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(54) Titre : PROTEINES IKK- α , ACIDES NUCLEIQUES ET PROCEDES
 (54) Title: IKK- α PROTEINS, NUCLEIC ACIDS AND METHODS

(57) **Abrégé/Abstract:**

The invention provides methods and compositions relating to an I κ B kinase, IKK- α , and related nucleic acids. The polypeptides may be produced recombinantly from transformed host cells from the disclosed IKK- α encoding nucleic acids or purified from human cells. The invention provides isolated IKK- α hybridization probes and primers capable of specifically hybridizing with the disclosed IKK- α genes, IKK- α -specific binding agents such as specific antibodies, and methods of making and using the subject compositions in diagnosis, therapy and in the biopharmaceutical industry.





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(57) Abstract <p>The invention provides methods and compositions relating to an IκB kinase, IKK-α, and related nucleic acids. The polypeptides may be produced recombinantly from transformed host cells from the disclosed IKK-α encoding nucleic acids or purified from human cells. The invention provides isolated IKK-α hybridization probes and primers capable of specifically hybridizing with the disclosed IKK-α genes, IKK-α-specific binding agents such as specific antibodies, and methods of making and using the subject compositions in diagnosis, therapy and in the biopharmaceutical industry.</p>		

IKK- α Proteins, Nucleic Acids and Methods

INTRODUCTION

Field of the Invention

The field of this invention is proteins involved in transcription factor activation.

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Background

Cytokines trigger changes in gene expression by modifying the activity of otherwise latent transcription factors (Hill and Treisman, 1995). Nuclear factor κ B (NF- κ B) is a prominent example of how such an external stimulus is converted into an active transcription factor (Verma et al., 1995). The NF- κ B system is composed of homo- and heterodimers of members of the Rel family of related transcription factors that control the expression of numerous immune and inflammatory response genes as well as important viral genes (Lenardo and Baltimore, 1989; Baeuerle and Henkel, 1994). The activity of NF- κ B transcription factors is regulated by their subcellular localization (Verma et al., 1995). In most cell types, NF- κ B is present as a heterodimer comprising of a 50 kDa and a 65 kDa subunit. This heterodimer is sequestered in the cytoplasm in association with I κ B α a member of the I κ B family of inhibitory proteins (Finco and Baldwin, 1995; Thanos and Maniatis, 1995; Verma et al., 1995). I κ B α masks the nuclear localization signal of NF- κ B and thereby prevents NF- κ B nuclear translocation. Conversion of NF- κ B into an active transcription factor that translocates into the nucleus and binds to cognate DNA sequences requires the phosphorylation and subsequent ubiquitin-dependent degradation of I κ B α in the 26s proteasome. Signal-induced phosphorylation of I κ B α occurs at serines 32 and 36. Mutation of one or both of these serines renders I κ B α resistant to ubiquitination and proteolytic degradation (Chen et al., 1995).

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The pleiotropic cytokines tumor necrosis factor (TNF) and interleukin-1 (IL-1) are among the physiological inducers of I κ B phosphorylation and subsequent NF- κ B activation (Osborn et al., 1989; Beg et al., 1993). Although TNF and IL-1 initiate signaling cascades leading to NF- κ B activation via distinct families of cell-surface receptors (Smith et al., 1994; Dinarello, 1996), both pathways utilize members of the TNF receptor-associated factor (TRAF) family of adaptor proteins as signal transducers (Rothe et al., 1995; Hsu et al., 1996; Cao et al., 1996b). TRAF proteins were originally found to

WO 99/01541

PCT/US98/13782

associate directly with the cytoplasmic domains of several members of the TNF receptor family including the 75 kDa TNF receptor (TNFR2), CD40, CD30, and the lymphotoxin- β receptor (Rothe et al., 1994; Hu et al., 1994; Cheng et al., 1995; Mosialos et al., 1995; Song and Donner, 1995; Sato et al., 1995; Lee et al., 1996; Gedrich et al., 1996; Ansieau et al., 1996). In addition, TRAF proteins are recruited indirectly to the 55 kDa TNF receptor (TNFR1) by the adaptor protein TRADD (Hsu et al., 1996). Activation of NF- κ B by TNF requires TRAF2 (Rothe et al., 1995; Hsu et al., 1996). TRAF5 has also been implicated in NF- κ B activation by members of the TNF receptor family (Nakano et al., 1996). In contrast, TRAF6 participates in NF- κ B activation by IL-1 (Cao et al., 1996b). Upon IL-1 treatment, TRAF6 associates with IRAK, a serine-threonine kinase that binds to the IL-1 receptor complex (Cao et al., 1996a).

The NF- κ B-inducing kinase (NIK) is a member of the MAP kinase kinase kinase (MAP3K) family that was identified as a TRAF2-interacting protein (Malinin et al., 1997). NIK activates NF- κ B when overexpressed, and kinase-inactive mutants of NIK comprising its TRAF2-interacting C-terminal domain (NIK₍₆₂₄₋₉₄₇₎) or lacking two crucial lysine residues in its kinase domain (NIK_(KK429-430AA)) behave as dominant-negative inhibitors that suppress TNF-, IL-1-, and TRAF2-induced NF- κ B activation (Malinin et al., 1997). Recently, NIK was found to associate with additional members of the TRAF family, including TRAF5 and TRAF6. Catalytically inactive mutants of NIK also inhibited TRAF5- and TRAF6-induced NF- κ B activation, thus providing a unifying concept for NIK as a common mediator in the NF- κ B signaling cascades triggered by TNF and IL-1 downstream of TRAFs.

Here, we disclose a novel human kinase I κ B Kinase, IKK- α , as a NIK-interacting protein. IKK- α has sequence similarity to the conceptual translate of a previously identified open reading frame (SEQ ID NO:5) postulated to encode a serine-threonine kinase of unknown function ('Conserved Helix-loop-helix Ubiquitous Kinase' or CHUK, Connelly and Marcu, 1995; Mock et al., 1995). Catalytically inactive mutants of IKK- α are shown to suppress NF- κ B activation induced by TNF and IL-1 stimulation as well as by TRAF and NIK overexpression; transiently expressed IKK- α is shown to associate with the endogenous I κ B α complex; and IKK- α is shown to phosphorylate I κ B α on serines 32 and 36.

SUMMARY OF THE INVENTION

The invention provides methods and compositions relating to isolated IKK- α polypeptides, related nucleic acids, polypeptide domains thereof having IKK- α -specific structure and activity and modulators of IKK- α function, particularly I κ B kinase activity. IKK- α polypeptides can regulate NF κ B activation and hence provide important regulators of cell function. The polypeptides may be produced recombinantly from transformed host cells from the subject IKK- α polypeptide encoding nucleic acids or purified from mammalian cells. The invention provides isolated IKK- α hybridization probes and primers capable of specifically hybridizing with the disclosed IKK- α gene, IKK- α -specific binding agents such as specific antibodies, and methods of making and using the subject compositions in diagnosis (e.g. genetic hybridization screens for IKK- α transcripts), therapy (e.g. IKK- α kinase inhibitors to inhibit TNF signal transduction) and in the biopharmaceutical industry (e.g. as immunogens, reagents for isolating other transcriptional regulators, reagents for screening chemical libraries for lead pharmacological agents, etc.).

According to a first aspect of the invention, there is provided an isolated IKK α polypeptide comprising at least 20 consecutive residues of the amino acid sequence set forth as SEQ ID NO:4, which consecutive amino acid residues comprise at least one of the amino acid residues 679, 680, 684, 686 and 687 of SEQ ID NO:4, wherein the polypeptide has an activity selected from at least one of: a kinase or kinase inhibitory activity, a NIK-binding or binding inhibitory activity, an I κ B-binding or binding inhibitory activity and an NF κ B activating or inhibiting activity.

