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(54) Title: METHODS FOR INCREASING IMMUNE RESPONSES USING AGENTS THAT DIRECTLY BIND TO AND ACTIVATE IRE-1

(57) Abstract: The invention provides, e.g., compositions and methods for increasing activation of immune cells.

**METHODS FOR INCREASING IMMUNE RESPONSES
USING AGENTS THAT DIRECTLY BIND TO AND ACTIVATE IRE-1**

REFERENCE TO RELATED APPLICATION

5 This application claims the benefit of U.S. Provisional Application Serial No.: 61/440,224 filed February 7, 2011; which is herein incorporated by reference.

Background of the Invention

10 The transcription factor XBP-1 was identified as a key regulator of the mammalian unfolded protein response (UPR) or endoplasmic reticulum (ER) stress response, which is activated by environmental stressors such as protein overload that require increased ER capacity (D. Ron, P. Walter (2007) *Nat Rev Mol Cell Biol* 8, 519). XBP-1 is activated by a post-transcriptional modification of its mRNA by IRE-1 alpha, an ER localizing proximal sensor of ER stress (M. Calton *et al.* (2002) *Nature* 415, 92; 15 H. Yoshida, *et al.* (2001) *Cell* 107, 881; X. Shen *et al.* (2001) *Cell* 107, 893). Upon ER stress, IRE-1 alpha induces an unconventional splicing of XBP-1 mRNA by using its endoribonuclease activity to generate a mature mRNA encoding an active transcription factor, XBP-1s, which directly binds to the promoter region of ER chaperone genes to promote transcription (A. L. Shaffer *et al.* (2004) *Immunity* 21, 81; A. H. Lee, *et al.* 20 (2003) *Mol Cell Biol* 23, 7448; D. Acosta-Alvear *et al.* (2007) *Mol Cell* 27, 53). Mice deficient in XBP-1 display severe abnormalities in the development and function of professional secretory cells, such as plasma B cells and pancreatic acinar cells (N. N. Iwakoshi *et al.* (2003) *Nat Immunol* 4, 321; A. H. Lee, *et al.* (2005) *Embo J* 24, 4368) and intestinal Paneth cells (Kaser, *et al.* (2008) *Cell*).

25 It has previously been shown that XBP-1 plays an important role in modulating toll-like receptor (TLR)-mediated responses and that enhancing XBP-1 activity can amplify the innate immune response. XBP-1 has also plays many other roles. For example, it been shown to activate the UPR, to increase proper protein folding and transport, to increase hepatocyte growth, and to increase plasma cell differentiation. The 30 identification of agents that can be used to increase XBP-1 activity, e.g., by directly binding to and activating IRE-1 would be of great benefit in increasing immune cell activation, e.g., in the context of natural infection, vaccination, and cancer, as well as in promoting XBP-1 activity in other cell types.

35

Figure Legends

Figure 1. HIV-protease inhibitors (PIs) trigger robust IRE1 and XBP1 activation and synergize with TLR4 activation to produce cytokines and co-stimulatory molecules. A) XBP1 mRNA maturation (XBP1s) in J774 cells stimulated with dose dependent concentrations of HIV-PIs (similar data were obtained in primary mouse M0s, and various M0 cell lines of human and mouse origin). B) Cell extracts of cells stimulated with Tunicamycin (TM) or HIV-protease inhibitors were monitored for IRE1 activation by phosphorylation in a Phos-tag SDS-PAGE gel, CHOP induction and ATF6a processing. C) Realtime PCR of CHOP induction by the ER-stress inducer TM and the HIV-PI Nelfinavir (NFR) was analyzed in PERK proficient and deficient MEFs. D) J774 cells were stimulated with HIV-PIs or TM as indicated in presence or absence of LPS and analyzed for IL-6 production by rtPCR. E) Increased IL-6 production and co-stimulatory ligand (CD86 and CD40) expression were observed in the presence of Nelfinavir and the synthetic TLR4 agonist MPLA compared to TLR4 agonist alone.

Figure 2. In vitro fluorescent splicing reporter assay with recombinant IRE1 protein reveals marked induction of xbp1 splicing with ritonavir and nelfinavir but not amprenavir at doses of PIs ranging from 20uM to 0.63uM

20

Figure 3. HIV PIs induce splicing of XBP-1 in mouse embryonic fibroblasts.

Summary of the Invention

25 The present invention demonstrates, *inter alia*, a role for agents that directly bind to and activate IRE-1, e.g., inhibitors of HIV proteases, in the activation of XBP-1, e.g., in immune cells and in other cell types. As described in the appended Examples, it has been discovered that agents that directly bind to IRE-1, e.g., at the interface between the subunits of the IRE-1 dimer, activate IRE-1 and thereby increase XBP-1 activity. These agents increase XBP-1 activity in cells that express IRE-1 and XBP-1. For example, these agents synergize with agonists of toll-like receptors to increase the production of cytokines and co-stimulatory molecules in immune cells, e.g., macrophages.

Surprisingly, certain of these agents activate IRE-1 and do not activate PERK or ATF6 (the two other branches of the UPR) selectively activating the IRE-1 pathway in a non-ER stress dependent fashion, similar to toll-like receptors. These data point to a role for IRE-1 and XBP-1 that is separate from their role in classical ER-stress mediated responses. The fact that these agents synergize with TLR agonists to induce immune cell activation was also surprising.

35

Accordingly, in one aspect, the invention pertains to a method for increasing activation of XPB-1 in a cell which comprises IRE-1 and XBP-1 (e.g., a cell in vitro or present in a subject), comprising administering an agent that directly binds to and activates IRE-1 in the cell thereby increasing the activation of XPB-1 in the cell. In one
5 embodiment, the cell is an immune cell. In another embodiment, the cell is a B cell. In another embodiment, the cell is a macrophage. In another embodiment, the cell expresses a heterologous protein.

In another aspect, the invention pertains to a method for increasing activation of immune cells in a subject, comprising administering an agent that directly binds to and
10 activates IRE-1 to the subject thereby increase activation of immune cells in the subject.

In one embodiment, the subject is infected with a pathogen that does not express an HIV protease.

In one embodiment, the agent is an HIV protease inhibitor.

In one embodiment, the pathogen is selected from the group consisting of a
15 bacterium, a virus, and a parasite.

In one embodiment, wherein the subject has cancer.

In one embodiment, the method further comprises administering the IRE1 agonist and at least one toll-like receptor agonist to the subject.

In one embodiment, the TLR agonist stimulates a TLR selected from the group
20 consisting of: TLR2, TLR4, and TLR5. In one embodiment, the TLR agonist stimulates TLR4.

In one embodiment, the method further comprises contacting the immune cells with an antigen to which an immune response is desired.

In one embodiment, the production of a proinflammatory cytokine by the
25 immune cells is increased. In one embodiment, the proinflammatory cytokine is IL-6.

In one embodiment, the expression of at least one costimulatory molecule is increased. In one embodiment, the expression of CD40 is increased.

In one embodiment, the immune cells comprise macrophages.

In on embodiment, the HIV protease inhibitor is selected from the group
30 consisting of: Nelfinavir, Atazanavir, Lopinavir, and Ritonavir. In one embodiment, the HIV protease inhibitor is Nelfinavir.

In one embodiment, the activation of immune cells is increased in vivo.

In another aspect, the invention pertains to a method for increasing activation of a population of immune cells in vitro, wherein the population of cells comprises
35 macrophages, comprising contacting the cells with an agent that directly binds to and activates IRE-1 thereby increasing activation of immune cells in vitro.

In one embodiment, the agent is an HIV protease inhibitor that binds to and activates IRE-1 such that XBP-1 is activated in the cells and the method further comprising determining the effects of XBP-1 activation on the cells in culture.

5 In another aspect, the invention pertains to a method for increasing protein production in vitro, comprising contacting cells which comprise a heterologous DNA molecule specifying a protein of interest with an agent that directly binds to and activates IRE-1 such that the amount of the protein of interest produced by the cells in vitro is increased.

10 In one embodiment, the invention pertains to a method of identifying compounds that enhance the innate immune response comprising,

- a) providing an immune cell comprising an IRE-1 polypeptide;
- b) contacting the immune cell with each member of a library of compounds;
- c) determining the ability of the compound to directly bind to IRE-1 and activate XBP-1 in the absence of activation of PERK or ATF6,
- 15 d) the effect of the compound on at least one parameter of activation of the immune cell;
- e) selecting a compound of interest that increases at least one parameter of activation of the immune cell to thereby identify the compound as useful in enhancing the innate immune response.

20 In one embodiment, the immune cell is a macrophage. In one embodiment, the immune cell is a B cell. In one embodiment, the immune cell is present in a mixed population of cells.

In another aspect, the invention pertains to a method of identifying improved HIV protease inhibitors comprising testing candidate HIV protease inhibitors for their 25 ability to bind to IRE-1, wherein those agents that bind to HIV protease but have reduced ability to bind to IRE-1 are identified as being improved HIV protease inhibitors.

In one embodiment, the method further comprises altering the candidate HIV protease inhibitor to reduce the ability of the HIV protease inhibitor to bind to IRE-1.

30 In one embodiment, the invention pertains to a method of identifying improved IRE-1 inhibitors comprising testing candidate HIV protease inhibitors for their ability to bind to IRE-1, altering the candidate HIV protease inhibitors to decrease their binding to IRE-1, to thereby identify improved IRE-1 inhibitors.

35 In one embodiment, the invention pertains to a method of identifying improved IRE-1 agonists comprising testing candidate HIV protease inhibitors for their ability to bind to IRE-1, altering the candidate HIV protease inhibitors to increase their binding to IRE-1, to thereby identify improved IRE-1 agonists.

DETAILED DESCRIPTION

The instant invention is based, at least in part, on the discovery that agents that directly bind to the IRE-1 dimeric interface activate IRE-1. More specifically, as
5 described in the appended Examples, it has been discovered that inhibitors of HIV proteases activate IRE-1 and thereby increase XBP-1 activity. In one embodiment, these agents increase immune cell activation. These same agents also activate IRE-1 and induce splicing of XBP-1 in other cell types which comprise IRE-1 and XBP-1 and are therefore useful in activating XBP-1 activity in other cells where it is desirable to do so.
10 These agents synergize with agonists of toll-like receptors to increase the production of cytokines and co-stimulatory molecules in macrophages.

Certain terms are first defined so that the invention may be more readily understood.
15

I. Definitions

In one embodiment, the subject methods modulate the activity of the innate immune system. The “innate immune system” comprises the cells and mechanisms that
20 defend the host from infection by other organisms, in a non-specific manner. The innate system, unlike the adaptive immune system, does not confer long-lasting or protective immunity to a host, *e.g.*, antibody protection, but rather provides immediate defense against infection. The innate system is an evolutionarily older defense strategy, and is the dominant immune system found in plants, fungi, insects, and in primitive
25 multicellular organisms, and in all classes of plant and animal life.

The major functions of the vertebrate innate immune system include recruiting immune cells to sites of infection and inflammation, through the production of cytokines; activation of the complement cascade to identify bacteria, activate cells and to promote clearance of dead cells or antibody complexes; identification and removal of
30 foreign substances present in organs, tissues, the blood and lymph; and activation of the adaptive immune system through antigen presentation.

The innate immune system recognizes key molecular signatures of pathogens or “pathogen associated molecular patterns” (PAMPs), also referred to as “microbe-associated molecular patterns” (MAMPs) (R. Medzhitov, *Nature* 449, 819 (Oct 18,
35 2007)) that include carbohydrates (*e.g.* structural components, *e.g.* lipopolysaccharide or LPS, mannose, peptidoglycans (PGN)), nucleic acids (*e.g.* bacterial or viral DNA or RNA, dsRNA, DNA), peptidoglycans and lipotechoic acids (from Gram positive bacteria), N-formylmethionine, lipoproteins and fungal glucans. The host organism

harbors a group of receptors referred to as “pathogen recognition receptors” (“PRRs”) that recognize these PAMPs, the best studied of which is the “Toll like receptors” (“TLRs”) (K. J. Ishii, S. Koyama, A. Nakagawa, C. Coban, S. Akira, *Cell Host Microbe* 3, 352 (Jun 12, 2008)).

5 Pathogen recognition receptors, also referred to as “primitive pattern recognition receptors” are proteins expressed by cells of the immune system to identify molecules associated with microbial pathogens or cellular stress. PRRs are classified according to their ligand specificity, function, localization and/or evolutionary relationships. On the basis of function, PRRs may be divided into endocytic PRRs or signaling PRRs.

10 Signaling PRRs include the large families of membrane-bound Toll-like receptors and cytoplasmic NOD-like receptors. Endocytic PRRs promote the attachment, engulfment and destruction of microorganisms by phagocytes, without relaying an intracellular signal. Endocytic PRRs recognize carbohydrates and include mannose receptors of macrophages, glucan receptors present on all phagocytes and scavenger receptors that
15 recognize charged ligands, are found on all phagocytes and mediate removal of apoptotic cells.

