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(54) **NOUVEAUX INHIBITEURS D'ACTIVATION NF-κB**
(54) **INHIBITORS OF NF-κB ACTIVATION**

(57) Cette invention concerne de nouveaux inhibiteurs de la voie d'activation du facteur nucléaire kappa B (NF-κB), lesquels sont utiles dans le traitement de maladies associées au NF-κB et/ou dans l'amélioration de traitements anti-tumoraux. Ces inhibiteurs interfèrent de manière précoce dans la voie de signalisation induite par TRAF, et sont ainsi plus spécifiques que le lκB.

(57) The present invention relates to novel inhibitors of the Nuclear factor kappa B (NF-κB) activating pathway useful in the treatment of NF-κB related diseases and/or in the improvement of anti-tumor treatments. These inhibitors interfere early in the TRAF induced signalling pathway and are therefore more specific than IκB.

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(54) Title: NOVEL INHIBITORS OF NF–κB ACTIVATION

(57) Abstract

The present invention relates to novel inhibitors of the Nuclear factor kappa B (NF–κB) activating pathway useful in the treatment of NF–κB related diseases and/or in the improvement of anti–tumor treatments. These inhibitors interfere early in the TRAF induced signalling pathway and are therefore more specific than IκB.

NOVEL INHIBITORS OF NF-κB ACTIVATION

Field of the invention

This invention relates to novel inhibitors of the Nuclear factor kappa B (NF-κB) activating pathway useful in the treatment of NF-κB related diseases and/or in the improvement of anti-tumor treatments.

The invention also relates to nucleic acids coding for said novel inhibitors.

The invention relates further to the use of polypeptides, derived from these inhibitors in the treatment of NF-κB related diseases and/or cancer.

Furthermore, the invention concerns pharmaceutical preparations, comprising the novel inhibitors or the polypeptides, derived from these inhibitors.

Background of the invention

NF-κB is an ubiquitously expressed transcription factor that controls the expression of a diverse range of genes involved in inflammation, immune response, lymphoid differentiation, growth control and development. NF-κB resides in the cytoplasm as an inactive dimer consisting of p50 and p65 subunits, bound to an inhibitory protein known as IκB. The latter becomes phosphorylated and degraded in response to various environmental stimuli, such as proinflammatory cytokines, viruses, lipopolysaccharides, oxidants, UV light and ionising radiation. This allows NF-κB to translocate to the nucleus where it activates genes that play a key role in the regulation of inflammatory and immune responses, including genes that encode proinflammatory cytokines (IL-1β, TNF, GM-CSF, IL-2, IL-6, IL-11, IL-17), chemokines (IL-8, RANTES, MIP-1α, MCP-2), enzymes that generate mediators of inflammation (NO synthetase, cyclo-oxygenase), immune receptors (IL-2 receptor) and adhesion molecules (ICAM-1, VCAM-1, E-selectin). Some of these induced proteins can on their turn activate NF-κB, leading to the further amplification and perpetuation of the inflammatory response. Recently, NF-κB has been shown to have an anti-apoptotic role in

certain cell types, most likely by inducing the expression of anti-apoptotic genes. This function may protect tumor cells against anti-cancer treatments and opens the possibility to use NF-κB inhibiting compounds to sensitize the tumor cells and to improve the efficiency of the anti-cancer treatment.

Because of its direct role in regulating responses to inflammatory cytokines and endotoxin, activation of NF-κB plays an important role in the development of different diseases (Barnes and Karin, 1997): chronic inflammatory diseases such as rheumatoid arthritis, asthma and inflammatory bowel disease (Brand *et al.,* 1996); acute diseases such as septic shock (Remick, 1995); Alzheimer's disease where the β-amyloid protein activates NF-κB (Behl *et al.,* 1997); atherosclerosis, where NF-κB may be activated by oxidised lipids (Brand *et al.*, 1997); autoimmune disease such as systemic lupus erythematosus (Kaltschmidt *et al.*, 1994); cancer by upregulating certain oncogenes or by preventing apoptosis (Luque *et al.*, 1997). In addition, NF-κB is also involved in viral infection since it is activated by different viral proteins, such as occurs upon infection with rhinovirus, influenzavirus, Epstein-Barr virus, HTLV, cytomegalovirus or adenovirus. Furthermore, several viruses such as HIV have NF-κB binding sites in their promoter/enhancer regions (Mosialos, 1997)

Because of the potential role of NF-κB in many of the above mentioned diseases, NF-κB and its regulators have drawn much interest as targets for the treatment of NF-κB related diseases. Glucocorticoids are effective inibitors of NF-κB, but they have endocrine and metabolic side effects when given systematically (Barnes *et al.,* 1993). Antioxidants may represent another class of NF-κB inhibitors, but currently available antioxidants such as acetylcysteine are relatively weak and unspecific (Schreck *et al.,* 1991). Aspirin and sodium salicylate also inhibit activation of NF-κB, but only at relatively high concentrations (Kopp and Gosh, 1994). There are some natural inhibitors of NF-κB such as glyotoxin, derived from *Aspergillus*, but these compounds are too toxic to be used as a drug (Pahl *et al.,* 1996). Finally, there may be endogenous inhibitors of NF-κB, such as IL-10, that blocks NF-κB through an effect on IκB (Wang *et al.*, 1995). However, total

inhibition of NF-κB in all cell types for prolonged periods is unwanted, because NF-κB plays a crucial role in the immune response and other defensive responses.

An important role in the induction of NF-κB by TNF and IL1 has recently been demonstrated for TNF-receptor associated factors, TRAF2 and TRAF6, which are recruited to the stimulated TNF-receptor and IL-1 receptor, respectively (Rothe *et al.*, 1995; Cao *et al.*, 1996). Overexpression of TRAF2 or TRAF6 activates NF-κB, whereas dominant negative mutants inhibit TNF or IL-1 induced activation of NF-κB in most cell types. TRAF2 knock out studies have recently shown that TRAF2 is not absolutely required for NF-κB activation, presumably because of redundancy within the TRAF family (Yeh *et al.*1997). The TRAF induced signalling pathway to NF-κB was further resolved by the identification of the TRAF-interacting protein NIK which mediates NF-κB activation upon TNF and IL-1 stimulation by its association and activation of IκB kinase-α and -β (IKK) (Malinin *et al,* 1997; Regnier *et al.,* 1997; DiDonato *et al.*,1997; Zandi *et al.*, 1997; Woronicz *et al.*, 1997). The latter are part of a large multiprotein NF-κB activation complex and are responsible for phosphorylation of IκB, leading to its subsequent degradation and to translocation of released, active NF-κB to the nucleus. This allows a more specific inhibition of NF-κB activation by stimuli (including TNF and IL-1) that activate TRAF pathways. Based on this principle, WO 97/37016 discloses the use of NIK and other TRAF interacting proteins for the modulation of NF-κB activity.

Another protein that can associate with TRAF2 is the zinc finger protein A20 (Song *et al.*, 1996). The latter is encoded by an immediate early response gene induced in different cell lines upon stimulation by TNF or IL-1 (Dixit *et al,* 1990). Interestingly, overexpression of A20 blocks both TNF and IL-1 induced NF-κB activation (Jaattela *et al.*, 1996). However, the mechanism by which A20 blocks NF-κB activation is totally unknown, but in contrast to NIK, A20 does not seem to act directly on IκB, and follows in this respect an alternative pathway to modulate NF-κB activation.

De Valck *et al.* (1997) isolated an A20 binding protein, so-called 14-3-3, using the yeast two-hybrid assay and demonstrated that NF-κB inhibition was independent from the binding of A20 to 14-3-3.

Aims and description of the invention

It is shown in the current invention that other new A20 interacting proteins unexpectedely can modulate and/or inhibit NF-κB activation.

To the invention belongs an isolated functional protein either comprising an amino acid sequence with 70-100% homology to the amino acid sequence depicted in SEQ ID NO. 2 or either comprising an amino acid sequence with 70-100% homology to the amino acid sequence depicted in SEQ ID NO. 3 or in the alternative comprising an amino acid sequence with 70-100% homology to the amino acid sequence depicted in SEQ ID NO. 5.

More specifically said functional protein comprises an amino acid sequence with 70-100% homology to the amino acids 54-647 of SEQ ID NO. 2, even more specifically said functional protein comprises an amino acid sequence with 70-100% homology to the amino acids 390-647 of SEQ ID NO. 2 or in the alternative and/or comprising an amino acid sequence with 70-100% homology to the amino acids 420-647 of SEQ ID NO.2.

Homology in this context means identical or similar to the referenced sequence while obvious replacements/modifications of any of the amino acids provided, are included as well. A homology search in this respect can be performed with the BLAST-P (Basic Local Alignment Search Tool) program well known to a person skilled in the art. For the corresponding nucleic acid sequence homology is referred to the BLASTX and BLASTN programs known in the art.

One aspect of the invention is to offer novel modulators and/or inhibitors of TNF and/or IL-1 induced NF-κB activation pathways.

An important embodiment of the invention is a protein comprising at least the amino acids of SEQ ID NO.2.

Another embodiment of the invention is a protein comprising at least the amino acids 54-647 of SEQ ID NO.2, as represented in SEQ ID NO.3.

A further embodiment of the invention is a protein comprising at least the amino acids of SEQ ID.NO.5.

A further aspect of the invention is the use of protein comprising the amino acids 420-647 of SEQ ID.NO. 2 to modulate and/or inhibit the NF-κB related pathway, especially the TNF and/or IL-1 induced pathways.

In addition the invention concerns the use of a protein, comprising the consensus sequence shown in SEQ ID NO.6 and/or SEQ ID.NO.7, to modulate and/or inhibit the TNF and/or IL-1 induced, NF-κB related pathway.

Another aspect of the invention is the use of above mentioned proteins in a screening method to screen compounds that interfere with the interaction of these protein(s) with other protein components of the NF-κB related pathway.

Another embodiment of the invention is the use of the above mentioned proteins, or the use of protein components screened by the above mentioned method to sensitize tumor cells and/or improve the anti-cancer treatment.

In the alternative, the present invention relates to a method for identifying and obtaining an activator or inhibitor of A20 interacting protein(s) comprising the steps of:

(a) combining a compound to be screened with a reaction mixture containing the protein of the invention and a read out system capable of interacting with the protein under suitable conditions;

(b) maintaining said reaction mixture in the presence of the compound or a sample comprising a plurality of compounds under conditions which permit interaction of the protein with said read out system;

(c) identifying or verifying a sample and compound, respectively, which leads to suppression or activation of the read out system.

The term "read out system" in context with the present invention means a DNA sequence which upon transcription and/or expression in a cell, tissue or

organism provides for a scorable and/or selectable phenotype. Such read out systems are well known to those skilled in the art and comprise, for example, recombinant DNA molecules and marker genes as described above.

The term "plurality of compounds" in a method of the invention is to be understood as a plurality of substances which may or may not be identical. Said compound or plurality of compounds may be comprised in, for example, samples, e.g., cell extracts from animals or microorganisms. Furthermore, said compound(s) may be known in the art but hitherto not known to be capable of suppressing or activating A20 interacting proteins. The reaction mixture may be a cell free extract or may comprise a cell or tissue culture. Suitable set ups for the method of the invention are known to the person skilled in the art and are, for example, generally described in Alberts et al., Molecular Biology of the Cell, third edition (1994). The plurality of compounds may be, e.g., added to the reaction mixture, culture medium or injected into the cell.

If a sample containing a compound or a plurality of compounds is identified in the method of the invention, then it is either possible to isolate the compound from the original sample identified as containing the compound capable of suppressing or activating A20 interacting proteins, or one can further subdivide the original sample, for example, if it consists of a plurality of different compounds, so as to reduce the number of different substances per sample and repeat the method with the subdivisions of the original sample. Depending on the complexity of the samples, the steps described above can be performed several times, preferably until the sample identified according to the method of the invention only comprises a limited number of or only one substance(s). Preferably said sample comprises substances of similar chemical and/or physical properties, and most preferably said substances are identical. The compounds which can be tested and identified according to a method of the invention may be expression libraries, e.g., cDNA expression libraries, peptides, proteins, nucleic acids, antibodies, small organic compounds, hormones, peptidomimetics, PNAs or the like (Milner, Nature

Medicine 1 (1995), 879-880; Hupp, Cell 83 (1995), 237-245; Gibbs, Cell 79 (1994), 193-198 and references cited supra).

In the alternative, the invention also relates to a DNA sequence encoding the above mentioned proteins or encoding an immunologically active and/or functional fragment of such a protein, selected from the group consisting of:

(a) DNA sequences comprising a nucleotide sequence encoding a protein comprising the amino acid sequence as given in SEQ ID NO: 2;

(b) DNA sequences comprising a nucleotide sequence as given in SEQ ID NO: 1;

(c) DNA sequences hybridizing with the complementary strand of a DNA sequence as defined in (a) or (b) and encoding an amino acid sequence which is at least 70% identical to the amino acid sequence encoded by the DNA sequence of (a) or (b);

(d) DNA sequences, the nucleotide sequence of which is degenerated as a result of the genetic code to a nucleotide sequence of a DNA sequence as defined in any one of (a) to (c); and

(e) DNA sequences encoding a fragment of a protein encoded by a DNA sequence of any one of (a) to (d).

So the invention consists of DNA molecules, also called nucleic acid sequences, encoding for the above mentioned proteins preferably a nucleic acid sequence with 70-100% homology to the DNA sequence depicted in SEQ ID NO. 1 and/or a nucleic acid sequence with 70-100% homology to the DNA sequence depicted in SEQ ID NO. 4.

Homology in this context means that the respective nucleic acid molecules or encoded proteins are functionally and/or structurally equivalent. The nucleic acid molecules that are homologous to the nucleic acid molecules described above and that are derivatives of said nucleic acid molecules are, for example, variations of said nucleic acid molecules which represent modifications having the same biological function, in particular encoding proteins with the same or substantially the same biological function. They may

be naturally occurring variations, such as sequences from other varieties or species, or mutations. These mutations may occur naturally or may be obtained by mutagenesis techniques. The allelic variations may be naturally occurring allelic variants as well as synthetically produced or genetically engineered variants.