According to a second aspect of the invention, there is provided an isolated or recombinant nucleic acid encoding the polypeptide described above.

According to a third aspect of the invention, there is provided an isolated or recombinant first nucleic acid comprising at least 24 consecutive nucleotides of SEQ ID NO:3, which consecutive nucleotides comprise at least one of nucleotides 1811 and 1812 of the sequence set forth as SEQ ID NO:3, wherein said first nucleic acid is sufficient to specifically hybridize with a second nucleic acid comprising the complementary strand of SEQ ID NO:3 in the presence of a third nucleic acid comprising (SEQ ID NO:5).

According to a fourth aspect of the invention, there is provided a cell into which a nucleic acid as described above is introduced.

According to a fifth aspect of the invention, there is provided a method of making an isolated polypeptide, said method comprising the steps of:

- 3a -

introducing a recombinant nucleic acid encoding the polypeptide as described above into a host cell or cellular extract,

incubating said host cell or cellular extract under conditions whereby said polypeptide is expressed; and

5 isolating said polypeptide.

According to a sixth aspect of the invention, there is provided a method of screening for an agent which modulates the interaction of an IKK polypeptide to a binding target, said method comprising the steps of:

incubating a mixture comprising:

10 an isolated polypeptide as described above,

a binding target of said polypeptide, wherein the binding target is an I κ B polypeptide, and

a candidate agent; under conditions whereby, but for the presence of said agent, said polypeptide specifically binds said binding target at a reference affinity;

15 detecting the binding affinity of said polypeptide to said binding target to determine an agent-biased affinity, wherein a difference between the agent-biased affinity and the reference affinity indicates that said agent modulates the binding of said polypeptide to said binding target.

According to a seventh aspect of the invention, there is provided a method of screening for an agent which modulates the interaction of an IKK polypeptide to a binding target, said method comprising the steps of:

20 incubating a mixture comprising: the isolated polypeptide as described above which retains I κ B kinase activity, an I κ B polypeptide comprising at least a six residue domain of a natural I κ B comprising at least one of Ser32 and Ser36, and a candidate agent; under conditions whereby, but for the presence of said agent, said polypeptide specifically phosphorylates said I κ B polypeptide at at least one of said Ser32 and Ser36 at a reference activity;

25 detecting the polypeptide-induced phosphorylation of said I κ B polypeptide at at least one of said Ser32 and Ser36 to determine an agent-biased activity, wherein a difference between the agent-biased activity and the reference activity indicates that said agent modulates the ability of said polypeptide to specifically phosphorylate an I κ B polypeptide.

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DETAILED DESCRIPTION OF THE INVENTION

The nucleotide sequence of a natural cDNA encoding a human IKK- α polypeptide is shown as SEQ ID NO:3, and the full conceptual translate is shown as SEQ ID NO:4. The IKK- α polypeptides of the invention include incomplete translates of SEQ ID NO:3, particularly of
5 SEQ ID NO:3, residues 1-638, which translates and deletion mutants of SEQ ID NO:4 have human IKK- α -specific amino acid sequence, binding specificity or function and comprise at least one of Cys30, Glu 543, Leu604, Thr679, Ser680, Pro684, Thr686, and Ser678. Preferred translates/deletion mutants comprise at least a 6 residue Cys30, Glu543, Leu604,
10 Thr679, Ser680, Pro684, Thr686 or Ser687-containing domain of SEQ ID NO:4, preferably including at least 8, more preferably at least 12, most preferably at least 20 contiguous residues which immediately flank said residue, with said residue preferably residing within said contiguous residues, see, e.g. Table 1; which mutants provide hIKK- α specific epitopes and immunogens.

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TABLE 1. Exemplary IKK- α polypeptides having IKK- α binding specificity

hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 1-30) hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 686-699)
hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 22-31) hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 312-345)
hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 599-608) hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 419-444)
hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 601-681) hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 495-503)
5 hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 604-679) hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 565-590)
hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 670-687) hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 610-627)
hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 679-687) hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 627-638)
hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 680-690) hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 715-740)
hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 684-695) hIKK- $\alpha\Delta$ 1 (SEQ ID NO:4, residues 737-745)

10 The subject domains provide IKK- α domain specific activity or function, such as
IKK- α -specific kinase or kinase inhibitory activity, NIK-binding or binding inhibitory
activity, I κ B-binding or binding inhibitory activity, NF κ B activating or inhibitory activity
or antibody binding. Preferred domains phosphorylate at least one and preferably both the
serine 32 and 36 of I κ B (Verma, I. M., et al. (1995)). As used herein, Ser32 and Ser36 of
15 I κ B refers collectively to the two serine residues which are part of the consensus sequence
DSGL/IXSM/L (e.g. ser 32 and 36 in I κ B α , ser 19 and 23 in I κ B β , and ser 157 and 161,
or 18 and 22, depending on the usage of methionines, in I κ B ϵ , respectively.

IKK- α -specific activity or function may be determined by convenient *in vitro*, cell-
based, or *in vivo* assays: e.g. *in vitro* binding assays, cell culture assays, in animals (e.g.
20 gene therapy, transgenics, etc.), etc. Binding assays encompass any assay where the
molecular interaction of an IKK- α polypeptide with a binding target is evaluated. The
binding target may be a natural intracellular binding target such as an IKK- α substrate, a
IKK- α regulating protein or other regulator that directly modulates IKK- α activity or its
localization; or non-natural binding target such a specific immune protein such as an
25 antibody, or an IKK- α specific agent such as those identified in screening assays such as
described below. IKK- α -binding specificity may assayed by kinase activity or binding
equilibrium constants (usually at least about 10^7 M $^{-1}$, preferably at least about 10^8 M $^{-1}$,
more preferably at least about 10^9 M $^{-1}$), by the ability of the subject polypeptide to function
as negative mutants in IKK- α -expressing cells, to elicit IKK- α specific antibody in a
30 heterologous host (e.g a rodent or rabbit), etc. In any event, the IKK- α binding specificity

of the subject IKK- α polypeptides necessarily distinguishes the murine and human CHUK sequences of Connelly and Marcu (1995) as well as IKK- β (SEQ ID NO:2).

The claimed IKK- α polypeptides are isolated or pure: an "isolated" polypeptide is unaccompanied by at least some of the material with which it is associated in its natural state, preferably constituting at least about 0.5%, and more preferably at least about 5% by weight of the total polypeptide in a given sample and a pure polypeptide constitutes at least about 90%, and preferably at least about 99% by weight of the total polypeptide in a given sample. In a particular embodiments, IKK- α polypeptides are isolated from a MKP-1 precipitable complex, isolated from a IKK complex, and/or isolated from IKK- β .

5 The IKK- α polypeptides and polypeptide domains may be synthesized, produced by recombinant technology, or purified from mammalian, preferably human cells. A wide variety of molecular and biochemical methods are available for biochemical synthesis, molecular expression and purification of the subject compositions, see e.g. Molecular Cloning, A Laboratory Manual (Sambrook, *et al.* Cold Spring Harbor Laboratory), Current

10 Protocols in Molecular Biology (Eds. Ausubel, *et al.*, Greene Publ. Assoc., Wiley-Interscience, NY) or that are otherwise known in the art.