TLRs are single membrane-spanning non-catalytic receptors that recognize structurally conserved molecules derived from microbes, *e.g.*, PAMPs. TLRs together with the Interleukin-1 receptor, *e.g.*, IL-1 and IL-18) form a receptor superfamily,
20 known as the "Interleukin-1 Receptor/Toll-Like Receptor Superfamily"; members of this family are characterized structurally by an extracellular leucine-rich repeat (LRR) domain, a conserved pattern of juxtamembrane cysteine residues, and an intracytoplasmic signaling domain (Toll/IL-1 resistance or Toll-IL-1 receptor (TIR))
25 interactions) TIR domain-containing adapters including MyD88, TIR domain-containing adaptor (TIRAP), and TIR domain-containing adaptor inducing IFN β (TRIF) (L. A. O'Neill, A. G. Bowie, *Nat Rev Immunol* 7, 353 (May 1, 2007)).

There are three subgroups of TIR domains. Proteins with subgroup 1 TIR domains are receptors for interleukins that are produced by macrophages, monocytes
30 and dendritic cells and all have extracellular Immunoglobulin (Ig) domains. Proteins with subgroup 2 TIR domains are classical TLRs, and bind directly or indirectly to molecules of microbial origin, *e.g.*, TLR5, TLR4 and TLR2. A third subgroup of proteins containing TIR domains consists of adaptor proteins that are exclusively cytosolic and mediate signaling from proteins of subgroups 1 and 2.

35 The nucleotide and amino acid sequences of TLRs are known and can be found at, for example, GenBank Accession Nos. gi:41350336, gi:13507602 (TLR1 human and mouse, respectively); gi:68160956, gi:158749637, gi:42476288 (TLR2 human, mouse, and rat, respectively); gi:19718735, GI:146149239, GI:38454315 (TLR3 human, mouse,

and rat, respectively); GI:88758616, GI:118130391, gi:25742798 (TLR4 human, mouse, and rat, respectively); gi:124248535, gi:124248589, gi:109498326 (TLR5 human, mouse, and rat, respectively); gi:20143970, gi:157057100, gi:46485392 (TLR6 human, mouse, and rat, respectively); gi:67944638, gi:141803199, gi:147900683 (TLR7 human, mouse, and rat, respectively); gi:156071526, gi:126723494 (TLR8 human and mouse, respectively); gi:20302169, gi:157057165 (TLR9 human and mouse, respectively); there are two isoforms of TLR 10 in human, gi:62865620 and gi:62865617, gi:109499688 (TLR10 rat); gi:148539899, gi:221307462 (TLR11 mouse and rat, respectively); gi:148539900 (TLR12 mouse); gi:45429998 (TLR13 mouse).

10 TLR-mediated signaling in response to PAMPs is a sequential cascade of transcriptional regulatory events that vary depending on the TLR agonists, cell types involved and pathogenicity of the microbe. Individual genes (notably proinflammatory cytokines, *e.g.*, IL-1 (alpha and beta), IL-6, IL-18, TNF- α) are induced transiently and then repressed reflecting the ability that the innate immune system has to interpret the
15 infection and orchestrate appropriate responses while promoting resolution (T. Ravasi, C. A. Wells, D. A. Hume, *Bioessays* 29, 1215 (Nov 15, 2007); J. C. Roach et al., *Proc Natl Acad Sci USA* 104, 16245 (Oct 9, 2007); M. Gilchrist et al., *Nature* 441, 173 (May 11, 2006)). Nuclear factor-kappaB (NF- κ B), the best characterized transcription factor downstream of TLRs, is activated by virtually all TLRs, *e.g.*, TLR5, TLR4 and TLR2,
20 through MyD88 or TRIF dependent pathways and is crucial for the production of proinflammatory cytokines. However, bacterial products are not the only signals that modulate innate immune responses- signals produced by stressed or damaged tissues have also been suggested to modulate the inflammatory response (H. Kono, K. L. Rock, *Nat Rev Immunol* 8, 279 (Apr 1, 2008); R. Medzhitov, *Nature* 454, 428 (Jul 24, 2008)).

25 The nucleotide and amino acid sequences of MyD88 are known and can be found at, for example, GenBank Accession Nos. gi:197276653, gi:31543276, gi:37693502 (human, mouse, rat, respectively).

The nucleotide and amino acid sequences of TIR domain-containing adaptor (TIRAP) are known and can be found at, for example, GenBank Accession Nos.
30 gi:89111121 and gi:89111123 (two isoforms in himan), gi:16905130 and gi:109483246 (mouse and rat).

The nucleotide and amino acid sequences of TIR domain-containing adaptor inducing IFN β (TRIF) are known and can be found at, for example, GenBank Accession Nos. gi:197209874 and gi:144227224 (human and mouse, respctcively).

35 As used herein, the term "XBP-1" refers to the X-box binding protein. XBP-1 is a basic region leucine zipper (b-zip) transcription factor isolated independently by its ability to bind to a cyclic AMP response element (CRE)-like sequence in the mouse

class II MHC A α gene or the CRE-like site in the HTLV-1 21 base pair enhancer, and subsequently shown to regulate transcription of both the DR α and HTLV-1 ltr gene.

Like other members of the b-zip family, XBP-1 has a basic region that mediates DNA-binding and an adjacent leucine zipper structure that mediates protein
5 dimerization. Deletional and mutational analysis has identified transactivation domains in the C-terminus of XBP-1 in regions rich in acidic residues, glutamine, serine/threonine and proline/glutamine. XBP-1 is present at high levels in plasma cells in joint synovium in patients with rheumatoid arthritis. In human multiple myeloma cells, XBP-1 is selectively induced by IL-6 treatment and implicated in the proliferation of
10 malignant plasma cells. XBP-1 has also been shown to be a key factor in the transcriptional regulation of molecular chaperones and to enhance the compensatory UPR (Calfon et al., Nature 415, 92 (2002); Shen et al., Cell 107:893 (2001); Yoshida et al., Cell 107:881 (2001); Lee et al., Mol. Cell Biol. 23:7448 (2003); each of which is incorporated herein by reference).

15 The amino acid sequence of XBP-1 is described in, for example, Liou, H-C. *et al.* (1990) *Science* 247:1581-1584 and Yoshimura, T. *et al.* (1990) *EMBO J.* 9:2537-2542. The amino acid sequence of mammalian homologs of XBP-1 are described in, for example, in Kishimoto T. *et al.*, (1996) *Biochem. Biophys. Res. Commun.* 223:746-751 (rat homologue). Exemplary proteins intended to be encompassed by the term "XBP-1"
20 include those having amino acid sequences disclosed in GenBank with accession numbers A36299 [gi:105867]; AF443192 [gi: 18139942] (spliced murine XBP-1); P17861 [gi:139787]; CAA39149 [gi:287645]; AF027963 [gi: 13752783] (murine unspliced XBP-1); BAB82982.1 [gi:18148382] (spliced human XBP-1); BAB82981 [gi:18148380] (human unspliced XBP-1); and BAA82600 [gi:5596360] or *e.g.*, encoded
25 by nucleic acid molecules such as those disclosed in GenBank with accession numbers AF027963 [gi: 13752783]; NM_013842 [gi:13775155] (spliced murine XBP-1); or M31627 [gi:184485] (unspliced murine XBP-1); AB076384 [gi:18148381] (spliced human XBP-1); or AB076383 [gi:18148379] (human unspliced XBP-1); gi:51948392 (rat). XBP-1 is also referred to in the art as TREB5 or HTF (Yoshimura *et al.* 1990.
30 *EMBO Journal.* 9:2537; Matsuzaki *et al.* 1995. *J. Biochem.* 117:303).

There are two forms of XBP-1 protein, unspliced and spliced, which differ markedly in their sequence and activity. Unless the form is referred to explicitly herein, the term "XBP-1" as used herein includes both the spliced and unspliced forms.

As used herein, the term "spliced XBP-1" or "XBP-1s" refers to the spliced,
35 processed form of the mammalian XBP-1 mRNA or the corresponding protein. Human and murine XBP-1 mRNA contain an open reading frame (ORF1) encoding bZIP proteins of 261 and 267 amino acids, respectively. Both mRNAs also contain another ORF, ORF2, partially overlapping but not in frame with ORF1. ORF2 encodes 222

amino acids in both human and murine cells. Human and murine ORF1 and ORF2 in the XBP-1 mRNA share 75% and 89% identity respectively. In response to ER stress, XBP-1 mRNA is processed by the ER transmembrane endoribonuclease and kinase IRE-1 which excises an intron from XBP-1 mRNA. In murine and human cells, a 26
5 nucleotide intron is excised. The boundaries of the excised introns are encompassed in an RNA structure that includes two loops of seven residues held in place by short stems. The RNA sequences 5' to 3' to the boundaries of the excised introns form extensive base-pair interactions. Splicing out of 26 nucleotides in murine and human cells results in a frame shift at amino acid 165 (the numbering of XBP-1 amino acids herein is based
10 on GenBank accession number NM_013842 [gi:13775155] (spliced murine XBP-1) and one of ordinary skill in the art can determine corresponding amino acid numbers for XBP-1 from other organisms, *e.g.*, by performing a simple alignment). This causes removal of the C-terminal 97 amino acids from the first open reading frame (ORF1) and addition of the 212 amino from ORF2 to the N-terminal 164 amino acids of ORF1
15 containing the b-ZIP domain. In mammalian cells, this splicing event results in the conversion of a 267 amino acid unspliced XBP-1 protein to a 371 amino acid spliced XBP-1 protein. The spliced XBP-1 then translocates into the nucleus where it binds to its target sequences to induce their transcription.

As used herein, the term "unspliced XBP-1" refers to the unprocessed XBP-1
20 mRNA or the corresponding protein. As set forth above, unspliced murine XBP-1 is 267 amino acids in length and spliced murine XBP-1 is 371 amino acids in length. The sequence of unspliced XBP-1 is known in the art and can be found, *e.g.*, Liou, H-C. *et al.* (1990) *Science* 247:1581-1584 and Yoshimura, T. *et al.* (1990) *EMBO J.* 9:2537-2542, or at GenBank accession numbers: AF443192 [gi: 18139942] (amino acid spliced
25 murine XBP-1); AF027963 [gi: 13752783] (amino acid murine unspliced XBP-1); NM_013842 [gi:13775155] (nucleic acid spliced murine XBP-1); or M31627 [gi:184485] (nucleic acid unspliced murine XBP-1).

As used herein, the term "ratio of spliced to unspliced XBP-1" refers to the amount of spliced XBP-1 present in a cell or a cell-free system, relative to the amount or
30 of unspliced XBP-1 present in the cell or cell-free system. "The ratio of unspliced to spliced XBP-1" refers to the amount of unspliced XBP-1 compared to the amount of unspliced XBP-1. "Increasing the ratio of spliced XBP-1 to unspliced XBP-1" encompasses increasing the amount of spliced XBP-1 or decreasing the amount of unspliced XBP-1 by, for example, promoting the degradation of unspliced XBP-1.
35 Increasing the ratio of unspliced XBP-1 to spliced XBP-1 can be accomplished, *e.g.*, by decreasing the amount of spliced XBP-1 or by increasing the amount of unspliced XBP-1. Levels of spliced and unspliced XBP-1 can be determined as described herein, *e.g.*, by comparing amounts of each of the proteins which can be distinguished on the basis of

their molecular weights or on the basis of their ability to be recognized by an antibody. In another embodiment described in more detail below, PCR can be performed employing primers with span the splice junction to identify unspliced XBP-1 and spliced XBP-1 and the ratio of these levels can be readily calculated.

5 In one embodiment, the subject methods can be used to activate the UPR in cells. As used herein, the term “Unfolded Protein Response” (UPR) or the “Unfolded Protein Response pathway” refers to an adaptive response to the accumulation of unfolded proteins in the ER and includes the transcriptional activation of genes encoding chaperones and folding catalysts and protein degrading complexes as well as
10 translational attenuation to limit further accumulation of unfolded proteins. Both surface and secreted proteins are synthesized in the endoplasmic reticulum (ER) where they need to fold and assemble prior to being transported.

 Since the ER and the nucleus are located in separate compartments of the cell, the unfolded protein signal must be sensed in the lumen of the ER and transferred across
15 the ER membrane and be received by the transcription machinery in the nucleus. The unfolded protein response (UPR) performs this function for the cell. Activation of the UPR can be caused by treatment of cells with reducing agents like DTT, by inhibitors of core glycosylation like tunicamycin or by Ca-ionophores that deplete the ER calcium stores. First discovered in yeast, the UPR has now been described in *C. elegans* as well
20 as in mammalian cells. In mammals, the UPR signal cascade is mediated by three types of ER transmembrane proteins: the protein-kinase and site—specific endoribonuclease IRE-1; the eukaryotic translation initiation factor 2 kinase, PERK/PEK; and the transcriptional activator ATF6. If the UPR cannot adapt to the presence of unfolded proteins in the ER, an apoptotic response is initiated leading to the activation of JNK
25 protein kinase and caspases 7, 12, and 3. The most proximal signal from the lumen of the ER is received by a transmembrane endoribonuclease and kinase called IRE-1. Following ER stress, IRE-1 initiates splicing of the XBP-1 mRNA, the spliced version of which, activates the UPR.