The proteins encoded by the various derivatives and variants of the above-described nucleic acid molecules have similar common characteristics, such as biological activity, molecular weight, immunological reactivity, conformation, etc., as well as physical properties, such as electrophoretic mobility, chromatographic behavior, sedimentation coefficients, pH optimum, temperature optimum, stability, solubility, spectroscopic properties, etc.

The present invention also relates to vectors, particularly plasmids, cosmids, viruses, bacteriophages and other vectors used conventionally in genetic engineering that contain a nucleic acid molecule according to the invention. Methods which are well known to those skilled in the art can be used to construct various plasmids and vectors; see, for example, the techniques described in Sambrook, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory (1989) N.Y.

Alternatively, the nucleic acid molecules and vectors of the invention can be reconstituted into liposomes for delivery to target cells.

In a preferred embodiment the nucleic acid molecule present in the vector is operably linked to (a) control sequence(s) which allow the expression of the nucleic acid molecule in prokaryotic and/or eukaryotic cells.

The term "control sequence" refers to regulatory DNA sequences which are necessary to affect the expression of coding sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism. In prokaryotes, control sequences generally include promoter, ribosomal binding site, and terminators. In eukaryotes generally control sequences include promoters, terminators and, in some instances, enhancers, transactivators or transcription factors. The term "control sequence" is intended to include, at a minimum, all components the presence

of which are necessary for expression, and may also include additional advantageous components.

The term "operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequences. In case the control sequence is a promoter, it is obvious for a skilled person that double-stranded nucleic acid is used.

Thus, the vector of the invention is preferably an expression vector. An "expression vector" is a construct that can be used to transform a selected host cell and provides for expression of a coding sequence in the selected host. Expression vectors can for instance be cloning vectors, binary vectors or integrating vectors. Expression comprises transcription of the nucleic acid molecule preferably into a translatable mRNA. Regulatory elements ensuring expression in prokaryotic and/or eukaryotic cells are well known to those skilled in the art.

The present invention furthermore relates to host cells comprising a vector as described above or a nucleic acid molecule according to the invention wherein the nucleic acid molecule is foreign to the host cell.

By "foreign" it is meant that the nucleic acid molecule is either heterologous with respect to the host cell, this means derived from a cell or organism with a different genomic background, or is homologous with respect to the host cell but located in a different genomic environment than the naturally occurring counterpart of said nucleic acid molecule. This means that, if the nucleic acid molecule is homologous with respect to the host cell, it is not located in its natural location in the genome of said host cell, in particular it is surrounded by different genes. In this case the nucleic acid molecule may be either under the control of its own promoter or under the control of a heterologous promoter. The vector or nucleic acid molecule according to the invention which is present in the host cell may either be integrated into the genome of

the host cell or it may be maintained in some form extrachromosomally. In this respect, it is also to be understood that the nucleic acid molecule of the invention can be used to restore or create a mutant gene via homologous recombination (Paszkowski (ed.), Homologous Recombination and Gene Silencing in Plants. Kluwer Academic Publishers (1994)).

The host cell can be any prokaryotic or eukaryotic cell, such as bacterial, insect, fungal, plant or animal cells. Preferred fungal cells are, for example, those of the genus Saccharomyces, in particular those of the species S. cerevisiae.

Another subject of the invention is a method for the preparation of A20 interacting proteins which comprises the cultivation of host cells according to the invention which, due to the presence of a vector or a nucleic acid molecule according to the invention, are able to express such a protein, under conditions which allow expression of the protein and recovering of the so-produced protein from the culture.

The term "expression" means the production of a protein or nucleotide sequence in the cell. However, said term also includes expression of the protein in a cell-free system. It includes transcription into an RNA product, post-transcriptional modification and/or translation to a protein product or polypeptide from a DNA encoding that product, as well as possible post-translational modifications. Depending on the specific constructs and conditions used, the protein may be recovered from the cells, from the culture medium or from both. For the person skilled in the art it is well known that it is not only possible to express a native protein but also to express the protein as fusion polypeptides or to add signal sequences directing the protein to specific compartments of the host cell, e.g., ensuring secretion of the peptide into the culture medium, etc. Furthermore, such a protein and fragments thereof can be chemically synthesized and/or modified according to standard methods.

The terms "protein" and "polypeptide" used in this application are interchangeable. "Polypeptide" refers to a polymer of amino acids (amino acid sequence) and does not refer to a specific length of the molecule. Thus peptides and oligopeptides are included within the definition of polypeptide. This term does also refer to or include post-translational modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like. Included within the definition are, for example, polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids, etc.), polypeptides with substituted linkages, as well as other modifications known in the art, both naturally occurring and non-naturally occurring.

The present invention furthermore relates to proteins encoded by the nucleic acid molecules according to the invention or produced or obtained by the above-described methods, and to functional and/or immunologically active fragments of such A20 interacting proteins. The proteins and polypeptides of the present invention are not necessarily translated from a designated nucleic acid sequence; the polypeptides may be generated in any manner, including for example, chemical synthesis, or expression of a recombinant expression system, or isolation from a suitable viral system. The polypeptides may include one or more analogs of amino acids, phosphorylated amino acids or unnatural amino acids. Methods of inserting analogs of amino acids into a sequence are known in the art. The polypeptides may also include one or more labels, which are known to those skilled in the art. In this context, it is also understood that the proteins according to the invention may be further modified by conventional methods known in the art. By providing the proteins according to the present invention it is also possible to determine fragments which retain biological activity, namely the mature, processed form. This allows the construction of chimeric proteins and peptides comprising an amino sequence derived from the protein of the invention, which is crucial for its binding activity. The other functional amino acid sequences may be either

physically linked by, e.g., chemical means to the proteins of the invention or may be fused by recombinant DNA techniques well known in the art.

The term "functional fragment of a sequence" or " functional part of a sequence" means a truncated sequence of the original sequence referred to. The truncated sequence (nucleic acid or protein sequence) can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 30 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids, up to a maximum of about 20 or 25 amino acids.

Furthermore, folding simulations and computer redesign of structural motifs of the protein of the invention can be performed using appropriate computer programs (Olszewski, Proteins 25 (1996), 286-299; Hoffman, Comput. Appl. Biosci. 11 (1995), 675-679). Computer modeling of protein folding can be used for the conformational and energetic analysis of detailed peptide and protein models (Monge, J. Mol. Biol. 247 (1995), 995-1012; Renouf, Adv. Exp. Med. Biol. 376 (1995), 37-45). In particular, the appropriate programs can be used for the identification of interactive sites of the inventive protein , its receptor, its ligand or other interacting proteins by computer assistant searches for complementary peptide sequences (Fassina, Immunomethods 5 (1994), 114-120. Further appropriate computer systems for the design of protein and peptides are described in the prior art, for example in Berry, Biochem. Soc. Trans. 22 (1994), 1033-1036; Wodak, Ann. N. Y. Acad. Sci. 501 (1987), 1-13; Pabo, Biochemistry 25 (1986), 5987-5991. The results obtained from the above-described computer analysis can be used for, e.g., the preparation of peptidomimetics of the protein of the invention or fragments thereof. Such

pseudopeptide analogues of the natural amino acid sequence of the protein may very efficiently mimic the parent protein (Benkirane, J. Biol. Chem. 271 (1996), 33218-33224). For example, incorporation of easily available achiral - amino acid residues into a protein of the invention or a fragment thereof results in the substitution of amide bonds by polymethylene units of an aliphatic chain, thereby providing a convenient strategy for constructing a peptidomimetic (Banerjee, Biopolymers 39 (1996), 769-777). Superactive peptidomimetic analogues of small peptide hormones in other systems are described in the prior art (Zhang, Biochem. Biophys. Res. Commun. 224 (1996), 327-331). Appropriate peptidomimetics of the protein of the present invention can also be identified by the synthesis of peptidomimetic combinatorial libraries through successive amide alkylation and testing the resulting compounds, e.g., for their binding and immunological properties. Methods for the generation and use of peptidomimetic combinatorial libraries are described in the prior art, for example in Ostresh, Methods in Enzymology 267 (1996), 220-234 and Dorner, Bioorg. Med. Chem. 4 (1996), 709-715.

Furthermore, a three-dimensional and/or crystallographic structure of the protein of the invention can be used for the design of peptidomimetic inhibitors of the biological activity of the protein of the invention (Rose, Biochemistry 35 (1996), 12933-12944; Rutenber, Bioorg. Med. Chem. 4 (1996), 1545-1558).

Furthermore, the present invention relates to antibodies specifically recognizing a A20 interacting protein according to the invention or parts, i.e. specific fragments or epitopes, of such a protein. The antibodies of the invention can be used to identify and isolate other A20 interacting proteins and genes in any organism. These antibodies can be monoclonal antibodies, polyclonal antibodies or synthetic antibodies as well as fragments of antibodies, such as Fab, Fv or scFv fragments etc. Monoclonal antibodies can be prepared, for example, by the techniques as originally described in Köhler and Milstein, Nature 256 (1975), 495, and Galfré, Meth. Enzymol. 73 (1981), 3, which comprise the fusion of mouse myeloma cells to spleen cells derived from immunized mammals. Furthermore, antibodies or fragments thereof to the

aforementioned peptides can be obtained by using methods which are described, e.g., in Harlow and Lane "Antibodies, A Laboratory Manual", CSH Press, Cold Spring Harbor, 1988. These antibodies can be used, for example, for the immunoprecipitation and immunolocalization of proteins according to the invention as well as for the monitoring of the synthesis of such proteins, for example, in recombinant organisms, and for the identification of compounds interacting with the protein according to the invention. For example, surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies selections, yielding a high increment of affinity from a single library of phage antibodies which bind to an epitope of the protein of the invention (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmborg, J. Immunol. Methods 183 (1995), 7-13). In many cases, the binding phenomena of antibodies to antigens is equivalent to other ligand/anti-ligand binding.

The invention also relates to a diagnostic composition comprising at least one of the aforementioned nucleic acid molecules, vectors, proteins, antibodies or compounds and optionally suitable means for detection.

Said diagnostic compositions may be used for methods for detecting expression of related A20 interacting proteins by detecting the presence of the corresponding mRNA which comprises isolation of mRNA from a cell and contacting the mRNA so obtained with a probe comprising a nucleic acid probe as described above under hybridizing conditions, detecting the presence of mRNA hybridized to the probe, and thereby detecting the expression of the protein in the cell. Further methods of detecting the presence of a protein according to the present invention comprises immunotechniques well known in the art, for example enzyme linked immunosorbent assay.

The invention also relates to a pharmaceutical composition comprising one or more compounds, obtained by the above mentioned screening method, in a biologically active amount, for the treatment of NF-κB related diseases such

as respiratory disorders, particularly adult respiratory distress syndrome, allograft rejection, chronic inflammatory diseases such as rheumatoid arthritis, asthma or inflammatory bowel disease, and/or autoimmune diseases such as systemic lupus erythematosus.

In another aspect, the invention relates to a pharmaceutical composition comprising one or more of the above mentioned proteins in a biologically active amount, for the treatment of NF-κB related diseases such as respiratory disorders, particularly adult respiratory distress syndrome, allograft rejection, chronic inflammatory diseases such as rheumatoid arthritis, asthma or inflammatory bowel disease, and/or autoimmune diseases such as systemic lupus erythematosus.

The invention also concerns a pharmaceutical composition comprising one or more of the above mentioned proteins and/or one or more of the above mentioned compounds in a biologically active amount, for a treatment to sensitize tumor cells.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1: Tissue distribution of ABIN transcripts. A Northern blot of poly(A)$^+$ RNA (2µg per lane) of various murine tissues (Clontech) was probed with the fragment of ABIN cloned by two hybrid analysis covering the C-terminal sequences ABIN (390-599). RNA size markers are indicated in kB. Expression of β-actin served as a control for the quantity of RNA loaded.

Figure 2 A: Co-immunoprecipitation of A20 and ABIN after transient transfection of the encoding plasmids of E-tagged ABIN and Green Fluorescent Protein (GFP), GFP-A20, GFP-A20(369-775), GFP-A20(1-368) or an empty expression vector as a negative control in 239T cells. Immunoprecipitation (upper panel) was performed with anti-GFP antibody and Western blot detection with anti E-tag antibody. To control expression levels of ABIN, 10 µl aliquots of lysates were separated by sodium dodecyl sulphate

polyacrylamide gel electrophoresis (SDS-PAGE) and Western blot detection with anti-E-tag antibody (lower panel).

B: Co-immunoprecipitation of the C-terminal fragment of ABIN lacking the putative leucine zipper structure with GFP-A20 upon transient overexpression in 293T cells. Immunoprecipitation and expression levels were detected as described for full length ABIN and are shown in the upper and lower panel, respectively.

Figure 3: Consensus sequences, derived from the comparison of the ABIN and ABIN2 sequences.

Figure 4 A: Effect of ABIN or fragments of ABIN on the TNF- and IL-1-induced activation of NF–κB, as measured by reporter gene activity. 293T cells were transiently transfected with 100 ng pUT651, 100 ng pNFconluc and 100 ng expression plasmid and stimulated with hTNF (1000 IU/ml) or mIL1β (20 ng/ml) during 6 hours. As a control, 100 ng of plasmids encoding GFP or GFP-A20 were transfected.

B: Effect of transient transfection of suboptimal quantities of expression plasmids encoding A20 (5ng) and ABIN (20 ng) on TNF mediated NF-κB induction in 293T cells. In both experiments, standard deviations were less than 10 %.

Figure 5: Effect of ABIN or fragments of ABIN on the TPA-induced activation of NF–κB, as measured by reporter gene activity. 293T cells were transiently transfected with 100 ng pUT651, 100 ng pNFconluc and 100 ng expression plasmid and stimulated with TPA (200 ng/ml) during 6 hours. As a control, 100 ng of plasmids encoding GFP or GFP-A20 were transfected.

Figure 6: Effect of ABIN2 on the TNF- and TPA-induced activation of NF–κB, as measured by reporter gene activity. 293T cells were transiently transfected with 100 ng pUT651, 100 ng pNFconluc and 600 ng expression plasmid and

stimulated with hTNF (1000IU/ml) or TPA (200 ng/ml) during 6 hours. As a control, 600 ng of plasmid encoding GFP or GFP-A20 was transfected

Figure 7 A: Effect of full length ABIN on NF-κB activation in 293T cells induced by overexpression of TRADD, RIP, TRAF2, NIK or p65 after transfection of 300 ng of their encoding plasmids, together with 100 ng pUT651, 100 ng pNFconluc and 500 ng pCAGGS-ABIN. Cells were lysed 24 hours after transfection, and luciferase and β-galactosidase activity were measured.