The invention provides binding agents specific to IKK polypeptides, preferably the claimed IKK- α polypeptides, including substrates, agonists, antagonists, natural intracellular binding targets, etc., methods of identifying and making such agents, and

20 their use in diagnosis, therapy and pharmaceutical development. For example, specific binding agents are useful in a variety of diagnostic and therapeutic applications, especially where disease or disease prognosis is associated with improper utilization of a pathway involving the subject proteins, e.g. NF- κ B activation. Novel IKK-specific binding agents include IKK-specific receptors, such as somatically recombined polypeptide

25 receptors like specific antibodies or T-cell antigen receptors (see, e.g Harlow and Lane (1988) Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory) and other natural intracellular binding agents identified with assays such as one-, two- and three-hybrid screens, non-natural intracellular binding agents identified in screens of chemical libraries such as described below, etc. Agents of particular interest modulate IKK

30 function, e.g. IKK-dependent transcriptional activation. For example, a wide variety of inhibitors of IKK I κ B kinase activity may be used to regulate signal transduction involving I κ B. Exemplary IKK I κ B kinase inhibitors include known classes of serine/threonine kinase (e.g. PKC)

WO 99/01541

PCT/US98/13782

inhibitors such as competitive inhibitors of ATP and substrate binding, antibiotics, IKK-derived peptide inhibitors, etc., see Tables II and III. IKK specificity and activity are readily quantified in high throughput kinase assays using panels of protein kinases (see cited references and Examples).

Preferred inhibitors include natural compounds such as staurosporine (Omura S, et al. J Antibiot (Tokyo) 1995 Jul;48(7):535-48), produced by a marine organism, and synthetic compounds such as PD 153035, which also potently inhibits the EGF receptor protein kinase (Fry DW et al. Science 1994 Aug 19;265(5175):1093-5). Members of the tyrphostin family of synthetic protein kinase inhibitors are also useful; these include compounds which are pure ATP competitors, compounds which are pure substrate competitors, and compounds which are mixed competitors: compete with both ATP and substrate (Levitzki A and Gazit A, Science 1995 Mar 24;267(5205):1782-8). Additional IKK inhibitors include peptide-based substrate competitors endogenously made by the mammalian cell, e.g. PKI (protein kinase inhibitor, Seasholtz AF et al., Proc Natl Acad Sci USA 1995 Feb 28;92(5):1734-8), or proteins inhibiting cdc kinases (Correa-Bordes J and Nurse P, Cell 1995 Dec 15;83(6):1001-9). Additional small peptide based substrate competitive kinase inhibitors and allosteric inhibitors (inhibitory mechanisms independent of ATP or substrate competition) are readily generated by established methods (Hvalby O, et al. Proc Natl Acad Sci USA 1994 May 24;91(11):4761-5; Barja P, et al., Cell Immunol 1994 Jan;153(1):28-38; Villar-Palasi C, Biochim Biophys Acta 1994 Dec 30;1224(3):384-8; Liu WZ, et al., Biochemistry 1994 Aug 23;33(33):10120-6).

TABLE II. Selected Small Molecule IKK Kinase Inhibitors

HA-100 ¹	Iso-H7 ¹²	A-3 ¹⁸
Chelerythrine ²	PKC 19-31	HA1004 ^{19,20}
Staurosporine ^{3,4,5}	H-7 ^{13,3,14}	K-252a ^{16,5}
Calphostin C ^{6,7,8,9}	H-89 ¹⁵	KT5823 ¹⁶
K-252b ¹⁰	KT5720 ¹⁶	ML-9 ²¹
PKC 19-36 ¹¹	cAMP-depPKinhib ¹⁷	KT5926 ²²

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WO 99/01541

PCT/US98/13782

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20 TABLE III. Selected Peptidyl IKK Kinase Inhibitors

hI κ B α , residues 24-39, 32Ala	hIKK- α , Δ 5-203
hI κ B α , residues 29-47, 36Ala	hIKK- α , Δ 1-178
hI κ B α , residues 26-46, 32/36Ala	hIKK- α , Δ 368-756
hI κ B β , residues 25-38, 32Ala	hIKK- α , Δ 460-748
25 hI κ B β , residues 30-41, 36Ala	hIKK- α , Δ 1-289
hI κ B β , residues 26-46, 32/36Ala	hIKK- α , Δ 12-219
hI κ B ϵ , residues 24-40, 32Ala	hIKK- α , Δ 307-745
hI κ B ϵ , residues 31-50, 36Ala	hIKK- α , Δ 319-644
hI κ B ϵ , residues 27-44, 32/36Ala	

30 Accordingly, the invention provides methods for modulating signal transduction

WO 99/01541

PCT/US98/13782

involving I κ B in a cell comprising the step of modulating IKK kinase activity, e.g. by contacting the cell with a serine/threonine kinase inhibitor. The cell may reside in culture or in situ, i.e. within the natural host. Preferred inhibitors are orally active in mammalian hosts. For diagnostic uses, the inhibitors or other IKK binding agents are frequently labeled, such as with fluorescent, radioactive, chemiluminescent, or other easily detectable molecules, either conjugated directly to the binding agent or conjugated to a probe specific for the binding agent.

The amino acid sequences of the disclosed IKK- α polypeptides are used to back-translate IKK- α polypeptide-encoding nucleic acids optimized for selected expression systems (Holler et al. (1993) Gene 136, 323-328; Martin et al. (1995) Gene 154, 150-166) or used to generate degenerate oligonucleotide primers and probes for use in the isolation of natural IKK- α -encoding nucleic acid sequences ("GCG" software, Genetics Computer Group, Inc, Madison WI). IKK- α -encoding nucleic acids used in IKK- α -expression vectors and incorporated into recombinant host cells, e.g. for expression and screening, transgenic animals, e.g. for functional studies such as the efficacy of candidate drugs for disease associated with IKK- α -modulated cell function, etc.

The invention also provides nucleic acid hybridization probes and replication / amplification primers having a IKK- α cDNA specific sequence comprising at least 12, preferably at least 24, more preferably at least 36 and most preferably at least contiguous 96 bases of a strand of SEQ ID NO:3, particularly of SEQ ID NO:2, nucleotides 1-1913, and preferably including at least one of bases 1-92, 1811, 1812, 1992, 1995, 2034, 2035, 2039, 2040, 2050, 2055 and 2060, and sufficient to specifically hybridize with a second nucleic acid comprising the complementary strand of SEQ ID NO:3 in the presence of a third nucleic acid comprising (SEQ ID NO:5). Demonstrating specific hybridization generally requires stringent conditions, for example, hybridizing in a buffer comprising 30% formamide in 5 x SSPE (0.18 M NaCl, 0.01 M NaPO₄, pH7.7, 0.001 M EDTA) buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with 0.2 x SSPE; preferably hybridizing in a buffer comprising 50% formamide in 5 x SSPE buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with 0.2 x SSPE buffer at 42°C. IKK- α nucleic acids can also be distinguished using alignment algorithms, such as BLASTX (Altschul *et al.* (1990) Basic Local Alignment Search Tool, J Mol Biol 215, 403-410).

The subject nucleic acids are of synthetic/non-natural sequences and/or are isolated, i.e. unaccompanied by at least some of the material with which it is associated in its natural state, preferably constituting at least about 0.5%, preferably at least about 5% by weight of total nucleic acid present in a given fraction, and usually recombinant, meaning they comprise a non-natural sequence or a natural sequence joined to
5 nucleotide(s) other than that which it is joined to on a natural chromosome. Recombinant nucleic acids comprising the nucleotide sequence of SEQ ID NO:3, or requisite fragments thereof, contain such sequence or fragment at a terminus, immediately flanked by (i.e. contiguous with) a sequence other than that which it is joined to on a natural chromosome, or flanked by a native flanking region fewer than 10 kb, preferably fewer than 2 kb, which
10 is at a terminus or is immediately flanked by a sequence other than that which it is joined to on a natural chromosome. While the nucleic acids are usually RNA or DNA, it is often advantageous to use nucleic acids comprising other bases or nucleotide analogs to provide modified stability, etc.

