US 20140045775A1

(19) **United States**

(12) **Patent Application Publication**

Arditi et al.

(10) **Pub. No.: US 2014/0045775 A1**

(43) **Pub. Date: Feb. 13, 2014**

(54) **SHORT-FORM HUMAN MD-2 AS A NEGATIVE REGULATOR OF TOLL-LIKE RECEPTOR 4 SIGNALING**

(71) Applicant: **Cedars-Sinai Medical Center**, Los Angeles, CA (US)

(72) Inventors: **Moshe Arditi**, Encino, CA (US); **Pearl S. Gray**, Los Angeles, CA (US)

(73) Assignee: **CEDARS-SINAI MEDICAL CENTER**, Los Angeles, CA (US)

(21) Appl. No.: **14/010,362**

(22) Filed: **Aug. 26, 2013**

Related U.S. Application Data

(63) Continuation of application No. 13/051,390, filed on Mar. 18, 2011, now Pat. No. 8,546,324, which is a continuation-in-part of application No. PCT/US09/50317, filed on Jul. 10, 2009.

(60) Provisional application No. 61/098,861, filed on Sep. 22, 2008.

Publication Classification

(51) **Int. Cl.**
C07K 14/47 (2006.01)

(52) **U.S. Cl.**
CPC ***C07K 14/47*** (2013.01)
USPC **514/21.2**

(57) **ABSTRACT**

The present invention is based on a novel, alternatively spliced human isoform of MD-2 (MD-2s). In addition, the present invention relates to modified MD-2 proteins, wherein one or more tyrosine residues have been mutated to phenylalanine. In various embodiments, the invention relates to methods and kits for preventing, reducing the likelihood of developing and/or treating various conditions using MD-2s. The invention also describes methods of determining the risk of a subject to various conditions.

FIG. 1A

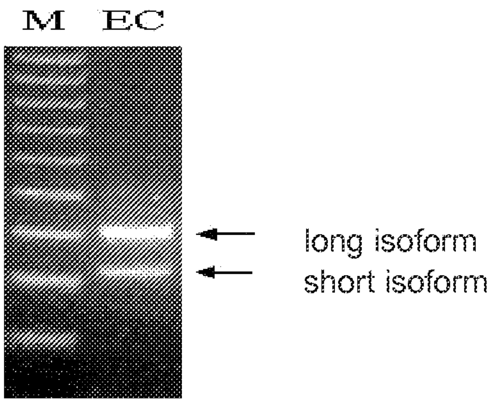


FIG. 1B

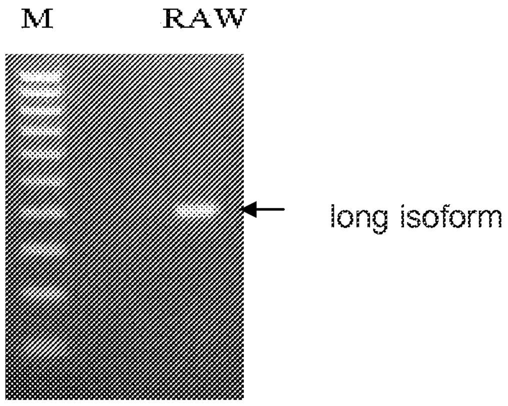


FIG. 1C

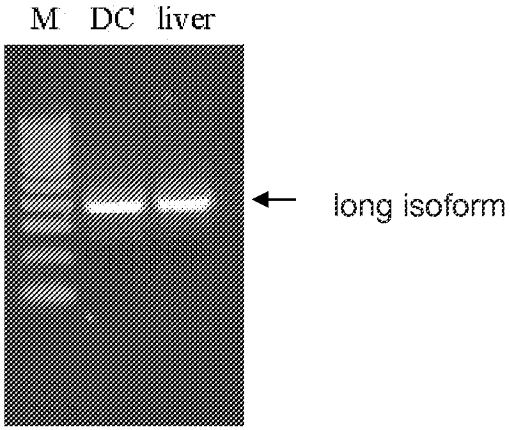
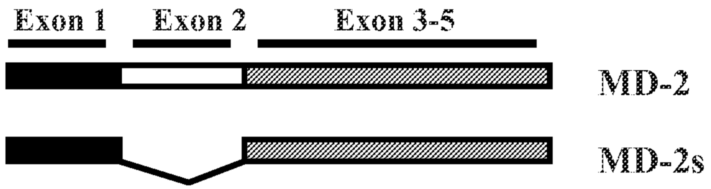


FIG. 1D



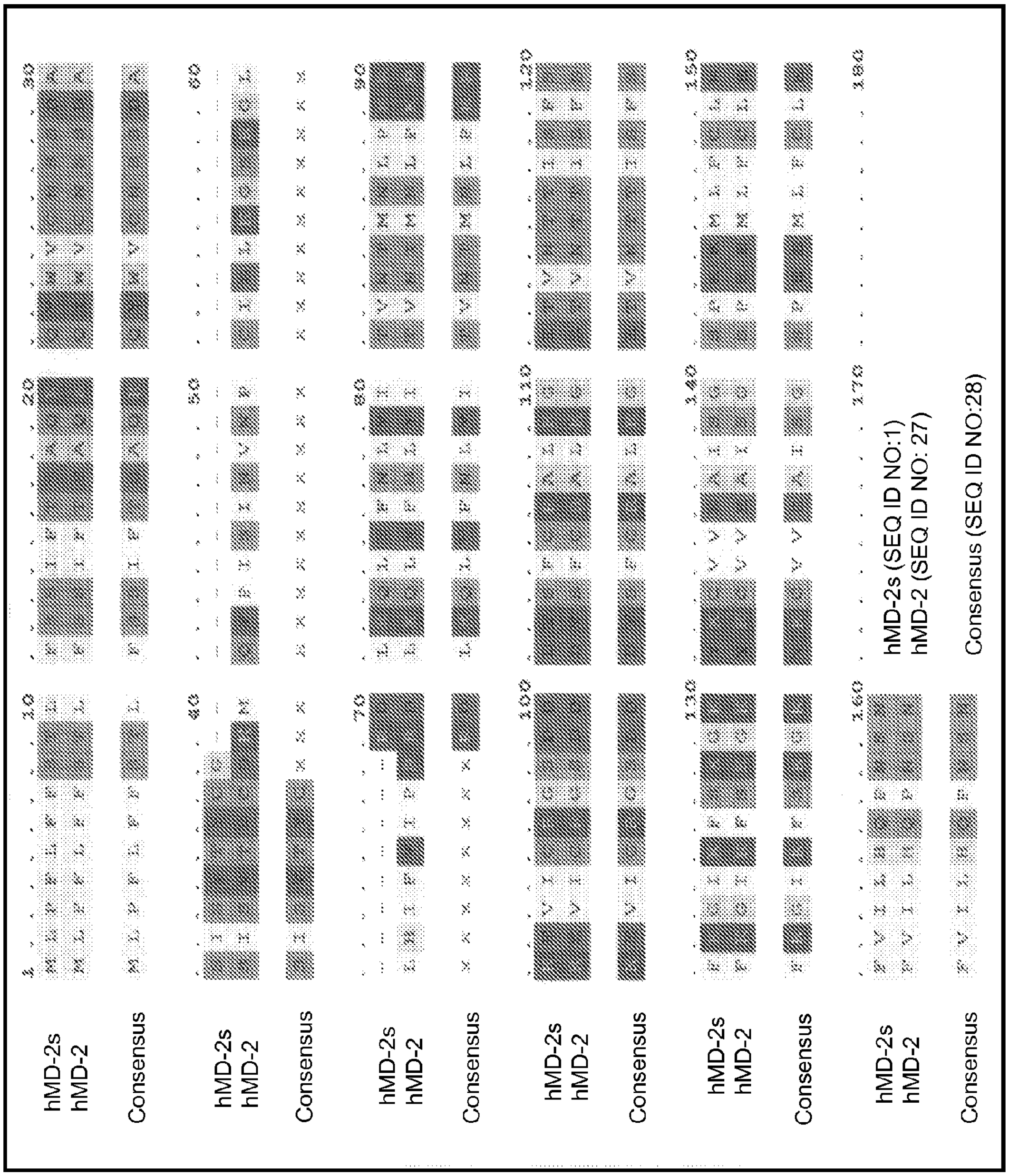

hMD-2s
hMD-2
Consensus
1
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
hMD-2s (SEQ ID NO:1)
hMD-2 (SEQ ID NO: 27)
Consensus (SEQ ID NO:28)

FIG. 1E

FIG. 1F

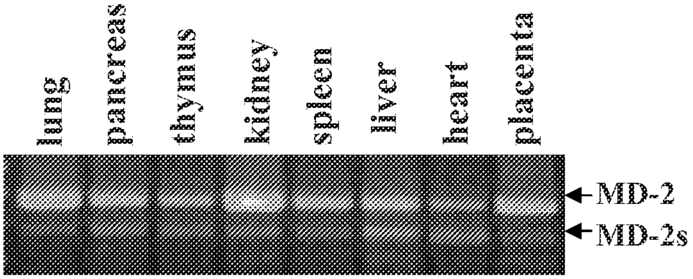

lung
pancreas
thymus
kidney
spleen
liver
heart
placenta
←MD-2
←MD-2s

FIG. 1G

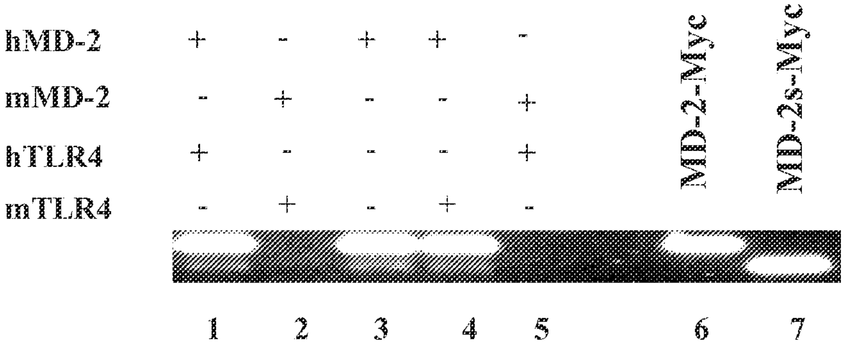

hMD-2 + - + + -
mMD-2 - + - - +
hTLR4 + - - - +
mTLR4 - + - + -
MD-2-Myc
MD-2s-Myc
1
2
3
4
5
6
7

FIG. 2A

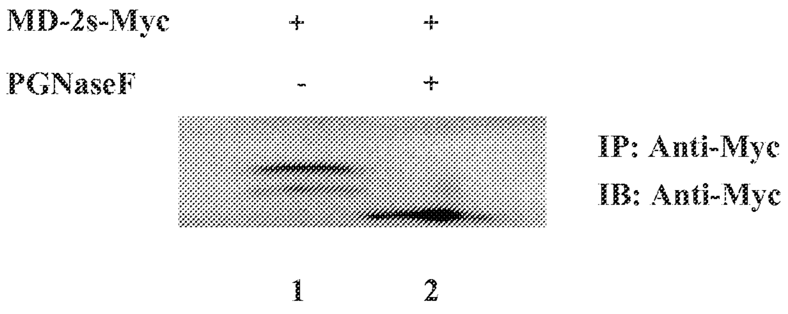

MD-2s-Myc
+
+
PGNaseF
-
+
IP: Anti-Myc
IB: Anti-Myc
1
2

FIG. 2B

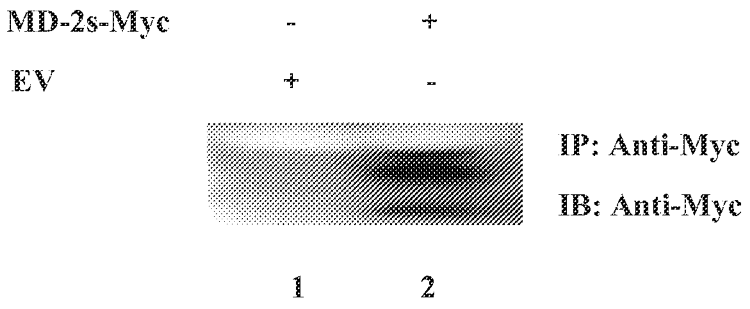

MD-2s-Myc
-
+
EV
+
-
IP: Anti-Myc
IB: Anti-Myc
1
2

FIG. 3B

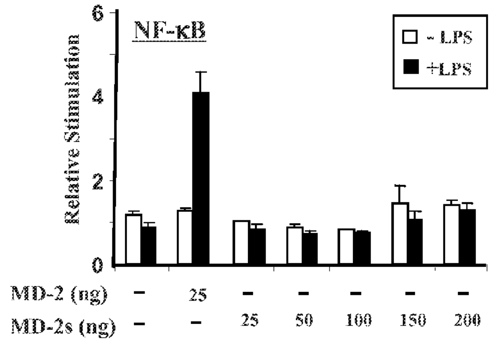


FIG. 3D

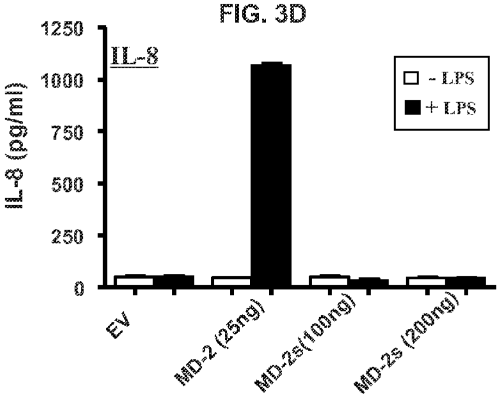


FIG. 3A

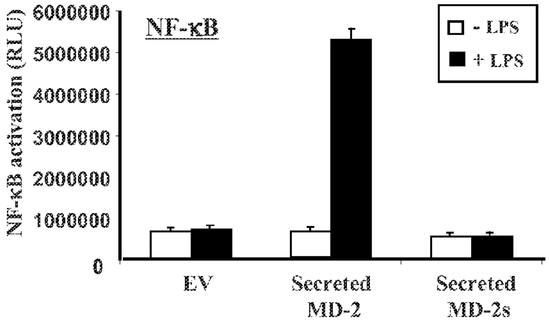


FIG. 3C

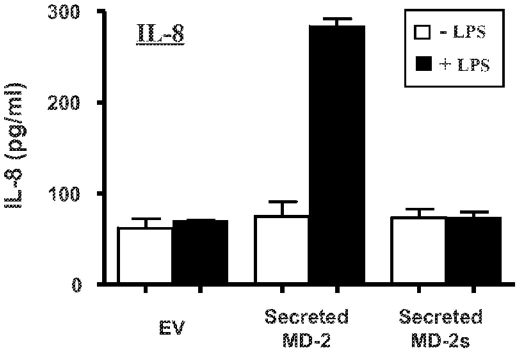


Fig. 4A

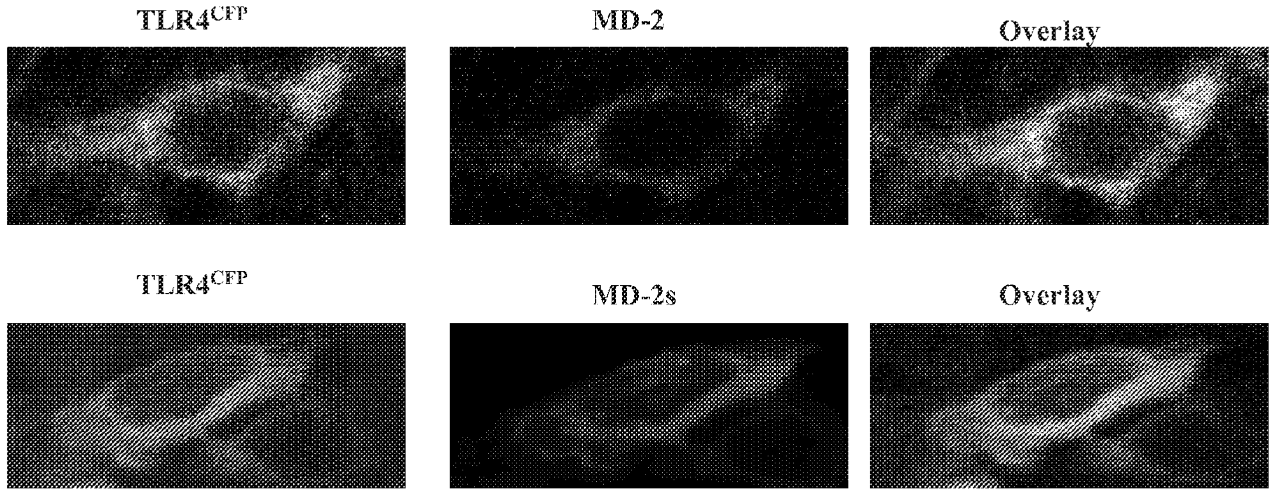

TLR4CFP
MD-2
Overlay
TLR4CFP
MD-2s
Overlay

Fig. 4B

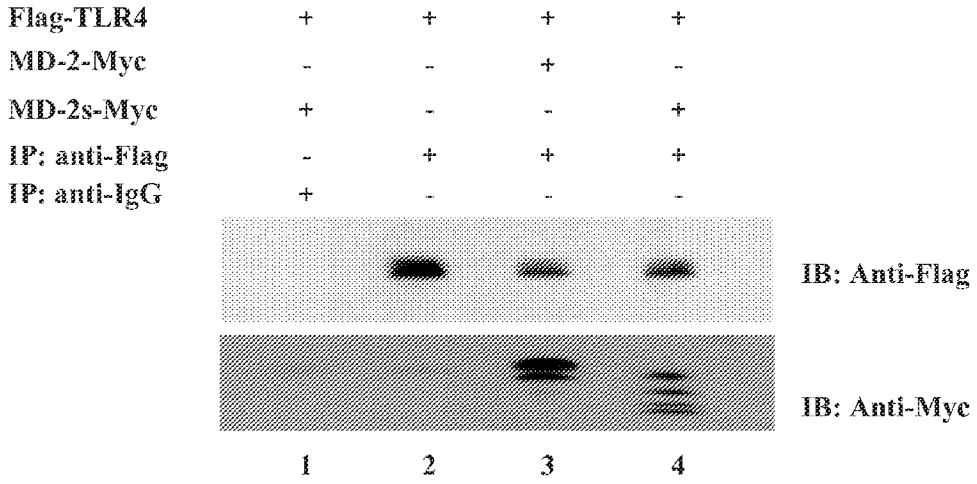

Flag-TLR4 + + + +
MD-2-Myc - - + -
MD-2s-Myc + - - +
IP: anti-Flag - + + +
IP: anti-IgG + - - -
IB: Anti-Flag
IB: Anti-Myc
1
2
3
4