 Eukaryotic cells respond to the presence of unfolded proteins by upregulating the
30 transcription of genes encoding ER resident protein chaperones such as the glucose-regulated BiP/Grp74, Grp94 and CHOP genes, folding catalysts and protein degrading complexes that assist in protein folding.

 As used herein, the term “modulation of the UPR” includes both upregulation and downregulation of the UPR. As used herein the term “UPRE” refers to UPR
35 elements upstream of certain genes which are involved in the activation of these genes in response, e.g., to signals sent upon the accumulation of unfolded proteins in the lumen of the endoplasmic reticulum, e.g., EDEM, Herp, e.g., ER stress-responsive cis-acting elements with the consensus sequence TGACGTGG/A (SEQ ID NO:XXX) (Wang, Y.,

et al. 2000. *J. Biol. Chem.* 275:27013–27020; Yoshida, H., et al. 2001. *Cell* 107:881–891). Such elements are suitable for use in the screening assays of the invention.

As used herein, the term “ER stress” includes conditions such as the presence of reducing agents, depletion of ER luminal Ca²⁺, inhibition of glycosylation or interference with the secretory pathway (by preventing transfer to the Golgi system), which lead to an accumulation of misfolded protein intermediates and increase the demand on the chaperoning capacity, and induce ER-specific stress response pathways. ER stress pathways involved with protein processing include the Unfolded Protein Response (UPR) and the Endoplasmic Reticulum Overload Response (EOR) which is triggered by certain of the same conditions known to activate UPR (e.g. glucose deprivation, glycosylation inhibition), as well as by heavy overexpression of proteins within the ER. The distinguishing feature of EOR is its association with the activation of the transcription factor NF- κ B. Modulation of both the UPR and the EOR can be accomplished using the methods and compositions of the invention. ER stress can be induced, for example, by inhibiting the ER Ca²⁺ ATPase, e.g., with thapsigargin. As used herein, the term “protein folding or transport” encompasses posttranslational processes including folding, glycosylation, subunit assembly and transfer to the Golgi compartment of nascent polypeptide chains entering the secretory pathway, as well as extracytosolic portions of proteins destined for the external or internal cell membranes, that take place in the ER lumen. Proteins in the ER are destined to be secreted or expressed on the surface of a cell. Accordingly, expression of a protein on the cell surface or secretion of a protein can be used as indicators of protein folding or transport.

As used herein, the term “IRE-1” refers to an ER transmembrane endoribonuclease and kinase called inositol requiring enzyme, that oligomerizes and is activated by autophosphorylation upon sensing the presence of unfolded proteins, see, e.g., Shamu et al., (1996) *EMBO J.* 15: 3028-3039. In *Saccharomyces cerevisiae*, the UPR is controlled by IREp. In the mammalian genome, there are two homologs of IRE-1, IRE1 α and IRE1 β . IRE1 α is expressed in all cells and tissue whereas IRE1 β is primarily expressed in intestinal tissue. The endoribonucleases of either IRE1 α and IRE1 β are sufficient to activate the UPR. Accordingly, as used herein, the term “IRE-1” includes, e.g., IRE1 α , IRE1 β and IREp. In a preferred embodiment, IRE-1 refers to IRE1 α .

IRE-1 is a large protein having a transmembrane segment anchoring the protein to the ER membrane. A segment of the IRE-1 protein has homology to protein kinases and the C-terminal has some homology to RNAses. Over-expression of the IRE-1 gene leads to constitutive activation of the UPR. Phosphorylation of the IRE-1 protein occurs at specific serine or threonine residues in the protein.

IRE-1 senses the overabundance of unfolded proteins in the lumen of the ER. The oligomerization of this kinase leads to the activation of a C-terminal endoribonuclease by trans-autophosphorylation of its cytoplasmic domains. IRE-1 uses its endoribonuclease activity to excise an intron from XBP-1 mRNA. Cleavage and
5 removal of a small intron is followed by re-ligation of the 5' and 3' fragments to produce a processed mRNA that is translated more efficiently and encodes a more stable protein (Calfon et al. (2002) Nature 415(3): 92-95). The nucleotide specificity of the cleavage reaction for splicing XBP-1 is well documented and closely resembles that for IRE-p mediated cleavage of HAC1 mRNA (Yoshida et al. (2001) Cell 107:881-891). In
10 particular, IRE-1 mediated cleavage of murine XBP-1 cDNA occurs at nucleotides 506 and 532 and results in the excision of a 26 base pair fragment (e.g., CAGCACTCAGACTACGTGCACCTCTG (SEQ ID NO:1) for mouse XBP-1). IRE-1 mediated cleavage of XBP-1 derived from other species, including humans, occurs at nucleotides corresponding to nucleotides 506 and 532 of murine XBP-1 cDNA, for
15 example, between nucleotides 502 and 503 and 528 and 529 of human XBP-1.

There are two transcript variants of human IRE-1, the sequence of which are known in the art and can be found at, e.g., at GenBank accession numbers: gi:50345998 and gi:153946420. The nucleotide and amino acid sequences of mouse and rat IRE-1 may be found at, e.g., at GenBank accession numbers: gi:15284149 and gi:109489193,
20 respectively.

XBP-1 controls expression of several other genes, for example, ERdj4, p58ipk, EDEM, PDI-P5, RAMP4, HEDJ, BiP, ATF6 α , XBP-1, Armet and DNAJB9, which encodes the 222 amino acid protein, mDj7 (GenBank Accession Number NM—013760 [gi:31560494]). These genes are important in a variety of cellular functions. For
25 example, Hsp70 family proteins including BiP/Grp78 which is a representative ER localizing HSP70 member, function in protein folding in mammalian cells. A family of mammalian DnaJ/Hsp40-like proteins has recently been identified that are presumed to carry out the accessory folding functions. Two of them, Erdj4 and p58ipk, were shown to be induced by ER stress, localize to the ER, and modulate HSP70 activity (Chevalier
30 et al. 2000 J Biol Chem 275: 19620-19627; Ohtsuka and Hata 2000 Cell Stress Chaperones 5: 98-112; Yan et al. 2002 Proc Natl Acad Sci USA 99: 15920-15925). ERdj4 has recently been shown to stimulate the ATPase activity of BiP, and to suppress ER stress-induced cell death (Kurusu et al. 2003 Genes Cells 8: 189-202; Shen et al. 2003 J Biol Chem 277: 15947-15956). ERdj4, p58IPK, EDEM, RAMP-4, PDI-P5 and
35 HEDJ, all appear to act in the ER. ERdj4 (Shen et al. 2003), p58IPK (Melville et al. 1999 J Biol Chem 274: 3797-3803) and HEDJ (Yu et al. 2000 Mol Cell 6: 1355-1364) are localized to the ER and display Hsp40-like ATPase augmenting activity for the HspTO family chaperone proteins. EDEM was shown to be critically involved in the

ERAD pathway by facilitating the degradation of ERAD substrates (Hosokawa et al. 2001 EMBO Rep 2:415-422; Molinari et al. 2003 Science 299 1397-1400; Oda et al. 2003 Science 299:1394-1397; Yoshida et al. 2003 Dev. Cell. 4:265-271). RAMP4 is a recently identified protein implicated in glycosylation and stabilization of membrane proteins in response to stress (Schroder et al. 1999 EMBO J 18:4804-4815; Wang and Dobberstein 1999 Febs Lett 457:316-322; Yamaguchi et al. 1999 J. Cell Biol 147:1195-1204). PDI-P5 has homology to protein disulfide isomerase, which is thought to be involved in disulfide bond formation (Kikuchi et al. 2002 J. Biochem (Tokyo) 132:451-455). Collectively, these results show that the IRE1/XBP-1 pathway is required for efficient protein folding, maturation and degradation in the ER.

Another UPR signaling pathway is activated by the PERK protein kinase. PERK phosphorylates eIF2 α , which induces a transient suppression of protein translation accompanied by induction of transcription factor(s) such as ATF4 (Harding et al. 2000 Mol Cell 6: 1099-1108). eIF2 α is also phosphorylated under various cellular stress conditions by specific kinases, double strand RNA activated protein kinase PKR, the amino acid control kinase GCN2 and the heme regulated inhibitor HRI (Samuel 1993 J. Biol. Chem 268:7603-76-6; Kaufman 1999 Genes Dev. 13: 1211-1233). Since genes that are induced by the PERK pathway are also induced by other stress signals, such as amino acid deprivation, it is likely that PERK dependent UPR target genes carry out common cellular defense mechanisms, such as cellular homeostasis, apoptosis and cell cycle (Harding et al. 2003 Mol. Cell 11619-633). Collectively, ER stress activates IRE/XBP-1 and PERK/eIF2 α pathways to ensure proper maturation and degradation of secretory proteins and to effect common cellular defense mechanisms, respectively.

The reliance of p58IPK gene expression on XBP-1 connects two of the UPR signaling pathways, IRE1/XBP-1 and PERK. P58IPK was originally identified as a 58 kD inhibitor of PKR in influenza virus-infected kidney cells (Lee et al. 1990 Proc Natl Acad Sci USA 87: 6208-6212) and described to downregulate the activity of PKR by binding to its kinase domain (Katze 1995 Trends Microbiol 3: 75-78). It also has a J domain in the C-terminus which has been shown to participate in interactions with Hsp70 family proteins Melville et al. 1999 J Biol Chem 274: 3797-380). Recently Katze and colleagues have demonstrated that p58IPK interacts with ERK which is structurally similar to PKR, inhibits its eIF2 α kinase activity and that it is induced during the UPR by virtue of an ER stress-response element in its promoter region (Yan et al. 2002 Proc Natl Acad Sci USA 99: 15920-15925).

As used herein the term “activating transcription factors 6” include ATF6 α and ATF6 β . ATF6 is a member of the basic-leucine zipper family of transcription factors. It contains a transmembrane domain and is located in membranes of the endoplasmic reticulum. ATF6 is constitutively expressed in an inactive form in the membrane of the

ER. Activation in response to ER stress results in proteolytic cleavage of its N-terminal cytoplasmic domain by the S2P serine protease to produce a potent transcriptional activator of chaperone genes (Yoshida *et al.* 1998 *J. Biol. Chem.* 273: 33741-33749; Li *et al.* 2000 *Biochem J* 350 Pt 1: 131-138; Ye *et al.* 2000 *Mol Cell* 6: 1355-1364; Yoshida *et al.* 2001 *Cell* 107: 881-891; Shen *et al.* 2002 *Dev Cell* 3: 99-111). The recently described ATF6 β is closely related structurally to ATF6 α and posited to be involved in the UPR (Haze *et al.* 2001 *Biochem J* 355: 19-28; Yoshida *et al.* 2001b *Mol Cell Biol* 21: 1239-1248). The third pathway acts at the level of posttranscriptional control of protein synthesis. An ER transmembrane component, PEK/PERK, related to PKR (interferon-induced double-stranded RNA-activated protein kinase) is a serine/threonine protein kinase that acts in the cytoplasm to phosphorylate eukaryotic initiation factor-2 α (eIF2 α). Phosphorylation of eIF2 α results in translation attenuation in response to ER stress (Shi *et al.* 1998 *Mol. Cell. Biol.* 18: 7499-7509; Harding *et al.* 1999 *Nature* 397: 271-274).

The nucleotide and amino acid sequences of ATF6 are known in the art and can be found at, *e.g.*, at GenBank accession number: gi:56786156, gi:124486810, gi:157821878 (human, mouse, rat, respectively).

As used herein, the various forms of the term "modulate" include stimulation (*e.g.*, increasing or upregulating a particular response or activity) and inhibition (*e.g.*, decreasing or downregulating a particular response or activity).

As used herein, the terms "a modulator of XBP-1" and "a modulator of IRE-1" include modulators of XBP-1 and/or IRE-1 expression, processing, post-translational modification, stability, and/or activity. The term includes agents, for example which bind to and directly activate IRE-1 and, thereby, increase the activity of XBP-1.

The term "interact" or "bind" as used herein is meant to include detectable interactions between molecules, such as can be detected using, for example, by virtue of the effect they have on a molecule to which they bind or by structural modeling methods. The term interact is also meant to include "binding" interactions between molecules. Binding interactions can be determined, *e.g.*, by isothermal titration calorimetry (ITC) and is read out as a change in the thermodynamic enthalpy of the reaction.

As used herein, the term "contacting" (*i.e.*, contacting a cell *e.g.* a cell, with a compound) includes incubating the compound and the cell together *in vitro* (*e.g.*, adding the compound to cells in culture) as well as administering the compound to a subject such that the compound and cells of the subject are contacted *in vivo*. The term "contacting" does not include exposure of cells to an XBP-1 and/or IRE-1 modulator that may occur naturally in a subject (*i.e.*, exposure that may occur as a result of a natural physiological process).

As used herein, the term "test compound" refers to a compound that has not previously been identified as, or recognized to be, a modulator of the activity being tested. The term "library of test compounds" refers to a panel comprising a multiplicity of test compounds.

5 As used herein with respect to screening methods and methods of modulating innate immune responses, the term "cell" includes mammalian cells. In a preferred embodiment, a cell of the invention is a murine or human cell.

As used herein, the term "engineered" (as in an engineered cell) refers to a cell into which a nucleic acid molecule *e.g.*, encoding a heterologous protein, *e.g.*, an XBP-1
10 protein (*e.g.*, a spliced and/or unspliced form of XBP-1) has been introduced.