The subject nucleic acids find a wide variety of applications including use as
15 translatable transcripts, hybridization probes, PCR primers, diagnostic nucleic acids, etc.; use in detecting the presence of IKK- α genes and gene transcripts and in detecting or amplifying nucleic acids encoding additional IKK- α homologs and structural analogs. In diagnosis, IKK- α hybridization probes find use in identifying wild-type and mutant IKK- α alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific
20 oligonucleotide (ASO) probes for high-throughput clinical diagnoses. In therapy, therapeutic IKK- α nucleic acids are used to modulate cellular expression or intracellular concentration or availability of active IKK- α .

The invention provides efficient methods of identifying agents, compounds or lead compounds for agents active at the level of a IKK modulatable cellular function.
25 Generally, these screening methods involve assaying for compounds which modulate IKK interaction with a natural IKK binding target, in particular, IKK phosphorylation of I κ B-derived substrates, particularly I κ B and NIK substrates. A wide variety of assays for binding agents are provided including labeled *in vitro* protein-protein binding assays, immunoassays, cell based assays, etc. The methods are amenable to automated, cost-
30 effective high throughput screening of chemical libraries for lead compounds. Identified reagents find use in the pharmaceutical industries for animal and human trials; for example,

the reagents may be derivatized and rescreened in *in vitro* and *in vivo* assays to optimize activity and minimize toxicity for pharmaceutical development.

In vitro binding assays employ a mixture of components including an IKK polypeptide, which may be part of a fusion product with another peptide or polypeptide, e.g. a tag for detection or anchoring, etc. The assay mixtures comprise a natural
5 intracellular IKK binding target. In a particular embodiment, the binding target is a substrate comprising I κ B serines 32 and/or 36. Such substrates comprise a I κ B α , β or ϵ peptide including the serine 32 and/or 36 residue and at least 5, preferably at least 10, and more preferably at least 20 naturally occurring immediately flanking residues on each side (e.g. for serine 36 peptides, residues 26-46, 22-42, or 12-32 or 151-171 for I κ B α , β or ϵ -
10 derived substrates, respectively). While native full-length binding targets may be used, it is frequently preferred to use portions (e.g. peptides) thereof so long as the portion provides binding affinity and avidity to the subject IKK polypeptide conveniently measurable in the assay. The assay mixture also comprises a candidate pharmacological agent. Candidate agents encompass numerous chemical classes, though typically they are organic
15 compounds; preferably small organic compounds and are obtained from a wide variety of sources including libraries of synthetic or natural compounds. A variety of other reagents may also be included in the mixture. These include reagents like ATP or ATP analogs (for kinase assays), salts, buffers, neutral proteins, e.g. albumin, detergents, protease inhibitors, nuclease inhibitors, antimicrobial agents, etc. may be used.

20 The resultant mixture is incubated under conditions whereby, but for the presence of the candidate pharmacological agent, the IKK polypeptide specifically binds the cellular binding target, portion or analog with a reference binding affinity. The mixture components can be added in any order that provides for the requisite bindings and incubations may be performed at any temperature which facilitates optimal binding. Incubation periods are likewise selected for optimal binding but also minimized to facilitate
25 rapid, high-throughput screening.

After incubation, the agent-biased binding between the IKK polypeptide and one or more binding targets is detected by any convenient way. For IKK kinase assays, 'binding' is generally detected by a change in the phosphorylation of a IKK- α substrate. In this
30 embodiment, kinase activity may be quantified by the transfer to the substrate of a labeled phosphate, where the label may provide for direct detection as radioactivity, luminescence,

WO 99/01541

PCT/US98/13782

optical or electron density, etc. or indirect detection such as an epitope tag, etc. A variety of methods may be used to detect the label depending on the nature of the label and other assay components, e.g. through optical or electron density, radiative emissions, nonradiative energy transfers, etc. or indirectly detected with antibody conjugates, etc.

5 A difference in the binding affinity of the IKK polypeptide to the target in the absence of the agent as compared with the binding affinity in the presence of the agent indicates that the agent modulates the binding of the IKK polypeptide to the IKK binding target. Analogously, in the cell-based assay also described below, a difference in IKK- α -dependent transcriptional activation in the presence and absence of an agent indicates the agent modulates IKK function. A difference, as used herein, is statistically significant and preferably represents at least a 50%, more preferably at least a 90% difference.

10 The following experimental section and examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

15 Identification of IKK- α

To investigate the mechanism of NIK-mediated NF- κ B activation, we identified proteins that associate directly with NIK by yeast two-hybrid protein interaction cloning (Fields and Song, 1989). An expression vector was generated that encodes NIK fused to the DNA-binding domain of the yeast transcription factor GAL4. This vector was used as bait in a two-hybrid screen of a human B cell cDNA library. From approximately six million transformants, eight positive clones were obtained, as determined by activation of *his* and *lacZ* reporter genes. Of these clones, three encoded a member of the TRAF family, TRAF3 (Hu et al., 1994; Cheng et al., 1995; Mosialos et al., 1995; Sato et al., 1995) and one encoded a novel protein we call IKK- α . Retransformation into yeast cells verified the interaction between NIK and IKK- α . A full-length human IKK- α clone was isolated by screening a Jurkat cDNA library with a probe generated from the 5'-end of the IKK- α two-hybrid clone. IKK- α comprises an N-terminal serine-threonine kinase catalytic domain, a C-terminal helix-loop-helix domain and a leucine zipper-like amphipathic α -helix juxtaposed in between the helix-loop-helix and kinase domain.

30 Interaction of IKK- α and NIK in Human Cells

The interaction of IKK- α with NIK was confirmed in mammalian cell

coimmunoprecipitation assays. Human IKK- α containing an N-terminal Flag epitope tag was transiently coexpressed in 293 human embryonic kidney cells with Myc epitope-tagged NIK or HA epitope-tagged TRAF proteins. Cell lysates were immunoprecipitated using a monoclonal antibody against the Flag epitope, and coprecipitating NIK or TRAF proteins were detected by immunoblot analysis with an anti-Myc or anti-HA monoclonal antibodies.

5 In this assay, IKK- α was able to coprecipitate NIK confirming the interaction between both proteins as detected for IKK- α by yeast two-hybrid analysis. Also, a deletion mutant IKK- α protein lacking most of the N-terminal kinase domain (IKK- $\alpha_{(307-745)}$) was able to associate with NIK, indicating that the α -helical C-terminal half of IKK- α mediates the interaction with NIK. In contrast to NIK, IKK- α failed to associate with either TRAF2 or TRAF3. However,

10 when NIK was coexpressed with IKK- α and TRAF2, strong coprecipitation of TRAF2 with IKK- α was detected, indicating the formation of a ternary complex between IKK- α , NIK and TRAF2.

Effect of IKK- α and IKK- α Mutants on NF- κ B Activation

To investigate a possible role for IKK- α in NF- κ B activation, we examined if transient

15 overexpression of IKK- α might activate an NF- κ B-dependent reporter gene. An E-selectin-luciferase reporter construct (Schindler and Baichwal, 1994) and a IKK- α expression vector were cotransfected into HeLa cells. IKK- α expression activated the reporter gene in a dose-dependent manner, with a maximal induction of luciferase activity of about 6 to 7-fold compared to vector control. Similar results were obtained in 293 cells, where IKK- α

20 overexpression induced reporter gene activity approximately 4-fold. TNF treatment did not stimulate the weak NF- κ B-inducing activity of overexpressed IKK- α in reporter gene assays. Thus, IKK- α induces NF- κ B activation when overexpressed.

We next determined the effect of overexpression of kinase-inactive IKK- $\alpha_{(307-745)}$ that still associates with NIK on signal-induced NF- κ B activation in reporter gene assays in

25 293 cells. Overexpression of IKK- $\alpha_{(307-745)}$ blocked TNF- and IL-1-induced reporter gene activation similar to overexpression of NIK $_{(624-947)}$. IKK- $\alpha_{(307-745)}$ was also found to inhibit NF- κ B-dependent reporter gene activity elicited by overexpression of TRAF2, TRAF6 and NIK. Taken together these results demonstrate that a catalytically inactive IKK- α mutant is a dominant-negative inhibitor of TNF-, IL-1, TRAF- and NIK-induced NF- κ B

30 activation. This indicates that IKK- α functions as a common mediator of NF- κ B activation by TNF and IL-1 downstream of NIK.