FIG. 5A

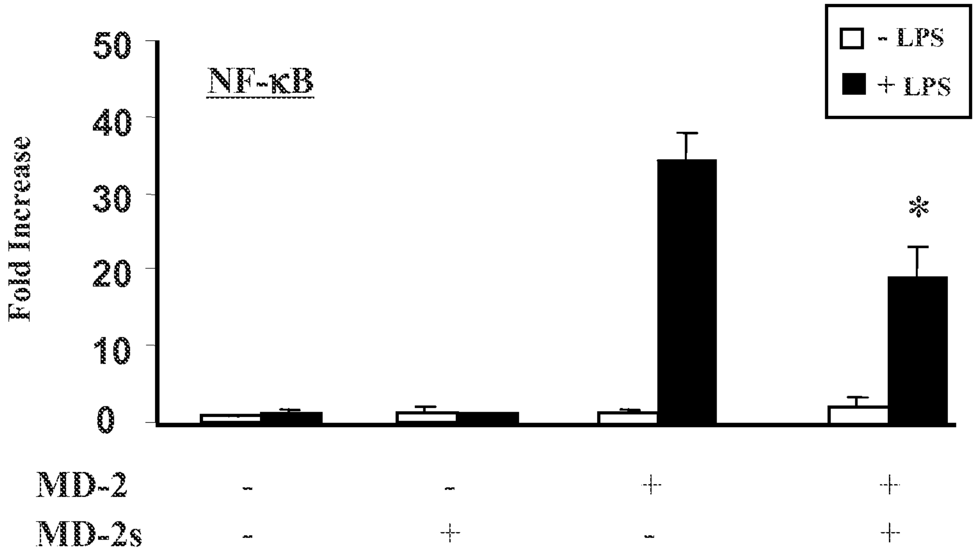

NF-κB
□ - LPS
■ + LPS
Fold Increase
50
40
30
20
10
0
*
MD-2 - - + +
MD-2s - + - +

FIG. 5B

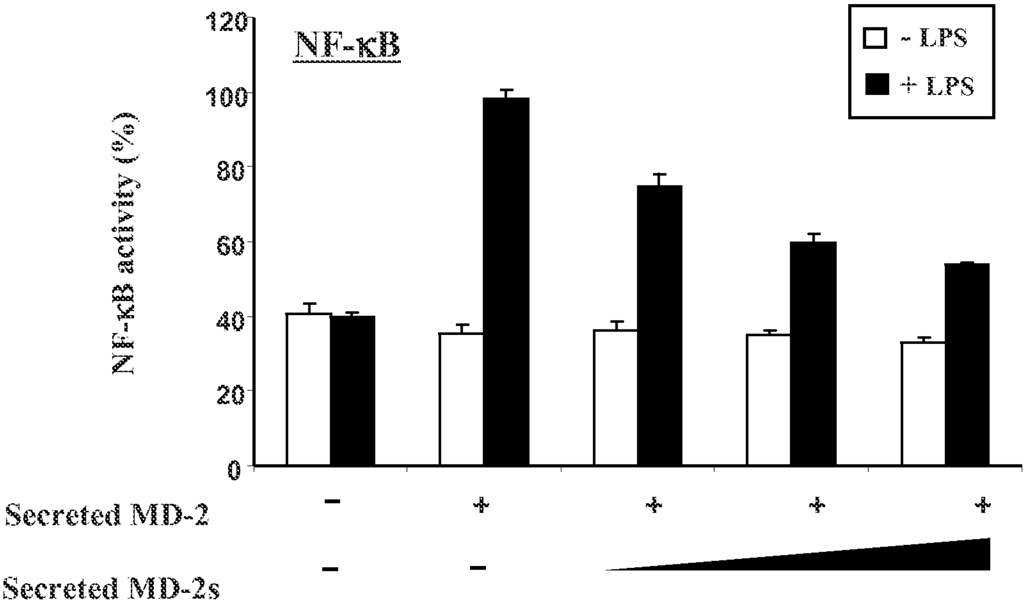

NF-κB
□ - LPS
■ + LPS
NF-κB activity (%)
120
100
80
60
40
20
0
Secreted MD-2 - + + + +
Secreted MD-2s - -

FIG. 6A

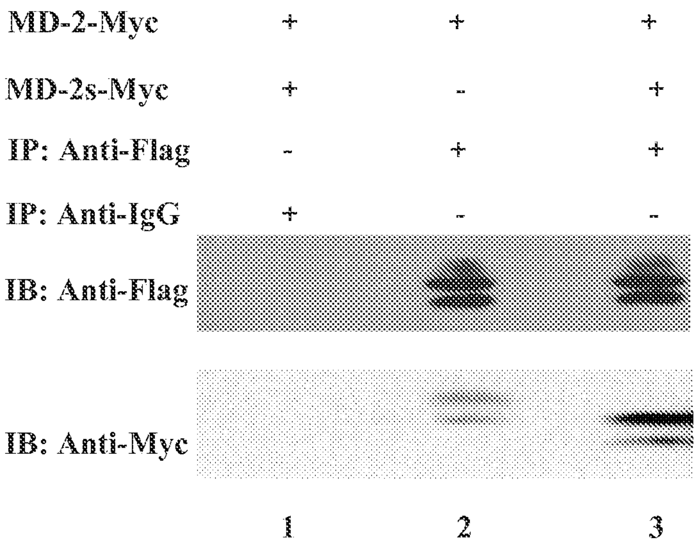

MD-2-Myc + + +
MD-2s-Myc + - +
IP: Anti-Flag - + +
IP: Anti-IgG + - -
IB: Anti-Flag
IB: Anti-Myc
1
2
3

FIG. 6B

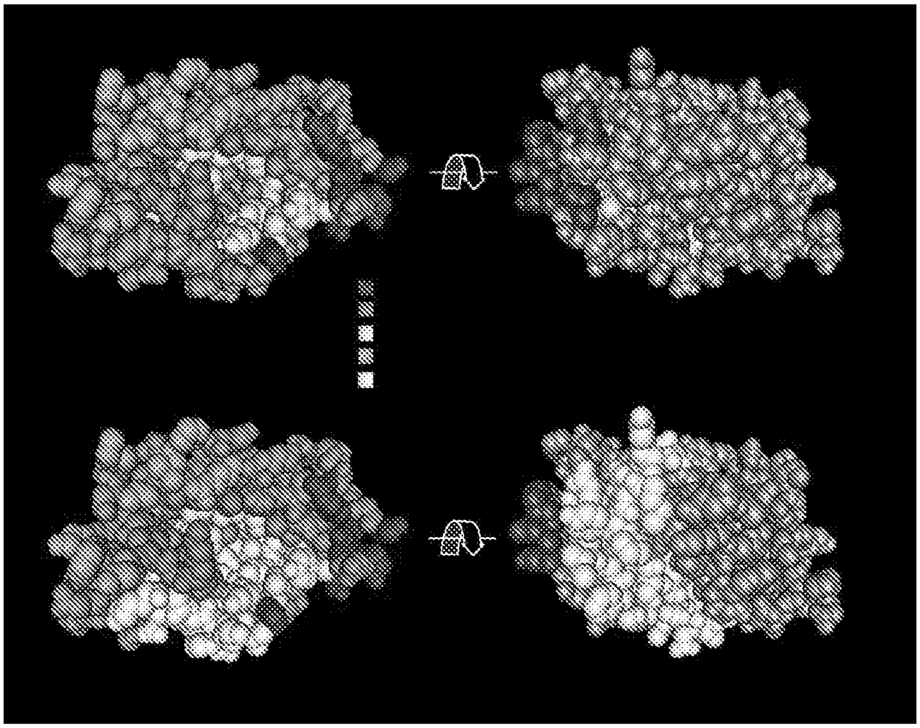


FIG. 6C

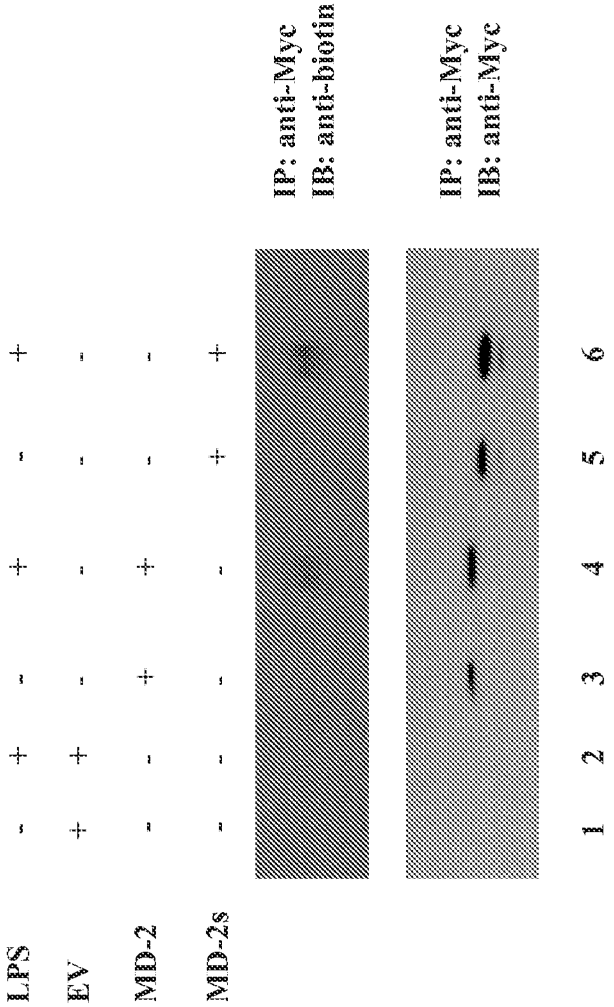

LPS - + - + - +
EV + + - - - -
MD-2 - - + + - -
MD-2s - - - - + +
IP: anti-Myc
IB: anti-biotin
IP: anti-Myc
IB: anti-Myc
1 2 3 4 5 6