As used herein, the term "reporter gene" refers to any gene that expresses a detectable gene product, *e.g.*, RNA or protein. As used herein the term "reporter protein" refers to a protein encoded by a reporter gene. Preferred reporter genes are those that are readily detectable. The reporter gene can also be included in a construct in
15 the form of a fusion gene with a gene that includes desired transcriptional regulatory sequences or exhibits other desirable properties. Examples of reporter genes include, but are not limited to CAT (chloramphenicol acetyl transferase) (Alton and Vapnek (1979), *Nature* 282: 864-869) luciferase, and other enzyme detection systems, such as beta-galactosidase; firefly luciferase (deWet *et al.* (1987), *Mol. Cell. Biol.* 7:725-737);
20 bacterial luciferase (Engebrecht and Silverman (1984), *PNAS* 1: 4154-4158; Baldwin *et al.* (1984), *Biochemistry* 23: 3663-3667); alkaline phosphatase (Toh *et al.* (1989) *Eur. J. Biochem.* 182: 231-238, Hall *et al.* (1983) *J. Mol. Appl. Gen.* 2: 101), human placental secreted alkaline phosphatase (Cullen and Malim (1992) *Methods in Enzymol.* 216:362-368) and green fluorescent protein (U.S. patent 5,491,084; WO 96/23898).

25 As used herein, the term "XBP-1-responsive element" refers to a DNA sequence that is directly or indirectly regulated by the activity of the XBP-1 (whereby activity of XBP-1 can be monitored, for example, via transcription of a reporter gene).

In one embodiment, small molecules can be used as test compounds. The term "small molecule" is a term of the art and includes molecules that are less than about
30 7500, less than about 5000, less than about 1000 molecular weight or less than about 500 molecular weight. In one embodiment, small molecules do not exclusively comprise peptide bonds. In another embodiment, small molecules are not oligomeric. Exemplary small molecule compounds which can be screened for activity include, but are not limited to, peptides, peptidomimetics, nucleic acids, carbohydrates, small organic
35 molecules (*e.g.*, Cane *et al.* 1998. *Science* 282:63), and natural product extract libraries. In another embodiment, the compounds are small, organic non-peptidic compounds. In a further embodiment, a small molecule is not biosynthetic. For example, a small molecule is preferably not itself the product of transcription or translation. In one

embodiment, small molecule compounds are present on a microarray, see, *e.g.*, Bradner JE, et al. 2006. *Chem Biol.* 13(5):493-504.

As used herein the term “antigen” refers to a molecule to which an immune response is desired. Such antigens may be purified or may be crude preparations
5 comprising multiple antigens or may be whole organisms (*e.g.*, inactivated or attenuated virus particles or non-lethal bacteria). In one embodiment, an antigen comprises a protein. In another embodiment, an antigen is administered in the form of a nucleic acid molecule encoding a protein.

As used herein the term “costimulatory molecule” refers to membrane-bound or
10 secreted product of accessory cells that is required for activation of T or B cells.

As used herein the term macrophage refers to white blood cells produced by the differentiation of monocytes in tissues. Human macrophages are about 21 micrometres (0.00083 in) in diameter. Monocytes and macrophages are phagocytes. Macrophages function in both non-specific defense (innate immunity) as well as help initiate specific
15 defense mechanisms (adaptive immunity) of vertebrate animals. Macrophages can be identified by specific expression of a number of proteins including CD14, CD11b, F4/80 (mice)/EMR1 (human), Lysozyme M, MAC-1/MAC-3 and CD68 by flow cytometry or immunohistochemical staining.

Various aspects of the present invention are described in further detail in the
20 following subsections.

25 **II. Agents That Directly Bind to and Activate IRE-1**

In one embodiment, agents that directly bind to and activate IRE-1 can be used to activate XBP-1 in cells that comprise both IRE-1 and XBP-1. In one embodiment, such cells endogenously express one or both of these molecules. In another embodiment,
30 such cells express exogenous or heterologous IRE-1 and/or XBP-1 molecules. In one embodiment, such agents bind to a site at the interface of the two subunits of the IRE-1 dimer, *i.e.*, at the dimerization interface. In one embodiment, such agents do not bind to the portion of the IRE-1 dimer that is bound by the IRE-1 inhibitor quercetin. In another embodiment, such agents bind to the portion of the IRE-1 dimer that is bound by
35 quercetin. In one embodiment, such agents contain a synthetic analog of the phenylalanine-proline sequence found at positions 167 and 168 of retroviral gag-pol polyprotein.

In one embodiment, agents that bind to and selectively activate IRE-1 do not activate PERK and ATF6, the two other branches of the UPR.

In one embodiment such agents are HIV protease inhibitors that prevent cleavage of gag and gag-pol protein precursors in acutely and chronically infected cells, arresting maturation and thereby blocking the infectivity of nascent virions. Exemplary such inhibitors include indinavir (Crixivan), nelfinavir (Viracept), ritonavir (Norvir), and saquinavir (Invirase and Fortovase), etazanavir (Reyataz) and the investigational protease inhibitor amprenavir.

In one embodiment, these agents may be administered to a subject at the same approximate dose currently used for HIV therapy (e.g., approximately between 600-800 mg every 8 hours, two time a day, or three times a day). In another embodiment, such agents may be administered at a lower dose than than currently administered for treatment of HIV, thereby reducing potential side effects associated with such administration. For example, such agents may be used at doses of about 1 mg, 3 mg, 10 mg, 30 mg, 100 mg, 300 mg, 400 mg, 500 mg, 600 mg, 700 mg, 800 mg, 900 mg, 1000 mg. Agents may be administered multiple times (e.g., multiple times per day, multiple times per week, multiple times per month).

III TLR Agonists

In one embodiment, an agent that binds to and activates IRE-1 can be used in combination with a TLR agonist, e.g., for contacting cells in vitro or in vivo. Exemplary TLR agonists are known in the art.

TLR2 mediates cellular responses to a large number of microbial products including peptidoglycan, bacterial lipopeptides, lipoteichoic acid, mycobacterial lipoarabinomannan and yeast cell wall components. In another embodiment, an agonist of TLR2 can be used in combination with an agent that binds to and directly activates IRE-1. Exemplary such TLR2 agonists include mycobacterial cell wall glycolipids, lipoarabinomannan (LAM) and mannosylated phosphatidylinositol (PIM), MALP-2 and Pam3Cys and synthetic variants thereof.

In another embodiment, an agonist of TLR4 can be used in combination with an agent that binds to and directly activates IRE-1. Exemplary such TLR4 agonists include lipopolysaccharide or synthetic variants thereof (e.g., MPL and RC529) and lipid A or synthetic variants thereof (e.g., aminoalkyl glucosaminide 4-phosphates). See, e.g., Cluff et al. 2005 *Infection and Immunity*, p. 3044-3052:73; Lembo et al. *The Journal of Immunology*, 2008, 180, 7574 -7581; Evans et al. 2003. *Expert Rev Vaccines* 2:219-29. Many such agents are commercially available.

In another embodiment, an agonist of TLR5 can be used in combination with an agent that binds to and directly activates IRE-1. Exemplary such TLR5 agonists include

flagellin or synthetic variants thereof (e.g., A pharmacologically optimized TLR5 agonist with reduced immunogenicity (such as CBLB502) made by deleting portions of flagellin that are non-essential for TLR5 activation).

5

IV. Methods of Activating XBP-1

Activation of XBP-1 has been shown to have a variety of effects in numerous cell types. For example, XBP-1 activation increases de novo hepatic lipogenesis, increases hepatocyte growth, increases plasma cell differentiation, increases T cell activation,
10 increases IL-6 production, increases the unfolded protein response, and increases protein folding and transport to thereby increase protein expression in cells. The subject methods employ agents that directly bind to IRE-1 and thereby increase XBP-1 activity. These agents may be used to increase XBP-1 activity in cells in which it is desirable to do so.

15 In one embodiment, XBP-1 can be activated in cells using an IRE-1 agonist of the invention to treat a disorder associated with protein trafficking. In one embodiment, the disorder is a synucleinopathy. Synucleins are a family of small, presynaptic neuronal proteins composed of alpha-, beta-, and gamma-synucleins, of which only alpha-synuclein aggregates have been associated with several neurological diseases (Ian
20 et al., *Clinical Neurosc. Res.* 1:445-455, 2001; Trojanowski and Lee, *Neurotoxicology* 23:457-460, 2002). The role of synucleins (and in particular, alpha-synuclein) in the etiology of a number of neurodegenerative and/or amyloid diseases has developed from several observations. Pathologically, alpha-synuclein was identified as a major
25 component of Lewy bodies, the hallmark inclusions of Parkinson's disease, and a fragment thereof was isolated from amyloid plaques of a different neurological disease, Alzheimer's disease. Biochemically, recombinant alpha-synuclein was shown to form amyloid-like fibrils that recapitulated the ultrastructural features of alpha-synuclein
isolated from patients with dementia with Lewy bodies, Parkinson's disease and multiple system atrophy. Additionally, the identification of mutations within the alpha-synuclein
30 gene, albeit in rare cases of familial Parkinson's disease, demonstrated an unequivocal link between synuclein pathology and neurodegenerative diseases. The common involvement of alpha-synuclein in a spectrum of diseases such as Parkinson's disease, dementia with Lewy bodies, multiple system atrophy and the Lewy body variant of
Alzheimer's disease has led to the classification of these diseases under the umbrella
35 term of "synucleinopathies."

In some embodiments, the disorder characterized by impaired protein trafficking is a lysosomal storage disorder such as Fabry disease, Farber disease, Gaucher disease, GM.sub.1-gangliosidosis, Tay-Sachs disease, Sandhoff disease, GM.sub.2 activator

disease, Krabbe disease, metachromatic leukodystrophy, Niemann-Pick disease (types A, B, and C), Hurler disease, Scheie disease, Hunter disease, Sanfilippo disease, Morquio disease, Maroteaux-Lamy disease, hyaluronidase deficiency, aspartylglucosaminuria, fucosidosis, mannosidosis, Schindler disease, sialidosis type 1, Pompe disease, Pycnodysostosis, ceroid lipofuscinosis, cholesterol ester storage disease, Wolman disease, Multiple sulfatase, galactosialidosis, mucopolysaccharidosis (types II, III, and IV), cystinosis, sialic acid storage disorder, chylomicron retention disease with Marinesco-Sjogren syndrome, Hermansky-Pudlak syndrome, Chediak-Higashi syndrome, Danon disease, or Geleophysic dysplasia. Lysosomal storage disorders are reviewed in, e.g., Wilcox (2004) J. Pediatr 144:S3-S14.

In some embodiments, the disorder characterized by impaired protein trafficking is characterized by an impaired delivery of cargo to a cellular compartment.

In some embodiments, the disorder characterized by impaired protein trafficking is characterized by a Rab27a mutation or a deficiency of Rab27a. The disorder can be, e.g., Griscelli syndrome.

In some embodiments, the disorder characterized by impaired protein trafficking is cystic fibrosis.

In some embodiments, the disorder characterized by impaired protein trafficking is diabetes (e.g., diabetes mellitus).

In some embodiments, the disorder characterized by impaired protein trafficking is hereditary emphysema, hereditary hemochromatosis, oculocutaneous albinism, protein C deficiency, type I hereditary angioedema, congenital sucrase-isomaltase deficiency, Crigler-Najjar type II, Laron syndrome, hereditary Myeloperoxidase, primary hypothyroidism, congenital long QT syndrome, tyroxine binding globulin deficiency, familial hypercholesterolemia, familial chylomicronemia, abeta-lipoproteinemia, low plasma lipoprotein a levels, hereditary emphysema with liver injury, congenital hypothyroidism, osteogenesis imperfecta, hereditary hypofibrinogenemia, alpha-1 antitrypsin deficiency, nephrogenic diabetes insipidus, neurohypophysial diabetes, insipidus, Charcot-Marie-Tooth syndrome, Pelizaeus Merzbacher disease, von Willebrand disease type IIA, combined factors V and VIII deficiency, spondyloepiphyseal dysplasia tarda, choroideremia, I cell disease, Batten disease, ataxia telangiectasia, acute lymphoblastic leukemia, acute myeloid leukemia, myeloid leukemia, ADPKD-autosomal dominant polycystic kidney disease, microvillus inclusion disease, tuberous sclerosis, oculocerebro-renal syndrome of Lowe, amyotrophic lateral sclerosis, myelodysplastic syndrome, Bare lymphocyte syndrome, Tangier disease, familial intrahepatic cholestasis, X-linked adrenoleukodystrophy, Scott syndrome, Hermansky-Pudlak syndrome types 1 and 2, Zellweger syndrome, rhizomelic chondrodysplasia punctata, autosomal recessive primary hyperoxaluria, Mohr Tranebjaerg

syndrome, spinal and bullar muscular atrophy, primary ciliary diskenesia (Kartagener's syndrome), Miller Dieker syndrome, lissencephaly, motor neuron disease, Usher's syndrome, Wiskott-Aldrich syndrome, Optiz syndrome, Huntington's disease, hereditary pancreatitis, anti-phospholipid syndrome, overlap connective tissue disease, Sjogren's syndrome, stiff-man syndrome, Brugada syndrome, congenital nephritic syndrome of the Finnish type, Dubin-Johnson syndrome, X-linked hypophosphatemia, Pendred syndrome, persistent hyperinsulinemic hypoglycemia of infancy, hereditary spherocytosis, aceruloplasminemia, infantile neuronal ceroid lipofuscinosis, pseudoachondroplasia and multiple epiphyseal, Stargardt-like macular dystrophy, X-linked Charcot-Marie-Tooth disease, autosomal dominant retinitis pigmentosa, Wolcott-Rallison syndrome, Cushing's disease, limb-girdle muscular dystrophy, mucopolysaccharidosis type IV, hereditary familial amyloidosis of Finish, Anderson disease, sarcoma, chronic myelomonocytic leukemia, cardiomyopathy, faciogenital dysplasia, Torsion disease, Huntington and spinocerebellar ataxias, hereditary hyperhomocysteinemia, polyneuropathy, lower motor neuron disease, pigmented retinitis, seronegative polyarthritis, interstitial pulmonary fibrosis, Raynaud's phenomenon, Wegner's granulomatosis, preteinuria, CDG-Ia, CDG-Ib, CDG-Ic, CDG-Id, CDG-Ie, CDG-If, CDG-IIa, CDG-IIb, CDG-IIc, CDG-IId, Ehlers-Danlos syndrome, multiple exostoses, Griscelli syndrome (type 1 or type 2), or X-linked non-specific mental retardation. Disorders characterized by impaired protein trafficking are reviewed in Aridor et al. (2000) *Traffic* 1:836-51 and Aridor et al. (2002) *Traffic* 3:781-90.