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EXAMPLES

1. Protocol for at IKK- α - I κ B α phosphorylation assay.
 - A. Reagents:
 - Neutralite Avidin: 20 μ g/ml in PBS.
 - 5 - kinase: 10^{-8} - 10^{-5} M IKK- α (SEQ ID NO:4) at 20 μ g/ml in PBS.
 - substrate: 10^{-7} - 10^{-4} M biotinylated substrate (21 residue peptide consisting of residues 26-46 of human I κ B α) at 40 μ g/ml in PBS.
 - Blocking buffer: 5% BSA, 0.5% Tween 20™ in PBS; 1 hour at room temperature.
 - Assay Buffer: 100 mM KCl, 10 mM MgCl₂, 1 mM MnCl₂, 20 mM HEPES pH 7.4, 0.25
10 mM EDTA, 1% glycerol, 0.5% NP-40, 50 mM BME, 1 mg/ml BSA, cocktail of protease inhibitors.
 - [³²P]γ-ATP 10x stock: 2×10^{-5} M cold ATP with 100 μ Ci [³²P]γ-ATP. Place in the 4°C microfridge during screening.
 - Protease inhibitor cocktail (1000X): 10 mg Trypsin Inhibitor (BMB # 109894), 10 mg
15 Aprotinin (BMB # 236624), 25 mg Benzamidine (Sigma # B-6506), 25 mg Leupeptin (BMB # 1017128), 10 mg APMSF (BMB # 917575), and 2mM NaVo₃ (Sigma # S-6508) in 10 ml of PBS.
 - B. Preparation of assay plates:
 - Coat with 120 μ l of stock N Avidin per well overnight at 4°C.
 - 20 - Wash 2 times with 200 μ l PBS.
 - Block with 150 μ l of blocking buffer.
 - Wash 2 times with 200 μ l PBS.
 - C. Assay:
 - Add 40 μ l assay buffer/well.
 - 25 - Add 40 μ l biotinylated substrate (2-200 pmoles/40 ul in assay buffer)
 - Add 40 μ l kinase (0.1-10 pmoles/40 ul in assay buffer)
 - Add 10 μ l compound or extract.
 - Add 10 μ l [³²P]γ-ATP 10x stock.
 - Shake at 25°C for 15 minutes.
 - 30 - Incubate additional 45 minutes at 25°C.
 - Stop the reaction by washing 4 times with 200 μ l PBS.
 - Add 150 μ l scintillation cocktail.

WO 99/01541

PCT/US98/13782

- Count in Topcount.

D. Controls for all assays (located on each plate):

- a. Non-specific binding
- b. cold ATP at 80% inhibition.

5 2. Protocol for high throughput IKK- α -NIK binding assay.

A. Reagents:

- Neutralite Avidin: 20 μ g/ml in PBS.
- Blocking buffer: 5% BSA, 0.5% Tween 20 in PBS; 1 hour at room temperature.
- Assay Buffer: 100 mM KCl, 20 mM HEPES pH 7.6, 1 mM MgCl₂, 1% glycerol,
10 0.5% NP-40, 50 mM β -mercaptoethanol, 1 mg/ml BSA, cocktail of protease inhibitors.
- ³³P IKK- α polypeptide 10x stock: 10⁻⁸ - 10⁻⁶ M "cold" IKK- α supplemented with 200,000-250,000 cpm of labeled IKK- α (Beckman counter). Place in the 4°C microfridge during screening.

15 - Protease inhibitor cocktail (1000X): 10 mg Trypsin Inhibitor (BMB # 109894), 10 mg Aprotinin (BMB # 236624), 25 mg Benzamidine (Sigma # B-6506), 25 mg Leupeptin (BMB # 1017128), 10 mg APMSF (BMB # 917575), and 2mM NaVO₃ (Sigma # S-6508) in 10 ml of PBS.

- NIK: 10⁻⁷ - 10⁻⁵ M biotinylated NIK in PBS.

B. Preparation of assay plates:

- 20
- Coat with 120 μ l of stock N-Avidin per well overnight at 4°C.
 - Wash 2 times with 200 μ l PBS.
 - Block with 150 μ l of blocking buffer.
 - Wash 2 times with 200 μ l PBS.

C. Assay:

- 25
- Add 40 μ l assay buffer/well.
 - Add 10 μ l compound or extract.
 - Add 10 μ l ³³P-IKK- α (20-25,000 cpm/0.1-10 pmoles/well = 10⁻⁹ - 10⁻⁷ M final conc).
 - Shake at 25°C for 15 minutes.
 - Incubate additional 45 minutes at 25°C.
- 30
- Add 40 μ M biotinylated NIK (0.1-10 pmoles/40 μ l in assay buffer)
 - Incubate 1 hour at room temperature.

- Stop the reaction by washing 4 times with 200 μ M PBS.
- Add 150 μ M scintillation cocktail.
- Count in Topcount.

D. Controls for all assays (located on each plate):

- 5 a. Non-specific binding
b. Soluble (non-biotinylated NIK) at 80% inhibition.

10 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Rothe, Mike
Cao, Zhaodan
R,gnier, Catherine
- (ii) TITLE OF INVENTION: IKK-à Proteins, Nucleic Acids and Methods
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
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 - (C) CITY: SAN FRANCISCO
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 - (E) COUNTRY: USA
 - (F) ZIP: 94104
- (v) 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
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
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 - (B) REGISTRATION NUMBER: 36,627
 - (C) REFERENCE/DOCKET NUMBER: T97-006-1
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 - (A) TELEPHONE: (415) 343-4341
 - (B) TELEFAX: (415) 343-4342

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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35          40          45
Glu Leu Ser Pro Arg Asn Arg Glu Arg Trp Cys Leu Glu Ile Gln Ile
50          55          60
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65          70          75          80
Glu Gly Met Gln Asn Leu Ala Pro Asn Asp Leu Pro Leu Leu Ala Met
85          90          95

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Gln	Cys	Ile	Ser	Asp	Gly	Lys	Leu	Asn	Glu	Gly	His	Thr	Leu	Asp	Met
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	610					615					620				
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			660				665						670		
Pro	Asp	Ser	Met	Asn	Ala	Ser	Arg	Leu	Ser	Gln	Pro	Gly	Gln	Leu	Met
		675					680					685			
Ser	Gln	Pro	Ser	Thr	Ala	Ser	Asn	Ser	Leu	Pro	Glu	Pro	Ala	Lys	Lys
	690					695					700				
Ser	Glu	Glu	Leu	Val	Ala	Glu	Ala	His	Asn	Leu	Cys	Thr	Leu	Leu	Glu
705					710				715						720
Asn	Ala	Ile	Gln	Asp	Thr	Val	Arg	Glu	Gln	Asp	Gln	Ser	Phe	Thr	Ala
				725					730					735	
Leu	Asp	Trp	Ser	Trp	Leu	Gln	Thr	Glu	Glu	Glu	Glu	His	Ser	Cys	Leu
			740					745					750		
Glu	Gln	Ala	Ser												
			755												