Fig. 7

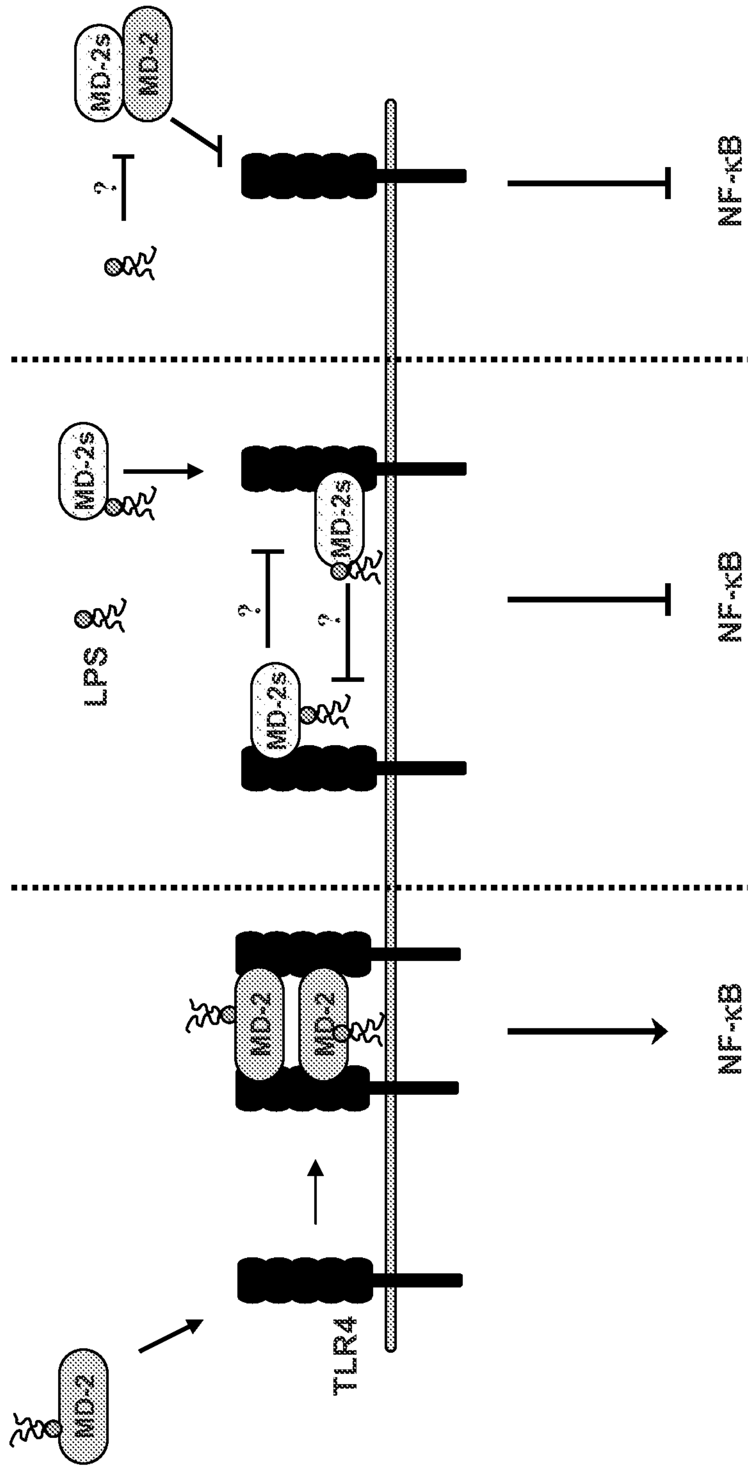


FIG. 8A

FIG. 8B

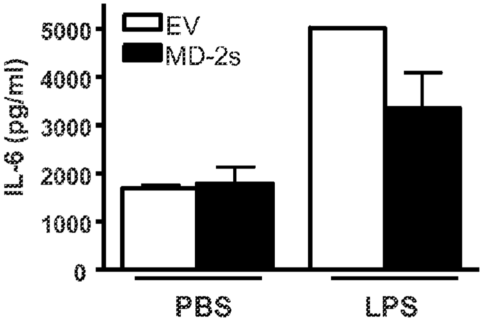


FIG. 8C

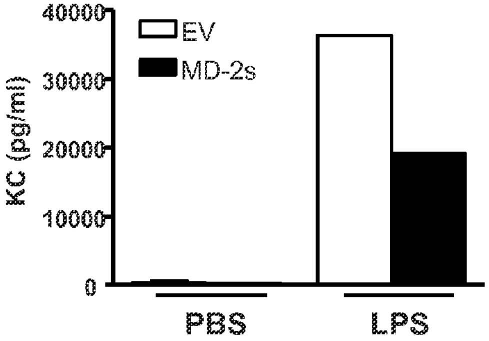


FIG. 8D

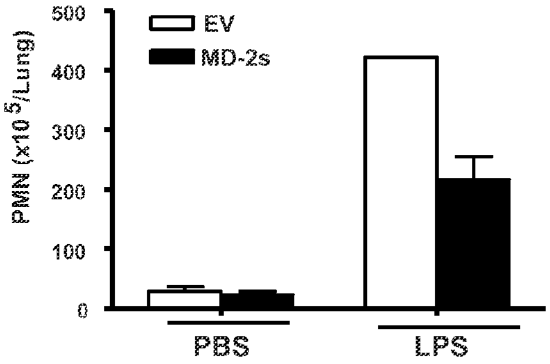


FIG. 8E

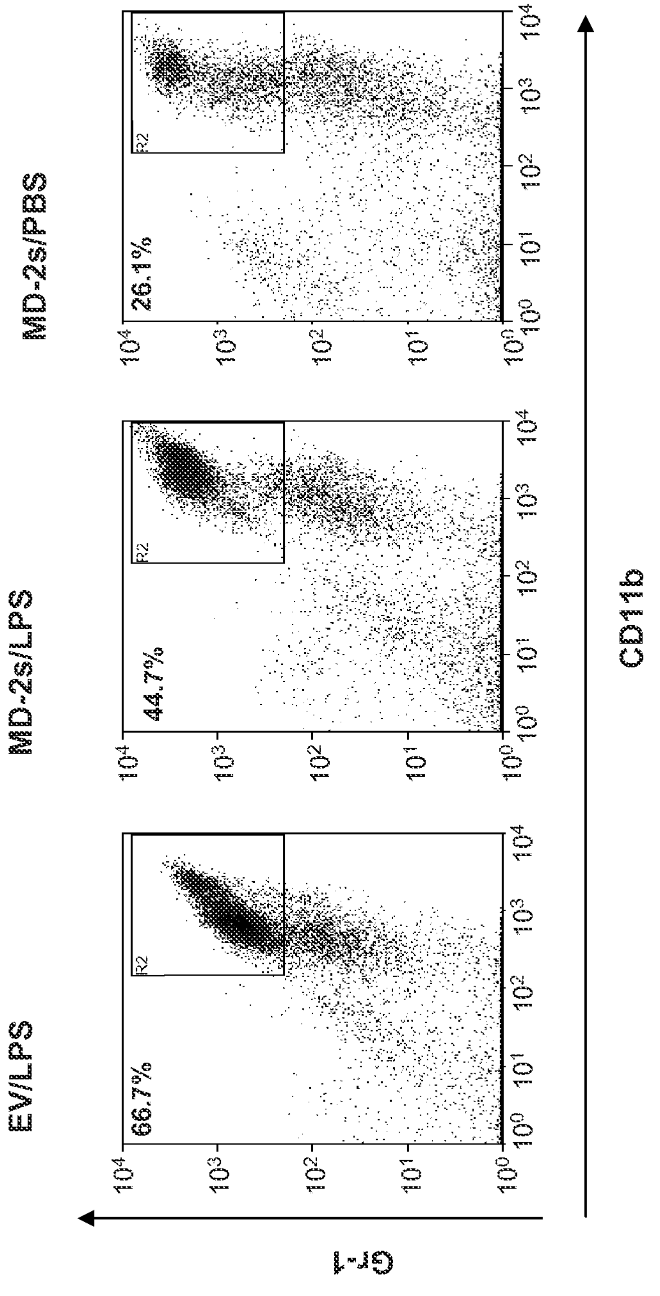

EV/LPS
MD-2s/LPS
MD-2s/PBS
66.7%
44.7%
26.1%
R2
10^0
10^1
10^2
10^3
10^4
Gr-1
CD11b

FIG. 9A

MD-2 Probes for Real-Time PCR

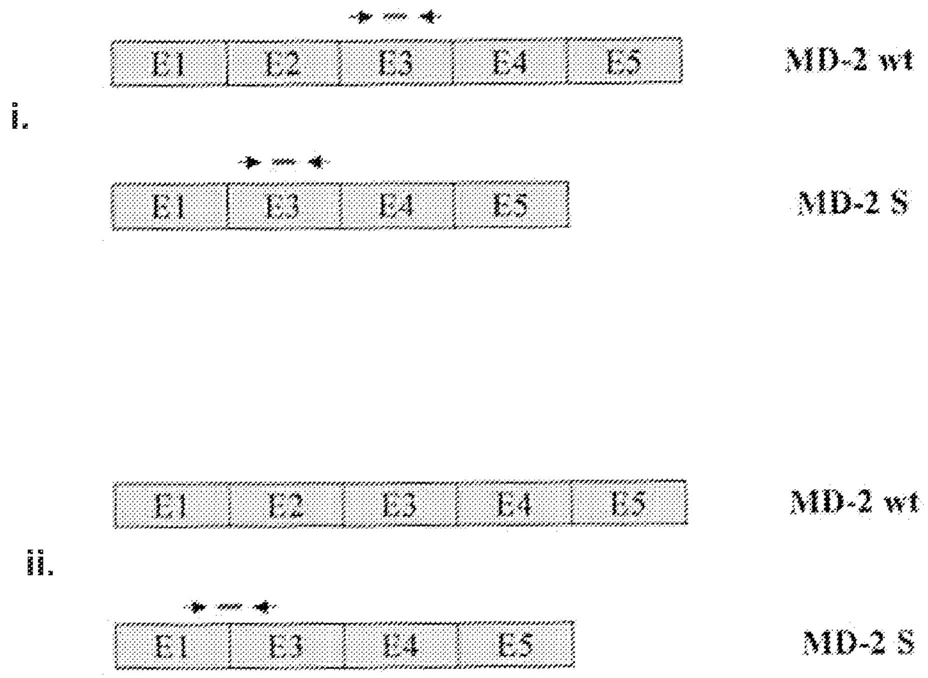


FIG. 9B

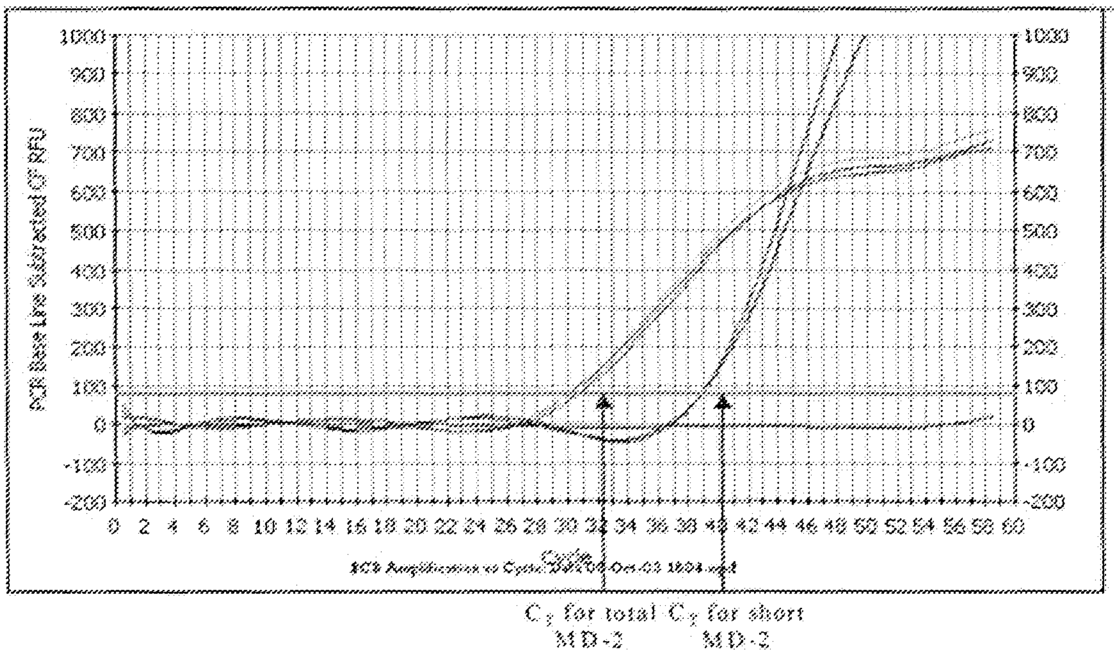

PCR Base Line Subtracted CF RFU
1000
900
800
700
600
500
400
300
200
100
0
-100
-200
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60
Cycle
PCR Amplification vs Cycle
C_T for total MD-2
C_T for short MD-2

FIG. 10

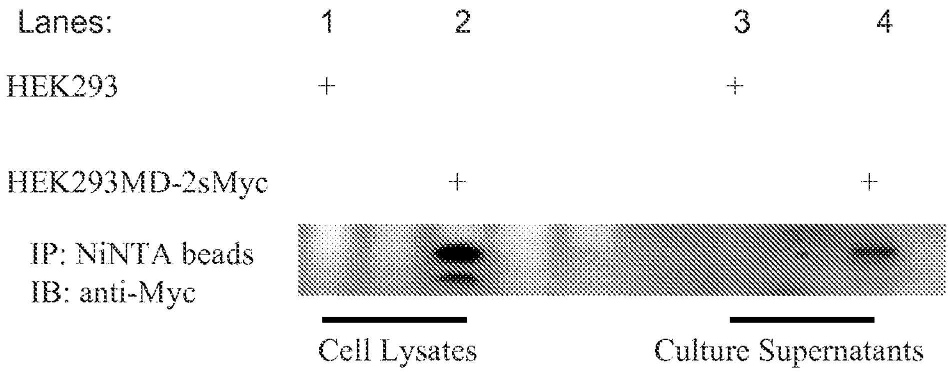

Lanes: 1 2 3 4
HEK293 + +
HEK293MD-2sMyc + +
IP: NiNTA beads
IB: anti-Myc
Cell Lysates
Culture Supernatants

FIG. 11

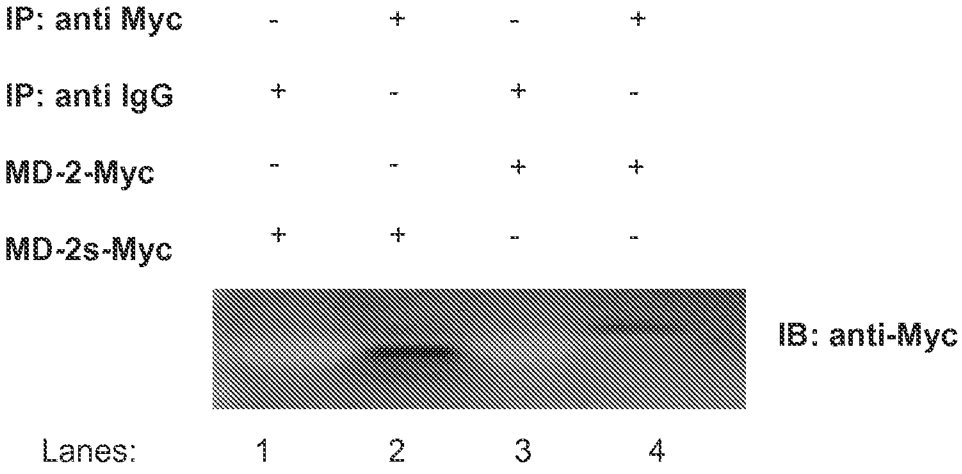

IP: anti Myc - + - +
IP: anti IgG + - + -
MD-2-Myc - - + +
MD-2s-Myc + + - -
IB: anti-Myc
Lanes: 1 2 3 4

FIG. 12A

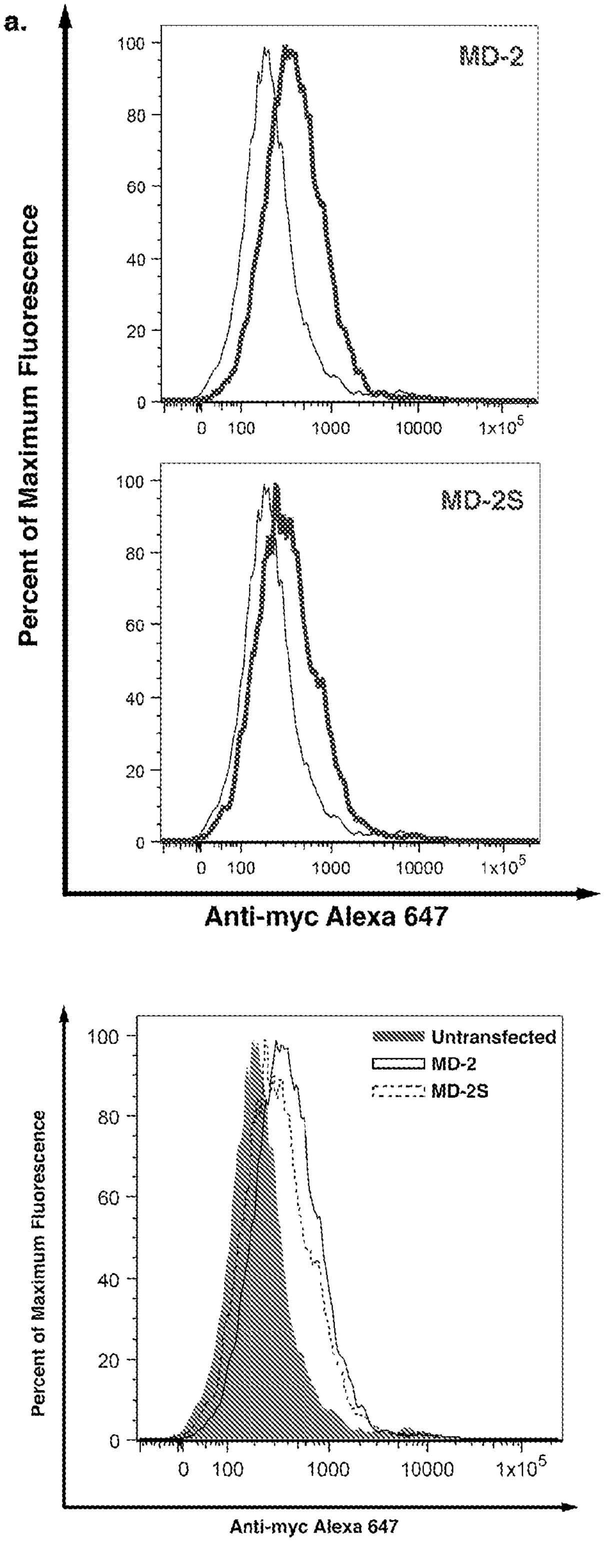

a.
Percent of Maximum Fluorescence
MD-2
100
80
60
40
20
0
0 100 1000 10000 1x10^5
MD-2S
100
80
60
40
20
0
0 100 1000 10000 1x10^5
Anti-myc Alexa 647
Untransfected
MD-2
MD-2S
Percent of Maximum Fluorescence
100
80
60
40
20
0
0 100 1000 10000 1x10^5
Anti-myc Alexa 647

FIG. 12B

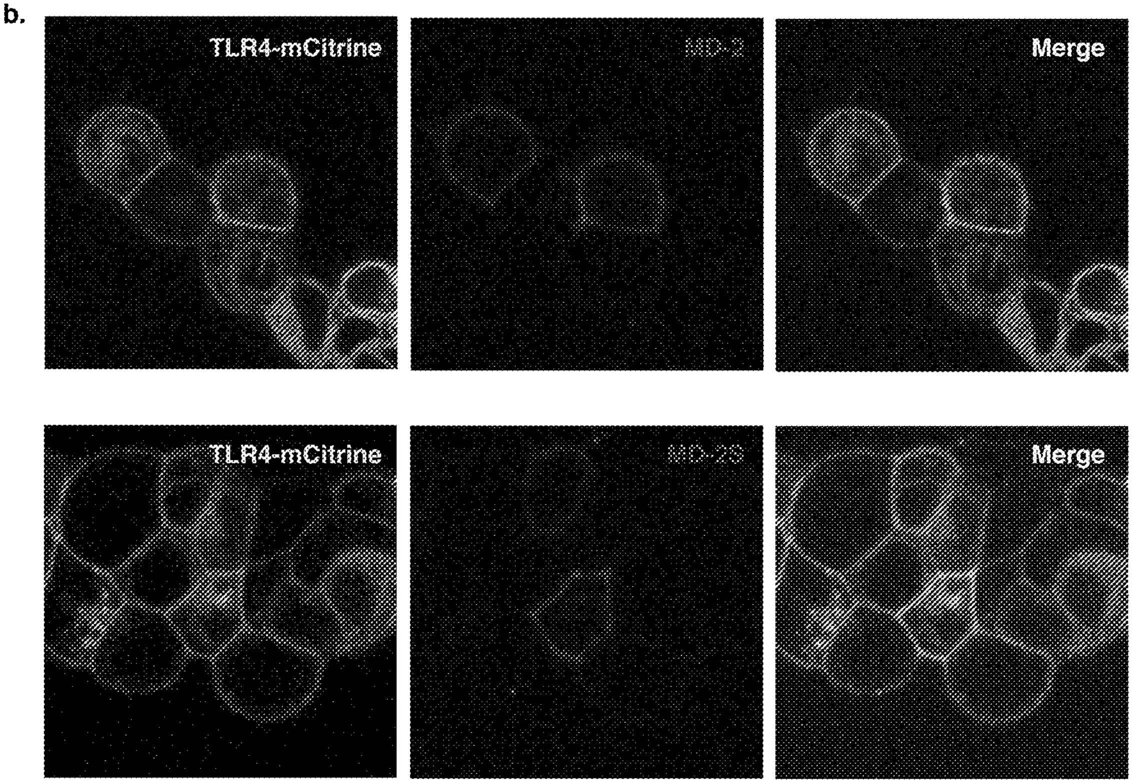


FIG. 13

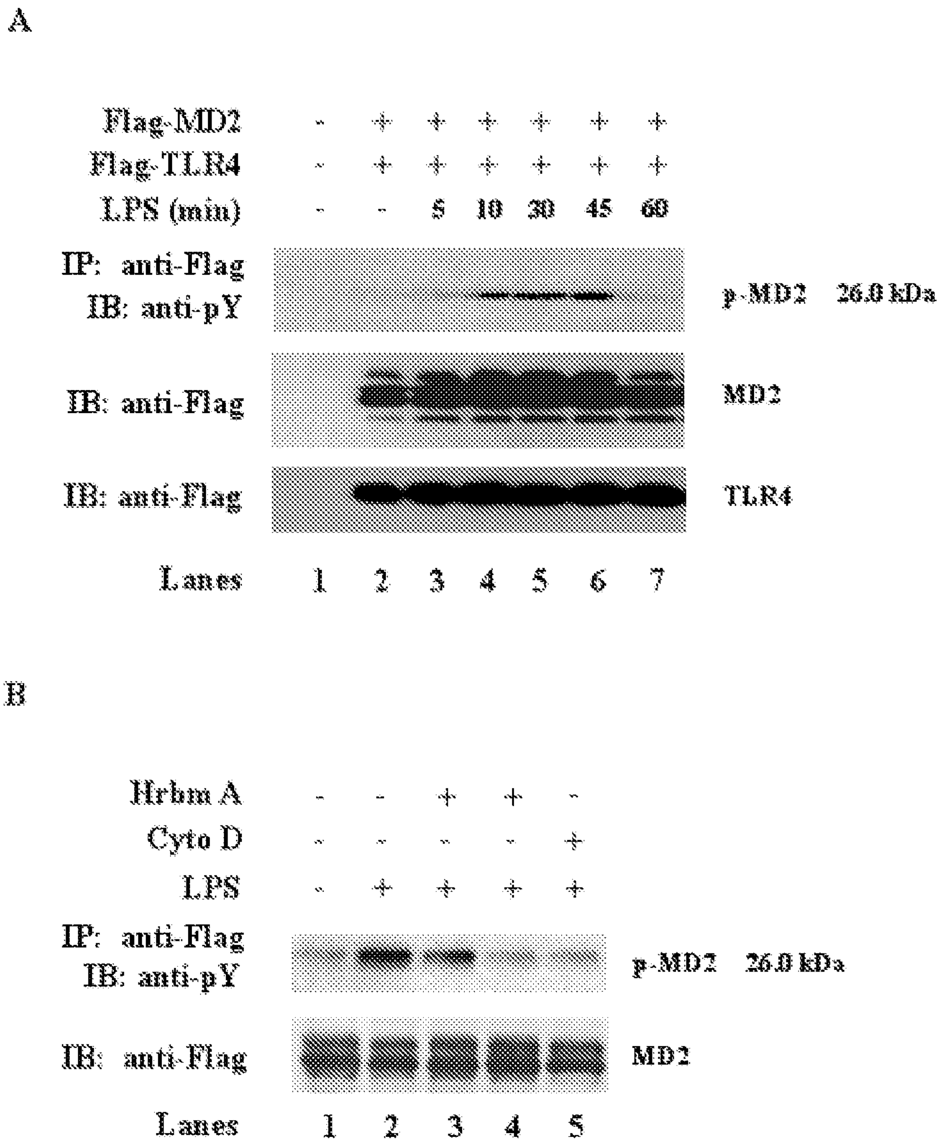

A
Flag-MD2 - + + + + + +
Flag-TLR4 - + + + + + +
LPS (min) - - 5 10 30 45 60
IP: anti-Flag
IB: anti-pY
p-MD2 26.0 kDa
IB: anti-Flag
MD2
IB: anti-Flag
TLR4
Lanes 1 2 3 4 5 6 7
B
Hrbm A - - + + -
Cyto D - - - - +
LPS - + + + +
IP: anti-Flag
IB: anti-pY
p-MD2 26.0 kDa
IB: anti-Flag
MD2
Lanes 1 2 3 4 5

FIG. 14

A

22 34 36 42

hMD-2 MLPFLFFSTLFSSIFTEAQKQYWVCNSSDASISYTYCDKMQYPISINVNPCIELKRSKGL 60

65 75 79 102

hMD-2 LHIFYIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFCRALKGETVNTTISFS 120

131

hMD-2 FKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVILHQPNSN 160 hMD-2 (SEQ ID NO: 27)