B: Effect of truncated ABIN containing the leucine zipper structure (ABIN(390-647)) on TRADD, RIP, TRAF2 or NIK induced NF-κB activation. In both experiments, standard deviations were less than 10 %.

Figuur 8: Effect of site specific mutations in 2 regions of ABIN on its binding with A20 and on its inhibition of NF-κB activation.

A. Amino acid comparison of two homologues sequences found in ABIN and ABIN-2. Identical amino acids are shown in bold. Site specific mutations (underlined) resulted in the mutants ABIN-MUT1, ABIN-MUT2, ABIN-MUT3 and ABIN-MUT4 as shown.

B. Coimmunoprecipitation of mutated ABIN with A20 after transient expression of these genes in 293T cells. Cells were transfected with the plasmids pCAGGS-GFP or pCAGGS-GFP/A20 together with the plasmids encoding ABIN or its site specific mutants (ABIN-MUT1, ABIN-MUT2, ABIN-MUT3 or ABIN-MUT4). Lysates of these cells were immunoprecipitated with polyclonal anti-GFP antibody and separated on SDS-PAGE. Western blot analysis was performed with monoclonal anti-E-tag antibody to look for the coimmunoprecipitation of ABIN or its mutants (upper panel). Lower panels show total expression levels of GFP, GFP/A20 and ABIN. In this case, a fraction of the total lysate was separated by SDS-PAGE and expression was detected with anti-GFP or anti-E-tag antibodies.

C. Effect of mutated ABIN on TNF-induced NF-κB activation. 293T cells were transiently transfected with 100 ng pUT651, 100 ng pNFconluc and 200 ng expression plasmid as indicated and stimulated with TNF (1000 IU/ml) during 6 hours. Cell extracts were analyzed for luciferase and β-galactosidase activity and plotted as luc/gal, which is representative for NF-κB activity. Each value is the mean (N=3) with standard deviations less than 10%.

D. Dominant negative effect of ABIN-MUT2, ABIN-MUT3 and ABIN-MUT4 on the NF-κB inhibiting function of ABIN. 293T cells were transiently transfected with 100 ng pUT651, 100 ng pNFconluc and 200 ng pCAGGS-ABIN or empty vector. In addition, 600 ng of the expression vectors encoding ABIN-MUT2, ABIN-MUT3, ABIN-MUT4 or empty vector were cotransfected, as indicated. Cells were stimulated with TNF (1000 IU/ml) during 6 hours. Cell extracts were analyzed for luciferase and β-galactosidase activity and plotted as luc/gal.

DEFINITIONS

The following definitions are provided in order to further illustrate and define the meaning and scope of the various terms used in the current description.

The term "treatment", "treating" or "treat" means any treatment of a disease in a mammal, including :(1) preventing the disease causing the clinical symptoms of the disease not to develop; (2) inhibiting the disease arresting the development of the clinical symptoms; and/or (3) relieving the disease causing the regression of clinical symptoms.

The term "effective amount" means a dosage sufficient to provide treatment for the disease state being treated. This will vary depending on the patient, the disease and the treatment being effected.

"Capable of interacting" means that a protein can form a complex with another protein, as can be measured using a yeast two hybrid system, or with co-immunoprecipitation, or with equivalent systems known to people skilled in the art.

"Functional" protein or fragment means a protein or fragment that is capable to interact with the zinc finger protein A20, or with another protein of the NF-κB related pathway

"Protein A20" ("A20") means the TNF induced zinc finger protein, described by (Dixit *et al.*, 1990; Opipari *et al.*, 1990; Tewari et al., 1995) , or an active fragment thereof, such as the zinc finger containing part (amino acids 387-790 of human A20; amino acids 369-775 of murine A20).

The terms "gene(s)", "polynucleotide", "nucleic acid sequence", "nucleotide sequence", "DNA sequence" or "nucleic acid molecule(s)" as used herein refers to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, this term includes double- and single-stranded DNA, and RNA. It also includes known types of modifications, for example, methylation, "caps" substitution of one or more of the naturally occuring nucleotides with an analog. Preferably, the DNA sequence of the invention comprises a coding sequence encoding the above defined A20 interacting protein.

A "coding sequence" is a nucleotide sequence which is transcribed into mRNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the 5'-terminus and a translation stop codon at the 3'-terminus. A coding sequence can include, but is not limited to mRNA, cDNA, recombinant nucleotide sequences or genomic DNA, while introns may be present as well under certain circumstances.

"Consensus sequence" means a stretch of at least 15 amino acids, showing 50-100% homology, preferably between 70-100% homology between ABIN and ABIN2.

"Compound" means any chemical or biological compound, including simple or complex inorganic or organic molecules, peptides, peptido-mimetics, proteins, antibodies, carbohydrates or nucleic acids, that interferes in the binding between a protein depicted in SEQ ID n° 2, 3, 5, 6 or 7 with a compound of the NF-κB related pathway, such as A20.

As used herein, the term "composition" refers to any composition such as a

pharmaceutical composition comprising as an active ingredient an isolated functional protein according to the present invention possibly in the presence of suitable excipients known to the skilled man and may thus be administered in the form of any suitable composition as detailed below by any suitable method of administration within the knowledge of a skilled man. The preferred route of administration is parenterally. In parenteral administration, the compositions of this invention will be formulated in a unit dosage injectable form such as a solution, suspension or emulsion, in association with a pharmaceutically acceptable excipient. Such excipients are inherently nontoxic and nontherapeutic. Examples of such excipients are saline, Ringer's solution, dextrose solution and Hank's solution. Nonaqueous excipients such as fixed oils and ethyl oleate may also be used. A preferred excipient is 5% dextrose in saline. The excipient may contain minor amounts of additives such as substances that enhance isotonicity and chemical stability, including buffers and preservatives.

The isolated functional protein of the invention is administered at a concentration that is therapeutically effective to prevent allograft rejection, GVHD, allergy and autoimmune diseases. The dosage and mode of administration will depend on the individual. Generally, the compositions are administered so that the isolated functional protein is given at a dose between 1 μg/kg and 10 mg/kg, more preferably between 10 μg/kg and 5 mg/kg, most preferably between 0.1 and 2 mg/kg. Preferably, it is given as a bolus dose. Continuous short time infusion (during 30 minutes) may also be used. The compositions comprising the isolated functional protein according to the invention may be infused at a dose between 5 and 20 μg/kg/minute, more preferably between 7 and 15 μg/kg/minute.

According to a specific case, the "therapeutically effective amount" of the isolated functional protein according to the invention needed should be determined as being the amount sufficient to cure the patient in need of treatment or at least to partially arrest the disease and its complications. Amounts effective for such use will depend on the severity of the disease and the general state of the patient's health. Single or multiple administrations

may be required depending on the dosage and frequency as required and tolerated by the patient.

With regard to the use of the isolated functional protein of the present invention to prevent allograft rejection, it should be stressed that said proteins of the present invention or the compositions comprising the same may be administered before, during or after the organ transplantation as is desired from case to case. In case the protein or the compositions comprising the same are administered directly to the host, treatment will preferably start at the time of the transplantation and continue afterwards in order to prevent the activation and differentiation of host T cells against the MHC on the allograft. In case the donor organ is *ex vivo* perfused with the functional protein according to the invention or the compositions comprising the same, treatment of the donor organ ex vivo will start before the time of the transplantation of the donor organ in order to prevent the activation and differentiation of host T cells against the MHC on the allograft.

The invention is hereunder further explained by way of examples without being restrictive in the scope of the current invention.

EXAMPLES

Example 1: Isolation of the novel inhibitors

The novel inhibitors of the NF-κB pathway were isolated using a yeast two-hybrid assay, with protein A20 as bait. The yeast two-hybrid assay was purchased from Clontech Laboratories (Palo Alto, CA). The screening of an L929r2 cDNA library with pAS2-A20 was described previously (De Valck *et al.* 1997). Yeast colonies expressing interacting proteins were selected by growth on minimal media lacking Tryptophan, Leucine and Histidine, in the presence of 5 mM 3-amino-1,2,4-triazole and by screening for β-gal activity. Plasmid DNA was extracted from the positive colonies and the pGAD424 vectors encoding candidate A20 interacting proteins were recovered by

electroporation in the *E.coli* strain HB101 and growth on media lacking Leucine.

From 1.3 x 10^6 transformants, 11 clones expressed A20 interacting proteins, including A20 itself (De Valck *et al.*, 1996) and 14-3-3 proteins (De Valck *et al.*, 1997). Three clones contained C-terminal fragments of the same cDNA encoding an unknown protein that herewith is named "A20 Binding Inhibitor of NF-κB activation (ABIN) and 1 clone contained the C-terminal fragment (1136 bp) of an unknown protein that herewith is called ABIN2.

Full length ABIN cDNA was subsequently isolated from the L929r2 cDNA library by colony hybridisation (De Valck *et al.*,1996) with an ABIN fragment (corresponding to amino acids 390-599) cloned by two-hybrid analysis as a probe. Several cDNA's were isolated and in the longest cDNA stop codons were identified in all three reading frames 5' of a potential initiator methionine. Two different splice variants were found of approximately 2800 and 2600 nucleotides long, with an open reading frame of 1941 and 1781 nucleotides respectively, initiating at two different methionines (ABIN (1-647) (SEQ ID NO.2) and ABIN (54-647) (SEQ ID NO.3)). These cDNA's encode proteins of 72 and 68 kDa containing an amphipathic helix with 4 consecutive repeats of a leucine followed by 6 random amino acids residues characteristic of a leucine zipper structure.

Full length cDNA of ABIN2 was isolated from murine heart by 5' RACE (SMART PCR cDNA synthesis kit, Clontech), using a 3' primer hybridising to an EST clone (572231) which corresponds to the ABIN2 fragment isolated by two hybrid analysis, but with 507 extra nucleotides at the 5' end. A 1967 nucleotides long cDNA was isolated, with an open reading frame of 1290 nucleotides long, encoding a protein of 430 amino acids (SEQ ID NO.5).

Example 2 : Expression pattern of ABIN and ABIN2.

Northern blot analysis revealed that both ABIN and ABIN2 are expressed in all murine tissues tested (heart, brain, spleen, lung, liver, skeletal muscle, kidney, testis: see Figure 1; only the data for ABIN are shown). ABIN is

present as mRNA of approximately 2800 bp which is in accordance with the length of the cloned full length cDNA. In contrast to A20, ABIN mRNA is constitutively expressed in both TNF-sensitive and TNF-resistant subclones derived from the parental cell line L929s, irrespective of TNF stimulation.

ABIN2 is present as mRNA of approximately 2000 bp which is in accordance with the length of the cloned, full length cDNA.

Example 3: Study of the interaction of the ABIN and ABIN2 proteins and protein fragments with A20.

Full length ABIN(1-647) and ABIN(54-647) were able to bind A20 in a yeast two hybrid assay, confirming the original interaction found with the 3 C-terminal fragments ABIN(390-599), ABIN(249-647) and ABIN(312-647). The latter contain the putative leucine zipper protein interaction motif (397-420).

Further analysis was carried out by co-immunoprecipitation. The eukaryotic plasmids for ABIN and its fragments as well as for ABIN2 were made by inserting the corresponding PCR fragment in frame with an N-terminal E-tag into the mammalian expression plasmid pCAGGS (Niwa *et al.*, 1991). cDNA encoding mutant GFP(S65T) and a fusion protein of GFP(S65T) with murine A20 were also cloned in pCAGGS.

2×10^6 human embryonic kidney 293T cells were plated on 10-cm Petri dishes and transiently transfected with the suitable plasmids by calcium phosphate-DNA coprecipitation. 24 hours after transfection, cells were lysed in 500 µl of lysis buffer (50 mM Hepes pH 7.6, 250 mM NaCl, 0.1% Nonidet P-40 and 5 mM EDTA). Lysates were incubated with 5 µl of rabbit anti-GFP antibody (Clontech) and immunocomplexes were immobilised on protein A-trisacryl (Pierce). The latter was washed twice with lysis buffer and twice with lysis buffer containing 1 M NaCl. Coprecipitating proteins were separated by SDS-PAGE and revealed by Western blotting with mouse anti-E-tag antibody (Pharmacia).

Full length ABIN as well as the C-terminal fragment lacking the leucine zipper motif (ABIN(420-647)) was still able to co-immunoprecipitate with A20 in 293T cells that were transiently transfected with an expression plasmid for chimeric

GFP-A20 protein and full length or truncated ABIN with an N-terminal E-tag (Figure 2). Interaction of ABIN with A20 required the C-terminal, zinc finger containing part of A20 (A20(369-775)). This domain was shown previously to be required for dimerisation of A20 and for the interaction of A20 with 14-3-3 protein (De Valck *et al.*, 1996; De Valck *et al.*, 1997). In contrast, the N-terminal part of human A20 (A20(1-386)) was previously shown to interact with TRAF2 (Song *et al.*, 1996), suggesting that A20 acts as an adapter protein between TRAF2 and ABIN. The interaction between A20 and ABIN was not influenced by stimulation with TNF.

To characterise the subcellular distribution of ABIN, we transiently transfected GFP-A20- and E-tagged ABIN cDNA in 293T cells and analysed their expression by means of GFP fluorescence and immunofluorescence via the anti-E tag antibody. 4 x 10^5 293T cells were seeded on coverslips in 6-well plates and transfected with 1 µg plasmid DNA. 24 hours after transfection, cells were fixed on the coverslips with 3% paraformaldehyde. Upon permeabilisation with 1% Triton X-100, the cells were incubated for 2 hours with mouse anti-E-tag antibody (1/1000) followed by a second incubation with anti-mouse Ig antibody coupled to biotin (Amersham, 1/1000). After subsequent incubation with streptavidine coupled to Texasred (Amersham), fluorescence can be analysed via fluorescence microscopy (Zeiss, Axiophot) using a filter set with excitation at 543 nm and emission at 600nm. In the same cells, fluorescence of GFP can be detected at a different wave length, namely absorption at 485 nm and emission at 510 nm.

ABIN colocalised with A20 throughout the cytoplasm, both in unstimulated and in TNF stimulated cells. This observation makes the existence of regulatory redistribution events rather unlikely.