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

ATGGAGCGGC	CCCCGGGGCT	GCGGCCGGGC	GCGGGCGGGC	CCTGGGAGAT	GCGGGAGCGG	60
CTGGGCACCG	GCGGCTTCGG	GAACGTCTGT	CTGTACCAGC	ATCGGGAACT	TGATCTCAAA	120
ATAGCAATTA	AGTCTTGTCG	CCTAGAGCTA	AGTACCAAAA	ACAGAGAACG	ATGGTGCCAT	180
GAAATCCAGA	TTATGAAGAA	GTTGAACCAT	GCCAATGTTG	TAAAGGCCTG	TGATGTTTCT	240
GAAGAATTGA	ATATTTTGAT	TCATGATGTG	CCTCTTCTAG	CAATGGAATA	CTGTTCTGGA	300
GGAGATCTCC	GAAAGCTGCT	CAACAAACCA	GAAAATTGTT	GTGGACTTAA	AGAAAGCCAG	360
ATACTTTCTT	TACTAAGTGA	TATAGGGTCT	GGGATTCGAT	ATTTGCATGA	AAACAAAATT	420
ATACATCGAG	ATCTAAAACC	TGAAAACATA	GTTCTTCAGG	ATGTTGGTGG	AAAGATAATA	480
CATAAAATAA	TTGATCTGGG	ATATGCCAAA	GATGTTGATC	AAGGAAGTCT	GTGTACATCT	540
TTTGTGGGAA	CACTGCAGTA	TCTGGCCCCA	GAGCTCTTTG	AGAATAAGCC	TTACACAGCC	600
ACTGTTGATT	ATTGGAGCTT	TGGGACCATG	GTATTTGAAT	GTATTGCTGG	ATATAGGCCT	660
TTTTTGCATC	ATCTGCAGCC	ATTTACCTGG	CATGAGAAGA	TTAAGAAGAA	GGATCCAAAG	720
TGTATATTTG	CATGTGAAGA	GATGTCAGGA	GAAGTTCGGT	TTAGTAGCCA	TTTACCTCAA	780
CCAAATAGCC	TTTGTAGTTT	AATAGTAGAA	CCCATGGAAA	ACTGGCTACA	GTTGATGTTG	840
AATTGGGACC	CTCAGCAGAG	AGGAGGACCT	GTTGACCTTA	CTTTGAAGCA	GCCAAGATGT	900
TTTGTATTAA	TGGATCACAT	TTTGAATTTG	AAGATAGTAC	ACATCCTAAA	TATGACTTCT	960
GCAAAGATAA	TTTCTTTTCT	GTTACCACCT	GATGAAAGTC	TTCATTCACT	ACAGTCTCGT	1020
ATTGAGCGTG	AAACTGGAAT	AAATACTGGT	TCTCAAGAAC	TTCTTTCAGA	GACAGGAATT	1080

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TCTCTGGATC CTCGGAAACC AGCCTCTCAA TGTGTTCTAG ATGGAGTTAG AGGCTGTGAT 1140
AGCTATATGG TTTATTTGTT TGATAAAAGT AAAACTGTAT ATGAAGGGCC ATTTGCTTCC 1200
AGAAGTTTAT CTGATTGTGT AAATTATATT GTACAGGACA GCAAATACA GCTTCCAATT 1260
ATACAGCTGC GTAAAGTGTG GGCTGAAGCA GTGCACTATG TGTCTGGACT AAAAGAAGAC 1320
TATAGCAGGC TCTTTCAGGG ACAAAGGGCA GCAATGTTAA GTCTTCTTAG ATATAATGCT 1380
AACTTAACAA AAATGAAGAA CACTTTGATC TCAGCATCAC AACAACTGAA AGCTAAATTG 1440
GAGTTTTTTC ACAAAGCAT TCAGCTTGAC TTGGAGAGAT ACAGCGAGCA GATGACGTAT 1500
GGGATATCTT CAGAAAAAAT GCTAAAAGCA TGGAAAGAAA TGGAAGAAAA GGCCATCCAC 1560
TATGCTGAGG TTGGTGTTCAT TGGATACCTG GAGGATCAGA TTATGTCTTT GCATGCTGAA 1620
ATCATGGAGC TACAGAAGAG CCCCTATGGA AGACGTCAGG GAGACTTGAT GGAATCTCTG 1680
GAACAGCGTG CCATTGATCT ATATAAGCAG TTAACACACA GACCTTCAGA TCACTCCTAC 1740
AGTGACAGCA CAGAGATGGT GAAAATCATT GTGCACACTG TGCAGAGTCA GGACCGTGTG 1800
CTCAAGGAGC TGTTTGGTCA TTTGAGCAAG TTGTTGGGCT GTAAGCAGAA GATTATTGAT 1860
CTACTCCCTA AGGTGGAAGT GGCCCTCAGT AATATCAAAG AAGCTGACAA TACTGTCATG 1920
TTCATGCAGG GAAAAAGGCA GAAAGAAATA TGGCATCTCC TTAAAATTGC CTGTACACAG 1980
AGTTCTGCCC GGTCCCTTGT AGGATCCAGT CTAGAAGGTG CAGTAACCCC TCAGACATCA 2040
GCATGGCTGC CCCCAGACTTC AGCAGAACAT GATCATTCTC TGTCATGTGT GGTAACCTCT 2100
CAAGATGGGG AGACTTCAGC ACAAATGATA GAAGAAAATT TGAAGTGCCT TGGCCATTTA 2160
AGCACTATTA TTCATGAGGC AAATGAGGAA CAGGGCAATA GTATGATGAA TCTTGATTGG 2220
AGTTGGTTAA CAGAATGA 2238

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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

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Met Glu Arg Pro Pro Gly Leu Arg Pro Gly Ala Gly Gly Pro Trp Glu
 1           5           10           15
Met Arg Glu Arg Leu Gly Thr Gly Gly Phe Gly Asn Val Cys Leu Tyr
          20           25           30
Gln His Arg Glu Leu Asp Leu Lys Ile Ala Ile Lys Ser Cys Arg Leu
          35           40           45
Glu Leu Ser Thr Lys Asn Arg Glu Arg Trp Cys His Glu Ile Gln Ile
          50           55           60
Met Lys Lys Leu Asn His Ala Asn Val Val Lys Ala Cys Asp Val Pro
          65           70           75           80
Glu Glu Leu Asn Ile Leu Ile His Asp Val Pro Leu Leu Ala Met Glu
          85           90           95
Tyr Cys Ser Gly Gly Asp Leu Arg Lys Leu Leu Asn Lys Pro Glu Asn
          100          105          110
Cys Cys Gly Leu Lys Glu Ser Gln Ile Leu Ser Leu Leu Ser Asp Ile
          115          120          125
Gly Ser Gly Ile Arg Tyr Leu His Glu Asn Lys Ile Ile His Arg Asp
          130          135          140
Leu Lys Pro Glu Asn Ile Val Leu Gln Asp Val Gly Gly Lys Ile Ile
          145          150          155          160
His Lys Ile Ile Asp Leu Gly Tyr Ala Lys Asp Val Asp Gln Gly Ser
          165          170          175
Leu Cys Thr Ser Phe Val Gly Thr Leu Gln Tyr Leu Ala Pro Glu Leu
          180          185          190