B

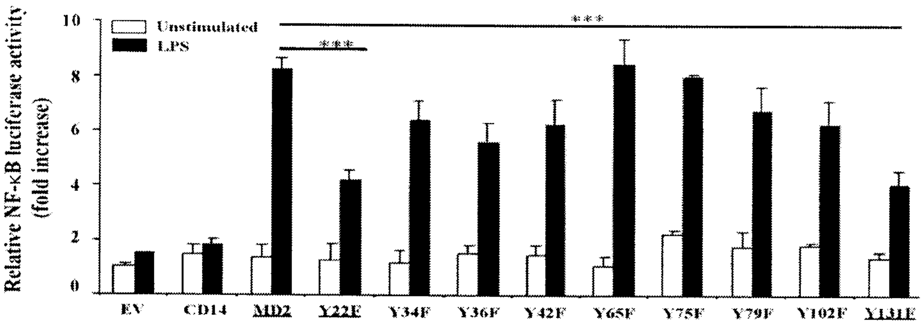


FIG. 14

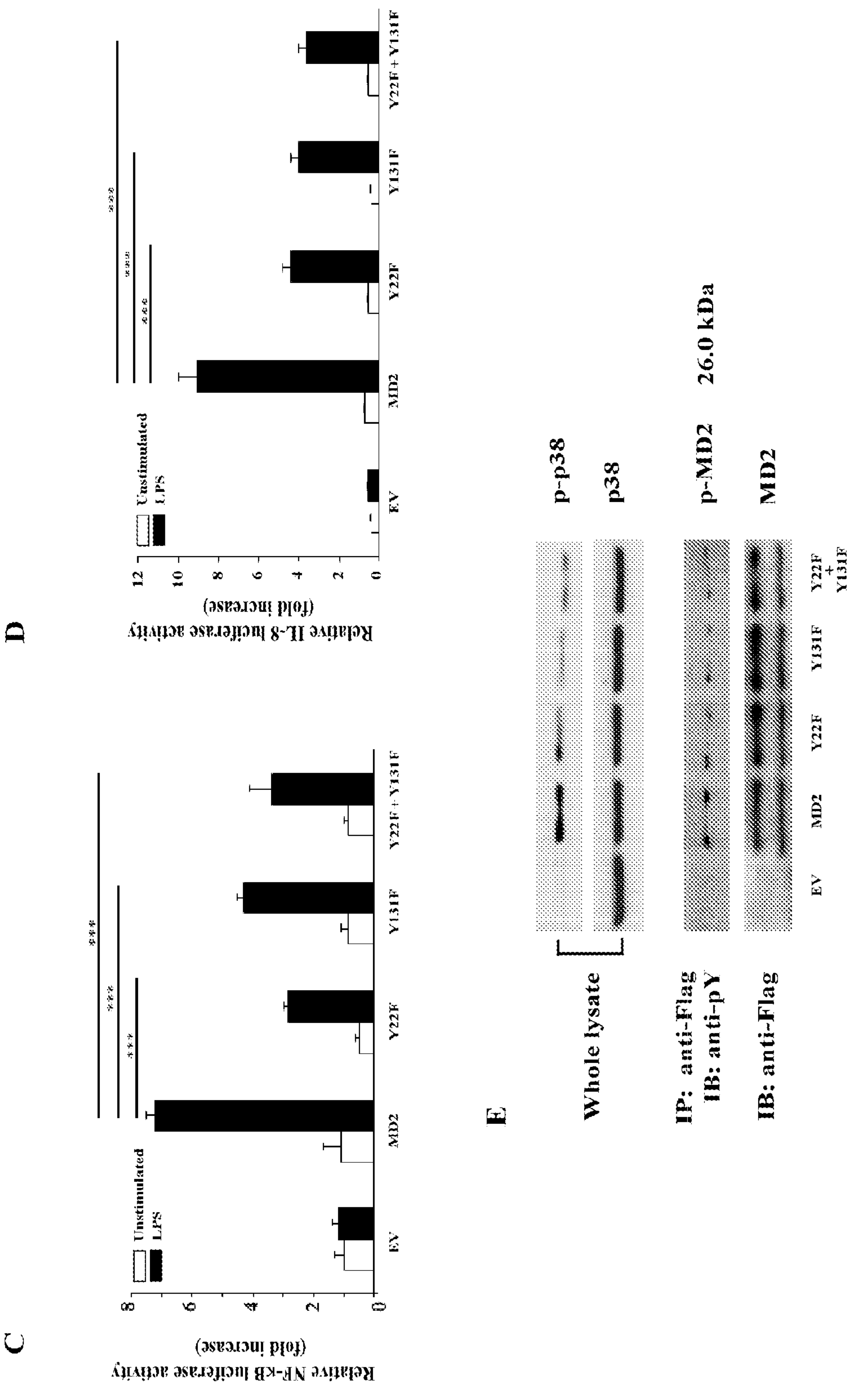

C
Relative NF-κB luciferase activity (fold increase)
0
2
4
6
8
□ Unstimulated
■ LPS
EV
MD2
Y22F
Y131F
Y22F + Y131F
***
***
***
D
Relative IL-8 luciferase activity (fold increase)
0
2
4
6
8
10
12
□ Unstimulated
■ LPS
EV
MD2
Y22F
Y131F
Y22F + Y131F
***
***
***
E
Whole lysate
p-p38
p38
IP: anti-Flag
IB: anti-pY
p-MD2
26.0 kDa
IB: anti-Flag
MD2
EV
MD2
Y22F
Y131F
Y22F + Y131F

FIG. 15

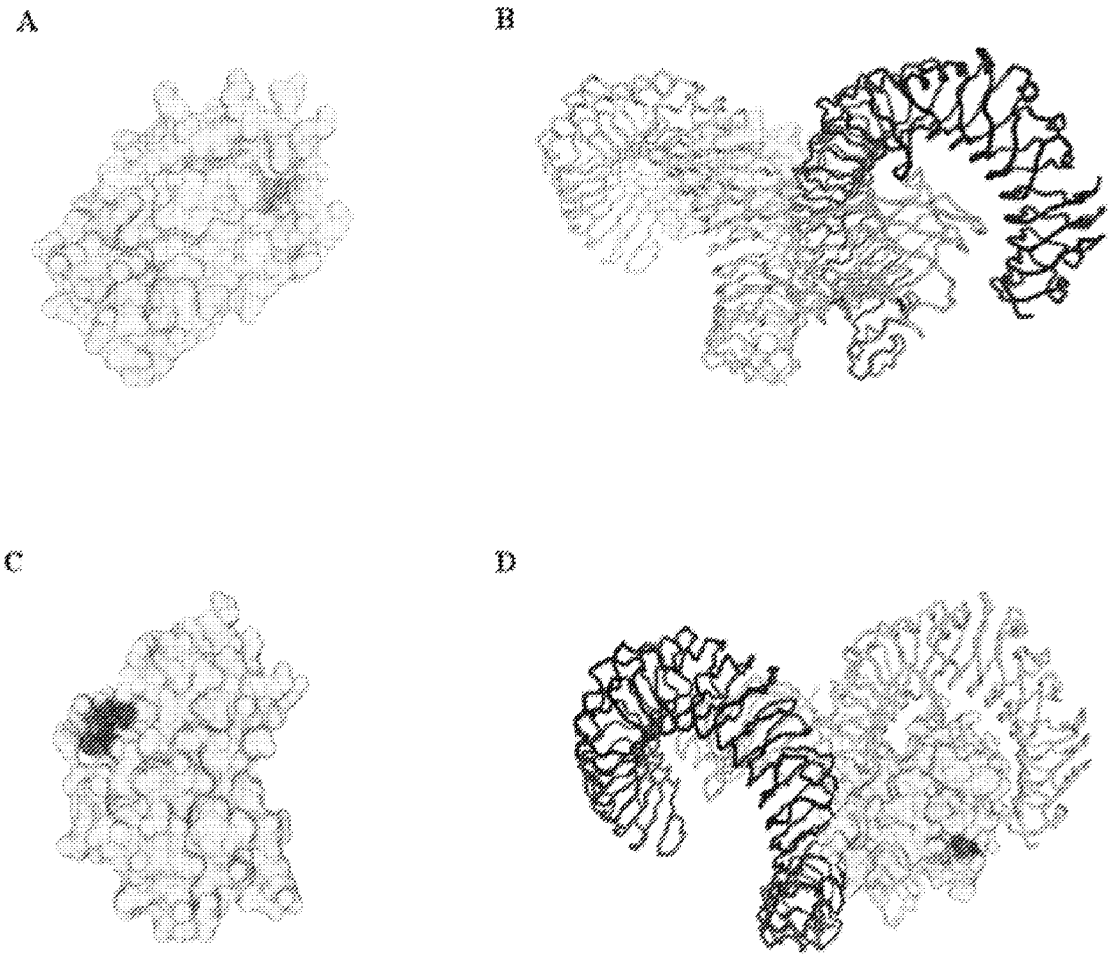


FIG. 16

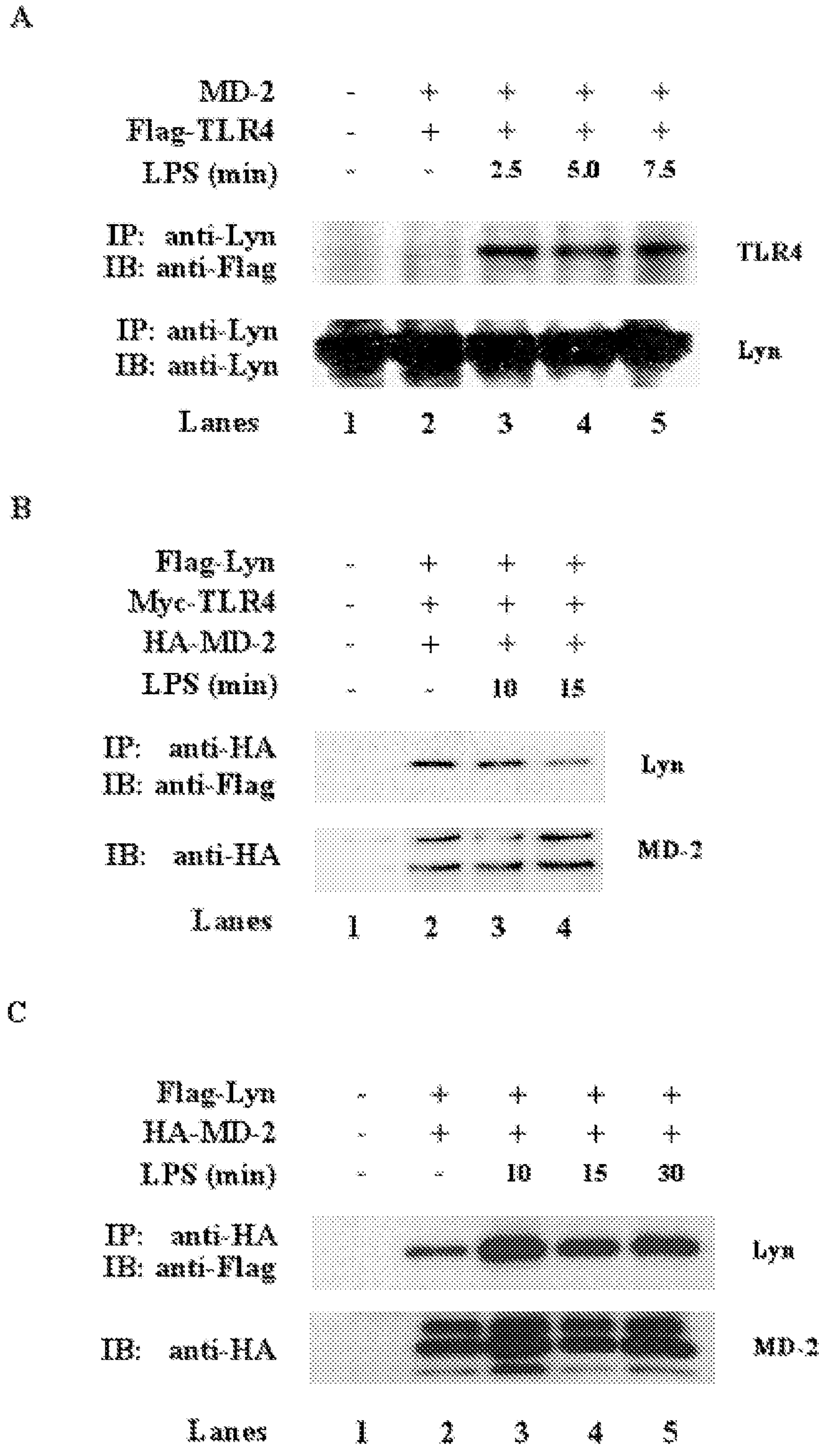
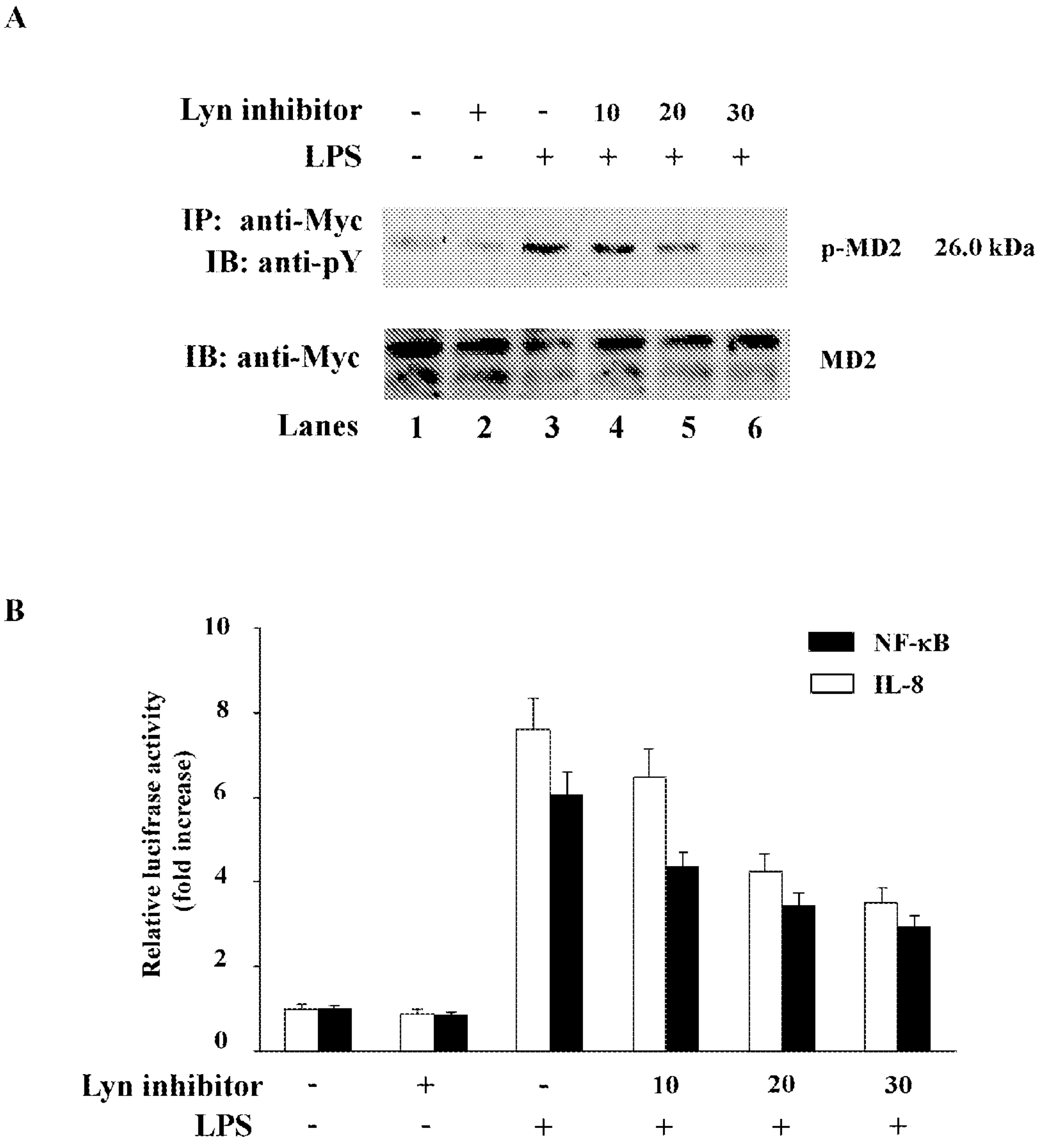

A
MD-2 - + + + +
Flag-TLR4 - + + + +
LPS (min) - - 2.5 5.0 7.5
IP: anti-Lyn
IB: anti-Flag
TLR4
IP: anti-Lyn
IB: anti-Lyn
Lyn
Lanes 1 2 3 4 5
B
Flag-Lyn - + + +
Myc-TLR4 - + + +
HA-MD-2 - + + +
LPS (min) - - 10 15
IP: anti-HA
IB: anti-Flag
Lyn
IB: anti-HA
MD-2
Lanes 1 2 3 4
C
Flag-Lyn - + + + +
HA-MD-2 - + + + +
LPS (min) - - 10 15 30
IP: anti-HA
IB: anti-Flag
Lyn
IB: anti-HA
MD-2
Lanes 1 2 3 4 5

FIG. 17


A
Lyn inhibitor - + - 10 20 30
LPS - - + + + +
IP: anti-Myc
IB: anti-pY
p-MD2 26.0 kDa
IB: anti-Myc
MD2
Lanes 1 2 3 4 5 6
B
NF-κB
IL-8
Relative lucifrase activity (fold increase)
0
2
4
6
8
10
Lyn inhibitor - + - 10 20 30
LPS - - + + + +

SHORT-FORM HUMAN MD-2 AS A NEGATIVE REGULATOR OF TOLL-LIKE RECEPTOR 4 SIGNALING

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation of application Ser. No. 13/051,390, filed Mar. 18, 2011, which is a continuation in part of International Application PCT/US09/50317, filed Jul. 10, 2009, which designated the U.S. and that International Application was published under PCT Article 21(2) in English, which claims the priority of U.S. Provisional Patent Application No. 61/098,861, filed Sep. 22, 2008.

[0002] This invention was made with U.S. Government support under NIAID Grant No. AI058128 and NHLBI Grant No. HL66436. Thus, the U.S. Government may have certain rights in the subject matter hereof.

FIELD OF INVENTION

[0003] This invention relates to myeloid differentiation-2 and its role in toll-like receptor 4 and lipopolysaccharide signaling.

BACKGROUND

[0004] All publications herein are incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference. The following description includes information that may be useful in understanding the present invention. It is not an admission that any of the information provided herein is prior art or relevant to the presently claimed invention, or that any publication specifically or implicitly referenced is prior art.

[0005] Microbial detection and instigation of an appropriate innate and subsequent adaptive immune response to a pathogenic assault, is highly reliant on toll-like receptors (TLRs) (Brikos et al. (2008) Handb Exp Pharmacol, 21-50). Members of the TLR family recognize specific conserved pathogen-associated molecular patterns (PAMPs) expressed by invading microorganisms. TLR4, one of the most widely studied TLRs, recognizes a repertoire of PAMPs, which includes lipopolysaccharide (LPS), a major component of the outer membrane of Gram-negative bacteria (Poltorak et al. (1998) Science 282, 2085-2088; Qureshi et al. (1999) J Exp Med 189, 615-625; Hoshino et al. (1999) J Immunol 162, 3749-3752; Medzhitov et al. (1997) Nature 388, 394-397). For optimal LPS-induced signal transduction to occur, a receptor complex is assembled consisting of the signaling subunit TLR4, the co-receptor myeloid differentiation (MD)-2, and two accessory proteins, LPS-binding protein (LBP) and CD14 (Schumann et al. (1990) Science 249, 1429-1431; Pugin et al. (1993) Proc Natl Acad Sci USA 90, 2744-2748; Frey et al. (1992) J Exp Med 176, 1665-1671; Shimazu et al. (1999) J Exp Med 189, 1777-1782).

[0006] MD-2 belongs to the MD-2-related lipid recognition (ML) family (Inohara et al. (2002) Trends Biochem Sci 27, 219-221). A secretion signal, the signature sequence of this group of proteins, is located at the N-terminal domain of MD-2 (Kato et al. (2000) Blood 96, 362-364). Although MD-2 lacks transmembrane and intracellular regions, it may be membrane-bound through its association with the extracellular portion of TLR4 (Akashi et al. (2000) J Immunol 164, 3471-3475). Studies with mice deficient in either MD-2 or that lacked a functional TLR4 have revealed that both proteins are absolutely required for LPS signaling (Poltorak et al. (1998) Science 282, 2085-2088; Qureshi et al. (1999) J Exp Med 189, 615-625; Hoshino et al. (1999) J Immunol 162, 3749-3752; Shimazu et al. (1999) J Exp Med 189, 1777-1782). Although TLR4 is critical to mount a response to gram-negative bacteria, tight regulation of the TLR4 signal transduction pathway is imperative to prevent excessive inflammation that could lead to collateral damage to the host (Liew et al. (2005) Nat Rev Immunol 5, 446-458). One method of control involves alternative splicing of specific genes that encode essential components of the TLR4 signaling pathway to produce inhibitory isoforms, examples include myeloid differentiation factor 88_S (MyD88_S) (Janssens et al. (2002) Curr Biol 12, 467-471), and smTLR4 (Iwami et al. (2000) J Immunol 165, 6682-6686; Jaresova et al. (2007) Microbes Infect 9, 1359-1367). Similarly, the murine MD-2 gene encodes two alternatively spliced isoforms. The truncated variant, MD-2B, generated by the splicing out of the first 54 amino acids of exon 3, downregulates LPS signaling (Ohta et al. (2004) Biochem Biophys Res Commun 323, 1103-1108). Given that mouse and human MD-2 are highly conserved, an alternative splicing of this gene in humans could also play an important regulatory role in humans.