Example 4: Sequence analysis of the cDNA's.

Nucleotide sequence analysis was carried out using cycle sequencing on an ABI373A sequencer (Applied Biosystems, Foster City, CA). The sequence of full length ABIN is shown in SEQ ID NO.1; the sequence of ABIN2 is shown in SEQ ID NO.4.

Database similarity searches (BLAST) showed that ABIN is the murine homologue of the partial human cDNA encoding a protein with an unknown function (Genbank accession number D30755; Nagase *et al.*, 1995). Moreover, ABIN shows homology with a partial human immunodeficiency virus (HIV) Nef interacting protein, NIP40-1 (no called Naf1=nef associated factor 1; Fukushi et al., FEBS Letters, 442 (1999), 83-88). HIV-Nef contributes substantially to disease pathogenesis by augmenting virus replication and markedly perturbing T-cell function. Interestingly, the effect of Nef on host cell activation has been explained in part by its interaction with specific cellular proteins involved in signal transduction (Harris, 1996) of which ABIN might be an example.

There are no proteins in the database that are clearly homologous with ABIN2. However, by comparing ABIN2 with ABIN, one can define two homologous regions and derive two consensus sequences (Figure 3, SEQ ID NOs. 6 and 7)) that may be important for the interaction of these proteins with A20, and/or for their further function in signal transduction.

Example 5: Role of ABIN, ABIN fragments and/or ABIN2 in the TNF-, IL-1- and/or TPA-induced transduction pathway leading to NF-κB activation, as measured by reporter gene activity.

The construction of the ABIN, ABIN-fragments and ABIN2 plasmids was carried out as described above. The plasmid pNFconluc, encoding a luciferase reporter gene driven by a minimal NF-κB responsive promoter described by Kimura *et al.* (1986) and the plasmid pUT651, encoding β-galactosidase was obtained from Eurogentec (Seraing, Belgium). NF-κB activity was determined by the NF-κB dependent expression of a luciferase reporter gene. Therefore, 293T cells were plated in 6-well plates at 4 x 10^5 cells per well and transiently transfected by the calcium phosphate-DNA coprecipitation method. Each transfection contained 800 ng of the expression plasmids, as well as 100 ng of pNFconluc plasmid as reporter and 100 ng pUT651 plasmid as a reference for transfection efficiency. 24 hours after transfection, these cells were trypsinised and seeded on a 24-well plate.

Another 24 hours later, cells were either stimulated with 1000 IU/ml hTNF, 20 ng/ml mIL1-β , 200 ng/ml TPA (Sigma) or left untreated. After 6 hours of stimulation, cells were lysed in 200 µl lysis buffer and analysed for luciferase and β-galactosidase activity as described in De Valck *et al.*, 1997. GFP and GFP-A20 served as negative and positive controls, respectively.

Similar to A20, both splice variants of ABIN were able to block TNF or IL-1 induced NF-κB activation in these cells, with the shorter N-terminal truncated isoform being slightly more effective (Figure 4 A). Moreover, structure-function analysis of ABIN deletion mutants revealed that the NF–κB inhibiting activity resides in the C-terminal 228 amino acids (ABIN(420-647) SEQ ID NO 8) which are also sufficient for interaction with A20. The latter ABIN-mutant no longer contains the leucine zipper structure, demonstrating that this protein domain is not involved in the interaction with A20 nor in the inhibition of NF-κB (Figure 4 A). Overexpression of a combination of suboptimal doses of A20 and ABIN, that on their own were not sufficient to inhibit NF-κB activation, diminished NF-κB activation upon stimulation with TNF (Figure 4 B) or IL-1 considerably. This suggests that ABIN mediates the NF-κB inhibiting effect of A20.

Total ABIN (1-647; SED.ID.NO.2), the shorter splice variant (54-647; SEQ.ID.NO.3) and the C-terminal fragment (390-647) are also able to block the TPA induced NF-κB activation (Figure 5).

Similar results were obtained when ABIN2 was used in the test instead of ABIN or ABIN-fragments (figuur 6).

Example 6: Effect of ABIN and/or ABIN fragments on NF-κB activation induced by overexpression of TRADD, RIP, TRAF2, NIK or p65.

Expression vectors for ABIN and ABIN fragments were constructed as described above. The expression vectors containing TRAF2, NIK and p65 have been described (Malinin *et al.*, 1997; Rothe *et al.*, 1994; Vanden Berghe *et al.*, 1998). PCR fragments encoding TRADD and RIP were cloned in pCDNA3 (Invitrogen, Carlsbad, CA) in frame with a C-terminal E-tag. Transfection and reporter assay was carried out as described above.

AMENDED SHEET

NF-κB can be activated in 293 T cells by TNF treatment as well as by overexpression of specific proteins of the TNF-receptor complex, including TRADD, RIP, TRAF2 and NIK (Rothe *et al.*,1995; Malinin *et al.*, 1997; Hsu *et al.*, 1995; Ting *et al.*, 1996). The latter associates with and activates IκB kinase complex which leads to IκB phosphorylation. This is a signal for ubiquitination and degradation of IκB, thus releasing NF-κB which then translocates to the nucleus. Co-transfection of expression plasmids encoding these TNF-receptor associated proteins together with the expression plasmids encoding full length ABIN, showed that the latter inhibited completely NF-κB activation induced by TRADD or RIP, and partially TRAF2-induced NF-κB activation. In contrast, no clear difference was observed when NF-κB-dependent reporter gene expression was induced by NIK or more directly by overexpression of the p65 subunit of NF-κB (Figure 7). These results suggest that ABIN inhibits TNF-induced NF-κB activation at a level preceding the activation of the NIK-IκB kinase steps, for example at the level of TRAF2 in the TNF-receptor complex,

As members of the TRAF family mediate NF-κB activation by several other stimuli, including IL-1, lymphotoxin β, CD30 and CD40 (Rothe *et al.*, 1995; Cao *et al.*, 1996; Nakano *et al.*, 1996; Aizawa *et al.*, 1997; Ishada *et al.*, 1996), ABIN might have the potential to inhibit NF-κB activation in response to a wide range of inducers. Therefore, drugs that mimic the activity of ABIN are likely to have therapeutic value in inflammatory and neurodegenerative diseases as well as in cancer and AIDS.

Example 7: Cell transfection, coimmunoprecipitation and Western blotting.

$2x10^6$ human embryonic kidney 293T cells were plated on 10 cm Petri dishes and transiently transfected by calcium phosphate-DNA coprecipitation. 24 hours after transfection, cells were lysed in 500 µl of lysis buffer (50 mM Hepes pH 7.6, 250 mM NaCl, 0.1% Nonidet P-40 and 5 mM EDTA). Lysates were incubated with 5 µl of rabbit anti-GFP antibody (Clontech) and immunocomplexes were immobilized on protein A-Trisacryl (Pierce). The

latter were washed twice with lysis buffer and twice with lysis buffer containing 1M NaCl. Coprecipitating proteins were separated by SDS-PAGE and analyzed by Western blotting with mouse anti-E-tag antibody (Pharmacia).

Example 8: NF-κB dependent reporter gene assay.

NF-κB activity was determined by the NF-κB dependent expression of a luciferase reporter gene. Therefore 293T cells were plated in 6-well plates at 4 x 10^5 cells per well and transiently transfected by the calcium phosphate-DNA coprecipitation method. Each transfection contained 800 ng of the specific expression plasmids, as well as 100 ng of pNFconluc plasmid and 100 ng pUT651 plasmid. 24 hours after transfection, these transfectants were trypsinized and seeded on a 24-well plate. Another 24 hours later, cells were either stimulated with 1000 IU/ml hTNF or 7000 IU/ml IL-1 or left untreated. After 6 hours of stimulation, cells were lysed in 200 µl lysis buffer and analyzed for luciferase and β-galactosidase activity. Luciferase values (luc) are normalized with β-galactosidase values (gal) and plotted as luc/gal.

Example 9: Site specific mutagenesis.

Site specific mutagenesis on ABIN was performed by overlap PCR reaction using primers which contain the desired mutations. The primers used were the mutation primers 5'-GAATACCAGGAGGCGCAGATCCAGCGGCTCAATAAAGCTTTGGAGGAGGC-3', 5'-GTTGCTGAAAGAGGACGTCAAAATCTTTGAAGAGG-3', 5'-GCAGGTAAAAATCTTTGAAGA GAATGCCCAGAGGGAACG-3', 5'-GCAGGTAAAAATCTTTGAAGAGGACTTCCAGAGGGAAC GGAGTGATGCGCAACGCATGCCC G-3', a forward primer located at the start codon and two reverse primers, one hybridizing in the 3' UTR and one in the coding region. The XhoI-BstEII fragment of wild type ABIN(54-647) in pCAGGS was exchanged with the same fragment of the PCR amplified mutated ABIN cDNA's.

Example 10: Binding of ABIN with A20 is not sufficient for its NF-κB inhibiting potential.

A two hybrid assay with A20 revealed another novel A20-binding protein which was also able to inhibit NF-κB activation upon overexpression. BLAST searches with this novel protein, named ABIN-2, revealed no homology with any known protein. However, by comparison of the protein sequence of ABIN-2 with ABIN, two boxes of 19 (AA 423-441) and 21 (AA 475-495) amino acids long with 68% and 67% homology were identified respectively (Fig. 8). Therefore the contribution of these regions to the binding with A20 and to the NF-κB inhibiting effects of ABIN were analysed by site specific mutagenesis of a number of conserved amino acids (Fig. 8A). Coimmunoprecipitation analysis after transient overexpression of GFP or GFP/A20 together with wild type ABIN or its site specific mutants (ABIN-MUT1, ABIN-MUT2, ABIN-MUT3 and ABIN-MUT4) in 293T cells, showed that all of these mutants can still bind A20 (Fig. 8B). On the other hand, point mutations in the second box (ABIN-MUT2, ABIN-MUT3 and ABIN-MUT4) completely abolished the ability of ABIN to block NF-κB activation upon stimulation of 293T cells with TNF, even when higher amounts of these expression plasmids were transfected. In contrast, the mutation in the first box (ABIN-MUT1) only slightly diminished the NF-κB inhibiting effect of ABIN (Fig. 8C). Furthermore, point mutations in the second conserved motif dominantly interfered with the NF-κB inhibiting effect of wild type ABIN (Fig. 8D). ABIN-MUT2 and ABIN-MUT3 exhibit a more potent function as dominant negative mutants of ABIN, compared to ABIN-MUT4. In these assays, comparable expression levels of the different mutants and of wild type ABIN were obtained as judged by Western blot analysis using anti-E tag antibody. These results suggest that the second conserved region is involved in the NF-κB inhibiting effects of ABIN, and that binding of ABIN with A20 as such is not sufficient for inhibition of NF-κB activation.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Vlaams Interuniversitair Instituut voor Biotechnologie
(B) STREET: Rijvisschestraat 120
(C) CITY: Zwijnaarde
(E) COUNTRY: Belgium
(F) POSTAL CODE (ZIP): B-9052
(G) TELEPHONE: +32 9 2446611
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(ii) TITLE OF INVENTION: Novel inhibitors of NF-kappaB activation

(iii) NUMBER OF SEQUENCES: 7

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2812 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mus musculus

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:117..2060

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:276..2060

(ix) FEATURE:
(A) NAME/KEY: intron
(B) LOCATION:81..252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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CACAGGGAGG CATGGCCGCA CTCACTGGGC ACATCTTCAG ATCACCTCGT GCATTCTCGG
60

ATGAGTGACC TGGGCTGAAG CTAGGCGGCC GTCACGGCAG GGGTTGAGCC ACCCTC
116

ATG GAA GGG AGA GGA CCC TAC CGG ATC TAC GAC CCA GGG GGC AGC ACG
164
Met Glu Gly Arg Gly Pro Tyr Arg Ile Tyr Asp Pro Gly Gly Ser Thr
  1               5                  10                  15

CCT CTG GGA GAG GTG TCC GCA GCT TTT GAA CGT CTA GTG GAG GAG AAT
212
Pro Leu Gly Glu Val Ser Ala Ala Phe Glu Arg Leu Val Glu Glu Asn
             20                  25                  30

ACT CGG CTG AAG GGA AAA ATG CAA GGG ATA AAG ATG TTA GGG GAG CTT
260
Thr Arg Leu Lys Gly Lys Met Gln Gly Ile Lys Met Leu Gly Glu Leu
         35                  40                  45

CTG GAG GAG TCT CAG ATG GAA GCG TCC AGA CTC CGG CAG AAG GCA GAG
308
Leu Glu Glu Ser Gln Met Glu Ala Ser Arg Leu Arg Gln Lys Ala Glu
     50                  55                  60

GAG CTG GTC AAG GAC AGC GAG CTG TCA CCA CCG ACA TCT GCC CCC TCC
356
Glu Leu Val Lys Asp Ser Glu Leu Ser Pro Pro Thr Ser Ala Pro Ser
 65                  70                  75                  80

TTG GTC TCC TTT GAT GAC CTG GCT GAG CTC ACA GGA CAG GAT ACA AAG
404
Leu Val Ser Phe Asp Asp Leu Ala Glu Leu Thr Gly Gln Asp Thr Lys
                 85                  90                  95

GTC CAG GTA CAT CCT GCT ACC AGC ACT GCC GCC ACC ACC ACC GCC ACC
452
Val Gln Val His Pro Ala Thr Ser Thr Ala Ala Thr Thr Thr Ala Thr
            100                 105                 110

GCC ACC ACG GGA AAC TCC ATG GAG AAG CCC GAG CCA GCC TCC AAA TCT
500
Ala Thr Thr Gly Asn Ser Met Glu Lys Pro Glu Pro Ala Ser Lys Ser
        115                 120                 125

CCG TCC AAT GGC GCC TCC TCG GAC TTT GAA GTG GTC CCT ACT GAG GAG
548
Pro Ser Asn Gly Ala Ser Ser Asp Phe Glu Val Val Pro Thr Glu Glu
    130                 135                 140

CAG AAT TCA CCC GAA ACT GGC AGC CAC CCT ACG AAC ATG ATG GAC CTG
596
Gln Asn Ser Pro Glu Thr Gly Ser His Pro Thr Asn Met Met Asp Leu
145                 150                 155                 160