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Phe	Glu	Asn	Lys	Pro	Tyr	Thr	Ala	Thr	Val	Asp	Tyr	Trp	Ser	Phe	Gly
		195					200					205			
Thr	Met	Val	Phe	Glu	Cys	Ile	Ala	Gly	Tyr	Arg	Pro	Phe	Leu	His	His
	210					215					220				
Leu	Gln	Pro	Phe	Thr	Trp	His	Glu	Lys	Ile	Lys	Lys	Lys	Asp	Pro	Lys
225					230					235					240
Cys	Ile	Phe	Ala	Cys	Glu	Glu	Met	Ser	Gly	Glu	Val	Arg	Phe	Ser	Ser
				245					250					255	
His	Leu	Pro	Gln	Pro	Asn	Ser	Leu	Cys	Ser	Leu	Ile	Val	Glu	Pro	Met
			260					265					270		
Glu	Asn	Trp	Leu	Gln	Leu	Met	Leu	Asn	Trp	Asp	Pro	Gln	Gln	Arg	Gly
		275					280					285			
Gly	Pro	Val	Asp	Leu	Thr	Leu	Lys	Gln	Pro	Arg	Cys	Phe	Val	Leu	Met
	290					295					300				
Asp	His	Ile	Leu	Asn	Leu	Lys	Ile	Val	His	Ile	Leu	Asn	Met	Thr	Ser
305				310						315					320
Ala	Lys	Ile	Ile	Ser	Phe	Leu	Leu	Pro	Pro	Asp	Glu	Ser	Leu	His	Ser
				325					330					335	
Leu	Gln	Ser	Arg	Ile	Glu	Arg	Glu	Thr	Gly	Ile	Asn	Thr	Gly	Ser	Gln
			340					345					350		
Glu	Leu	Leu	Ser	Glu	Thr	Gly	Ile	Ser	Leu	Asp	Pro	Arg	Lys	Pro	Ala
		355					360					365			
Ser	Gln	Cys	Val	Leu	Asp	Gly	Val	Arg	Gly	Cys	Asp	Ser	Tyr	Met	Val
	370					375					380				
Tyr	Leu	Phe	Asp	Lys	Ser	Lys	Thr	Val	Tyr	Glu	Gly	Pro	Phe	Ala	Ser
385				390						395					400
Arg	Ser	Leu	Ser	Asp	Cys	Val	Asn	Tyr	Ile	Val	Gln	Asp	Ser	Lys	Ile
				405					410					415	
Gln	Leu	Pro	Ile	Ile	Gln	Leu	Arg	Lys	Val	Trp	Ala	Glu	Ala	Val	His
			420					425					430		
Tyr	Val	Ser	Gly	Leu	Lys	Glu	Asp	Tyr	Ser	Arg	Leu	Phe	Gln	Gly	Gln
		435					440					445			
Arg	Ala	Ala	Met	Leu	Ser	Leu	Leu	Arg	Tyr	Asn	Ala	Asn	Leu	Thr	Lys
	450					455					460				
Met	Lys	Asn	Thr	Leu	Ile	Ser	Ala	Ser	Gln	Gln	Leu	Lys	Ala	Lys	Leu
465					470					475					480
Glu	Phe	Phe	His	Lys	Ser	Ile	Gln	Leu	Asp	Leu	Glu	Arg	Tyr	Ser	Glu
				485					490					495	
Gln	Met	Thr	Tyr	Gly	Ile	Ser	Ser	Glu	Lys	Met	Leu	Lys	Ala	Trp	Lys
			500					505					510		
Glu	Met	Glu	Glu	Lys	Ala	Ile	His	Tyr	Ala	Glu	Val	Gly	Val	Ile	Gly
		515					520					525			
Tyr	Leu	Glu	Asp	Gln	Ile	Met	Ser	Leu	His	Ala	Glu	Ile	Met	Glu	Leu
	530					535					540				
Gln	Lys	Ser	Pro	Tyr	Gly	Arg	Arg	Gln	Gly	Asp	Leu	Met	Glu	Ser	Leu
545					550					555					560
Glu	Gln	Arg	Ala	Ile	Asp	Leu	Tyr	Lys	Gln	Leu	Lys	His	Arg	Pro	Ser
				565					570					575	
Asp	His	Ser	Tyr	Ser	Asp	Ser	Thr	Glu	Met	Val	Lys	Ile	Ile	Val	His
			580					585						590	
Thr	Val	Gln	Ser	Gln	Asp	Arg	Val	Leu	Lys	Glu	Leu	Phe	Gly	His	Leu
		595					600					605			
Ser	Lys	Leu	Leu	Gly	Cys	Lys	Gln	Lys	Ile	Ile	Asp	Leu	Leu	Pro	Lys
	610					615					620				
Val	Glu	Val	Ala	Leu	Ser	Asn	Ile	Lys	Glu	Ala	Asp	Asn	Thr	Val	Met
625					630					635					640
Phe	Met	Gln	Gly	Lys	Arg	Gln	Lys	Glu	Ile	Trp	His	Leu	Leu	Lys	Ile

				645					650					655		
Ala	Cys	Thr	Gln	Ser	Ser	Ala	Arg	Ser	Leu	Val	Gly	Ser	Ser	Leu	Glu	
			660					665						670		
Gly	Ala	Val	Thr	Pro	Gln	Thr	Ser	Ala	Trp	Leu	Pro	Pro	Thr	Ser	Ala	
		675					680						685			
Glu	His	Asp	His	Ser	Leu	Ser	Cys	Val	Val	Thr	Pro	Gln	Asp	Gly	Glu	
	690					695					700					
Thr	Ser	Ala	Gln	Met	Ile	Glu	Glu	Asn	Leu	Asn	Cys	Leu	Gly	His	Leu	
705					710					715					720	
Ser	Thr	Ile	Ile	His	Glu	Ala	Asn	Glu	Glu	Gln	Gly	Asn	Ser	Met	Met	
			725						730					735		
Asn	Leu	Asp	Trp	Ser	Trp	Leu	Thr	Glu								
			740					745								