[0007] There is still a need for therapeutic strategies that may be used to treat human pathologies characterized by an overly exuberant or chronic immune response to LPS. Therefore, novel mechanisms to further regulate TLR4 signaling would be beneficial and the protein MD-2s described herein may be used to treat these human pathologies.

SUMMARY OF THE INVENTION

[0008] The following embodiments and aspects thereof are described and illustrated in conjunction with compositions and methods which are meant to be exemplary and illustrative, not limiting in scope.

[0009] The present invention provides a purified polypeptide comprising an amino acid sequence that is at least 80% identical to SEQ ID NO:1 or SEQ ID NO:2. In one embodiment, the amino acid sequence is as disclosed by SEQ ID NO:1 or SEQ ID NO:2. In another embodiment, the polypeptide is glycosylated.

[0010] In another embodiment, the amino acid sequence is as disclosed by SEQ ID NO:1 or SEQ ID NO:2 but with 1-20 conservative amino acid substitutions. Alternatively, the amino acid sequence is as disclosed by SEQ ID NO:1 or SEQ ID NO:2 but with 1-20 amino acid insertions, deletions and/or substitutions.

[0011] The present invention also provides an isolated nucleic acid comprising a nucleotide sequence that encodes the polypeptide of the present invention.

[0012] The present invention also provides a method of inhibiting toll-like receptor 4 signaling ("TLR4"), inhibiting lipopolysaccharide ("LPS") signaling, treating a condition mediated by TLR4 signaling, or reducing a likelihood of developing a condition mediated by TLR4 signaling in a subject in need thereof, comprising: providing a polypeptide of the present invention; and administering the polypeptide to the subject to inhibit TLR4 signaling, inhibit LPS signaling, treat the condition mediated by TLR4 signaling, or reduce the likelihood of developing the condition mediated by TLR4 signaling. In various embodiments, the condition mediated by TLR signaling may be selected from the group consisting of sepsis, septic shock, inflammation, gram negative bacterial infection, gram negative bacterial lung infection, immune response such as atherosclerosis and combinations thereof.

[0013] The present invention also provides a purified polypeptide comprising an amino acid sequence of an alternatively spliced human myeloid differentiation-2 protein ("MD-2s").

[0014] The present invention also provides an isolated nucleic acid comprising a nucleotide sequence at least 80% identical to SEQ ID NO:4 or SEQ ID NO:5. In one embodiment, the isolated nucleic acid encodes a polypeptide that binds to toll-like receptor 4 ("TLR4") and/or or lipopolysaccharide ("LPS").

[0015] In another embodiment, the nucleotide sequence is as disclosed by SEQ ID NO:4 or SEQ ID NO:5. In another embodiment, nucleotide sequence is a degenerate variant of SEQ ID NO:4 or SEQ ID NO:5.

[0016] The present invention also provides for an expression vector comprising a nucleic acid of the present invention, operably linked to an expression control sequence.

[0017] The present invention also provides a cultured cell comprising an expression vector of the present invention.

[0018] The present invention also provides a method of producing a polypeptide of the present invention, comprising: providing a cultured cell of the present invention; and culturing the cell under conditions permitting expression of the polypeptide to produce the polypeptide. In one embodiment, the method further comprises purifying the polypeptide from the cell or from the medium of the cell.

[0019] The present invention also provides a nucleic acid comprising a nucleotide sequence at least 80% identical to SEQ ID NO:7, SEQ ID NO:8 or SEQ ID NO:9. In one embodiment, the nucleotide sequence is as disclosed by SEQ ID NO:7, SEQ ID NO:8 or SEQ ID NO:9. In another embodiment, the nucleic acid hybridizes under highly stringent conditions to a region comprising exon 1 and exon 3 or a fragment thereof of MD-2s.

[0020] The present invention also provides a method of detecting the presence or absence of a nucleic acid that encodes an alternatively spliced myeloid differentiation 2 ("MD-2s") in a human subject, comprising: providing a first nucleic acid comprising a nucleotide sequence that is at least 80% identical to SEQ ID NO:7, SEQ ID NO:8 or SEQ ID NO:9; and detecting the presence or absence of a second nucleic acid sequence that encodes MD-2s, wherein the presence of the second nucleic acid indicates the presence of MD-2s and the absence of the second nucleic acid indicates the absence of MD-2s.

[0021] In one embodiment, detecting comprises: contacting the first nucleic acid with a biological sample from the subject; and determining whether the first nucleic acid hybridizes under highly stringent conditions with the second nucleic acid, wherein the presence of a binding complex comprising the first and second nucleic acid indicates the presence of the second nucleic acid and the absence of the binding complex indicates the absence of the second nucleic acid. In another embodiment, detecting comprises performing real time polymerase chain reaction on the sample.

[0022] The present invention also provides a method of determining a risk factor of a subject to lipopolysaccharide ("LPS") induced inflammation or an inflammatory disease, comprising: detecting the presence or absence of a nucleic acid that encodes an alternatively spliced myeloid differentiation 2 ("MD-2s"); and correlating the presence of MD-2s with a lower risk of having the LPS induced inflammation or the inflammatory disease or correlating the absence of MD-2s with a higher risk of having the LPS induced inflammation or the inflammatory disease.

[0023] In one embodiment, detecting comprises: contacting a first nucleic acid comprising a nucleotide sequence of at least 80% identical to SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9 with a biological sample from the subject; and determining whether the first nucleic acid hybridizes under highly stringent conditions with a second nucleic acid that encodes MD-2s, wherein the presence of a binding complex comprising the first and second nucleic acid indicates the presence of the second nucleic acid. In another embodiment, detecting comprises performing real time polymerase chain reaction on the sample.

[0024] In one embodiment, the lipopolysaccharide induced inflammation or the inflammatory disease may be selected from the group consisting of sepsis, septic shock, gram negative bacterial infection, gram negative bacterial lung infection, immune response such as atherosclerosis and combinations thereof.

[0025] The present invention also provides a polypeptide consisting of an amino acid sequence at least 80% identical to SEQ ID NO:3. In one embodiment, the amino acid sequence is as disclosed by SEQ ID NO:3. The present invention also provides a nucleotide sequence that encodes the polypeptide. In one embodiment, the nucleotide sequence is as disclosed by SEQ ID NO:6.

[0026] The present invention also provides a purified polypeptide comprising an amino acid sequence comprising at least 10 consecutive amino acid residues of SEQ ID NO:1 or SEQ ID NO:2.

[0027] In one embodiment, the amino acid sequence comprises amino acid residues N26 to N84 of SEQ ID NO:1 or amino acid residues N10 to N68 of SEQ ID NO:2. In a particular embodiment, the amino acid sequence comprises N-glycosylated sites at positions N26 and N84 of SEQ ID NO:1 or N-glycosylated sites at positions N10 and N68 of SEQ ID NO:2.

[0028] In another embodiment, the amino acid sequence comprises one or more residues involved in the dimerization interface of the TLR4/MD-2/LPS complex. In another embodiment, the amino acid sequence comprises residue V52 to residue F96 of SEQ ID NO:1, or residue V36 to residue F80 of SEQ ID NO:2. In another particular embodiment, the amino acid sequence comprises one or more residues selected from the group consisting of V52, M55, L57, R60, S88, K92, G93, 194, K95, F96 and combinations thereof of SEQ ID NO:1; or one or more residues selected from the group consisting of V36, M39, L41, R44, S72, K76, G77, I78, K79, F80 and combinations thereof of SEQ ID NO:2.

[0029] In another embodiment, the amino acid sequence comprises residue C37 to C118 involved in the second disulphide bond or a residue C65 to C75 involved in the third disulphide bond of SEQ ID NO: 1. In another embodiment, amino acid sequence comprises residue C37 and/or C118 involved in the second disulphide bond or a residue C65 and/or C75 involved in the third disulphide bond of SEQ ID NO:1.

[0030] In another embodiment, the polypeptide is an immunogenic polypeptide comprising an immunogenic domain comprising at least 10 consecutive residues of SEQ ID NO:1 or SEQ ID NO:2.

[0031] In further embodiments, a purified polypeptide, the amino acid sequence of which comprises SEQ ID NO:17 is provided. In a particular embodiment, the purified polypeptide consists of the amino acid sequence as set forth in SEQ ID NO:17. In a further embodiment, the purified polypeptide is glycosylated. In another embodiment, a purified polypeptide, the amino acid sequence of which comprises a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:17 is provided. These polypeptides may be useful for modulating LPS-induced signaling and/or TLR signaling.

[0032] In another embodiments, a purified polypeptide, the amino acid sequence of which comprises SEQ ID NO:25 is provided. In a particular embodiment, the purified polypeptide consists of the amino acid sequence as set forth in SEQ ID NO:25. In a further embodiment, the purified polypeptide is glycosylated. In another embodiment, a purified polypeptide, the amino acid sequence of which comprises a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:25 is provided. These polypeptides may be useful for modulating LPS-induced signaling and/or TLR signaling.

[0033] In further embodiments, a purified polypeptide, the amino acid sequence of which comprises SEQ ID NO:26 is provided. In a particular embodiment, the purified polypeptide consists of the amino acid sequence as set forth in SEQ ID NO:26. In a further embodiment, the purified polypeptide is glycosylated. In another embodiment, a purified polypeptide, the amino acid sequence of which comprises a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:25 is provided. These polypeptides may be useful for modulating LPS-induced signaling and/or TLR signaling.

[0034] Other features and advantages of the invention will become apparent from the following detailed description, taken in conjunction with the accompanying drawings, which illustrate, by way of example, various features of embodiments of the invention.

BRIEF DESCRIPTION OF THE FIGURES

[0035] Exemplary embodiments are illustrated in referenced figures. It is intended that the embodiments and figures disclosed herein are to be considered illustrative rather than restrictive.

[0036] FIG. **1** depicts detection of an alternatively spliced isoform of MD-2 in human, but not mouse cells in accordance with an embodiment of the present invention. RNA from (A) HMECs, (B) RAW 246.7 cells, or (C) murine liver tissue, and dendritic cells were isolated and reverse transcribed into cDNA. Following cDNA synthesis, RT-PCR using human or mouse MD-2-specific primers, was performed. (D) A schematic representation depicting the mature human MD-2 protein shown above the alternatively spliced MD-2s isoform. MD-2s is generated by skipping exon 2. An amino acid substitution, D38G, also occurs at the junction between exons 2 and 3. (E) Sequence alignment of wild-type MD-2 and MD-2s. (F) Expression profiles of MD-2 and MD-2s in different human tissues. MD-2 and MD-2s were amplified by RT-PCR from the indicated human tissues, as described herein. (G) Detection of MD-2s in BMDMs derived from transgenic mice that contain human MD-2 (lanes 1, 3, and 4).

[0037] FIG. **2** shows that MD-2s is N-linked glycosylated and secreted in accordance with an embodiment of the present invention. (A) Myc-MD-2s was immunoprecipitated (IP) from cell lysates prepared from HEK293 cells transiently transfected with a plasmid encoding Myc-MD-2s. Immunoprecipitants were either left untreated (lane 1) or treated with peptide N-glycosidase F (PNGase F) (lane 2). Samples were subsequently analyzed by SDS-PAGE and immunoblotted with an anti-Myc antibody. (B) Myc-MD-2s was immunoprecipitated (IP) from culture supernatants that were obtained from HEK293 cells transiently transfected with a plasmid encoding Myc-MD-2s. Samples were subsequently analyzed by SDS/PAGE and immunoblotted (IB) with an anti-Myc antibody. Mock transfected culture supernatants were used as a negative control.

[0038] FIG. **3** shows that MD2-s fails to mediate either LPS-dependent NF-κB activation or IL-8 secretion in accordance with an embodiment of the present invention. (A) HEK-293 cells stably transfected with TLR4 and a NF-κB reporter gene were treated with supernatants containing either MD-2 or MD-2s as described in the examples herein. Cells were left untreated or stimulated with LPS for 24 h. Mean relative stimulation of luciferase activity±S.D. for a representative experiment, each performed in triplicate, is shown. (B) HEK-293 cells stably transfected with TLR4 and a NF-κB reporter gene were transiently transfected with plasmids encoding for either MD-2, MD-2s or CD14 as shown. 24 h later, cells were left untreated or stimulated with LPS (250 ng/ml) for 6 h. Mean relative stimulation of luciferase activity±SD for a representative experiment, each performed in triplicate, is shown. (C) and (D) Supernatants were also collected and measured for IL-8 secretion.

[0039] FIG. **4** shows that MD-2s colocalizes and interacts with TLR4 in accordance with an embodiment of the present invention. (A) Cells stably expressing CFP-tagged TLR4 were transiently transfected with plasmids encoding wild-type MD-2 (upper panels) or MD-2s (lower panels). 24 h later, cells were incubated with an anti-Myc antibody and cross-liked with Alexa 647-conjugated anti-mouse polyclonal secondary antibody. (B) HEK293 cells were transiently transfected with a plasmid encoding for Flag-tagged TLR4 (lane 2) and cotransfected with either a Myc-tagged MD-2 (lane 3) or a Myc-tagged MD-2s (lanes 1 and 4) expressing plasmid. Co-immunoprecipitation experiments were then performed using an anti-Flag antibody (lanes 2-4) or an IgG isotype control antibody (lane 1). Samples were fractionated by SDS-PAGE and immunoblotting with an anti-Myc antibody was performed. Experiment shown is representative of 4 separate experiments.

[0040] FIG. **5** shows that MD-2s inhibits LPS-induced NF-κB activation in accordance with an embodiment of the present invention. (A) HEK293 cells were transiently transfected with plasmids encoding TLR4 and a NF-κB reporter gene in combination with MD-2 and MD-2s as indicated. 24 h later, cells were left untreated or incubated with LPS (250 ng/ml) for 5 h. Mean relative stimulation of luciferase activity±S.D. for a representative experiment from three separate experiments, each performed in triplicate, is shown. (B) HEK-293 cells stably transfected with TLR4 and a NF-κB reporter gene were treated with supernatants containing either MD-2 and MD-2s as depicted and left untreated or incubated with LPS for 24 h. Mean relative stimulation of luciferase activity±S.D. for a representative experiment from three separate experiments, each performed in triplicate, is shown.

[0041] FIG. **6** shows that MD-2s interacts with wild-type MD-2 and LPS in accordance with an embodiment of the present invention. (A) HEK293 cells were transiently transfected with plasmids encoding for Flag-tagged MD-2 (lanes

1-4) in combination with either a Myc-tagged MD-2 (lanes 1 and 3) or a Myc-tagged MD-2s (lanes 2 and 4) expressing plasmid. Co-immunoprecipitation experiments were then performed using an anti-Flag antibody (lanes 3-4) or an IgG isotype control antibody (lane 1-2). Samples were fractionated by SDS-PAGE and immunoblotting with an anti-Myc antibody was performed. (B) Structural analysis of MD-2. Structural features representing the TLR4 binding sites (red); the ligand contacts (dark blue); the ligand binding pocket (light blue) and the TLR4 secondary contacts (pink) are illustrated. The residues deleted in MD-2s (yellow) are also shown. (C) HEK293 cells were transiently transfected with plasmids encoding for Myc-tagged MD-2 (lanes 3 and 4) or a Myc-tagged MD-2s (lanes 5 and 6) expressing plasmid and treated with LPS-biotin as indicated. Co-immunoprecipitation experiments were then performed using an anti-Myc antibody. Samples were fractionated by SDS-PAGE and immunoblotting with an anti-biotin (upper panel) and anti-Myc antibody (lower panel) were performed.

[0042] FIG. **7** depicts schematic diagram representing the possible mechanisms employed by which MD-2s negatively regulates LPS signaling in accordance with an embodiment of the present invention.

[0043] FIG. **8** shows that MD-2s inhibits lung inflammation induced by LPS in vivo in accordance with an embodiment of the present invention. (A) MD-2s expression can be detected following in vivo transfection. RNA was isolated from lung tissue of wild-type mice at 48 h post in vivo transfection with control vector (lane 1), Myc-MD2 (lane 2) or a plasmid encoding MycMD-2s (lane 3) and reverse transcribed into cDNA. RT-PCR using human MD-2-specific primers (lanes 1-3) or murine GAPDH primers (lanes 4-6), was then performed. (B-E) Wild-type mice were transfected with control vector (EV, open bars) or a plasmid encoding MD-2s (black bars) 48 h before being challenged intratracheally with PBS or 10 μg of LPS, for 24 h. MD-2s expression reduced (B) IL-6 concentration in bronchoalveolar lavage fluid (BALF), (C) KC concentration in the lung homogenate, and (D) recruitment of polymorphonuclear leukocytes (PMN) into the lung. (E) Flow cytometry analysis demonstrated that following LPS challenge the percentage of $GR-1^{+}CD11b^{+}$ cells in the lung decreased from 66.7% to 26.1% with MD-2s expression.

[0044] FIG. **9** depicts the detection of MD-2s in accordance with an embodiment of the present invention. (A) MD-2 probes for real time PCR; (i) MD-2 total probe recognizes both wild-type and MD-2s; (ii) MD-2s probe recognizes only the short isoform of MD-2. (B) Real-time polymerase chain reaction analysis for MD-2 expression: shown are the threshold cycles for total MD-2 (wild-type and short isoform) and short MD-2 in epithelial cells stimulated with IFN-γ and TNF-α. The short MD-2 isoform is not expressed in unstimulated cells (flat blue line). MD-2s (blue=unstimulated; dark blue=IFN-γ; purple=TNF-α stimulation for 8 h). Total MD-2 (red=unstimulated; light blue IFN-γ; blue=TNF-α).

[0045] FIG. **10** depicts HEK293 cells transiently transfected with a plasmid expressing MD-2s-Myc (lane 2 and 4) and subsequently treated with G418 in accordance with an embodiment of the present invention. Cell lysates were prepared (lanes 1 and 2) or culture supernatants were collected (lanes 3 and 4). Immunoprecipitations (IP) were performed using Ni-NTA beads. Samples were subsequently analyzed by SDS/PAGE and immunoblotted (IB) with an anti-Myc antibody. HEK293 cells were used as a negative control.