GGG CCC CCA CCC CCA GAG GAC AGC AAC CTG AAG CTC CAC CTG CAG CGC
644
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Gly Pro Pro Pro Pro Glu Asp Ser Asn Leu Lys Leu His Leu Gln Arg
                    165                 170                 175

CTG GAG ACC ACC CTT AGC GTG TGT GCA GAG GAG CCA GAC CAC AGC CAG
692
Leu Glu Thr Thr Leu Ser Val Cys Ala Glu Glu Pro Asp His Ser Gln
            180                 185                 190

CTC TTC ACC CAC CTG GGC CGC ATG GCC CTC GAG TTC AAC AGG TTG GCC
740
Leu Phe Thr His Leu Gly Arg Met Ala Leu Glu Phe Asn Arg Leu Ala
        195                 200                 205

TCC AAA GTG CAT AAA AAT GAG CAG CGC ACC TCC ATC CTG CAG ACC TTA
788
Ser Lys Val His Lys Asn Glu Gln Arg Thr Ser Ile Leu Gln Thr Leu
    210                 215                 220

TGT GAG CAG CTG CGC CAG GAG AAT GAA GCC CTG AAG GCC AAG CTG GAC
836
Cys Glu Gln Leu Arg Gln Glu Asn Glu Ala Leu Lys Ala Lys Leu Asp
225                 230                 235                 240

AAG GGC CTG GAA CAG CGG GAT CTG GCT GCT GAG AGG CTG CGG GAG GAA
884
Lys Gly Leu Glu Gln Arg Asp Leu Ala Ala Glu Arg Leu Arg Glu Glu
                245                 250                 255

AAC ACG GAG CTC AAG AAA CTG TTG ATG AAC AGC AGC TGC AAA GAG GGA
932
Asn Thr Glu Leu Lys Lys Leu Leu Met Asn Ser Ser Cys Lys Glu Gly
            260                 265                 270

CTC TGT GGG CAG CCC AGC TCC CCA AAG CCA GAG GGT GCT GGC AAG AAG
980
Leu Cys Gly Gln Pro Ser Ser Pro Lys Pro Glu Gly Ala Gly Lys Lys
        275                 280                 285

GGC GTG GCT GGA CAG CAG CAG GCC AGT GTG ATG GCG AGT AAA GTC CCT
1028
Gly Val Ala Gly Gln Gln Gln Ala Ser Val Met Ala Ser Lys Val Pro
    290                 295                 300

GAA GCG GGG GCC TTT GGA GCA GCT GAG AAG AAA GTG AAG TTG CTA GAA
1076
Glu Ala Gly Ala Phe Gly Ala Ala Glu Lys Lys Val Lys Leu Leu Glu
305                 310                 315                 320

CAG CAA CGC ATG GAG CTG CTG GAA GTG AAC AAG CAG TGG GAC CAG CAT
1124
Gln Gln Arg Met Glu Leu Leu Glu Val Asn Lys Gln Trp Asp Gln His
                325                 330                 335

TTC CGG TCC ATG AAG CAG CAG TAT GAG CAG AAG ATC ACA GAG CTT CGC
1172
Phe Arg Ser Met Lys Gln Gln Tyr Glu Gln Lys Ile Thr Glu Leu Arg
            340                 345                 350
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CAG AAG CTG GTG GAC CTG CAG AAA CAG GTA ACT GAG CTG GAG GCC GAA
1220
Gln Lys Leu Val Asp Leu Gln Lys Gln Val Thr Glu Leu Glu Ala Glu
        355                 360                 365

CGG GAG CAG AAG CAG CGT GAC TTT GAC CGG AAA CTC CTC CTG GCC AAA
1268
Arg Glu Gln Lys Gln Arg Asp Phe Asp Arg Lys Leu Leu Leu Ala Lys
    370                 375                 380

TCG AAG ATA GAG ATG GAA GAG ACC GAC AAG GAG CAG CTG ACA GCA GAG
1316
Ser Lys Ile Glu Met Glu Glu Thr Asp Lys Glu Gln Leu Thr Ala Glu
385                 390                 395                 400

GCC AAG GAA CTG CGC CAG AAG GTC AGG TAC CTA CAG GAT CAG CTG AGC
1364
Ala Lys Glu Leu Arg Gln Lys Val Arg Tyr Leu Gln Asp Gln Leu Ser
                405                 410                 415

CCG CTC ACA AGG CAA CGA GAA TAC CAG GAG AAG GAG ATC CAG CGG CTC
1412
Pro Leu Thr Arg Gln Arg Glu Tyr Gln Glu Lys Glu Ile Gln Arg Leu
            420                 425                 430

AAT AAG GCC CTG GAG GAG GCC CTC AGC ATC CAG GCC TCT CCA TCA TCT
1460
Asn Lys Ala Leu Glu Glu Ala Leu Ser Ile Gln Ala Ser Pro Ser Ser
        435                 440                 445

CCG CCT GCA GCT TTT GGG AGT CCA GAA GGC GTT GGG GGC CAT CTG AGG
1508
Pro Pro Ala Ala Phe Gly Ser Pro Glu Gly Val Gly Gly His Leu Arg
    450                 455                 460

AAG CAG GAA CTA GTG ACA CAG AAT GAG TTG CTG AAA CAG CAG GTA AAG
1556
Lys Gln Glu Leu Val Thr Gln Asn Glu Leu Leu Lys Gln Gln Val Lys
465                 470                 475                 480

ATC TTT GAA GAG GAC TTC CAG AGG GAA CGG AGT GAC CGT GAA CGC ATG
1604
Ile Phe Glu Glu Asp Phe Gln Arg Glu Arg Ser Asp Arg Glu Arg Met
                485                 490                 495

AAT GAA GAG AAG GAG GAG CTG AAG AAG CAA GTA GAG AAG CTG CAG GCC
1652
Asn Glu Glu Lys Glu Glu Leu Lys Lys Gln Val Glu Lys Leu Gln Ala
            500                 505                 510

CAG GTC ACC CTG ACT AAT GCC CAG CTC AAA ACT CTC AAA GAG GAG GAG
1700
Gln Val Thr Leu Thr Asn Ala Gln Leu Lys Thr Leu Lys Glu Glu Glu
        515                 520                 525

AAG GCC AAG GAA GCC CTC AAA CAG CAG AAG AGG AAA GCA AAG GCT TCG
1748
Lys Ala Lys Glu Ala Leu Lys Gln Gln Lys Arg Lys Ala Lys Ala Ser
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     530                 535                 540

     GGA GAG CGC TAC CAC ATG GAA CCC CAC CCT GAG CAC GTC TGC GGC GCC
     1796
     Gly Glu Arg Tyr His Met Glu Pro His Pro Glu His Val Cys Gly Ala
     545                 550                 555                 560

     TAT CCC TAT GCC TAC CCA CCC ATG CCA GCC ATG GTA CCT CAC CAT GCC
     1844
     Tyr Pro Tyr Ala Tyr Pro Pro Met Pro Ala Met Val Pro His His Ala
                     565                 570                 575

     TAC AAG GAC TGG TCC CAG ATC CGA TAC CCT CCA CCC CCT GTG CCC ATG
     1892
     Tyr Lys Asp Trp Ser Gln Ile Arg Tyr Pro Pro Pro Pro Val Pro Met
                 580                 585                 590

     GAG CAC CCG CCC CCA CAC CCC AAC TCT CGC CTC TTC CAT CTG CCG GAG
     1940
     Glu His Pro Pro Pro His Pro Asn Ser Arg Leu Phe His Leu Pro Glu
             595                 600                 605

     TAC ACC TGG CGT CCA CCC TGT GCA GGG ATT CGG AAT CAG AGC TCT CAA
     1988
     Tyr Thr Trp Arg Pro Pro Cys Ala Gly Ile Arg Asn Gln Ser Ser Gln
         610                 615                 620

     GTG ATG GAC CCG CCC CCA GAC AGG CCT GCA GAG CCA GAG TCT GCA GAC
     2036
     Val Met Asp Pro Pro Pro Asp Arg Pro Ala Glu Pro Glu Ser Ala Asp
     625                 630                 635                 640

     AAT GAC TGT GAT GGG CCC CAG TGA GGCTGCAGTG GGTCATTTGG TTCCACCTTC
     2090
     Asn Asp Cys Asp Gly Pro Gln  *
                     645

     ATCTTTCAGA GCCAGCTGAC CTCAGATTGC CAAAAGTTTG AAGGCCATGT GCATGTTCTG
     2150

     TGTGACCCAA GCCTTGGCAG AGGAGAGGCT GGGATGGGTA GCTGGCTCAC ATCCCCAGCC
     2210

     AAGCCTCGAA CTGTTGACAA GACCAGGGAG AATCCACCCA TGGGCGCCCA CCAGGTTCTT
     2270

     ATGGATGCAA GCAGGAGAAG CTCAACACCC TGCCTCTTGC CAAGACAAGG AAGCCTCACC
     2330

     TGGCTTTGAC CTGCCATCCG TTGCTGAGGC CACTGGCTTC CATCCTAAGA ATGAGGTGCA
     2390

     ACAAGACCCC ATTCTCACAG AACCTCAAAG ACTTGGTTCC AGGCTCTCCA GAGACCATAC
     2450

     CCAACTCATG TGCATGTGCC GTTTTTGCTT CAAGCTCAGT AGCAGGACCT GCCCCGAGCC
     2510
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CCCTGCTCCT TGCCCCTCTG TGAGGAGTTA CGGAGAGGGC TTTGTCTCTA GAGCAGAAGA
2570

GAATGATGGG ACGGCCTGAT GCTGTCATGC TCTCCACTGC ACCTGTGGCA GCCTCCTGAG
2630

AGCCACCAAG ATCTGGGATG AAGGCCACAC CAGCCATGTC TGCTGAAGGG CCCCAGACTG
2690

AGATGACTCC GGCCTCCACA GTTAGATGTT TATGGTGCCA GAGGTCTATA TTAAGGTAGC
2750

TGTCTGTTGC TAGGCAGCCG TTTGCACAAA TCTTGGACAT AAATCCAACT TGAAGATCAA
2810

AA
2812

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 648 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Glu Gly Arg Gly Pro Tyr Arg Ile Tyr Asp Pro Gly Gly Ser Thr
1 5 10 15

Pro Leu Gly Glu Val Ser Ala Ala Phe Glu Arg Leu Val Glu Glu Asn
20 25 30

Thr Arg Leu Lys Gly Lys Met Gln Gly Ile Lys Met Leu Gly Glu Leu
35 40 45

Leu Glu Glu Ser Gln Met Glu Ala Ser Arg Leu Arg Gln Lys Ala Glu
50 55 60

Glu Leu Val Lys Asp Ser Glu Leu Ser Pro Pro Thr Ser Ala Pro Ser
65 70 75 80

Leu Val Ser Phe Asp Asp Leu Ala Glu Leu Thr Gly Gln Asp Thr Lys
85 90 95

Val Gln Val His Pro Ala Thr Ser Thr Ala Ala Thr Thr Thr Ala Thr
100 105 110

Ala Thr Thr Gly Asn Ser Met Glu Lys Pro Glu Pro Ala Ser Lys Ser
115 120 125

Pro Ser Asn Gly Ala Ser Ser Asp Phe Glu Val Val Pro Thr Glu Glu
130 135 140

Gln Asn Ser Pro Glu Thr Gly Ser His Pro Thr Asn Met Met Asp Leu
145 150 155 160

Gly Pro Pro Pro Pro Glu Asp Ser Asn Leu Lys Leu His Leu Gln Arg
165 170 175

Leu Glu Thr Thr Leu Ser Val Cys Ala Glu Glu Pro Asp His Ser Gln
180 185 190

Leu Phe Thr His Leu Gly Arg Met Ala Leu Glu Phe Asn Arg Leu Ala
195 200 205

Ser Lys Val His Lys Asn Glu Gln Arg Thr Ser Ile Leu Gln Thr Leu
210 215 220

Cys Glu Gln Leu Arg Gln Glu Asn Glu Ala Leu Lys Ala Lys Leu Asp
225 230 235 240

Lys Gly Leu Glu Gln Arg Asp Leu Ala Ala Glu Arg Leu Arg Glu Glu
245 250 255

Asn Thr Glu Leu Lys Lys Leu Leu Met Asn Ser Ser Cys Lys Glu Gly
260 265 270

Leu Cys Gly Gln Pro Ser Ser Pro Lys Pro Glu Gly Ala Gly Lys Lys
275 280 285

Gly Val Ala Gly Gln Gln Gln Ala Ser Val Met Ala Ser Lys Val Pro
290 295 300

Glu Ala Gly Ala Phe Gly Ala Ala Glu Lys Lys Val Lys Leu Leu Glu
305 310 315 320

Gln Gln Arg Met Glu Leu Leu Glu Val Asn Lys Gln Trp Asp Gln His
325 330 335

Phe Arg Ser Met Lys Gln Gln Tyr Glu Gln Lys Ile Thr Glu Leu Arg
340 345 350

Gln Lys Leu Val Asp Leu Gln Lys Gln Val Thr Glu Leu Glu Ala Glu
355 360 365

Arg Glu Gln Lys Gln Arg Asp Phe Asp Arg Lys Leu Leu Leu Ala Lys
370 375 380

Ser Lys Ile Glu Met Glu Glu Thr Asp Lys Glu Gln Leu Thr Ala Glu
385 390 395 400

Ala Lys Glu Leu Arg Gln Lys Val Arg Tyr Leu Gln Asp Gln Leu Ser
405 410 415

Pro Leu Thr Arg Gln Arg Glu Tyr Gln Glu Lys Glu Ile Gln Arg Leu
420 425 430

Asn Lys Ala Leu Glu Glu Ala Leu Ser Ile Gln Ala Ser Pro Ser Ser
435 440 445

Pro Pro Ala Ala Phe Gly Ser Pro Glu Gly Val Gly Gly His Leu Arg
450 455 460

Lys Gln Glu Leu Val Thr Gln Asn Glu Leu Leu Lys Gln Gln Val Lys
465 470 475 480

Ile Phe Glu Glu Asp Phe Gln Arg Glu Arg Ser Asp Arg Glu Arg Met
485 490 495

Asn Glu Glu Lys Glu Glu Leu Lys Lys Gln Val Glu Lys Leu Gln Ala
500 505 510

Gln Val Thr Leu Thr Asn Ala Gln Leu Lys Thr Leu Lys Glu Glu Glu
515 520 525

Lys Ala Lys Glu Ala Leu Lys Gln Gln Lys Arg Lys Ala Lys Ala Ser
530 535 540

Gly Glu Arg Tyr His Met Glu Pro His Pro Glu His Val Cys Gly Ala
545 550 555 560

Tyr Pro Tyr Ala Tyr Pro Pro Met Pro Ala Met Val Pro His His Ala
565 570 575

Tyr Lys Asp Trp Ser Gln Ile Arg Tyr Pro Pro Pro Pro Val Pro Met
580 585 590

Glu His Pro Pro Pro His Pro Asn Ser Arg Leu Phe His Leu Pro Glu
595 600 605

Tyr Thr Trp Arg Pro Pro Cys Ala Gly Ile Arg Asn Gln Ser Ser Gln
610 615 620

Val Met Asp Pro Pro Pro Asp Arg Pro Ala Glu Pro Glu Ser Ala Asp
625 630 635 640

Asn Asp Cys Asp Gly Pro Gln *
645

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 594 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Glu Ala Ser Arg Leu Arg Gln Lys Ala Glu Glu Leu Val Lys Asp