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

GTACCAGCAT	CGGGA	ACTTG	ATCTC	AAAAT	AGCAAT	TAAG	TCTTG	TCGCC	TAGAG	CTAAG	60	
TACCAAAAAC	AGAGA	ACGAT	GGTGC	CATGA	AATCC	CAGATT	ATGA	AAGAAGT	TGAAC	CATGC	120	
CAATGTTGTA	AAGGC	CTGTG	ATGTT	CCTGA	AGAAT	TGAAT	ATTTT	GATTC	ATGAT	GTGCC	180	
TCTTCTAGCA	ATGGA	ATACT	GTTCT	GGAGG	AGATC	TCCGA	AAGCT	GCTCA	ACAA	ACCAGA	240	
AAATTGTTGT	GGACT	TAAAG	AAAGC	CAGAT	ACTTT	CTTTA	CTAAG	TGATA	TAGG	GTCTGG	300	
GATTCGATAT	TTGC	ATGAAA	ACAAA	ATTAT	ACATC	CAGAT	CTAAA	ACCTG	AAA	CATAGT	360	
TCTTCAGGAT	GTTGG	TGGAA	AGATA	AATACA	TAAA	AATAATT	GATCT	GGGAT	ATGC	CAAAGA	420	
TGTTGATCAA	GGAAG	TCTGT	GTAC	ATCTTT	TGTGG	GGAACA	CTGC	AGTATC	TGGC	CCCAGA	480	
GCTCTTTGAG	AATA	AGCCTT	ACAC	AGCCAC	TGTT	GATTAT	TGG	AGCTTTG	GGAC	CATGGT	540	
ATTTGAATGT	ATTG	CTGGAT	ATAG	GCCTTT	TTTGC	ATCAT	CTGC	AGCCAT	TTAC	CTGGCA	600	
TGAGAAGATT	AAGA	AGAAGG	ATCC	AAAGT	TATAT	TTGCA	TGTG	AAGAGA	TGTC	CAGGAGA	660	
AGTTCGGTTT	AGTAG	CCATT	TACCT	CAACC	AAAT	AGCCTT	TGTAG	TTTAA	TAGT	AGAACC	720	
CATGGAAAAC	TGGCT	ACAGT	TGAT	GTTGAA	TTGG	GACCCT	CAGC	AGAGAG	GAGG	ACCTGT	780	
TGACCTTACT	TTGA	AGCAGC	CAAG	ATGTTT	TGTAT	TAAATG	GATCA	CATTT	TGA	ATTTGAA	840	
GATAGTACAC	ATCCT	AAATA	TGACT	TCTGC	AAAG	AATAATT	TCTTT	TCTGT	TACC	ACCTGA	900	
TGAAAGTCTT	CATTC	ACTAC	AGTCT	CGTAT	TGAG	CGTGAA	ACTG	GAAATAA	ATACT	GGTTC	960	
TCAAGA	ACTT	CTTTC	CAGAG	A	TTC	TCTGG	ATCCT	CGGAA	ACCAG	CCTCT	CAATG	1020
TGTTCTAGAT	GGAG	TAGAG	GCTGT	GATAG	CTAT	ATGGTT	TATTT	GTTTG	ATA	AAAAGTAA	1080	
AACTGTATAT	GAAGG	GCCAT	TTGCT	TCCAG	AAGTT	TATCT	GATT	GTGTA	ATT	TATTGT	1140	
ACAGGACAGC	AAAAT	ACAGC	TTCCA	ATTAT	ACAG	CTGCGT	AAAG	TGTGG	CTGA	AGCAGT	1200	
GCACTATGTG	TCTGG	ACTAA	AAGA	AGACTA	TAGC	AGGCTC	TTTC	AGGGAC	AAAG	GGCAGC	1260	
AATGTTAAGT	CTTCT	TAGAT	ATAAT	GCTAA	CTTA	ACAAA	ATGA	AGAACA	CTTT	GATCTC	1320	
AGCATCACAA	CAACT	GAAAG	CTAA	ATTGGA	GTTTT	TTTTCAC	AAA	AGCATT	AGCT	TGACTT	1380	
GGAGAGATAC	AGCG	AGCAGA	TGAC	GTATGG	GATAT	CCTTCA	GAAAA	AATGC	TAAA	AGCATG	1440	
GAAAGAAATG	GAAGA	AAAAGG	CCAT	CCACTA	TGCT	GAGGTT	GGTGT	CATTG	GATA	CCTGGA	1500	
GGATCAGATT	ATGT	CTTTGC	ATGCT	GAAAT	CATG	GAGCTA	CAGA	AGAGCC	CCT	ATGGAAG	1560	
ACGTCAGGGA	GACT	TGATGG	AATCT	CTGGA	ACAG	CGTGCC	ATTG	ATCTAT	ATA	AGCAGTT	1620	
AAAACACAGA	CCTTC	CAGATC	ACTC	TACAG	TGAC	AGCACA	GAGAT	GGTGA	AAAT	CATTGT	1680	
GCACACTGTG	CAGAG	TCAGG	ACCG	TGTGCT	CAAG	GAGCGT	TTTG	GTCATT	TGAG	CAAGTT	1740	
GTTGGGCTGT	AAGC	AGAAGA	TTATT	GATCT	ACTC	CCCTAAG	GTGG	AAGTGG	CCCT	CAGTAA	1800	
TATCAAAGAA	GCTG	ACAATA	CTGT	CATGTT	CATG	CAGGGA	AAA	AGGCAGA	AAG	AAATATG	1860	
GCATCTCCTT	AAAAT	TGCCT	GTAC	ACAGAG	TTCT	GCCCCG	TCTCT	TGTAG	GATC	CAGTCT	1920	

AGAAGGTGCA	GTAACCCCTC	AAGCATACGC	ATGGCTGGCC	CCCGACTTAG	CAGAACATGA	1980
TCATTCTCTG	TCATGTGTGG	TAACTCCTCA	AGATGGGGAG	ACTTCAGCAC	AAATGATAGA	2040
AGAAAATTTG	AACTGCCTTG	GCCATTTAAG	CACTATTATT	CATGAGGCAA	ATGAGGAACA	2100
GGGCAATAGT	ATGATGAATC	TTGATTGGAG	TTGGTTAACA	GAATGA		2146

I hereby declare that the content of the paper and computer readable copies of this document are the same.


Dr. Michael Williams

Date: *March 1, 2000*

WHAT IS CLAIMED IS:

1. An isolated IKK α polypeptide comprising at least 20 consecutive residues of the amino acid sequence set forth as SEQ ID NO:4, which consecutive amino acid residues comprise at least one of the amino acid residues 679, 680, 684, 686 and 687 of SEQ ID
5 NO:4, wherein the polypeptide has an activity selected from at least one of: a kinase or kinase inhibitory activity, a NIK-binding or binding inhibitory activity, an I κ B-binding or binding inhibitory activity and an NF κ B activating or inhibiting activity.
2. An isolated polypeptide according to claim 1, wherein the consecutive amino acid residues comprise the amino acid residues of SEQ ID NO:4.
- 10 3. An isolated polypeptide according to claim 1, wherein said polypeptide has kinase activity.
4. An isolated or recombinant nucleic acid encoding the polypeptide of claim 1, 2 or 3.
5. An isolated or recombinant first nucleic acid comprising at least 24 consecutive
15 nucleotides of SEQ ID NO:3, which consecutive nucleotides comprise at least one of nucleotides 1811 and 1812 of the sequence set forth as SEQ ID NO:3, wherein said first nucleic acid is sufficient to specifically hybridize with a second nucleic acid comprising the complementary strand of SEQ ID NO:3 in the presence of a third nucleic acid comprising (SEQ ID NO:5).
- 20 6. An isolated or recombinant nucleic acid according to claim 5, comprising at least 36 consecutive nucleotides of SEQ ID NO:3, which consecutive nucleotides comprise at least one of nucleotides 1811 and 1812 of the sequence set forth as SEQ ID NO:3.
7. An isolated or recombinant nucleic acid according to claim 5, comprising at least 96 consecutive nucleotides of SEQ ID NO:3, which consecutive nucleotides comprise at
25 least one of nucleotides 1811 and 1812 of the sequence set forth as SEQ ID NO:3.
8. An isolated or recombinant nucleic acid according to claim 5, comprising the sequence set forth as SEQ ID NO:3.
9. A cell into which a nucleic acid according to any one of claims 4, 5, 6, 7 or 8 is introduced.
- 30 10. A method of making an isolated polypeptide, said method comprising the steps of:
introducing a recombinant nucleic acid encoding the polypeptide of claim 1, 2 or 3 into a host cell or cellular extract,

incubating said host cell or cellular extract under conditions whereby said polypeptide is expressed; and

isolating said polypeptide.

11. A method of screening for an agent which modulates the interaction of an IKK polypeptide to a binding target, said method comprising the steps of:

incubating a mixture comprising:

an isolated polypeptide of claim 1, 2 or 3,

a binding target of said polypeptide, wherein the binding target is an I κ B polypeptide, and

10 a candidate agent; under conditions whereby, but for the presence of said agent, said polypeptide specifically binds said binding target at a reference affinity;

detecting the binding affinity of said polypeptide to said binding target to determine an agent-biased affinity, wherein a difference between the agent-biased affinity and the reference affinity indicates that said agent modulates the binding of said polypeptide to said binding target.

15

12. A method according to claim 11, wherein said reference and agent-biased binding affinity is detected as phosphorylation of said substrate.

13. A method of screening for an agent which modulates the interaction of an IKK polypeptide to a binding target, said method comprising the steps of:

20 incubating a mixture comprising: the isolated polypeptide of claim 3 which retains I κ B kinase activity, an I κ B polypeptide comprising at least a six residue domain of a natural I κ B comprising at least one of Ser32 and Ser36, and a candidate agent; under conditions whereby, but for the presence of said agent, said polypeptide specifically phosphorylates said I κ B polypeptide at at least one of said Ser32 and Ser36 at a reference activity;

25 detecting the polypeptide-induced phosphorylation of said I κ B polypeptide at at least one of said Ser32 and Ser36 to determine an agent-biased activity, wherein a difference between the agent-biased activity and the reference activity indicates that said agent modulates the ability of said polypeptide to specifically phosphorylate an I κ B polypeptide.