[0046] FIG. **11** depicts HEK293 cells that stably express MD-2 or MD-2s in accordance with an embodiment of the present invention. HEK293 cells were transiently transfected with plasmids expressing either MD-2-Myc or MD-2s-Myc and subsequently selected with G418. Culture supernatants from cells stably expressing MD-2s (lanes 1 and 2) or MD-2 (lanes 3 and 4) were collected and immunoprecipitations were performed using a control antibody (lanes 1 and 3) or with an anti-myc antibody (lanes 2 and 4). Samples were subsequently analyzed by SDS/PAGE and immunoblotted (IB) with an anti-Myc antibody.

[0047] FIG. **12** shows that MD-2 and MD-2S bind to the surface of TLR4-expressing cells in accordance with an embodiment of the present invention. HEK293T cells stably expressing fluorescent TLR4-mCitrine were transiently transfected with myc-tagged wild-type MD-2 or MD-2s and surface-stained with anti-myc antibody. (a) Cells analyzed by flow cytometry were gated to select single cells and the TLR4-positive population. Anti-myc staining of TLR4-mCitrine positive cells expressing MD-2 (top panel, thick line) or MD-2s (middle panel, thick line) and untransfected cells (thin line) is shown. (b) Confocal imaging shows that a subpopulation of cells expressing mCitrine-tagged TLR4 (green) co-express transfected MD-2 (red, top panel) or MD-2S (red, bottom panel). Co-localization of TLR4 and MD-2 isoforms on the cell surface is visualized in yellow.

[0048] FIG. **13** shows that MD-2 is tyrosine phosphorylated and that this phosphorylation is inhibited by herbimycin A and cytochalasin D. (A) HEK293 cells were transiently transfected with Flag-TLR4, Flag-MD-2 and CD14 constructs (lanes 2-7) or mock transfected (lane 1). 24 h later cells were left untreated (lanes 1 and 2) or stimulated with LPS (lanes 3-7). Flag-tagged proteins were immunoprecipitated with an anti-Flag Ab in cell lysates and analyzed by SDS-PAGE and immunoblotted with an anti-phosphotyrosine Ab (top panel), or an anti-Flag Ab (middle and lower panels). (B) HEK293 cells were transiently transfected with Flag-TLR4 and Flag-MD-2 (lanes 1-5). 24 hrs later, cells were pretreated for 2 hrs with herbimycin A at 0.5 μg/ml (lane 3) or 2.5 μg/ml (lane 4), or for 1 hr with 2 μM cytochalasin D (lane 5) prior to stimulation with LPS for 5 mins.

[0049] FIG. **14** shows that the mutant proteins MD-2-Y22F, MD-2-Y131F, and MD-2-Y22FY131F do not activate NF-κB as strongly as wild-type MD-2. (A) Schematic diagram showing the location of the tyrosine residues of MD-2. (B) HEK293 cells stably transfected with a NF-κB reporter gene and TLR4 were transiently transfected with wild-type MD-2, MD-2-Y22F, MD-2-Y34F, MD-2-Y36F, MD-2-Y42F, MD-2-Y65F, MD-2-Y75F, MD-2-Y79F, or MD-2-Y131F constructs, for 24 h. Cells were left untreated or stimulated with LPS for 6 hours and luciferase activity measured in cell lysates and expressed as fold induction relative to mock-transfected cells (EV). (C) and (D) HEK293 cells stably transfected with a NF-κB and IL-8 reporter gene and TLR4 were transiently transfected with wild-type MD-2, MD-2-Y22F, MD-2-Y131F, or MD-2-Y22FY131F constructs. Cells were left untreated or stimulated with LPS for 6 hours and luciferase activity measured in cell lysates and expressed as fold induction relative to mock-transfected cells (EV). (E) HEK293 cells were transfected with plasmids expressing the indicated mutant Flag-MD-2 proteins, wild type Flag-MD-2 or empty vector, plus Myc-TLR4 and CD14 constructs. The cells were stimulated with LPS for 15 minutes. Cell lysates were prepared and samples were analyzed by immunoblotting with an p38 or an anti-phospho-p38 antibody. Flag-tagged proteins were immunoprecipitated with an anti-Flag Ab in cell lysates and analyzed by SDS-PAGE and immunoblotted with an anti-phosphotyrosine Ab, or an anti-Flag Ab.

[0050] FIG. **15** depicts the structure of the TLR4-MD-2 complex. All figures are based on the published crystal structure of the TLR4-MD-2 receptor complex. The structure with PDB ID: 3FXI was modified with 3-D molecule viewer (a component of vector NTI Advance 11.0-Invitrogen). The surface was calculated using the Conolly method. (A) The structure of MD-2 (yellow) with the location of Y131 depicted in purple. (B) The structure of MD-2 as shown in (A) in complex with TLR-4 (Cyan) and with one more copy of the TLR-4 (blue)-MD-2 (green) complex. (C) Y131 is shown in purple, the overall structure of MD-2 (yellow) with the location of Y22 depicted in purple. (D) The structure of MD-2 as shown in (C) in complex with TLR-4 (Cyan) and with one more copy of TLR-4 (blue)-MD-2 (green) complex. The position of Y22 is shown in purple.

[0051] FIG. **16** shows that Lyn interacts with MD-2. (A) HEK293 cells were transiently transfected with MD-2, Flag-TLR4 and CD14 construct. 24 h later, cells were left untreated (lanes 1 and 2) or stimulated with LPS (lanes 3-5). Lyn proteins were immunoprecipitated with an anti-Lyn antibody in cell lysates and analyzed by SDS-PAGE and immunoblotted with an anti-Flag Ab (top panel), or an anti-Lyn Ab (lower panel). (B) HEK293 cells were transiently transfected with Flag-Lyn, Myc-TLR4 and HA-MD-2 and CD14 constructs. 24 h later, cells were left untreated (lanes 1 and 2) or stimulated with LPS (lanes 3-4). HA-tagged proteins were immunoprecipitated with an anti-HA Ab in cell lysates, and analyzed by SDS-PAGE and immunoblotted with an anti-Flag Ab. (C) HEK293 cells were transiently transfected with Flag-Lyn and HA-MD-2 construct. 24 h later, cells were left untreated (lanes 1 and 2) or stimulated with LPS (lanes 3-5). HA-tagged proteins were immunoprecipitated with an anti-HA Ab in cell lysates and analyzed by SDS-PAGE and immunoblotted with an anti-Flag Ab.

[0052] FIG. **17** shows that MD-2 tyrosine phosphorylation is inhibited by Lyn peptide inhibitor. (A) HEK293 cells were transiently transfected with TLR4 and Myc-MD-2 (lanes 1-6). 24 hrs later, cells were pretreated for 2 hrs with Lyn peptide inhibitor at 10, 20 or 30 μM, prior to stimulation with LPS for 10 mins (lanes 3-6). Myc-tagged proteins were immunoprecipitated with an anti-Myc Ab in cell lysates, and analyzed by SDS-PAGE and immunoblotted with an anti-phosphotyrosine Ab (top panel), or an anti-Myc Ab (lower panel). (B) HEK293 cells stably transfected with a NF-κB or IL-8 reporter gene and TLR4 were transiently transfected with wild-type MD-2 24 hrs later, cells were pretreated for 2 hrs with Lyn peptide inhibitor (μM) at indicated doses. Cells were left untreated or stimulated with LPS for 6 hours and luciferase activity measured in cell lysates and expressed as fold induction relative to untreated cells.

DESCRIPTION OF THE INVENTION

[0053] All references cited herein are incorporated by reference in their entirety as though fully set forth. Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Singleton et al., *Dictionary of Microbiology and Molecular Biology* 3rd ed., J. Wiley & Sons (New York, N.Y. 2001); March, *Advanced Organic Chemistry Reactions, Mechanisms and Structure* 5th ed., J. Wiley & Sons (New York, N.Y. 2001); and Sambrook and Russel, *Molecular Cloning: A Laboratory Manual* 3rd ed., Cold Spring Harbor Laboratory Press (Cold Spring Harbor, N.Y. 2001), provide one skilled in the art with a general guide to many of the terms used in the present application.

[0054] One skilled in the art will recognize many methods and materials similar or equivalent to those described herein, which could be used in the practice of the present invention. Indeed, the present invention is in no way limited to the methods and materials described. For purposes of the present invention, the following terms are defined below.

[0055] "Therapeutically effective amount" as used herein refers to that amount which is capable of achieving beneficial results in a patient in need of treatment. A therapeutically effective amount can be determined on an individual basis and will be based, at least in part, on consideration of the physiological characteristics of the mammal, the type of delivery system or therapeutic technique used and the time of administration relative to the progression of the disease.

[0056] "Treatment" and "treating," as used herein refer to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent, slow down and/or lessen the disease, even if the treatment is ultimately unsuccessful.

[0057] "Conditions," as used herein, may include, but are in no way limited to any condition or disease in which modulation of TLR4 signaling would be beneficial, including partial or complete TLR4 inhibition. Conditions may include, but are in no way limited to, sepsis, septic shock, inflammation, gram negative bacterial infections, gram negative bacterial lung infections, immune responses such as atherosclerosis and other diseases or conditions resulting from or characterized by TLR4 activation and/or an over-exaggerated MD2/TLR4-induced immune response.

[0058] "Isolated" nucleic acid as used herein refers to nucleic acids (e.g., DNA or RNA) that are isolated relative to other nucleic acids in the source material. For example, "isolated DNA" that encodes MD-2s (including cDNA) refers to DNA isolated relative to DNA which encodes polypeptides other than MD-2s.

[0059] "Purified" protein or polypeptide as used herein refer to proteins or polypeptides that are purified relative to other proteins or polypeptides in the source material. For example, "purified MD-2s" refers to MD-2s purified relative to proteins and polypeptides other than MD-2s.

[0060] "Binds specifically" as used herein refers to the act of an antibody binding to its antigen and is intended to exclude low-level, non-specific binding that may occur between random proteins. "Binds specifically" as used herein is not intended and does not imply that the antibody will not bind to any protein other than the proteins or polypeptides as disclosed herein since antibodies can cross-react with any protein that includes the relevant epitope.

[0061] An inappropriately excessive immune response causes considerable morbidity and mortality in a number of diseases. For example, sepsis is among the most common causes of death in the United States, with over 750,000 cases presenting annually, of which more than one-quarter are fatal (Angus et al. (2001) Crit Care Med 29, 1303-1310). Excessive inflammation is the hallmark of a number of related infectious pathologies as well, including acute respiratory distress syndrome and multiple organ failure (Miller et al. (2005) Nat Rev Micro 3, 36-46). LPS derived from bacterial sources can contribute to these diseases, and does so by interacting with a complex consisting of TLR4, CD14, LBP, and MD-2. To circumvent an excessive host immune response to LPS, it is imperative that TLR4 signal transduction be tightly regulated, but the precise molecular mechanisms by which this is accomplished are only partly understood.

[0062] The most direct way to attenuate TLR4 signaling is by targeting specific proteins at the extracellular level, akin to the method employed by the soluble TLR4 decoy receptors. Another mechanism dispatches the LPS receptor complex for endosomal trafficking, which results in lysosomal degradation of TLR4 and termination of LPS signal transduction (Husebye et al. (2006) EMBO J 25, 683-692; Latz et al. (2002) J Biol Chem 277, 47834-47843). In addition, the relative levels of LBP, CD14, MD-2 and TLR4 all have a direct effect on the potency of the host response to LPS (Abreu et al. (2001) J Immunol 167, 1609-1616; Kitchens et al. (2003) J Endotoxin Res 9, 113-118). However, despite the elucidation of the MD-2 and TLR4 crystalline structures (Kim et al. (2007) Cell 130, 906-917; Ohto et al. (2007) Science 316, 1632-1634), it remains unclear as to the precise mechanism by which LPS interacts with the MD-2/TLR4 complex. While numerous studies have shown that LPS directly associates with both TLR4 and MD-2 (Poltorak et al. (2000) Proc Natl Acad Sci USA 97, 2163-2167; da Silva Correia et al. (2001) J Biol Chem 276, 21129-21135), it has also been proposed that a monomeric LPS:MD-2 complex, rather than LPS alone, is the true ligand for TLR4 (Gioannini et al. (2004) Proc Natl Acad Sci USA 101, 4186-4191; Visintin et al. (2005) J Immunol 175, 6465-6472; Prohinar et al. (2007) J Biol Chem 282, 1010-1017).

[0063] It is clear that myeloid differentiation-2 (MD-2) is an essential component of the signaling receptor complex that recognizes and initiates an innate immune response to bacterial LPS (Shimazu et al. (1999) J Exp Med 189, 1777-1782). At the receptor level, LPS binding protein (Schumann et al. (1990) Science 249, 1429-1431), CD14 (Wright et al. (1990) Science 249, 1431-1433) and TLR4 (Inohara et al. (2002) Trends Biochem Sci 27, 219-221; Kato et al. (2000) Blood 96, 362-364; Visintin et al. (2001) Proc Natl Acad Sci USA 98, 12156-12161) are the also required in this signaling event, as is evidenced by the fact that mice deficient in either of these proteins or MD-2 (Shimazu et al. (1999) J Exp Med 189, 1777-1782) display a similar hyporesponsiveness to LPS challenge. For signaling to occur, LPS is first extracted from the bacterial membrane by LBP, which is then transferred to CD14 in its monomeric form. CD14 subsequently delivers LPS to MD-2, which is a secreted glycoprotein that belongs to the MD-2-related lipid recognition (ML) family (Inohara et al. (2002) Trends Biochem Sci 27, 219-221), the signature sequence of which is a secretion signal. MD-2 may be present in a soluble form or bound to the ectodomain of TLR4 (Kato et al. (2000) BLOOD 96, 362-364; Visintin et al. (2001) Proc Natl Acad Sci USA 98, 12156-12161)). Upon LPS binding, a receptor multimer composed of two copies of the TLR4-MD-2-LPS complex is formed (Park et al. (2009) Nature 458, 1191-1195), which triggers a downstream signaling cascade, culminating in the activation of transcription factors such as nuclear factor-κB (NF-κB) and the interferon regulatory factors (IRFs), which in turn induce various immune and inflammatory genes.

[0064] Upon ligand binding, the TLR signaling pathway initiates a cascade of serine, threonine and tyrosine phosphorylation events. Interestingly, several members of the TLR family are also tyrosine phosphorylated, including TLR2 (Arbibe et al. (2000) Nat Immunol 1, 533-540), TLR3 (Sarkar et al. (2004) Nat Struct Mol Biol 11, 1060-1067; Sarkar et al. (2007) J Biol Chem 282, 3423-3427; Sarkar et al. (2003) J Biol Chem 278, 4393-4396), and TLR4 (Medvedev et al. (2007) J Biol Chem 282, 16042-16053; Chen et al. (2003) Am J Physiol Lung Cell Mol Physiol 284, 607-613). To date the identity of the kinases involved have yet to be elucidated, however, in the case of TLR4, the Src kinase Lyn has been implicated in this posttranslational modification (Medvedev et al. (2007) J Biol Chem 282, 16042-16053). In addition to TLRs, the TLR adapter proteins, MyD88 (Ojaniemi et al. (2003) Eur J Immunol 33, 597-605), MyD88-adapter like (Gray et al. (2006) J Biol Chem 281, 10489-10495), TRIF (Bin et al. (2003) J Biol Chem 278, 24526-24532) and TRAM (McGettrick et al. (2006) Proc Natl Acad Sci USA 103, 9196-9201) have also been shown to be phosphorylated.

[0065] Described herein, the inventors further elucidate the complexities involved in averting an excessive and dysregulated immune response to LPS by the identification of a naturally occurring alternatively spliced isoform of human MD-2, which the inventors have termed MD-2s. The inventors report that human MD-2s is generated by the removal of exon 2 from MD-2, which leads to an in-frame deletion of 30 amino acids spanning positions 39-69, and one amino acid substitution (D38G). Under similar conditions and using primers homologous to the murine MD-2 gene, a corresponding murine splice variant was not detected. The mRNA expression profile of MD-2s revealed that it is ubiquitously expressed, suggesting that this isoform may perform a widespread role in regulating LPS signal transduction. The inventors also detected MD-2s protein, indicating that MD-2s mRNA is not subject to nonsense-mediated decay, and found that similar to wild type MD-2, multiple forms of MD-2s were detected upon overexpression. Glycosidase treatment established that the slower migrating forms of MD-2s represented glycosylated MD-2s protein. The glycosylation sites of MD-2 are located to the extremity of the cavity region and are believed to play a role in the secretion and stability of the protein (Ohto et al. (2007) Science 316, 1632-1634). Closer analysis of MD-2s confirmed that it is also stably secreted.

[0066] The functional studies provide significant insights into a novel regulatory mechanism employed to control TLR4 signaling upon exposure to LPS. Ectopic expression of the MD-2s isoform failed to trigger NF-κB activation following LPS treatment, suggesting that MD-2s interferes with normal LPS-induced signaling. Interaction studies demonstrated that MD-2s maintains the ability to bind TLR4. This may have been predicted, given that MD-2s retains most of the residues reported to be essential in mediating a MD-2/TLR4 interaction, with the exception of 166 and R68 (Kim et al. (2007) Cell 130, 906-917; Re et al. (2003) J Immunol 171, 5272-5276). In addition, MD-2s interacts directly with both MD-2 and LPS. Thus, MD-2s binds to LPS, TLR4, and MD-2.

[0067] Two theoretical models of LPS-induced MD-2/TLR4 dimerization have been proposed. Model 1 proposes that MD-2 first binds LPS, which induces a structural change in MD-2 that in turn facilitates an interaction between a second TLR4 molecule. In model 2, the remaining chains of LPS that are not accommodated in the ligand binding pocket are predicted to interact with a second TLR4 (Kim et al. (2007) Cell 130, 906-917). An independent study also predicts that the binding of LPS promotes TLR4 homodimerization of the TLR4 ectodomains (Walsh et al. (2008) J Immunol

181, 1245-1254). It is thought unlikely that MD-2 homodimerization is required for receptor dimerization (Kim et al. (2007) Cell 130, 906-917), which concurs with previous reports indicating that monomeric MD-2 preferentially binds TLR4 and confers LPS responsiveness more efficiently than MD-2 multimers (Re et al. (2002) J Biol Chem 277, 23427-23432).

[0068] The results showing that MD-2s suppresses LPS-induced TLR4 activation are most consistent with at least two possibilities. First, MD-2s could be forming a complex with MD-2; this would reduce the amount of active monomeric MD-2 available to bind both LPS and TLR4, which could in turn suppress TLR4 activation. Secondly, MD-2s could interact directly with LPS, and then compete with the MD-2:LPS complex for binding to TLR4. These possibilities are not mutually exclusive, and either or both could be operative, the net effect is still the same: MD-2s suppresses LPS-induced TLR4 activation by acting as a competitive inhibitor of the active MD2:LPS:TLR4 signaling assembly.

[0069] In addition, there is another possible mechanism by which MD-2s could interfere with TLR4 activation. MD-2s retains the His155 and Phe126 residues, both of which are required for TLR4 dimerization. However, the missing exon may alter the tertiary structure such that these essential residues are no longer able to promote an effective interaction between MD-2s and a second TLR4 molecule, and the subsequently reduced TLR4 dimerization might reduce TLR4-dependent signaling. Also this could minimize the formation of a TLR4:MD-2 heterodimer due to the number of TLR4:MD2 complexes being proportionally reduced as the number of TLR4:MD-2s complexes increase.