1 5 10 15

Ser Glu Leu Ser Pro Pro Thr Ser Ala Pro Ser Leu Val Ser Phe Asp
20 25 30

Asp Leu Ala Glu Leu Thr Gly Gln Asp Thr Lys Val Gln Val His Pro
35 40 45

Ala Thr Ser Thr Ala Ala Thr Thr Thr Ala Thr Ala Thr Thr Gly Asn
50 55 60

Ser Met Glu Lys Pro Glu Pro Ala Ser Lys Ser Pro Ser Asn Gly Ala
65 70 75 80

Ser Ser Asp Phe Glu Val Val Pro Thr Glu Glu Gln Asn Ser Pro Glu
85 90 95

Thr Gly Ser His Pro Thr Asn Met Met Asp Leu Gly Pro Pro Pro Pro
100 105 110

Glu Asp Ser Asn Leu Lys Leu His Leu Gln Arg Leu Glu Thr Thr Leu
115 120 125

Ser Val Cys Ala Glu Glu Pro Asp His Ser Gln Leu Phe Thr His Leu
130 135 140

Gly Arg Met Ala Leu Glu Phe Asn Arg Leu Ala Ser Lys Val His Lys
145 150 155 160

Asn Glu Gln Arg Thr Ser Ile Leu Gln Thr Leu Cys Glu Gln Leu Arg
165 170 175

Gln Glu Asn Glu Ala Leu Lys Ala Lys Leu Asp Lys Gly Leu Glu Gln
180 185 190

Arg Asp Leu Ala Ala Glu Arg Leu Arg Glu Glu Asn Thr Glu Leu Lys
195 200 205

Lys Leu Leu Met Asn Ser Ser Cys Lys Glu Gly Leu Cys Gly Gln Pro
210 215 220

Ser Ser Pro Lys Pro Glu Gly Ala Gly Lys Lys Gly Val Ala Gly Gln
225 230 235 240

Gln Gln Ala Ser Val Met Ala Ser Lys Val Pro Glu Ala Gly Ala Phe
245 250 255

Gly Ala Ala Glu Lys Lys Val Lys Leu Leu Glu Gln Gln Arg Met Glu
260 265 270

Leu Leu Glu Val Asn Lys Gln Trp Asp Gln His Phe Arg Ser Met Lys
275 280 285

Gln Gln Tyr Glu Gln Lys Ile Thr Glu Leu Arg Gln Lys Leu Val Asp
290 295 300

Leu Gln Lys Gln Val Thr Glu Leu Glu Ala Glu Arg Glu Gln Lys Gln
305 310 315 320

Arg Asp Phe Asp Arg Lys Leu Leu Leu Ala Lys Ser Lys Ile Glu Met
325 330 335

Glu Glu Thr Asp Lys Glu Gln Leu Thr Ala Glu Ala Lys Glu Leu Arg
340 345 350

Gln Lys Val Arg Tyr Leu Gln Asp Gln Leu Ser Pro Leu Thr Arg Gln
355 360 365

Arg Glu Tyr Gln Glu Lys Glu Ile Gln Arg Leu Asn Lys Ala Leu Glu
370 375 380

Glu Ala Leu Ser Ile Gln Ala Ser Pro Ser Ser Pro Pro Ala Ala Phe
385 390 395 400

Gly Ser Pro Glu Gly Val Gly Gly His Leu Arg Lys Gln Glu Leu Val
405 410 415

Thr Gln Asn Glu Leu Leu Lys Gln Gln Val Lys Ile Phe Glu Glu Asp
420 425 430

Phe Gln Arg Glu Arg Ser Asp Arg Glu Arg Met Asn Glu Glu Lys Glu
435 440 445

Glu Leu Lys Lys Gln Val Glu Lys Leu Gln Ala Gln Val Thr Leu Thr
450 455 460

Asn Ala Gln Leu Lys Thr Leu Lys Glu Glu Glu Lys Ala Lys Glu Ala
465 470 475 480

Leu Lys Gln Gln Lys Arg Lys Ala Lys Ala Ser Gly Glu Arg Tyr His
485 490 495

Met Glu Pro His Pro Glu His Val Cys Gly Ala Tyr Pro Tyr Ala Tyr
500 505 510

Pro Pro Met Pro Ala Met Val Pro His His Ala Tyr Lys Asp Trp Ser
515 520 525

Gln Ile Arg Tyr Pro Pro Pro Pro Val Pro Met Glu His Pro Pro Pro
530 535 540

His Pro Asn Ser Arg Leu Phe His Leu Pro Glu Tyr Thr Trp Arg Pro
545 550 555 560

Pro Cys Ala Gly Ile Arg Asn Gln Ser Ser Gln Val Met Asp Pro Pro
565 570 575

Pro Asp Arg Pro Ala Glu Pro Glu Ser Ala Asp Asn Asp Cys Asp Gly
580 585 590

Pro Gln

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1967 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mus musculus

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:83..1375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AAACTTTCCG GGAAGGCTGG TTTTCGCTCC CCCTGTGTGG AGAAGTTGGA GACGCCCAAG
60

TCCCCACGGA AGGCCTACAG CC ATG TCG TCT GGG GAC CCA AGG TCT GGT AGA
112
Met Ser Ser Gly Asp Pro Arg Ser Gly Arg
650 655

CAG GAC GGG GCC CCG CGT GCG GCC GCA GCG CTC TGT GGC CTG TAC CAC
160
Gln Asp Gly Ala Pro Arg Ala Ala Ala Ala Leu Cys Gly Leu Tyr His
660 665 670

GAG GCC GGC CAG CAA CTA CAG CGC CTG AAG GAT CAG CTG GCC GCG CGT
208
Glu Ala Gly Gln Gln Leu Gln Arg Leu Lys Asp Gln Leu Ala Ala Arg
675 680 685 690

GAC GCC CTC ATC GCG AGC CTC CGC ACC CGC CTC GCG GCT CTG GAA GGG
256
Asp Ala Leu Ile Ala Ser Leu Arg Thr Arg Leu Ala Ala Leu Glu Gly
695 700 705

CAC ACG GCG CCG TCA CTC GTG GAC GCA CTT CTG GAT CAG GTG GAG CGC
304
His Thr Ala Pro Ser Leu Val Asp Ala Leu Leu Asp Gln Val Glu Arg
710 715 720

TTC CGT GAG CAG CTG CGA CGA CAG GAG GAA GGC GCT TCG GAG ACC CAG
352
Phe Arg Glu Gln Leu Arg Arg Gln Glu Glu Gly Ala Ser Glu Thr Gln
725 730 735

CTG CGG CAG GAA GTT GAA AGA CTT ACG GAG CGT CTA GAG GAA AAA GAG
400
Leu Arg Gln Glu Val Glu Arg Leu Thr Glu Arg Leu Glu Glu Lys Glu
740 745 750

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AGG GAG ATG CAA CAG CTG ATG AGC CAG CCT CAG CAT GAG CAA GAG AAG
448
Arg Glu Met Gln Gln Leu Met Ser Gln Pro Gln His Glu Gln Glu Lys
755                 760                 765                 770

GAG GTA GTC TTG CTT CGG CGA AGT GTG GCA GAG AAG GAG AAA GCC AGG
496
Glu Val Val Leu Leu Arg Arg Ser Val Ala Glu Lys Glu Lys Ala Arg
                775                 780                 785

GCC GCC AGT GAT GTT CTG TGC CGC TCC TTG GCT GAT GAG ACC CAC CAA
544
Ala Ala Ser Asp Val Leu Cys Arg Ser Leu Ala Asp Glu Thr His Gln
            790                 795                 800

CTG CGC AGG ACA TTG GCA GCC ACT GCC CAC ATG TGC CAA CAT CTG GCC
592
Leu Arg Arg Thr Leu Ala Ala Thr Ala His Met Cys Gln His Leu Ala
        805                 810                 815

AAA TGT CTG GAT GAA CGA CAG TGT GCA CAG GGA GAC GCT GGG GAG AAA
640
Lys Cys Leu Asp Glu Arg Gln Cys Ala Gln Gly Asp Ala Gly Glu Lys
    820                 825                 830

AGC CCT GCT GAG CTA GAG CAA ACA AGC AGC GAT GCT TCT GGC CAG AGT
688
Ser Pro Ala Glu Leu Glu Gln Thr Ser Ser Asp Ala Ser Gly Gln Ser
835                 840                 845                 850

GTT ATT AAG AAG TTA CAG GAA GAA AAT CGA CTG TTA AAA CAG AAG GTG
736
Val Ile Lys Lys Leu Gln Glu Glu Asn Arg Leu Leu Lys Gln Lys Val
                855                 860                 865

ACT CAT GTA GAA GAC CTC AAT GCT AAG TGG CAG CGT TAT GAT GCA AGT
784
Thr His Val Glu Asp Leu Asn Ala Lys Trp Gln Arg Tyr Asp Ala Ser
            870                 875                 880

AGG GAC GAA TAT GTG AAG GGG TTG CAT GCC CAG CTA AAG AGG CGG CAG
832
Arg Asp Glu Tyr Val Lys Gly Leu His Ala Gln Leu Lys Arg Arg Gln
        885                 890                 895

GTC CCT CTG GAG CCT GAG CTG ATG AAG AAG GAG ATT TCC CGA CTT AAC
880
Val Pro Leu Glu Pro Glu Leu Met Lys Lys Glu Ile Ser Arg Leu Asn
    900                 905                 910

AGA CAG TTG GAG GAG AAA ATA AGT GAC TGT GCG GAA GCA AAC CAG GAG
928
Arg Gln Leu Glu Glu Lys Ile Ser Asp Cys Ala Glu Ala Asn Gln Glu
915                 920                 925                 930

CTG ACA GCC ATG AGG ATG TCC CGG GAC ACT GCG CTG GAG CGA GTG CAG
976
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Leu Thr Ala Met Arg Met Ser Arg Asp Thr Ala Leu Glu Arg Val Gln
                  935                 940                 945

ATG CTA GAA CAG CAG ATT CTT GCT TAC AAG GAT GAC TTC AAA TCA GAA
1024
Met Leu Glu Gln Gln Ile Leu Ala Tyr Lys Asp Asp Phe Lys Ser Glu
             950                 955                 960

AGG GCA GAT CGG GAA CGA GCG CAC AGT AGG ATT CAA GAG CTG GAG GAA
1072
Arg Ala Asp Arg Glu Arg Ala His Ser Arg Ile Gln Glu Leu Glu Glu
         965                 970                 975

AAG ATC ATG TCC TTG ATG TAC CAA GTG TCC CAG AGA CAG GAC TCC CGG
1120
Lys Ile Met Ser Leu Met Tyr Gln Val Ser Gln Arg Gln Asp Ser Arg
     980                 985                 990

GAG CCA GGA CCC TGT CGG ATT CAT ACG GGG AAC AAA ACT GCC AAG TAC
1168
Glu Pro Gly Pro Cys Arg Ile His Thr Gly Asn Lys Thr Ala Lys Tyr
995                 1000                1005                1010

TTA GAG ATG GAT GCA CTG GAG CAT GTG ACC CCT GGC GGC TGG AGG CCT
1216
Leu Glu Met Asp Ala Leu Glu His Val Thr Pro Gly Gly Trp Arg Pro
                 1015                1020                1025

GAG TCT AGG TCC CAA CAG ATG GAA CCT TCT GCA GAG GGT GGG CAT GTG
1264
Glu Ser Arg Ser Gln Gln Met Glu Pro Ser Ala Glu Gly Gly His Val
            1030                1035                1040

TGC ACA GCC CAG AGA GGT CAG GGT GAC CTT CAG TGC CCT CAT TGC CTG
1312
Cys Thr Ala Gln Arg Gly Gln Gly Asp Leu Gln Cys Pro His Cys Leu
        1045                1050                1055

CGG TGC TTC AGT GAT GAG CAA GGC GAG GCA TTC CTC AGG CAC CTG TCT
1360
Arg Cys Phe Ser Asp Glu Gln Gly Glu Ala Phe Leu Arg His Leu Ser
    1060                1065                1070