In one embodiment, the subject IRE-1 agonists can be used to activate XBP-1 in a cell expressing an endogenous protein to thereby increase production of properly folded protein molecules. In one embodiment, the agonists can be used to activate XBP-1 in a cell expressing an exogenous protein (e.g., one that has been transfected into the cell) to thereby increase production of a commercially valuable properly folded protein molecule. The protein molecule can be obtained by culture of the cell *in vitro* and recovery of the protein molecule from the medium or from the cells.

XBP-1 also plays a key role in TLR-mediated signaling in cells of the innate immune system. Accordingly, in one embodiment, the invention features methods for enhancing the TLR-mediated activation of cells of the innate immune system or of enhancing an innate immune response in a subject.

The claimed methods are not meant to include naturally occurring events. For example, the step of contacting includes administering the modulator in a treatment protocol and, in one embodiment the term "agent" or "modulator" is not meant to embrace endogenous mediators produced by the cells of a subject.

The methods can be practiced either *in vitro* or *in vivo*. For practicing the method *in vitro*, cells can be obtained from a subject by standard methods and incubated

(i.e., cultured) *in vitro* with an agent that binds directly to IRE-1 and, optionally a TLR agonist. Methods for isolating immune cells are known in the art.

Cells treated *in vitro* can be administered to a subject. For administration of cells to a subject, it may be preferable to first remove residual compounds in the culture from
5 the cells before administering them to the subject. This can be done for example by gradient centrifugation of the cells or by washing.

In one embodiment, the cell is a mammalian cell. In another embodiment, the cell is a human cell.

The term "subject" is intended to include living organisms but preferred subjects
10 are mammals. Examples of subjects include mammals such as, e.g., humans, monkeys, dogs, cats, mice, rats cows, horses, goats, and sheep.

In one embodiment, the subject does not have HIV and is not undergoing therapy with HIV protease inhibitors to reduce retroviral proliferation.

15 Vaccination

In one embodiment, agents that bind to and directly activate IRE-1 can be used as part of a vaccine. As used herein, "vaccine" means an organism or material that contains an antigen in an innocuous form. The vaccine is designed to trigger an immunoprotective response. The vaccine may be recombinant or non-recombinant.
20 When inoculated into a non-immune host, the vaccine will provoke active immunity to the organism or material, but will not cause disease. Vaccines may take the form, for example, of a toxoid, which is defined as a toxin that has been detoxified but that still retains its major immunogenic determinants; or a killed organism, such as typhoid, cholera and poliomyelitis; or attenuated organisms, that are the live, but non-virulent,
25 forms of pathogens, or it may be antigen encoded by such organism, or it may be a live tumor cell or an antigen present on a tumor cell. Vaccines may also take the form, for example, of nucleic acid which, when administered to a subject, specifies an antigenic determinant to which an immune response is desired.

In one embodiment, the invention provides for the use of an effective amount of
30 an agent that directly binds to and activates IRE-1 (e.g., an HIV protease inhibitor) to increase XBP-1 activation in cells. In one embodiment, the agent increases the activation of immune cells or the production of proteins (e.g., cytokines or antibodies) by immune cells, e.g., B cells or macrophages. In one embodiment, the agent is administered in combination with an antigen. In yet another embodiment, such an agent
35 is administered with a TLR agonist. In yet another embodiment, the agent is administered with an antigen and a TLR agonist. As a vaccine adjuvant, IRE-1 activating agents (with or without TLR agonists) improve the activation of the immune

system (e.g., the innate immune system and/or the acquired immune system) and result, e.g., in enhanced activation of T and/or B cells as well as macrophages.

5

Natural infection

In one embodiment, the invention provides for the use of an effective amount of an agent that directly binds to and activates IRE-1 (e.g., an HIV protease inhibitor) to increase the activation of immune cells, e.g., macrophages and/or B cells in the context of an infection. In one embodiment, such an agent is administered with a TLR agonist to a subject having an infection. As an agent for use in treating infection, IRE-1 activating agents (with or without TLR agonists) improve the activation of the immune cells and result, e.g., in enhanced clearance of and/or response to the infectious agent. Exemplary infectious agents include viruses (other than HIV), bacteria, and parasites.

Cancer

In one embodiment, the subject agents that bind to and activate IRE-1 can be used to improve the immune response to cancer cells. For example, in one embodiment, agents that activate IRE-1 can be administered to a subject to increase immune responses to cancer cells or molecules associated with cancer cells. Such agents may be administered with or without a TLR agonist or with or without a cancer antigen or with or without a cancer antigen and a TLR agonist.

Cancer antigens include antigens or antigenic determinant which is present on (or associated with) a tumor cell and not typically on normal cells, or an antigen or antigenic determinant which is present on or associated with tumor cells in greater amounts than on normal (non-tumor) cells, or an antigen or antigenic determinant which is present on tumor cells in a different form than that found on normal (non-tumor) cells. Such antigens include tumor-specific antigens, including tumor-specific membrane antigens, tumor-associated antigens, including tumor-associated membrane antigens, embryonic antigens on tumors, growth factor receptors, growth factor ligands, and any other type of antigen that is associated with cancer. A tumor antigen may be, for example, an epithelial cancer antigen, (e.g., breast, gastrointestinal, lung), a prostate specific cancer antigen (PSA) or prostate specific membrane antigen (PSMA), a bladder cancer antigen, a lung (e.g., small cell lung) cancer antigen, a colon cancer antigen, an ovarian cancer antigen, a brain cancer antigen, a gastric cancer antigen, a renal cell carcinoma antigen, a

pancreatic cancer antigen, a liver cancer antigen, an esophageal cancer antigen, a head and neck cancer antigen, or a colorectal cancer antigen. For example, the antigen may include a tumor antigen, such as β hCG, gp100 or Pmel17, CEA, gp100, TRP-2, NY-BR-1, NY-CO-58, MN (gp250), idiotype, Tyrosinase, Telomerase, SSX2, MUC-1, 5 MAGE-A3, and high molecular weight-melanoma associated antigen (HMW-MAA) MART1, melan-A, NY-ESO-1, MAGE-1, MAGE-3, WT1, Her2, mesothelin or high molecular weight-melanoma associated antigen (HMW-MAA). In another embodiment, a tumor antigen may be a composition which comprises a number of such molecules, e.g., in unpurified form or may be administered in the form of tumor cells or extract 10 thereof.

III. Pharmaceutical Compositions

15

In one embodiment, agents that directly bind to IRE-1 (e.g., with or without a TLR agonist or with or without an antigen) can be administered to a subject as a pharmaceutical composition. In another embodiment, such an agent can be formulated with an acceptable carrier to be compatible with mammalian cells for use in vitro. 20 Pharmaceutically acceptable carriers and methods of administration to a subject are described herein.

A pharmaceutical composition is formulated to be compatible with its intended route of administration. For example, solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile 25 diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial compounds such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating compounds such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and compounds for the adjustment of tonicity such as 30 sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the 35 extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition will preferably be sterile and should be fluid to the extent that

easy syringability exists. It will preferably be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, 5 propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal compounds, for example, parabens, 10 chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic compounds, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an compound which delays absorption, for example, aluminum monostearate and gelatin.

15 Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those 20 enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They 25 can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically 30 compatible binding compounds, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating compound such as alginic acid, Primogel, or corn starch; a 35 lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening compound such as sucrose or saccharin; or a flavoring compound such as peppermint, methyl salicylate, or orange flavoring.

In one embodiment, preparations comprising carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems are used. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, 5 polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from, *e.g.*, Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected 10 cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

15

V. Methods of Identifying Agents

Screening Methods

In one embodiment, the invention provides methods (also referred to herein as 20 "screening assays") for identifying agents that enhance the innate immune response. In one embodiment, such methods comprise,

- a) providing an immune cell comprising an IRE-1 and an XBP-1 polypeptide;
- b) contacting the immune cell with each member of a library of compounds;
- c) determining the ability of the compound to directly bind to IRE-1 and activate 25 XBP-1 in the absence of activation of PERK or ATF6,
- d) the effect of the compound on at least one parameter of activation of the immune cell;
- e) selecting a compound of interest that increases at least one parameter of activation of the immune cell to thereby identify the compound as useful in enhancing 30 the innate immune response. In one embodiment, compounds are selected based on their ability to synergize with a TLR agonist in the activation of immune cells

In one embodiment a cell that naturally expresses or, more preferably, a cell that has been engineered to express the IRE-1 protein by introducing into the cell an 35 expression vector encoding the protein is used. Preferably, the cell is a mammalian cell, *e.g.*, a human cell. In another embodiment, the cell is a cell of the innate immune system, *e.g.*, a hematopoietic cell. In one embodiment, the cell is a macrophage or a dendritic cell. In one embodiment, the cell is under ER stress. In another embodiment,

the cell is stimulated with a TLR agonist, *e.g.*, lipopolysaccharide (LPS), lipoteichoic acid, PAM3CSK4, and FSL1.

Compounds identified in the assays described herein are useful in modulating IRE-1 activity, and thereby modulating XBP-1 activity, in cells comprising IRE-1 and
5 XBP-1. XBP-1 has been shown to play a role in numerous cell types.

In one embodiment, compounds identified the assays described herein are useful for modulating activation in cells of the innate immune system.

The subject screening assays can be performed in the presence or absence of other agents. In one embodiment, the subject assays are performed in the presence of an
10 agent that affects the unfolded protein response, *e.g.*, tunicamycin, which evokes the UPR by inhibiting N-glycosylation, or thapsigargin, or HIV protease inhibitors. In another embodiment, the subject assays are performed in the presence of an agent that inhibits degradation of proteins by the ubiquitin-proteasome pathway (*e.g.*, peptide aldehydes, such as MG132). In another embodiment, the screening assays can be
15 performed in the presence or absence of a molecule that enhances cell activation.

A modulating agent can be identified using an assay, and the ability of the agent to modulate the activity of XBP-1 or a molecule in a signal transduction pathway involving XBP-1 can be confirmed *in vivo*, *e.g.*, in an animal model for immune cell activation or inflammation.

In another embodiment, modulation of the UPR or ER stress can also be determined and used as an indicator of modulation of XBP-1 and/or IRE-1 activity. Transcription of genes encoding molecular chaperones and folding enzymes in the endoplasmic reticulum (ER) is induced by accumulation of unfolded proteins in the ER. This intracellular signaling, known as the unfolded protein response (UPR), is mediated
25 by the cis-acting ER stress response element (ERSE) or unfolded protein response element (UPRE) in mammals.

The activation of the kinase PERK can also be measured to determine whether an agent modulates ER stress by measuring the induction of CHOP. The processing of ATF6 alpha can also be measured to determine whether an agent modulates ER stress.
30 The basic leucine zipper protein ATF6 alpha isolated as a CCACG-binding protein is synthesized as a transmembrane protein in the ER, and ER stress-induced proteolysis produces a soluble form of ATF6 alpha that translocates into the nucleus.

In one embodiment, compounds that modulate TLR-mediated signaling and do not activate ER stress and/or the UPR are identified. In another embodiment,
35 compounds that modulate TLR-mediated signaling and do activate ER stress and/or the UPR are identified.

In one embodiment, the ability of a compound to modulate proinflammatory cytokine production, *e.g.*, IL-6, IFN β , ISG15, can be determined. Production of

proinflammatory cytokine can be monitored, for example, using RT-PCR, Northern or Western blotting. Proinflammatory cytokine can also be detected using an ELISA assay or in a bioassay, *e.g.*, employing cells which are responsive to proinflammatory cytokine (*e.g.*, cells which proliferate in response to the cytokine or which survive in the presence of the cytokine), such as plasma cells or multiple myeloma cells using standard techniques.