[0070] Based on these results and while not wishing to be bound to any particular theory, the inventors believe that MD-2s functionally behaves like a decoy co-receptor by binding LPS and TLR4 to form a non-functional complex that does not activate NF-κB (FIG. **7**, left panel). In addition, MD-2s heterodimerizes with MD-2, thus decreasing the availability of the more active monomeric MD-2, which in turn would be predicted to further dampen LPS-induced NF-κB activation (FIG. **7**, right panel). The inventors are currently investigating whether or not MD-2s interferes with formation of TLR4:TLR4 dimers (FIG. **7**, middle panel). Nevertheless, collectively, the results define an important role for MD-2s in regulating the LPS/TLR4 signal transduction pathway.

[0071] According to embodiments disclosed herein, the inventors determined the role of MD-2 in TLR4 signaling and demonstrated that MD-2 undergoes tyrosine phosphorylation upon LPS stimulation and that this phosphorylation event is required for LPS-induced NF-κB activation. Phosphorylation is a highly conserved mechanism that can be employed to regulate protein function. Indeed several studies have illustrated that the TLR signaling pathway is dependent on a series of phosphorylation events. As disclosed herein, the inventors discovered that similar to TLR2, TLR3, and TLR4, MD-2 also undergoes tyrosine phosphorylation in response to LPS. Furthermore, the disclosed results suggest that phosphorylation of MD-2 on specific tyrosines are required for NF-κB activation and can be a regulatory step employed to curtail an over exuberant host immune response. Furthermore, the inventors confirmed that this MD-2 tyrosine phosphorylation was specific to LPS stimulation, as it did not occur following stimulation with IL-1β or TNFα.

[0072] As described herein, this phosphorylation event is inhibited by the tyrosine kinase inhibitor herbimycin A. Furthermore, an endocytosis inhibitor, cytochalasin D, blocks the tyrosine phosphorylation of MD-2 in cells stimulated with LPS. The inventors have identified two residues, located at positions 22 and 131, as possible phospho-accepting tyrosines. Mutant proteins in which these tyrosines were altered to phenylalanine have a significantly reduced ability to activate LPS-induced NF-κB and IL-8. In addition, the inventors determined that Lyn interacts with MD2 and that a Lyn-binding peptide inhibitor specifically abolishes MD-2 tyrosine phosphorylation, thus according to certain embodiments Lyn is the kinase required for MD-2 tyrosine phophorylation. The inventors have shown that MD-2 as a phosphoprotein and have demonstrated the importance of this posttranslational event as a mechanism required for MD-2-TLR4-LPS signaling.

[0073] Based on these results and while not wishing to be bound to any particular theory, the inventors believe that Lyn is responsible for LPS stimulated MD-2 tyrosine phosphorylation. LPS-induced tyrosine phosphorylation of MD-2 is specific, it is blocked by the tyrosine kinase inhibitor, Herbimycin A, and by an inhibitor of endocytosis, Cytochalsin-D, suggesting that MD-2 phosphorylation occurs during trafficking of MD2 and not on cell surface. Furthermore, the inventors have identified two possible phospho-accepting tyrosine residues at positions 22 and 131. Mutant proteins in which these tyrosines were changed to phenylalanine have significantly diminished ability to activate NF-κB in response to LPS. In addition, MD2 co-precipitates with Lyn kinase and pretreatment with a Lyn-binding peptide inhibitor abolished MD2 tyrosine phosphorylation, suggesting that Lyn is a likely candidate to be the kinase required for MD-2 tyrosine phophorylation. The currently disclosed studies demonstrate that tyrosine phosphorylation of MD-2 is important for signaling following exposure to LPS and underscores the importance of this event in mediating an efficient and prompt immune response.

[0074] Embodiments of the present invention are based on the inventors' identification of the alternatively spliced isoform of human MD-2. Similar to wild-type MD-2, it is demonstrated herein that MD-2s is secreted and glycosylated. In addition, despite its ability to interact with TLR4 and LPS, MD-2s fails to mediate NF-κB activation following LPS exposure. Importantly, MD-2s is identified as a negative regulator of LPS-induced NF-κB activation. The inventors' results therefore, define a novel mechanism that can curtail excessive activation of the innate immune response following initiation of the LPS/TLR4 signal transduction pathway.

[0075] Further embodiments of the present invention are based on the inventors' discovery that MD-2 is phosphorylated on certain tyrosine residues. In particular, two of the substitutions, MD-2-Y22F and MD-2-Y131F, resulted in a 50% decrease in NF-κB activity upon LPS stimulation, indicating that these residues were critical for maximal NF-κB activation and could possibly be phospho-accepting residues. Importantly, by analyzing the published crystal structure of MD-2, the inventors determined that the hydroxyl groups of both MD2 tyrosine residues, located at positions 22 and 131, are surface exposed thereby permitting phosphorylation of the aforementioned residues to occur.

Still further embodiments of the present invention relate to the kinase for MD-2 phosphorylation, Lyn kinase. Lyn kinase is recruited to TLR4 as well as to CD14 upon LPS stimulation and has also been implicated as the kinase involved in the tyrosine phosphorylation of TLR4. According to embodiments described herein, MD-2 has been determined to also be present in a complex with TLR4 and Lyn and that MD-2 can immunoprecipitate Lyn in the absence of CD14 and TLR4. Furthermore the inventors determined that LPS-induced MD-2 tyrosine phosphorylation is strongly abolished following pre-treatment with a Lyn-binding peptide inhibitor. Since MD-2 and Lyn appear to directly interact with one another, and MD-2 tyrosine phosphorylation is diminished following Lyn kinase inactivation, according to certain embodiments, that similar to TLR4, Lyn kinase is involved in the tyrosine phosphorylation of MD-2

TABLE 1

Sequences relating to human MD-2s.

SEQ ID NO.	Sequence	Description
1	MLPFLFFSTLFSSIFTEAQKQYWVCNSSDASISYTYC GRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDY SFCRALKGETVNTTISFSFKGIKFSKGKYKCVVEAIS GSPEEMLFCLEFVILHQPNSN	Expressed protein
2	EAQKQYWVCNSSDASISYTYCGRDLKQLYFNLYIT VNTMNLPKRKEVICRGSDDDYSFCRALKGETVNTT ISFSFKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVIL HQPNSN	Secreted protein
3	KMQYPISINVNPCIELKGSKGLLHIFYIP	Polypeptide encoded by Exon 2
4	atgttacca tttctgtttt tttccaccct gttttcttcc atatttactg aagctcagaa gcagtattgg gtctgcaact catccgatgc aagtatttca tacacctact gtgggagaga tttaaagcaa ttatatttca atctctatat aactgtcaac accatgaatc ttccaaagcg caaagaagtt atttgccgag gatctgatga cgattactct ttttgcagag ctctgaaggg agagactgtg aatacaacaa tatcattctc cttcaaggga ataaaatttt ctaagggaaa atacaaatgt gttgttgaag ctatttctgg gagcccagaa gaaatgctct tttgcttgga gtttgtcatc ctacaccaac ctaattcaaa ttag	Nucleotide sequence for expressed protein
5	gaagctcagaa gcagtattgg gtctgcaact catccgatgc aagtatttca tacacctact gtgggagaga tttaaagcaa ttatatttca atctctatat aactgtcaac accatgaatc ttccaaagcg caaagaagtt atttgccgag gatctgatga cgattactct ttttgcagag ctctgaaggg agagactgtg aatacaacaa tatcattctc cttcaaggga ataaaatttt ctaagggaaa atacaaatgt gttgttgaag ctatttctgg gagcccagaa gaaatgctct tttgcttgga gtttgtcatc ctacaccaac ctaattcaaa ttag	Nucleotide sequence for secreted protein
6	ataaaatgcaatacccaatttcaattaatgttaacccctgtctagaattgaaaagatc caaaggattattgcacattttctacattccaa	Nucleotide sequence of Exon 2

[0076] One embodiment of the present invention provides for a purified MD-2s protein.

[0077] In one embodiment, a purified polypeptide, the amino acid sequence of which comprises SEQ ID NO:1 is provided. In a particular embodiment, the purified polypeptide consists of the amino acid sequence as set forth in SEQ ID NO: 1. In a further embodiment, the purified polypeptide is glycosylated.

[0078] In another embodiment, a purified polypeptide, the amino acid sequence of which comprises SEQ ID NO:2 is provided. In a particular embodiment, the purified polypeptide consists of the amino acid sequence as set forth in SEQ ID NO:2. In a further embodiment, the purified polypeptide is glycosylated.

[0079] In another embodiment, a purified polypeptide comprising 10, 20 or 30 consecutive residues of SEQ ID NO:1 or SEQ ID NO:2 is provided. One of ordinary skill in the art will readily be able to screen for the purified polypeptide's ability to modulate (e.g., inhibit, induce) TLR signaling without undue burden using methods known in the art and as described herein.

[0080] In another embodiment, a purified immunogenic polypeptide comprising an immunogenic domain comprising ten consecutive residues of SEQ ID NO:1 or SEQ ID NO:2. These purified immunogenic polypeptides can be useful for producing antibodies that bind specifically to MD-2s.

[0081] In other embodiments, the present invention provides a purified polypeptide comprising residues N26 to N84 of SEQ ID NO:1 or residues N10 to N68 of SEQ ID NO:2. In additional embodiments, the present invention provides a purified polypeptide comprising N-glycosylated sites at positions N26 and N84 of SEQ ID NO:1 or N-glycosylated sites at positions N10 and N68 of SEQ ID NO:2.

[0082] In additional embodiments, the present invention provides a purified polypeptide comprising residues involved in the dimerization interface of the TLR4/MD-2/LPS complex. In one embodiment, the purified polypeptide comprises residues V52 to F96 of SEQ ID NO:1, or residues V36 to F80 of SEQ ID NO:2. In another embodiment, purified polypeptide comprising one or more residues selected from the group consisting of V52, M55, L57, R60, S88, K92, G93, I94, K95, and F96 of SEQ ID NO:1; or one or more residues selected from the group consisting of V36, M39, L41, R44, S72, K76, G77, I78, K79, and F80 of SEQ ID NO:2: (Park et al., *The structural basis of lipopolysaccharide recognition by the TLR4-MD-2 complex*, doi:10.1038/nature07830).

[0083] In further embodiments, the present invention provides a purified polypeptide comprising residues C37 to

C118, or residues C65 and/or C75. In additional embodiments, the present invention provides a purified polypeptide comprising C37 and/or C118, which are residues involved in the second disulphide bond; or C65 and/or C75, which are residues involved in the third disulphide bond of SEQ ID NO:1.

[0084] In another embodiment, a purified polypeptide, the amino acid sequence of which comprises a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:1 or SEQ ID NO:2 is provided. In a further embodiment, the purified polypeptide is glycosylated.

[0085] In another embodiment, a purified polypeptide comprising the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2, but with 0 to 29 conservative amino acid substitution is provided. In particular embodiments, the purified polypeptides have 0 to 20, 1-20, 0-10, or 1-10 conservative amino acid substitutions. In a further embodiment, the purified polypeptide is glycosylated.

[0086] In another embodiment, a purified polypeptide comprising the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2, but with 0 to 29 amino acid insertions, deletions and/or substitutions is provided. In a particular embodiment, the purified polypeptide has 0 to 20, 1-20, 0-10, or 1-10 amino acid insertions, deletions and/or substitutions. In a further embodiment, the purified polypeptide is glycosylated.

[0087] In another embodiment, a purified polypeptide consisting of the amino acid sequence of SEQ ID NO:3 is provided. In another embodiment, a purified polypeptide, the amino acid sequence of which comprises a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:3 is provided. These polypeptides may be useful for modulating LPS-induced signaling and/or TLR signaling.

[0088] In further embodiments, a purified polypeptide, the amino acid sequence of which comprises SEQ ID NO:17 is provided. In a particular embodiment, the purified polypeptide consists of the amino acid sequence as set forth in SEQ ID NO:17. In a further embodiment, the purified polypeptide is glycosylated. In another embodiment, a purified polypeptide, the amino acid sequence of which comprises a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:17 is provided. These polypeptides may be useful for modulating LPS-induced signaling and/or TLR signaling.

[0089] In another embodiments, a purified polypeptide, the amino acid sequence of which comprises SEQ ID NO:25 is provided. In a particular embodiment, the purified polypeptide consists of the amino acid sequence as set forth in SEQ ID NO:25. In a further embodiment, the purified polypeptide is glycosylated. In another embodiment, a purified polypeptide, the amino acid sequence of which comprises a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:25 is provided. These polypeptides may be useful for modulating LPS-induced signaling and/or TLR signaling.

[0090] In further embodiments, a purified polypeptide, the amino acid sequence of which comprises SEQ ID NO:26 is provided. In a particular embodiment, the purified polypeptide consists of the amino acid sequence as set forth in SEQ ID NO:26. In a further embodiment, the purified polypeptide is glycosylated. In another embodiment, a purified polypeptide, the amino acid sequence of which comprises a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:25 is provided. These polypeptides may be useful for modulating LPS-induced signaling and/or TLR signaling.

[0091] In various embodiments, the present invention provides pharmaceutical compositions including a pharmaceutically acceptable excipient along with a therapeutically effective amount of MD-2s or a polypeptide as described above. "Pharmaceutically acceptable excipient" means an excipient that is useful in preparing a pharmaceutical composition that is generally safe, non-toxic, and desirable, and includes excipients that are acceptable for veterinary use as well as for human pharmaceutical use. Such excipients may be solid, liquid, semisolid, or, in the case of an aerosol composition, gaseous.

[0092] In various embodiments, the pharmaceutical compositions according to the invention may be formulated for delivery via any route of administration. "Route of administration" may refer to any administration pathway known in the art, including but not limited to aerosol, nasal, oral, transmucosal, transdermal or parenteral. "Transdermal" administration may be accomplished using a topical cream or ointment or by means of a transdermal patch. "Parenteral" refers to a route of administration that is generally associated with injection, including intraorbital, infusion, intraarterial, intracapsular, intracardiac, intradermal, intramuscular, intraperitoneal, intrapulmonary, intraspinal, intrasternal, intrathecal, intrauterine, intravenous, subarachnoid, subcapsular, subcutaneous, transmucosal, or transtracheal. Via the parenteral route, the compositions may be in the form of solutions or suspensions for infusion or for injection, or as lyophilized powders. Via the enteral route, the pharmaceutical compositions can be in the form of tablets, gel capsules, sugar-coated tablets, syrups, suspensions, solutions, powders, granules, emulsions, microspheres or nanospheres or lipid vesicles or polymer vesicles allowing controlled release. Via the parenteral route, the compositions may be in the form of solutions or suspensions for infusion or for injection. Via the topical route, the pharmaceutical compositions based on compounds according to the invention may be formulated for treating the skin and mucous membranes and are in the form of ointments, creams, milks, salves, powders, impregnated pads, solutions, gels, sprays, lotions or suspensions. They can also be in the form of microspheres or nanospheres or lipid vesicles or polymer vesicles or polymer patches and hydrogels allowing controlled release. These topical-route compositions can be either in anhydrous form or in aqueous form depending on the clinical indication. Via the ocular route, they may be in the form of eye drops.

[0093] The pharmaceutical compositions according to the invention can also contain any pharmaceutically acceptable carrier. "Pharmaceutically acceptable carrier" as used herein refers to a pharmaceutically acceptable material, composition, or vehicle that is involved in carrying or transporting a compound of interest from one tissue, organ, or portion of the body to another tissue, organ, or portion of the body. For example, the carrier may be a liquid or solid filler, diluent, excipient, solvent, or encapsulating material, or a combination thereof. Each component of the carrier must be "pharmaceutically acceptable" in that it must be compatible with the other ingredients of the formulation. It must also be suitable for use in contact with any tissues or organs with which it may come in contact, meaning that it must not carry a risk of toxicity, irritation, allergic response, immunogenicity, or any other complication that excessively outweighs its therapeutic benefits.

[0094] The pharmaceutical compositions according to the invention can also be encapsulated, tableted or prepared in an emulsion or syrup for oral administration. Pharmaceutically acceptable solid or liquid carriers may be added to enhance or stabilize the composition, or to facilitate preparation of the composition. Liquid carriers include syrup, peanut oil, olive oil, glycerin, saline, alcohols and water. Solid carriers include starch, lactose, calcium sulfate, dihydrate, terra alba, magnesium stearate or stearic acid, talc, pectin, acacia, agar or gelatin. The carrier may also include a sustained release material such as glyceryl monostearate or glyceryl distearate, alone or with a wax.

[0095] The pharmaceutical preparations are made following the conventional techniques of pharmacy involving milling, mixing, granulation, and compressing, when necessary, for tablet forms; or milling, mixing and filling for hard gelatin capsule forms. When a liquid carrier is used, the preparation will be in the form of a syrup, elixir, emulsion or an aqueous or non-aqueous suspension. Such a liquid formulation may be administered directly p.o. or filled into a soft gelatin capsule.

[0096] The pharmaceutical compositions according to the invention may be delivered in a therapeutically effective amount. The precise therapeutically effective amount is that amount of the composition that will yield the most effective results in terms of efficacy of treatment of a condition in a given subject. This amount will vary depending upon a variety of factors, including but not limited to the characteristics of the therapeutic compound (including activity, pharmacokinetics, pharmacodynamics, and bioavailability), the physiological condition of the subject (including age, sex, disease type and stage, general physical condition, responsiveness to a given dosage, and type of medication), the nature of the pharmaceutically acceptable carrier or carriers in the formulation, and the route of administration. One skilled in the clinical and pharmacological arts will be able to determine a therapeutically effective amount through routine experimentation, for instance, by monitoring a subject's response to administration of a compound and adjusting the dosage accordingly. For additional guidance, see Remington: The Science and Practice of Pharmacy (Gennaro ed. 20th edition, Williams & Wilkins PA, USA) (2000).

[0097] Typical dosages of an effective amount of MD-2s or a polypeptide as described above can be as indicated to the skilled artisan by the in vitro responses or responses in animal models. Such dosages typically can also be reduced by up to about one order of magnitude in concentration or amount without losing the relevant biological activity. Thus, the actual dosage can depend upon the judgment of the physician, the condition of the patient, and the effectiveness of the therapeutic method based, for example, on the in vitro responsiveness of the relevant primary cultured cells or histocultured tissue sample or the responses observed in the appropriate animal models.

[0098] Another embodiment of the present invention provides for a nucleic acid or an isolated nucleic acid encoding the MD-2s protein or a polypeptide as described above.

[0099] In one embodiment, a nucleic acid, the nucleotide sequence of which comprises SEQ ID NO:4 is provided. In another embodiment, the nucleic acid is isolated and/or consists of SEQ ID NO:4.

[0100] In another embodiment, a nucleic acid, the nucleotide sequence of which comprises SEQ ID NO:5 is provided. In another embodiment, the nucleic acid is isolated and/or consists of SEQ ID NO:5.