GAG TGC TGC CAA TGA GCCAGACATT GCCCGTGTGA CCCATGACCA CCATAGCTGC
1415
Glu Cys Cys Gln  *
1075

TCTAAGGGAC TGGGAGGGGT CCTCAGACTC AGTTTTCAAC TCAGTGTGTT GCATTCTCCT
1475

GGGATCTAGG GCCCAAATGG GCAGGGTCAC TGGAAGGTCA TCTTGTTTTC ATTTGACCAT
1535

GGTGAGACTT GGTCAGAGGG AACTATTGAC AGAGCAGGAG GAAGAGGGTG GGGTCAGGGA
1595
```

CATCAAGTGG ACATCAGTTT TGTCTCACGT AGAGTTTGGA GTGAGCTGTC AATTCAAAGC
1655

TGCAAGCTAT CAGTTGTGGG AATATTCTGA AGCCTGCTTG CACCTAGAGT TATGCCACTT
1715

GCTGGAAGGG GAAGTTGCTG TGGGAGCAGT GTGTCCTCTT TCTAGGGTGG TAGCTCCATC
1775

CTGTTGAGTA GTGAGATACA CTCCCTGACT GGTCTGTGCT GCATTACAGT TACATGATAC
1835

ACTAGAACCT TCCCAAACTC AGCAGAGCCA CACAGCTGCA TCCAGTACCA TCACCCTGCA
1895

AAACACTTGT ATTTCCAAAA GGGAAAGCAC CTTTATTTCC TAATCATTTA TTTTTATAAT
1955

AAATGGCTTT AC
1967

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Ser Ser Gly Asp Pro Arg Ser Gly Arg Gln Asp Gly Ala Pro Arg
1 5 10 15

Ala Ala Ala Ala Leu Cys Gly Leu Tyr His Glu Ala Gly Gln Gln Leu
20 25 30

Gln Arg Leu Lys Asp Gln Leu Ala Ala Arg Asp Ala Leu Ile Ala Ser
35 40 45

Leu Arg Thr Arg Leu Ala Ala Leu Glu Gly His Thr Ala Pro Ser Leu
50 55 60

Val Asp Ala Leu Leu Asp Gln Val Glu Arg Phe Arg Glu Gln Leu Arg
65 70 75 80

Arg Gln Glu Glu Gly Ala Ser Glu Thr Gln Leu Arg Gln Glu Val Glu
85 90 95

Arg Leu Thr Glu Arg Leu Glu Glu Lys Glu Arg Glu Met Gln Gln Leu
100 105 110

Met Ser Gln Pro Gln His Glu Gln Glu Lys Glu Val Val Leu Leu Arg
115 120 125

Arg Ser Val Ala Glu Lys Glu Lys Ala Arg Ala Ala Ser Asp Val Leu
130 135 140

```
Cys Arg Ser Leu Ala Asp Glu Thr His Gln Leu Arg Arg Thr Leu Ala
145                 150                 155                 160

Ala Thr Ala His Met Cys Gln His Leu Ala Lys Cys Leu Asp Glu Arg
                165                 170                 175

Gln Cys Ala Gln Gly Asp Ala Gly Glu Lys Ser Pro Ala Glu Leu Glu
            180                 185                 190

Gln Thr Ser Ser Asp Ala Ser Gly Gln Ser Val Ile Lys Lys Leu Gln
        195                 200                 205

Glu Glu Asn Arg Leu Leu Lys Gln Lys Val Thr His Val Glu Asp Leu
    210                 215                 220

Asn Ala Lys Trp Gln Arg Tyr Asp Ala Ser Arg Asp Glu Tyr Val Lys
225                 230                 235                 240

Gly Leu His Ala Gln Leu Lys Arg Arg Gln Val Pro Leu Glu Pro Glu
                245                 250                 255

Leu Met Lys Lys Glu Ile Ser Arg Leu Asn Arg Gln Leu Glu Glu Lys
            260                 265                 270

Ile Ser Asp Cys Ala Glu Ala Asn Gln Glu Leu Thr Ala Met Arg Met
        275                 280                 285

Ser Arg Asp Thr Ala Leu Glu Arg Val Gln Met Leu Glu Gln Gln Ile
    290                 295                 300

Leu Ala Tyr Lys Asp Asp Phe Lys Ser Glu Arg Ala Asp Arg Glu Arg
305                 310                 315                 320

Ala His Ser Arg Ile Gln Glu Leu Glu Glu Lys Ile Met Ser Leu Met
                325                 330                 335

Tyr Gln Val Ser Gln Arg Gln Asp Ser Arg Glu Pro Gly Pro Cys Arg
            340                 345                 350

Ile His Thr Gly Asn Lys Thr Ala Lys Tyr Leu Glu Met Asp Ala Leu
        355                 360                 365

Glu His Val Thr Pro Gly Gly Trp Arg Pro Glu Ser Arg Ser Gln Gln
    370                 375                 380

Met Glu Pro Ser Ala Glu Gly Gly His Val Cys Thr Ala Gln Arg Gly
385                 390                 395                 400

Gln Gly Asp Leu Gln Cys Pro His Cys Leu Arg Cys Phe Ser Asp Glu
                405                 410                 415