In one embodiment, the effect of a test compound on sustained production of a proinflammatory cytokine may be determined. For example, the production of a proinflammatory cytokine may be determined at multiple time points, *e.g.*, a time course assay, *e.g.*, at about 0, 0.5, 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 10.5, 11, 11.5, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 hours, following exposure to a test compound.

The techniques for assessing the ratios of unspliced to spliced XBP-1 and spliced to unspliced XBP-1 are routine in the art. For example, the two forms can be distinguished based on their size, *e.g.*, using northern blots or western blots. Because the spliced form of XBP-1 comprises an exon not found in the unspliced form, in another embodiment, antibodies that specifically recognize the spliced or unspliced form of XBP-1 can be developed using techniques well known in the art (Yoshida *et al.* 2001. *Cell*. 107:881). In addition, PCR can be used to distinguish spliced from unspliced XBP-1. For example, as described herein, primer sets can be used to amplify XBP-1 where the primers are derived from positions 410 and 580 of murine XBP-1, or corresponding positions in related XBP-1 molecules, in order to amplify the region that encompasses the splice junction. A fragment of 171 base pairs corresponds to unspliced XBP-1 mRNA. An additional band of 145 bp corresponds to the spliced form of XBP-1. The ratio of the different forms of XBP-1 can be determined using these or other art recognized methods.

Compounds that alter the ratio of unspliced to spliced XBP-1 or spliced to unspliced XBP-1 can be useful to modulate TLR-mediated signaling and/or the activity of XBP-1, and the levels of these different forms of XBP-1 can be measured using various techniques described above, or known in the art, and a ratio determined.

The cells of the invention can express endogenous XBP-1 and/or IRE-1, or can be engineered to do so. For example, a cell that has been engineered to express the XBP-1 protein and/or a non XBP-1 protein can be produced by introducing into the cell an expression vector encoding the protein.

A variety of test compounds can be evaluated using the screening assays described herein. The term "test compound" includes any reagent or test agent which is employed in the assays of the invention and assayed for its ability to influence the expression and/or activity of XBP-1 and/or IRE-1. More than one compound, *e.g.*, a

plurality of compounds, can be tested at the same time for their ability to modulate the expression and/or activity of, *e.g.*, XBP-1, in a screening assay. The term "screening assay" preferably refers to assays which test the ability of a plurality of compounds to influence the readout of choice rather than to tests which test the ability of one

5 compound to influence a readout. Preferably, the subject assays identify compounds not previously known to have the effect that is being screened for. In one embodiment, high throughput screening can be used to assay for the activity of a compound.

In certain embodiments, the compounds to be tested can be derived from libraries (*i.e.*, are members of a library of compounds). While the use of libraries of peptides is well established in the art, new techniques have been developed which have allowed the production of mixtures of other compounds, such as benzodiazepines (Bunin *et al.* (1992). *J. Am. Chem. Soc.* 114:10987; DeWitt *et al.* (1993). *Proc. Natl. Acad. Sci. USA* 90:6909) peptoids (Zuckermann. (1994). *J. Med. Chem.* 37:2678) oligocarbamates (Cho *et al.* (1993). *Science.* 261:1303), and hydantoins (DeWitt *et al. supra*). An approach for the synthesis of molecular libraries of small organic molecules with a diversity of 10⁴-10⁵ as been described (Carell *et al.* (1994). *Angew. Chem. Int. Ed. Engl.* 33:2059- ; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061-).

The compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries, synthetic library methods requiring deconvolution, the 'one-bead one-compound' library method, and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S. (1997) *Anticancer Drug Des.* 12:145). Other exemplary methods for the synthesis of molecular libraries can be found in the art, for example in: Erb *et al.* (1994). *Proc. Natl. Acad. Sci. USA* 91:11422; Horwell *et al.* (1996) *Immunopharmacology* 33:68- ; and in Gallop *et al.* (1994); *J. Med. Chem.* 37:1233-.

Libraries of compounds can be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner USP 5,223,409), spores (Ladner USP '409), plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and Smith (1990) *Science* 249:386-390); (Devlin (1990) *Science* 249:404-406); (Cwirlla *et al.* (1990) *Proc. Natl. Acad. Sci.* 87:6378-6382); (Felici (1991) *J. Mol. Biol.* 222:301-310). In still another embodiment, the combinatorial polypeptides are produced from a cDNA library.

Exemplary compounds which can be screened for activity include, but are not limited to, peptides, nucleic acids, carbohydrates, small organic molecules, and natural product extract libraries.

Candidate/test compounds include, for example, 1) peptides such as soluble
5 peptides, including Ig-tailed fusion peptides and members of random peptide libraries
(see, *e.g.*, Lam, K.S. *et al.* (1991) *Nature* 354:82-84; Houghten, R. *et al.* (1991) *Nature*
354:84-86) and combinatorial chemistry-derived molecular libraries made of D- and/or
L- configuration amino acids; 2) phosphopeptides (*e.g.*, members of random and
partially degenerate, directed phosphopeptide libraries, see, *e.g.*, Songyang, Z. *et al.*
10 (1993) *Cell* 72:767-778); 3) antibodies (*e.g.*, polyclonal, monoclonal, humanized, anti-
idiotypic, chimeric, and single chain antibodies as well as Fab, F(ab')₂, Fab expression
library fragments, and epitope-binding fragments of antibodies); 4) small organic and
inorganic molecules (*e.g.*, molecules obtained from combinatorial and natural product
libraries); 5) enzymes (*e.g.*, endoribonucleases, hydrolases, nucleases, proteases,
15 synthetases, isomerases, polymerases, kinases, phosphatases, oxido-reductases and
ATPases), and 6) mutant forms of XBP-1 (or *e.g.*, IRE-1 molecules, *e.g.*, dominant
negative mutant forms of the molecules).

The test compounds of the present invention can be obtained using any of the
numerous approaches in combinatorial library methods known in the art, including:
20 biological libraries; spatially addressable parallel solid phase or solution phase libraries;
synthetic library methods requiring deconvolution; the 'one-bead one-compound' library
method; and synthetic library methods using affinity chromatography selection. The
biological library approach is limited to peptide libraries, while the other four
approaches are applicable to peptide, non-peptide oligomer or small molecule libraries
25 of compounds (Lam, K.S. (1997) *Anticancer Drug Des.* 12:145).

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30 *Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and Gallop
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35 '409), plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or phage
(Scott and Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406;
Cwirla *et al.* (1990) *Proc. Natl. Acad. Sci.* 87:6378-6382; Felici (1991) *J. Mol. Biol.*
222:301-310; Ladner *supra.*).

Compounds identified in the subject screening assays can be used in methods of modulating one or more of the biological responses regulated by XBP-1. It will be understood that it may be desirable to formulate such compound(s) as pharmaceutical compositions (described supra) prior to contacting them with cells.

5 Once a test compound is identified that directly or indirectly modulates, *e.g.*, XBP-1 expression or activity, by one of the variety of methods described hereinbefore, the selected test compound (or "compound of interest") can then be further evaluated for its effect on cells, for example by contacting the compound of interest with cells either *in vivo* (*e.g.*, by administering the compound of interest to a subject) or *ex vivo* (*e.g.*, by
10 isolating cells from the subject and contacting the isolated cells with the compound of interest or, alternatively, by contacting the compound of interest with a cell line) and determining the effect of the compound of interest on the cells, as compared to an appropriate control (such as untreated cells or cells treated with a control compound, or carrier, that does not modulate the biological response).

15

Computer Based Design of IRE-1 Inhibitors/HIV Protease Inhibitors

Computer-based analysis of IRE-1 can also be used to identify molecules which bind to the protein or to identify variants of HIV protease inhibitors with improved binding, *e.g.*, with improved binding to IRE-1 and reduced binding to HIV protease or
20 with improved binding to HIV protease and reduced binding to IRE-1.

Molecular modeling may use computers to model the molecular structure of IRE-1 and/or HIV protease and/or HIV protease inhibitors. Non-limiting examples of such methods include molecular graphics (*i.e.*, 3-D representations) to computational chemistry (*i.e.*, calculations of the physical and chemical properties). Using molecular
25 modeling, rational drug design programs can look at a range of molecular structures that may fit into an active site of the enzyme or interact at the interface between the IRE-1 subunits. By using computer programs, for example, a determination can be made as to which compounds actually fit into or bind a given site. U.S. patents that provide additional information on molecular modeling include U.S. Pat. Nos. 6,093,573;
30 6,080,576; 5,612,894; 5,583,973; 5,030,103; 4,906,122; and 4,812,128, each of which is incorporated herein by reference in its entirety. As used in the methods described herein, the term "computer fitting analysis" or "modeling" refers to a schematic or other work that is prepared using a computer algorithms or computer programs that can process and provide information about protein structure and conformation. A number of such
35 programs and algorithms are readily available and known to those of skill in the art. They can configure a protein sequence into a 3-dimensional molecule and additionally configure it with a ligand or other substrate.

For example, using a 3-D database, a program such as DOCK can be used to identify molecules which will bind to XBP-1 or a molecule in a signal transduction pathway involving XBP-1. See DesJarlias et al. (1988) J. Med. Chem. 31:722; Meng et al. (1992) J. Computer Chem. 13:505; Meng et al. (1993) Proteins 17:266; Shoichet et al. (1993) Science 259:1445. In addition, the electronic complementarity of a molecule to a targeted protein can also be analyzed to identify molecules which bind to the target. This can be determined using, for example, a molecular mechanics force field as described in Meng et al. (1992) J. Computer Chem. 13:505 and Meng et al. (1993) Proteins 17:266. Other programs which can be used include CLIX which uses a GRID force field in docking of putative ligands. See Lawrence et al. (1992) Proteins 12:31; Goodford et al. (1985) J. Med. Chem. 28:849; Boobbyer et al. (1989) J. Med. Chem. 32:1083

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patents and published patent applications cited throughout this application are hereby incorporated by reference.

EXAMPLES

20

Example 1. HIV-protease inhibitors (PIs) trigger robust IRE1 and XBP1 activation and synergize with TLR4 activation to produce cytokines and co-stimulatory molecules.

25 XBP1 mRNA maturation (XBP1s) in J774 cells stimulated with dose dependent concentrations of HIV-PIs (similar data were obtained in primary mouse M0s, and various M0 cell lines of human and mouse origin) see Figure 1, panel A. Cell extracts of cells stimulated with Tunicamycin (TM) or HIV-protease inhibitors were monitored for IRE1 activation by phosphorylation in a Phos-tag SDS-PAGE gel, CHOP induction and
30 ATF6a processing, see Figure 1, panel B. . Realtime PCR of CHOP induction by the ER-stress inducer TM and the HIV-PI Nelfinavir (NFR) was analyzed in PERK proficient and deficient MEFs see Figure 1, panel C. J774 cells were stimulated with HIV-PIs or TM as indicated in presence or absence of LPS and analyzed for IL-6 production by rtPCR, see Figure 1, panel D. Increased IL-6 production and co-
35 stimulatory ligand (CD86 and CD40) expression were observed in the presence of Nelfinavir and the synthetic TLR4 agonist MPLA compared to TLR4 agonist alone, see Figure 1, panel E.

Example 2. In vitro fluorescent splicing reporter assay with recombinant IRE1 protein reveals marked induction of xbp1 splicing with ritonavir and nelfinivir but not amprenivir at doses of PIs ranging from 20uM to 0.63uM, see Figure 2. As shown in Figure 3, these PIs also induce XBP-1 splicing in mouse embryonic fibroblasts.

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EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods
15 described herein. Such equivalents are intended to be encompassed by the scope of the following claims.

What is claimed is:

1. A method for increasing activation of XBP-1 in a subject, comprising administering an agent that directly binds to and activates IRE-1 in the subject thereby
5 increasing the activation of XBP-1 in the subject.

2. A method for increasing activation of immune cells in a subject, comprising administering an agent that directly binds to and activates IRE-1 to the subject thereby increasing activation of immune cells in the subject.
10

3. The method of claim 2, wherein the subject is infected with a pathogen that does not express an HIV protease.

4. The method of claim 2, wherein the agent is an HIV protease inhibitor.
15

5. The method of claim 2, wherein the pathogen is selected from the group consisting of a bacterium, a virus, and a parasite.

6. The method of claim 2, wherein the subject has cancer.
20

7. The method of claim 2, further comprising administering the activator and at least one toll-like receptor agonist to the subject.

8. The method of claim 7, wherein the TLR agonist stimulates a TLR selected
25 from the group consisting of: TLR2, TLR4, and TLR5.

9. The method of claim 8, wherein the TLR agonist stimulates TLR4.

10. The method of claim 2, further comprising contacting the immune cells with
30 an antigen to which an immune response is desired.

11. The method of claim 10, wherein the agent is an HIV protease inhibitor.

12. The method of claim 11, further comprising contacting the cells with at least
35 one toll-like receptor (TLR) agonist.

