoblastic leukemia, [chronic lymphocytic leukemias](#), and [multiple myelomas](#). Chromosomal translocation generated a fusion NF-kB2-[IGHA1](#) or NF-kB2- [TCRa](#) or [TCRd](#) transcriptional unit.

## External links

### Nomenclature

[Hugo](#)

[NFKB2](#)

[GDB](#)

[NFKB2](#)

[Entrez Gene](#)

[NFKB2\\_4791](#) nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)

### Cards

[Atlas](#)

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[eGenome](#) [NFkB2](#)  
[euGene](#) [4791](#)

### Genomic and cartography

[GoldenPath](#) [NFkB2](#) - [10q24](#) [chr10:104145453-104152257](#) + [10q24.32](#)  
(hg17-May\_2004)  
[Ensembl](#) [NFkB2](#) - [10q24.32](#) [[CytoView](#)]  
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[HomoloGene](#) [NFkB2](#)

### Gene and transcription

[Genbank](#) [AL121928](#) [SRS] [AL121928](#) [ENTREZ]  
[Genbank](#) [U20816](#) [SRS] [U20816](#) [ENTREZ]  
[Genbank](#) [AK098415](#) [SRS] [AK098415](#) [ENTREZ]  
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[RefSeq](#) [NT\\_086775](#) [SRS] [NT\\_086775](#) [ENTREZ]  
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[TRASER](#) [NFkB2](#) Traser - Stanford  
[Unigene](#) [Hs.73090](#) [SRS] [Hs.73090](#) [NCBI] [HS73090](#) [spliceNest]

### Protein : pattern, domain, 3D structure

[SwissProt](#) [Q00653](#) [SRS] [Q00653](#) [EXPASY] [Q00653](#) [INTERPRO]  
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[Pfam](#) [PF00023 Ank](#) [SRS] [PF00023 Ank](#) [Sanger] [pfam00023](#) [NCBI-CDD]  
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[Blocks](#) [Q00653](#)  
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### Polymorphism : SNP, mutations, diseases

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### General knowledge

[Family Browser](#) [NFKB2](#) [UCSC Family Browser]  
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[SAGE](#) [Hs.73090](#)  
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[Amigo](#) [function|protein binding](#)  
[Amigo](#) [process|regulation of transcription, DNA-dependent](#)  
[Amigo](#) [process|signal transduction](#)  
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### Other databases

### Probes

[Probe](#) [NFKB2 Related clones \(RZPD - Berlin\)](#)

### PubMed

[PubMed](#) [74 Pubmed reference\(s\) in LocusLink](#)

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