Gln Gly Glu Ala Phe Leu Arg His Leu Ser Glu Cys Cys Gln  *
            420                 425                 430
```

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:1..19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Xaa Xaa Xaa Lys Glu Ile Xaa Arg Leu Asn Xaa Xaa Leu Glu Glu
1 5 10 15

Xaa Xaa Ser

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION:1..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Xaa Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa Asp Phe Xaa Xaa Glu Arg
1 5 10 15

Xaa Asp Arg Glu Arg
20

Claims

1. An isolated protein comprising an amino acid sequence with 70-100% homology to the amino acid sequence depicted in SEQ ID NO.2, that is capable of interacting with the protein A20 and modulating and/or inhibiting NF-κB activation, and that is not Nef-associated factor 1.
2. An isolated protein comprising an amino acid sequence with 70-100% homology to the amino acids 54-647 of SEQ ID NO.2, as represented in SEQ ID NO. 3, that is capable of interacting with the protein A20 and modulating and/or inhibiting NF-κB activation.
3. An isolated protein comprising an amino acid sequence with 70-100% homology to the amino acids 420-647 of SEQ ID NO.2, as represented in SEQ ID NO. 8, that is capable of interacting with the protein A20 and modulating and/or inhibiting NF-κB activation.
4. An isolated protein comprising an amino acid sequence with 70-100% homology to the amino acid sequence depicted in SEQ ID NO.5, that is capable of interacting with the protein A20 and modulating and/or inhibiting NF-κB activation.
5. An isolated protein according to claim 1-4 comprising the consensus amino acid sequence depicted in SEQ ID NO. 6 and/or SEQ ID NO.7.
6. A nucleic acid encoding a protein according to any of the claims 1-5.
7. A nucleic acid according to claim 6 with about 70-100% homology to the DNA sequence depicted in SEQ ID NO.1.
8. A nucleic acid according to claim 6 with about 70-100% homology to the DNA sequence depicted in SEQ ID NO.4.
9. An isolated protein and/or a functional fragment thereof according to any of the claims 1-5 for use as a medicament.
10. Use of an isolated protein and/or a functional fragment thereof according to any of the claims 1-5 for the manufacture of a medicament to treat NF-κB related diseases.
11. Use according to claim 10, wherein the NF-κB related disease is a respiratory disorder, particularly adult respiratory distress syndrome, allograft rejection, a chronic inflammatory disease such as rheumatoid arthritis, asthma or

inflammatory bowel disease, and/or an autoimmune disease such as systemic lupus erythematosus.

12. Use of an isolated functional protein according to claim 1-5 and/or a functional fragment thereof for the manufacture of a medicament to sensitize tumor cells to anti-tumor treatments.

13. Use of an isolated functional protein and/or a functional fragment thereof according to any of the claims 10-12 wherein the protein at least comprises the amino acids 54-647, preferably 390-647, of SEQ ID NO.2.

14. Use of a functional protein and/or a functional fragment thereof according to claim 13, wherein the protein comprises at least the amino acids 420-647 of SEQ ID NO. 2.

15. Use of a functional protein according to any of the claims 1-5 and/or a functional fragment thereof to screen for compounds that interfere with the interaction of said protein(s) with other protein components of the NF-κB related pathway.

16. A method of screening compounds comprising the use of a protein according to claim 15.

17. A compound isolated with the method according to claim 16.

18. A pharmaceutical composition comprising one or more isolated functional proteins according to any of the claims 1-5 and/or functional fragments thereof and a pharmaceutically acceptable carrier material.

19. A pharmaceutical composition comprising one or more compounds according to claim 17 and a pharmaceutical acceptable carrier material.

20. A method of inhibiting activation of NF-κB comprising administering an effective amount of a protein according to any of the claims 1-5 and/or functional fragments thereof.

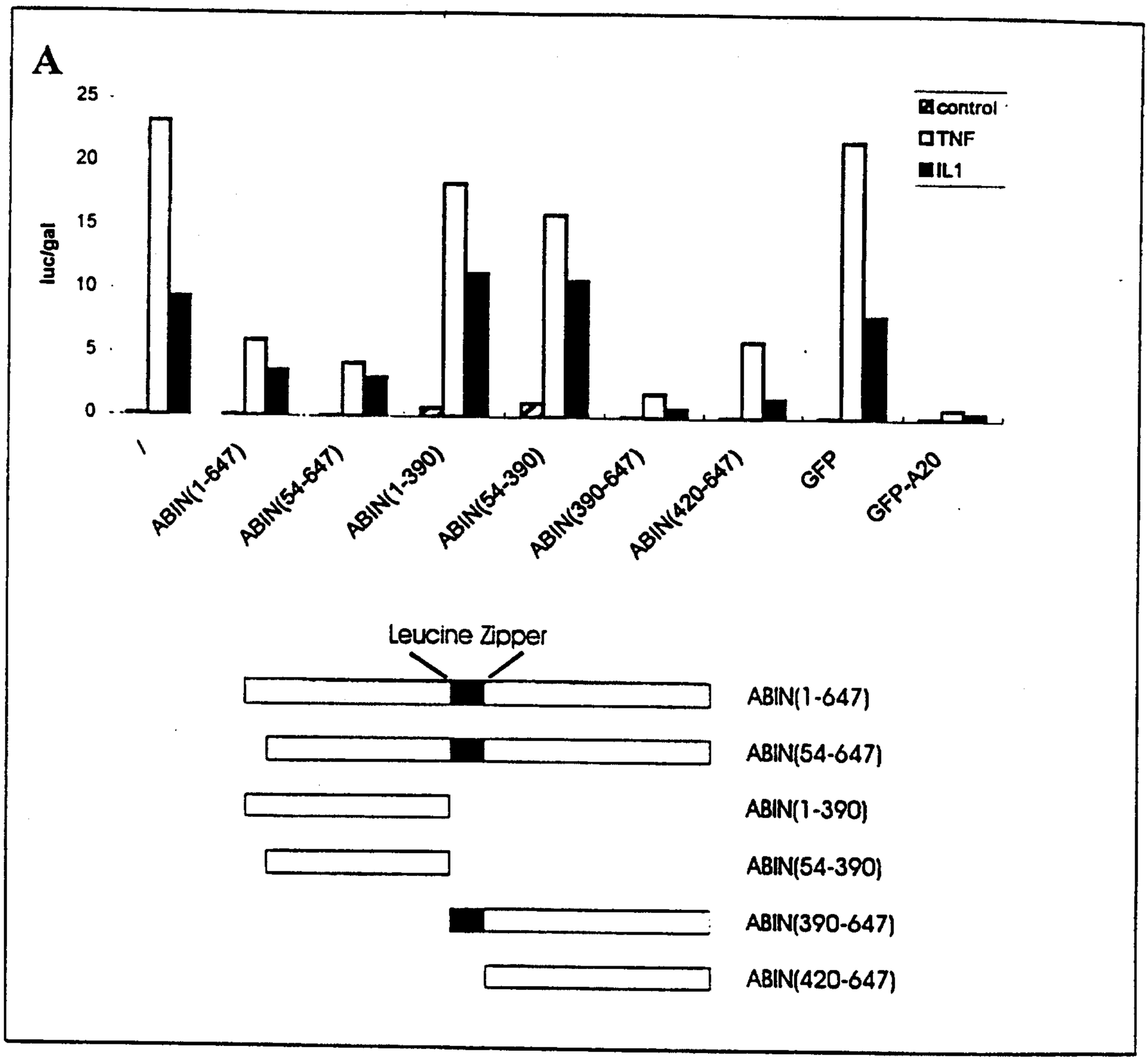
SEQUENCE 1

ABIN	^{423}E Y Q E K E I Q R L N K A L E E A L S^{441}
ABIN-2	^{256}E L M K K E I S R L N R Q L E E K I S^{274}
CONSENSUS	E x x x K E I x R L N K/R x L E E x L/I S

SEQUENCE 2

ABIN	^{475}L K Q Q V K I F E E D F Q R E R S D R E R^{495}
ABIN-2	^{300}L E Q Q I L A Y K D D F K S E R A D R E R^{320}
CONSENSUS	L x Q Q V/I x I/A x x E/D D F x x E R x D R E R

FIGURE 3


A
25
20
15
10
5
0
luc/gal
control
TNF
IL1
ABIN(1-647)
ABIN(54-647)
ABIN(1-390)
ABIN(54-390)
ABIN(390-647)
ABIN(420-647)
GFP
GFP-A20
Leucine Zipper
ABIN(1-647)
ABIN(54-647)
ABIN(1-390)
ABIN(54-390)
ABIN(390-647)
ABIN(420-647)

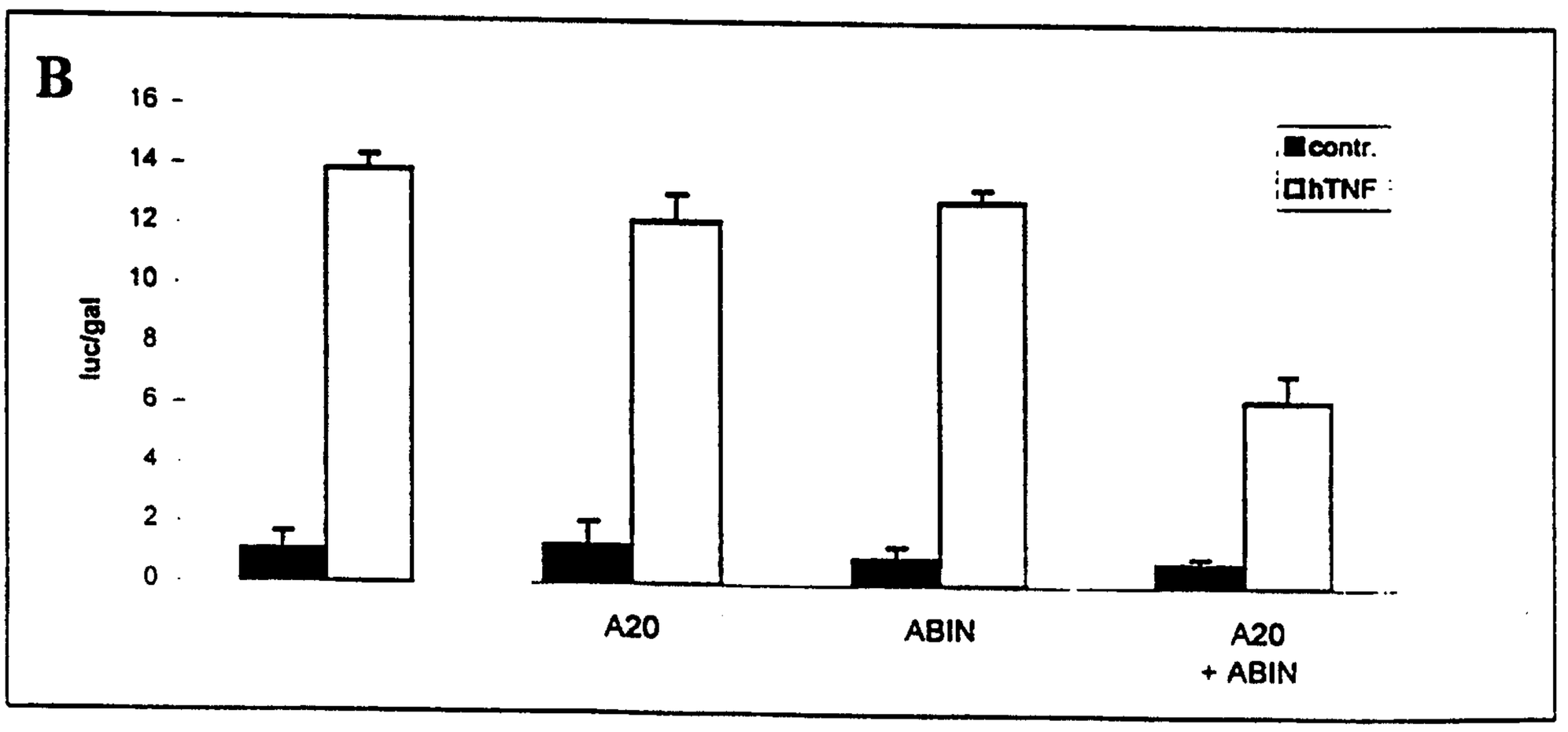

B
16
14
12
10
8
6
4
2
0
luc/gal
contr.
hTNF
A20
ABIN
A20
+ ABIN

FIGURE 4

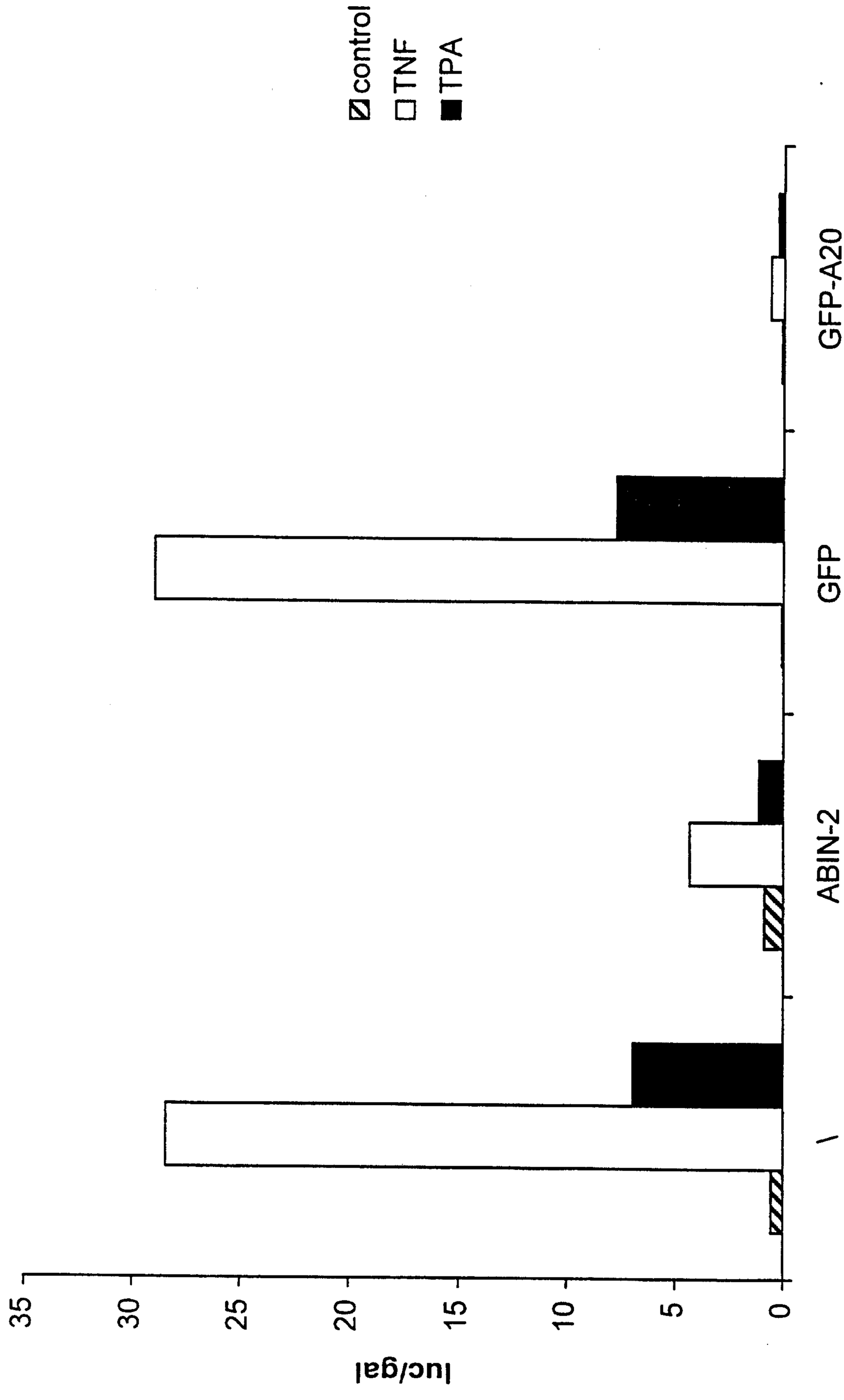
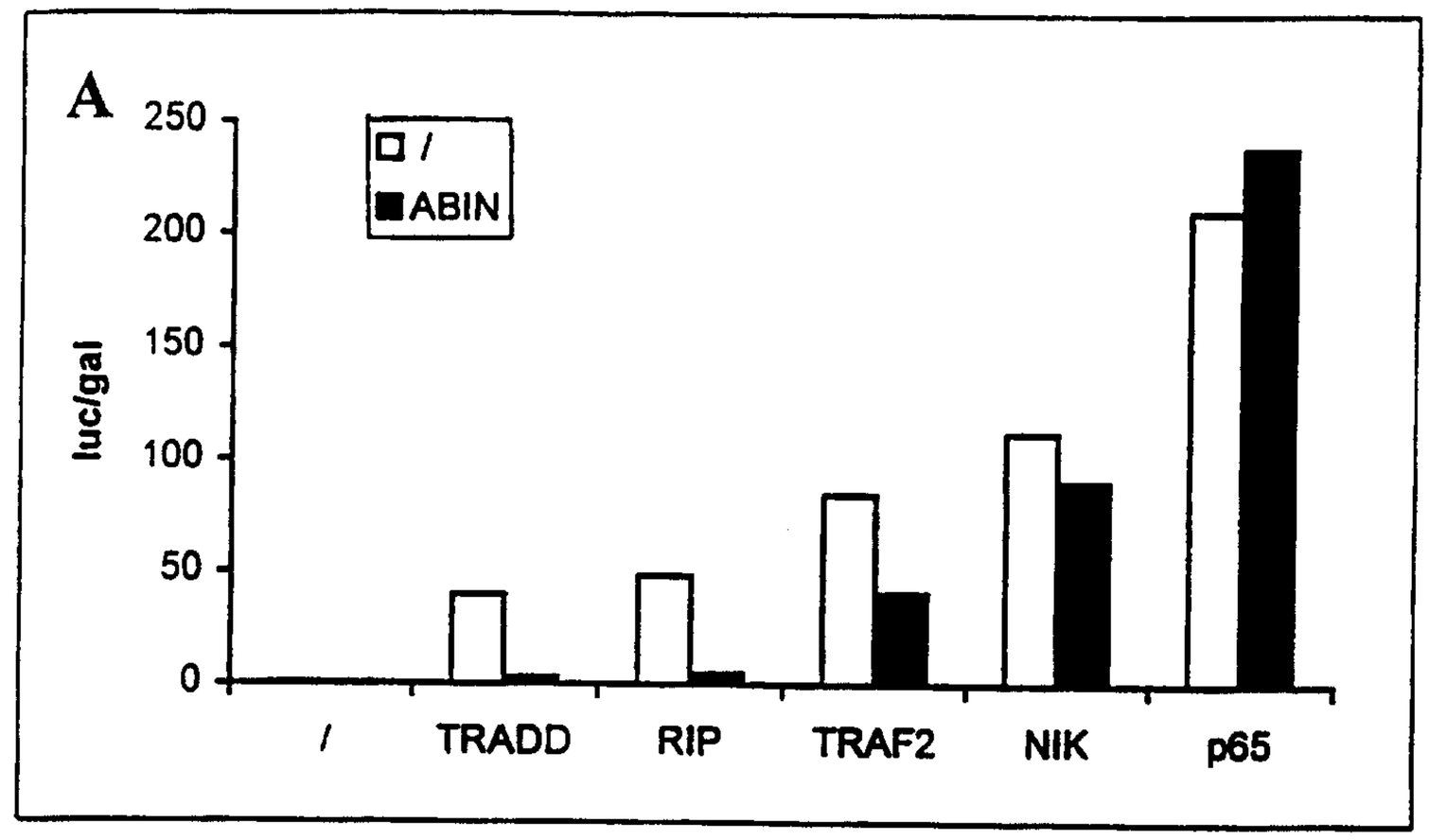


FIGURE 6


A
250
200
150
100
50
0
luc/gal
/
ABIN
/
TRADD
RIP
TRAF2
NIK
p65

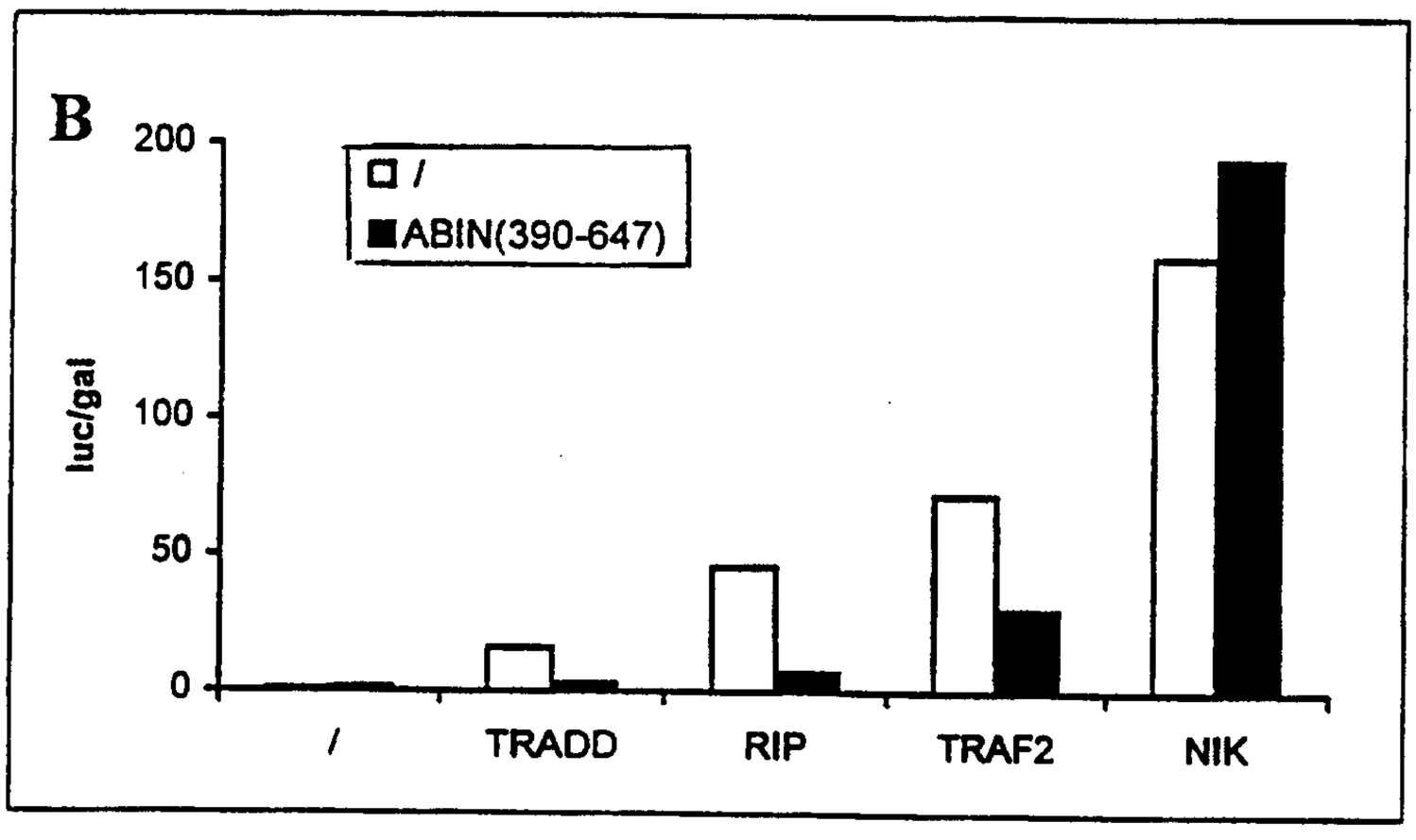

B
200
150
100
50
0
luc/gal
/
ABIN(390-647)
/
TRADD
RIP
TRAF2
NIK

FIGURE 7

UNSCANNABLE ITEM

RECEIVED WITH THIS APPLICATION

(ITEM ON THE 10TH FLOOR ZONE 5 IN THE FILE PREPARATION SECTION)

2328483

DOCUMENT REÇU AVEC CETTE DEMANDE

NE POUVANT ÊTRE BALAYÉ

(DOCUMENT AU 10 IÈME ÉTAGE AIRE 5 DANS LA SECTION DE LA

PRÉPARATION DES DOSSIERS)