13. The method of claim 12, wherein the agent that stimulates at least one TLR agonist stimulates a TLR selected from the group consisting of: TLR2, TLR4, and TLR5.
- 5 14. The method of claim 13, wherein the TLR is TLR4.
15. The method of claim 4 or 11, wherein production of a proinflammatory cytokine by the immune cells is increased.
- 10 16. The method of claim 15, wherein the proinflammatory cytokine is IL-6.
17. The method of claim 4 or 11, wherein the expression of at least one costimulatory molecule is increased.
- 15 18. The method of claim 17, wherein the expression of CD40 is increased.
19. The method of claim 4 or 11, wherein the immune cells comprise macrophages.
- 20 20. The method of claim 4 or 11, wherein the HIV protease inhibitor is selected from the group consisting of: Atazanavir, Loprenavir, Nelfinavir and Ritonavir.
21. The method of claim 20, wherein the HIV protease inhibitor is Nelfinavir.
- 25 22. The method of claim 4 or 11, wherein the activation of immune cells is increased in vivo.
23. A method for increasing activation of a population of immune cells in vitro, wherein the population of cells comprises macrophages, comprising contacting the cells
30 with an agent that directly binds to and activates IRE-1 thereby increasing activation of immune cells in vitro.
24. The method of claim 23, wherein the agent is an HIV protease inhibitor that binds to and activates IRE-1 such that ER stress is induced in the cells further
35 comprising determining the effects of ER stress on the cells in culture.
25. A method of identifying compounds that enhance the innate immune response comprising,

a) providing an immune cell comprising an IRE-1 polypeptide;
b) contacting the immune cell with each member of a library of compounds;
c) determining the ability of the compound to directly bind to IRE-1 and activate XBP-1 in the absence of activation of PERK or ATF6,

5 d) the effect of the compound on at least one parameter of activation of the immune cell;

e) selecting a compound of interest that increases at least one parameter of activation of the immune cell to thereby identify the compound as useful in enhancing the innate immune response.

10

26. The method of claim 25, wherein the immune cell is selected from the group consisting of a macrophage and a B cell.

15 27. The method of claim 25, wherein the immune cell is present in a mixed population of cells.

28. A method of identifying improved HIV protease inhibitors comprising testing candidate HIV protease inhibitors for their ability to bind to IRE-1, wherein those
20 agents that bind to HIV protease but have reduced ability to bind to IRE-1 are identified as being improved HIV protease inhibitors.

29. The method of claim 28, further comprising altering the candidate HIV protease inhibitor to reduce the ability of the HIV protease inhibitor to bind to IRE-1.

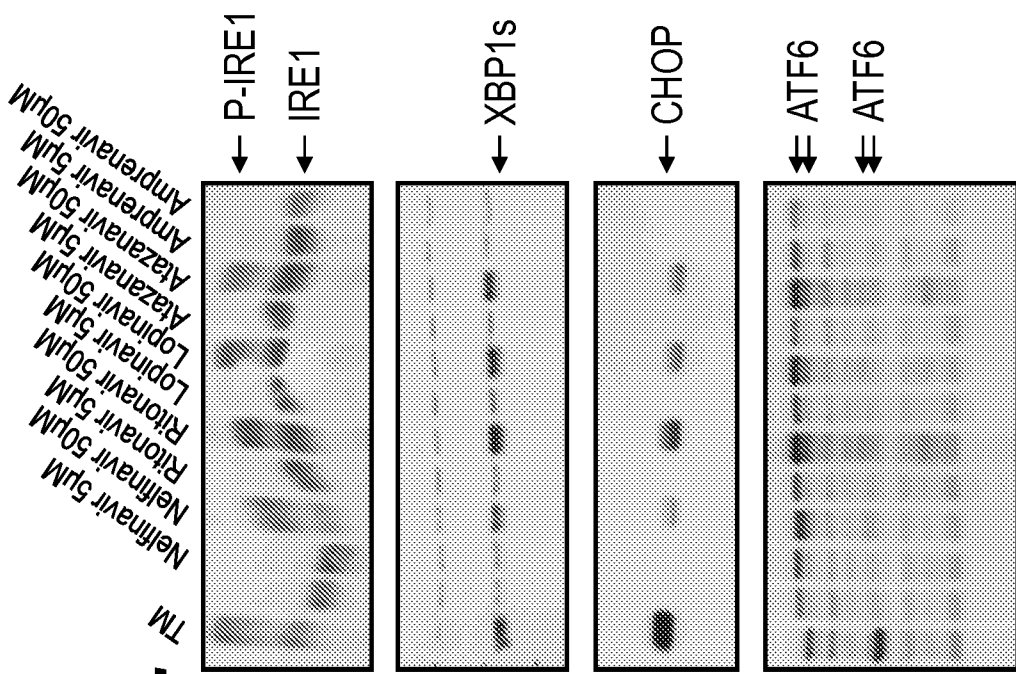
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30. A method of identifying improved IRE-1 inhibitors comprising testing candidate HIV protease inhibitors for their ability to bind to IRE-1, altering the candidate HIV protease inhibitors to increase their binding to IRE-1, to thereby identify improved IRE-1 agonists.

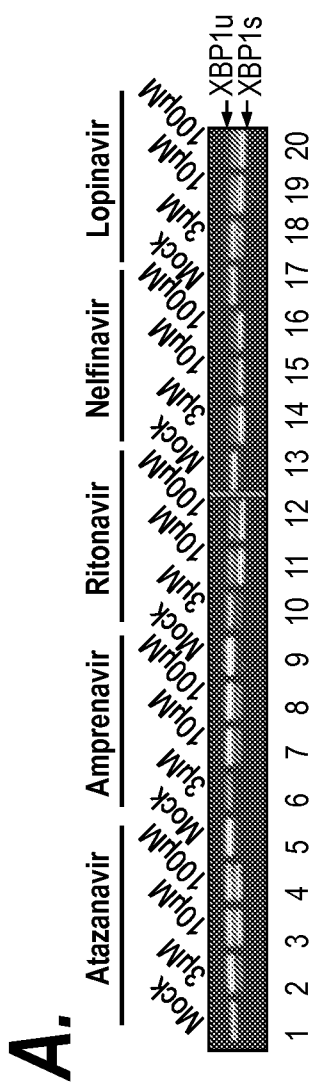
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31. In one embodiment, the invention pertains to a method of identifying improved IRE-1 inhibitors comprising testing candidate HIV protease inhibitors for their ability to bind to IRE-1, altering the candidate HIV protease inhibitors to decrease their binding to IRE-1, to thereby identify improved IRE-1 inhibitors.

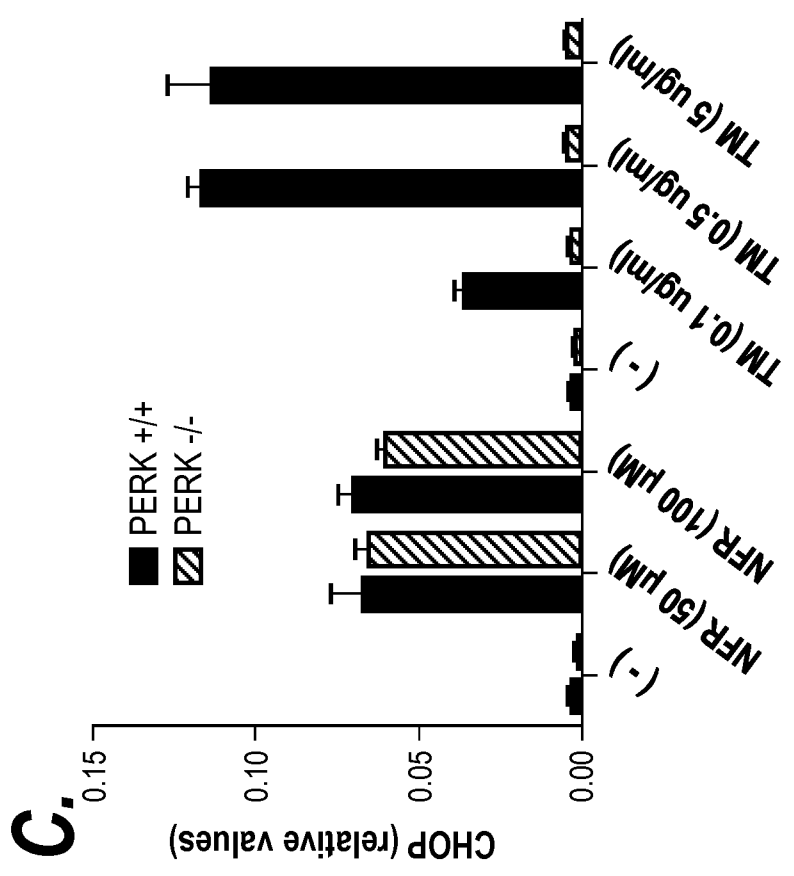
35



B.



A.

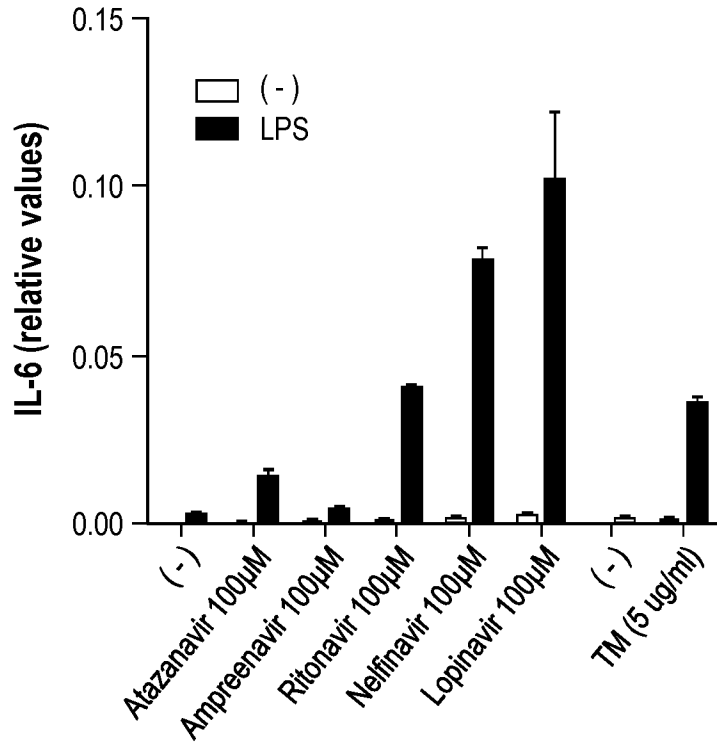


C.

Fig. 1

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D.



E.

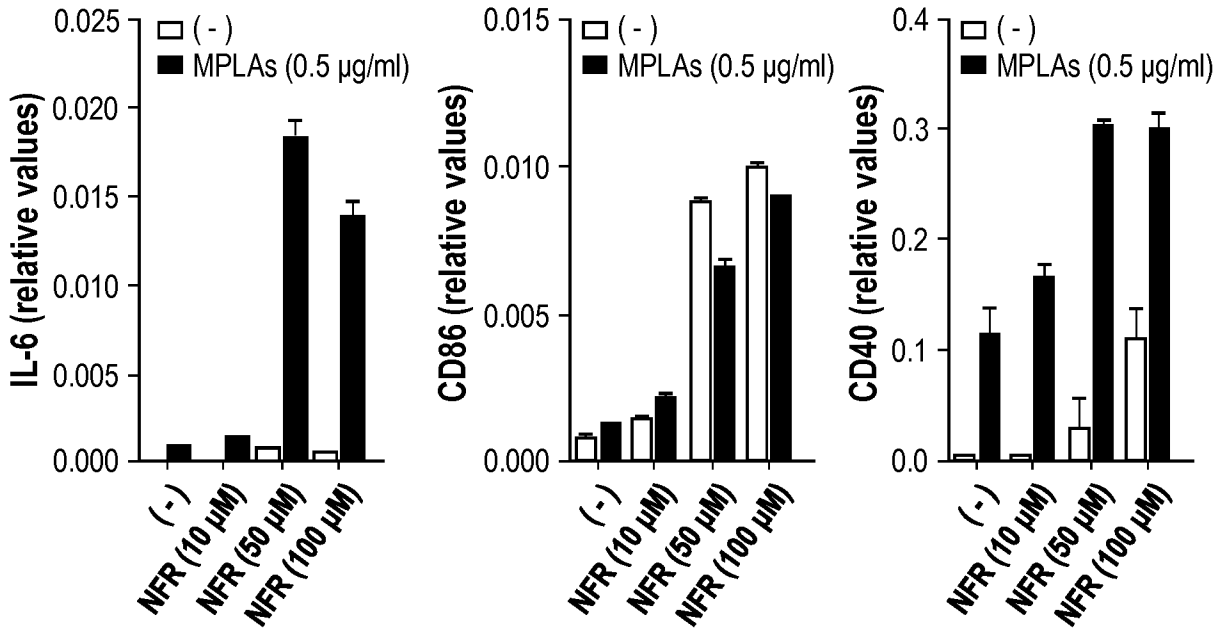
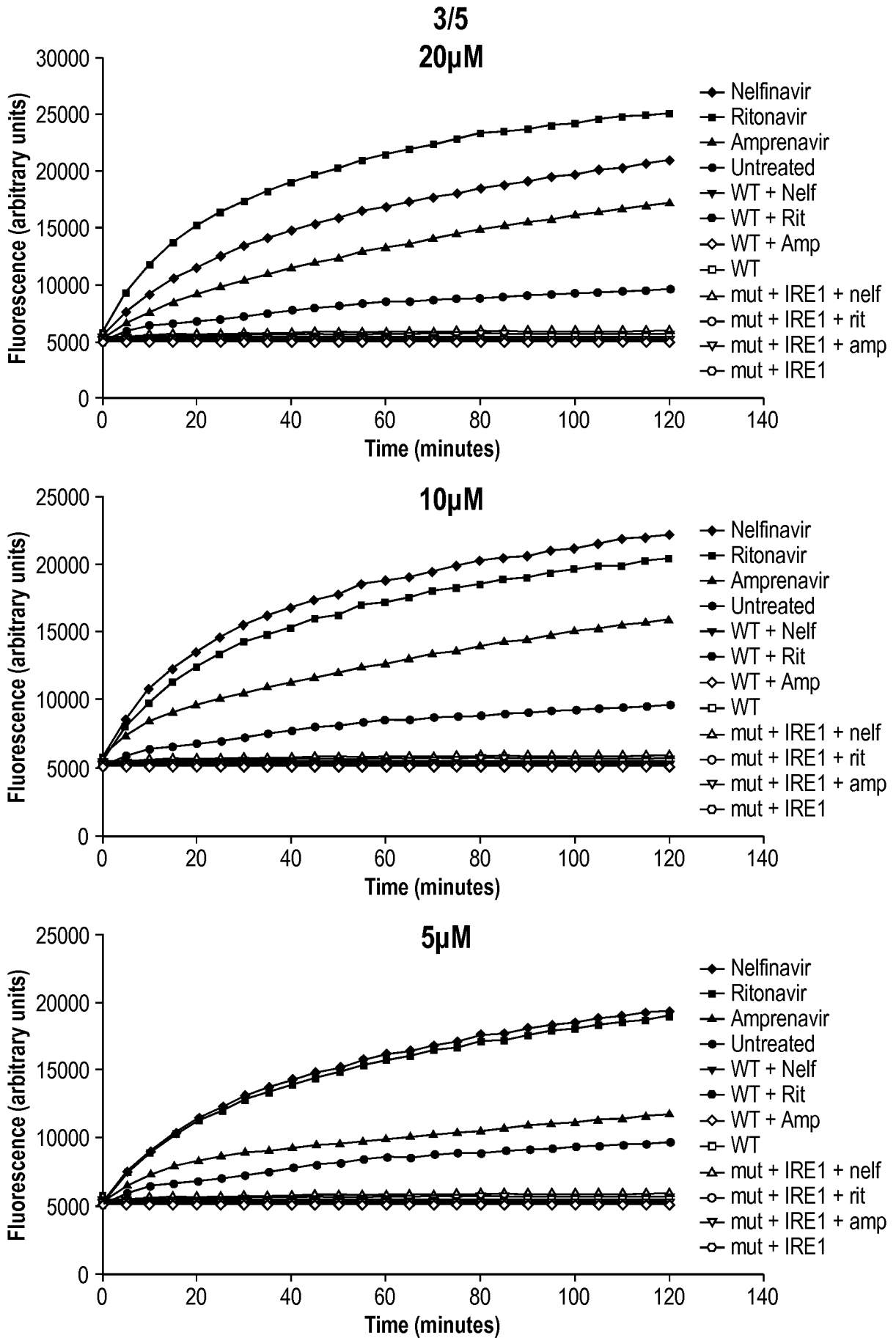


Fig. 1



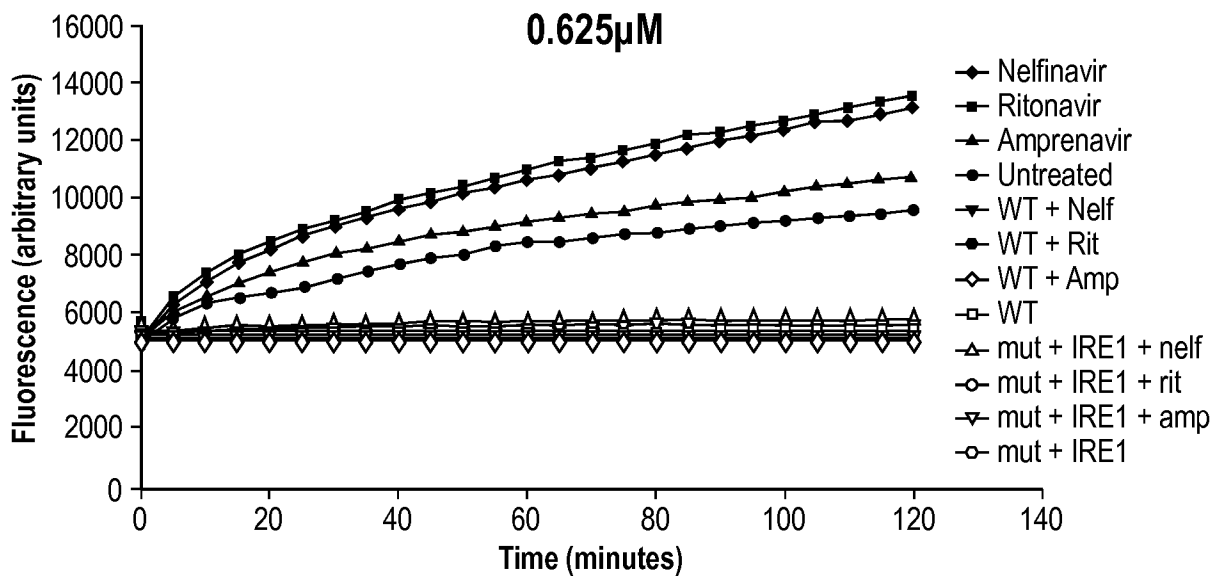
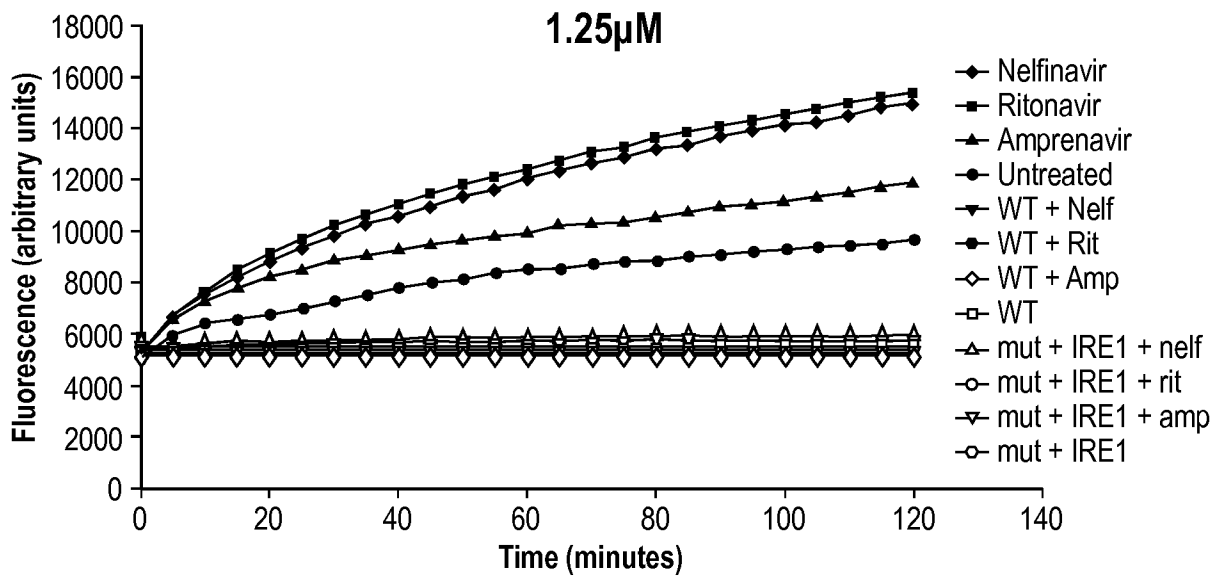
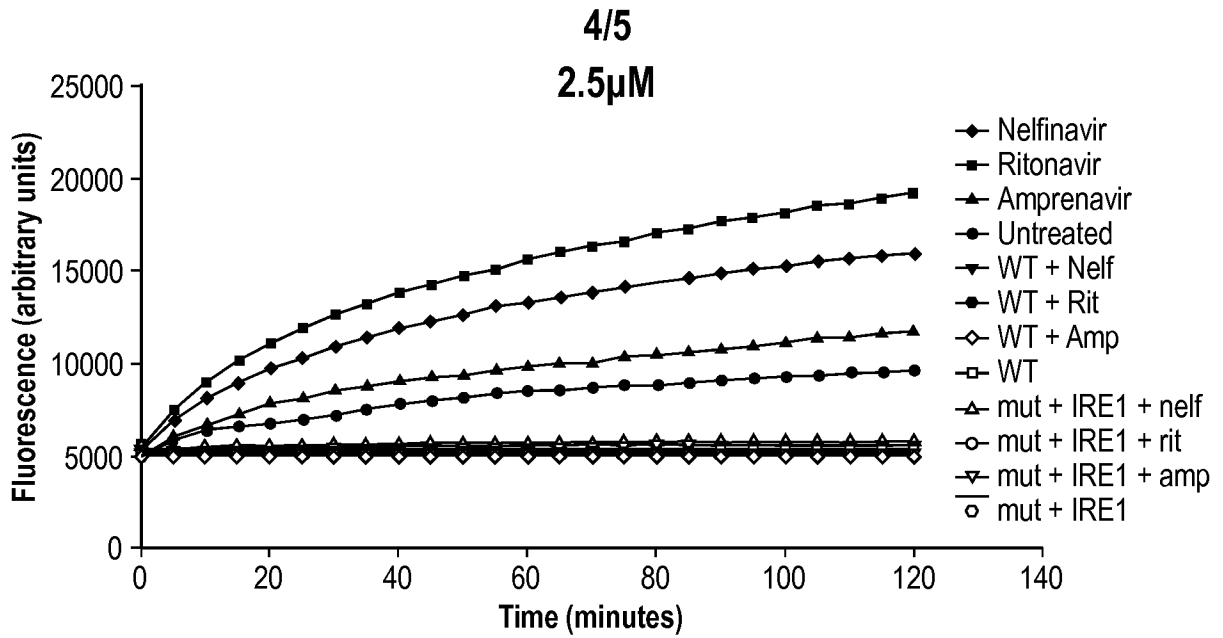


Fig. 2

HIV-PIs trigger XBP1 splicing in MEFs

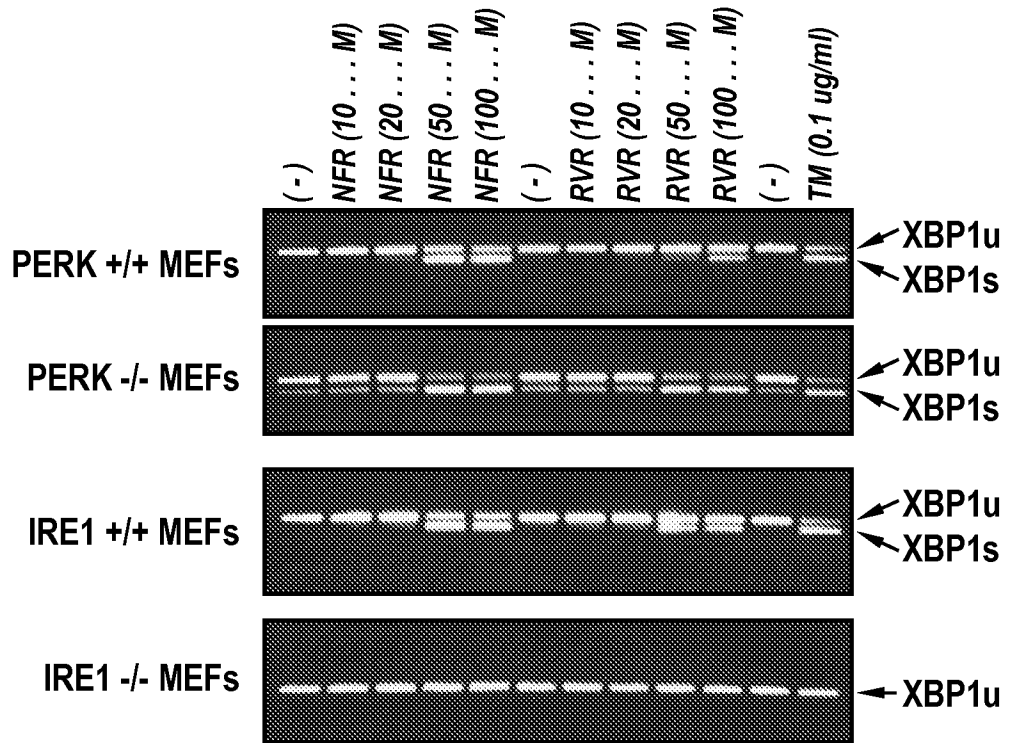


Fig. 3