[0101] In another embodiment, an isolated DNA, the nucleotide sequence of which consists of SEQ ID NO:4 or SEQ ID NO:5 is provided.

[0102] In another embodiment, a nucleic acid, the nucleotide sequence of which comprises a degenerate variant of SEQ ID NO:4 or SEQ ID NO:5 is provided. In another embodiment, the nucleic acid is isolated and/or consists of SEQ ID NO:4 or SEQ ID NO:5.

[0103] In another embodiment, an isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, the nucleotide sequence of which consists of SEQ ID NO:4, SEQ ID NO:5 or a complement of SEQ ID NO:4 or SEQ ID NO:5 is provided. In a particular embodiment, the hybridization probe comprises SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9.

[0104] In another embodiment, an isolated nucleic acid comprising a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:4 or SEQ ID NO:5, wherein the nucleic acid encodes a polypeptide that binds to TLR4 or LPS is provided. In another embodiment, the isolated nucleic acid consists of a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:4 or SEQ ID NO:5.

[0105] In another embodiment, an isolated nucleic acid, the nucleotide sequence of which encodes a polypeptide at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:1 or SEQ ID NO:2, wherein the polypeptide binds to TLR4 or LPS is provided.

[0106] In another embodiment, an isolated nucleic acid comprising a sequence that encodes a polypeptide comprising the sequence of SEQ ID NO:1 or SEQ ID NO:2 with up to 10, 15, 20 or 25 conservative amino acid substitutions, wherein the polypeptide binds TLR4 or LPS, is provided. In a particular embodiment, the isolated nucleic acid consists of the sequence that encodes a polypeptide comprising the sequence of SEQ ID NO:1 or SEQ ID NO:2 with up to 10, 15, 20 or 25 conservative amino acid substitutions.

[0107] In another embodiment, an isolated nucleic acid comprising a sequence that encodes a polypeptide comprising the sequence of SEQ ID NO:1 or SEQ ID NO:2 with up to 10, 15, 20 or 25 amino acid insertions, deletions and/or substitutions, wherein the polypeptide binds to TLR4 or LPS, is provided. In another embodiment, the isolated nucleic acid consists of the sequence that encodes a polypeptide comprising the sequence of SEQ ID NO:1 or SEQ ID NO:2 with up to 10, 15, 20 or 25 amino acid insertions, deletions and/or substitutions.

[0108] Another embodiment provides for a nucleic acid comprising exon 2 of human MD-2 gene. In one embodiment, a nucleic acid, the nucleotide sequence of which comprises SEQ ID NO:6 is provided. In another embodiment, the nucleic acid is isolated and consists of SEQ ID NO:6.

[0109] In another embodiment, an isolated nucleic acid comprising a sequence that encodes a polypeptide comprising the sequence of SEQ ID NO:3 is provided.

[0110] Another embodiment of the present invention provides for a PCR primer and/or a nucleic acid probe. The primer and/or probe can be used to identify the presence or absence of MD2s. In one embodiment, the PCR primer and/or nucleic acid probe is a nucleic acid comprising SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9. In another embodiment, the

PCR primer and/or nucleic acid probe comprises a nucleic acid at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9. In another embodiment, the PCR primer and/or nucleic acid probe hybridizes under highly stringent conditions to a region comprising exon 1 and exon 3 or a fragment thereof of MD-2s. In one particular embodiment, the PCR primer and/or nucleic acid probe hybridizes under highly stringent conditions to about 20 nucleotides of exon 1 and about 20 nucleotides of exon 3. In other particular embodiments, the PCR primer and/or nucleic acid probe hybridizes under highly stringent conditions to about 10 to 20 nucleotides of exon 1 and about 10 to 20 nucleotides of exon 3. In other particular embodiments, the PCR primer and/or nucleic acid probe hybridizes under highly stringent conditions to about 15 to 20 nucleotides of exon 1 and about 15 to 20 nucleotides of exon 3. In another particular embodiment, the PCR primer and/or nucleic acid probe hybridizes under highly stringent conditions to about 15, 14, 13, 12, 11 or 10 nucleotides of exon 1 and about 15, 14, 13, 12, 11 or 10 nucleotides of exon 3.

[0111] In another embodiment, an expression vector comprising a nucleic acid as described above operably linked to an expression control sequence is provided. In various embodiments, the expression vector and expression control sequence may be any expression vector or expression control sequence known in the art or as described herein. Examples of expression vectors include but are not limited to pCDNA3.1, pCMV-HA and pEF-BOS. Examples of expression control sequences include but are not limited to human cytomegalovirus immediate early (CMV) promoter and EF 1-α promoter region.

[0112] In another embodiment, a cultured cell comprising the expression vector comprising a nucleic acid as described above is provided.

[0113] In another embodiment, a cultured cell comprising a nucleic acid as described above, operably linked to an expression control sequence is provided. In various embodiments, the expression control sequence may be any expression control sequence known in the art or as described herein.

[0114] In another embodiment, a cultured cell transfected with an expression vector comprising a nucleic acid as described above or a progeny of said cell, wherein the cell expresses a polypeptide as described above is provided.

[0115] Another embodiment of the present invention provides for a method of producing MD-2s or a polypeptide as described above is provided.

[0116] In one embodiment, the method comprises culturing a cultured cell described above under conditions permitting expression of the polypeptide. In a further embodiment, the method comprises purifying the polypeptide from the cell or the medium of the cell.

[0117] In another embodiment, the method comprises culturing a cultured cell described above under conditions permitting expression under the control of the expression control sequence, and purifying the polypeptide from the cell or the medium of the cell.

[0118] Another embodiment of the present invention provides for methods of using the isolated MD-2s protein, or compositions comprising the isolated MD-2s protein.

[0119] In one embodiment, the method is for inhibiting TLR4 signaling in a subject in need thereof. The method comprises providing a purified MD-2s protein or polypeptide as described above and administering the purified MD-2s protein or polypeptide as described above to the subject. The purified MD-2s protein or polypeptide as described above may be in a composition that further comprises a pharmaceutically acceptable carrier or a pharmaceutically acceptable excipient.

[0120] In one embodiment, the method is for inhibiting LPS signaling in a subject in need thereof. The method comprises providing a purified MD-2s protein or polypeptide as described above and administering the purified MD-2s protein or polypeptide as described above to the subject. The purified MD-2s protein or polypeptide as described above may in a composition that further comprises a pharmaceutically acceptable carrier or a pharmaceutically acceptable excipient.

[0121] In another embodiment, the method is for treating a condition mediated by TLR4 signaling or reducing the likelihood of developing a condition mediated by TLR signaling in a subject in need thereof. The method comprises providing a purified MD-2s protein or a polypeptide as described above and administering the purified MD-2s protein or polypeptide as described above to the subject. The purified MD-2s protein or polypeptide may be in a composition that further comprises a pharmaceutically acceptable carrier and/or a pharmaceutically acceptable excipient. In various embodiments, the condition is sepsis, septic shock, inflammation, gram negative bacterial infection, gram negative bacterial lung infection and/or immune response such as atherosclerosis.

[0122] Another embodiment of the present invention provides a method of detecting the presence or absence of a nucleic acid that encodes MD-2s in a subject. The method comprises providing a PCR primer or nucleic acid probe as described above; and detecting the presence or absence of a second nucleic acid that encodes MD-2s in a biological sample of the subject, wherein the presence of the second nucleic acid indicates the presence of MD-2s and the absence of the second nucleic acid indicates the absence of MD-2s. In one embodiment, the method comprises providing a first nucleic acid, the nucleotide sequence of which comprises SEQ ID NO:7, SEQ ID NO: 8, or SEQ ID NO:9; and detecting the presence or absence of a second nucleic acid that encodes MD-2s in a biological sample of the subject, wherein the presence of the second nucleic acid indicates the presence of MD-2s and the absence of the second nucleic acid indicates the absence of MD-2s. These methods may further comprise reporting the presence or absence of the second nucleic acid. For example, a laboratory performing the test may report the results to a medical practitioner, such as the subject's doctor and/or the subject's doctor may report the results to the subject. In other non-limiting examples, reporting may comprise recording the results on an electronic storage medium, displaying the results on a computer screen, or printing the results on a piece of paper.

[0123] Examples of "biological sample" include but are not limited to mammalian body fluids, sera such as blood (including whole blood as well as its plasma and serum), CSF (spinal fluid), urine, sweat, saliva, tears, pulmonary secretions, breast aspirate, prostate fluid, seminal fluid, stool, cervical scraping, cysts, amniotic fluid, intraocular fluid, mucous, moisture in breath, animal tissue, cell lysates, tumor tissue, hair, skin, buccal scrapings, nails, bone marrow, cartilage, prions, bone powder, ear wax, etc. or even from external or archived sources such as tumor samples (i.e., fresh, frozen or paraffin-embedded).

[0124] In one embodiment, detecting the presence or absence of the second nucleic acid comprises contacting the

PCR primer or nucleic acid probe with a biological sample of the subject and performing real time polymerase chain reaction on the sample. In a particular embodiment, detecting the presence or absence of the second nucleic acid comprises contacting the first nucleic acid with a biological sample of the subject and performing real time polymerase chain reaction on the sample.

[0125] In another embodiment, detecting the presence or absence of the second nucleic acid comprises contacting the PCR primer or nucleic acid probe with a biological sample from the subject and determining whether the PCR primer or nucleic acid probe hybridizes under highly stringent conditions with the second nucleic acid in the biological sample, wherein the presence of a first and second nucleic acid binding complex indicates the presence of the second nucleic acid. In a particular embodiment, detecting the presence or absence of the second nucleic acid comprises contacting the first nucleic acid with a biological sample from the subject and determining whether the first nucleic acid hybridizes under highly stringent conditions with the second nucleic acid in the biological sample, wherein the presence of a first and second nucleic acid binding complex indicates the presence of the second nucleic acid.

[0126] Individuals who do not have MD-2s may have a higher risk of developing LPS-induced inflammation or an inflammatory disease. For example, an individual without MD-2s may develop severe sepsis when they are infected with gram negative bacteria. Therefore, another embodiment of the present invention provides for a method to determine a subject's risk of developing LPS-induced inflammation or an inflammatory disease. In one embodiment, the method comprises detecting the presence or absence of a nucleic acid that encodes MD-2s or a polypeptide as described above; and correlating the presence of the nucleic acid with a lower risk of developing LPS-induced inflammation or an inflammatory disease or correlating the absence of the second nucleic acid with a higher risk of developing LPS-induced inflammation or an inflammatory disease. These methods may further comprise reporting the presence or absence of the nucleic acid that encodes MD-2s, or reporting the low or high level of risk of developing LPS-induced inflammation an inflammatory disease. For example, a laboratory performing the test may report the results to a medical practitioner, such as the subject's doctor and/or the subject's doctor may report the results to the subject. In other non-limiting examples, reporting may comprise recording the results on an electronic storage medium, displaying the results on a computer screen, or printing the results on a piece of paper. Examples of LPS-induced inflammation or an inflammatory disease include but are not limited to sepsis, septic shock, gram negative bacterial infection, gram negative bacterial lung infection and immune response such as atherosclerosis.

[0127] Alternatively, the method comprises detecting the expression level of a nucleic acid that encodes MD-2s or a polypeptide as described above; comparing the expression level of the nucleic acid to a standardized expression level of a nucleic acid that encodes MD-2s determined from individuals who have MD-2s; and correlating an expression level that is equal or higher than the standardized expression level to a lower risk of developing LPS-induced inflammation or an inflammatory disease or correlating an expression level that is lower than the standardized expression level to a higher risk of developing LPS-induced inflammation or an inflammatory disease. These methods may further comprise reporting the low or high level of risk of developing LPS-induced inflammation an inflammatory disease. For example, a laboratory performing the test may report the results to a medical practitioner, such as the subject's doctor and/or the subject's doctor may report the results to the subject. In other non-limiting examples, reporting may comprise recording the results on an electronic storage medium, displaying the results on a computer screen, or printing the results on a piece of paper. Examples of LPS-induced inflammation or an inflammatory disease include but are not limited to sepsis, septic shock, gram negative bacterial infection, gram negative bacterial lung infection and immune response such as atherosclerosis.

[0128] The present invention describes kits for preventing or reducing the likelihood of developing and/or treating a condition using MD-2s and kits for determining a subject's risk of developing severe sepsis. Various embodiments of the present invention thus provides for kits for preventing or reducing the likelihood of developing and/or treating a condition in a mammal in need thereof, comprising: a quantity of MD-2s or a polypeptide as described above and instructions for administering the quantity of MD-2s or the polypeptide as described above to the mammal to prevent, reduce the likelihood of developing and/or treat the condition. Another embodiment of the present invention provides for a kit for determining a subject's risk of developing these diseases or disease conditions, comprising: a quantity of a PCR primer or nucleic acid probe as described above; and instructions for using the quantity PCR primer or nucleic acid probe to determine the subject's risk of developing these diseases or disease conditions. References herein to MD-2s include synthetic, recombinant, naturally-occurring and any other forms of the protein. In one embodiment, the condition is sepsis or septic shock. In another embodiment, the condition is inflammation. In another embodiment, the condition is a lung infection.

EXAMPLES

[0129] The following examples are provided to better illustrate the claimed invention and are not to be interpreted as limiting the scope of the invention. To the extent that specific materials are mentioned, it is merely for purposes of illustration and is not intended to limit the invention. One skilled in the art may develop equivalent means or reactants without the exercise of inventive capacity and without departing from the scope of the invention.

Example 1

Biological Reagents and Cell Culture

[0130] Immortalized human dermal microvessel endothelial cells (HMEC) (a kind gift from F. J. Candal, Center for Disease Control and Prevention, Atlanta, Ga.) were cultured in MCDB-131 medium, supplemented with 10% heat-inactivated fetal bovine serum, 2 mM glutamine, and 100 μg/ml penicillin and streptomycin. The HEK293 cell line and the mouse RAW 264.7 macrophage cell line were cultured in Dulbecco's modified Eagle's medium, supplemented with 10% heat-inactivated FBS and 2 mM glutamine. The plasmid encoding human wild-type Flag MD-2 was a generous gift from Kensuke Miyake. LPS (TLRGrade) was from (Alexis) and biotin-LPS (Ultrapure) was from Invivogen. Protein tyrosine kinase inhibitor herbimycin A was purchased from Sigma-Aldrich. Lyn peptide inhibitor was purchased from

Tocris Cookson. 4G10 anti-phosphotyrosine Ab was purchased from Upstate. Anti-Flag agarose affinity gel and anti-Flag Ab were from Sigma Aldrich. Anti-Myc and Anti-HA Abs were from Santa Cruz Biothecnology and Zymed Labs respectively.

Example 2

RT-PCR

[0131] Total cellular RNA was isolated from HMEC, RAW 264.7, murine dendritic cells, and murine liver tissue using RNeasy mini kit (Qiagen, Valencia, Calif.). RNA from human lung, pancreas, thymus, kidney, spleen, liver, heart, and placenta was purchased from Ambion (Austin, Tex.). Following reverse transcription with Omniscript cDNA synthesis kit (Qiagen), PCR analysis was performed using primers specific for the human MD-2 (sense: ATGTTACCATTTCTGTTT (SEQ ID NO:10)), antisense: CTAATTTGAATTAGGTTG (SEQ ID NO:11)) or mouse MD-2 (sense: TCTGCAACTCCTCCGATG (SEQ ID NO:12), antisense: GGCGGTGAATGATGGTGA (SEQ ID NO:13)). The PCR was performed using Taq DNA polymerase (Invitrogen, Carlsbad, Calif.). Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) served as a loading control.

Example 3

Immunoprecipitation and Immunoblotting

[0132] HEK 293 cells were seeded into 100 mm dishes (1.5×10^6) 24 h prior to transfection. Transfections were performed according to the manufacturer's instructions using lipofectamine. For co-immunoprecipitations, 4 μg of each construct was transfected. For competition experiments where the effect of increasing sMD-2 expression on complex formation between two signaling molecules was examined, 2 μg of each signaling molecule expression plasmid was transfected in the presence of increasing amounts of the sMD-2 expression plasmid. The total amount of DNA in each sample was kept constant by using empty vector cDNA. In all cases, cells were harvested 24 h following transfection in 600 μl of lysis buffer (50 mM HEPES, pH 7.5, 100 mM NaCl, 1 mM EDTA, 10% glycerol, 0.5% NP-40 containing protease inhibitor cocktail, and 1 mM sodium orthovanadate). For immunoprecipitations, the indicated antibodies were incubated with the cell lysates overnight at 4° C. Subsequently, Trueblot™ IgG beads were added and the samples were incubated at 4° C. for 1 hr. The immune complexes were then washed and the associated proteins were eluted from the beads by boiling in 35 μl of sample buffer, and then fractionated by SDS-PAGE. For immunoblotting, primary antibodies were detected using horseradish peroxidase-conjugated secondary antibodies, followed by enhanced chemiluminescence (Amersham Biosciences).

Example 4

NF-κB and IL-8 Promoter Luciferase Activation in HEK 293 Cells

[0133] HEK293 cells were transiently transfected with the expression vectors noted in combination with constructs encoding the NF-κB- and IL-8-luciferase reporter gene, and either the β-galactosidase gene or the phRL-TK report gene to normalize for transfection efficiency. In all cases, total DNA concentration was kept constant by supplementation with empty vector control. Following overnight incubation, cells were stimulated for 6 hours with 50 ng/ml LPS and then lysed, and luciferase activity was measured as described previously (Ohta et al. (2004) Biochem Biophys Res Commun 323, 1103-1108). Data are shown as mean±SD of three or more independent experiments and are reported as a percentage of LPS-stimulated NF-κB and IL-8 promoter activity, or relative luciferase activity.

Example 5

Identification of a Novel Human MD-2 Splice Variant

[0134] During the inventors' analysis of MD-2 expression in HMECs, two cDNA products approximately 390 and 480 bp in length (FIG. **1**A) were detected by RT-PCR. The expression of murine MD-2 was also examined by performing RT-PCR on cDNA derived from the murine cell line, RAW 246.7 (FIG. **1**B). In contrast, using primers homologous to the same region in the mouse as in the human, only the larger RT-PCR product was detected. To confirm that the absence of the smaller fragment was not specific to the murine cell line selected, cDNA from murine bone marrow derived dendritic cells and liver tissues obtained from C57BL/6 mice were also amplified. Again only the larger cDNA fragment was observed in the murine tissues tested (FIG. **1**C).

[0135] Upon sequencing the larger cDNA fragment detected in HMECs, it was determined that this PCR product corresponded to the published sequence of full-length human MD-2. Sequence analysis of the smaller cDNA fragment (subsequently referred to as MD-2s), revealed that this was a splice variant of human MD-2, which lacked the region encoded by exon 2 of the MD-2 gene (FIGS. **1**D and E). This isoform is putatively translated into a 114-residue protein with no frame shift, however, one amino acid substitution, D38G, occurs at the junction between exons 2 and 3.

[0136] To further characterize the expression profile of MD-2s, RT-PCR analysis on a variety of human tissues was performed. As shown in FIG. **1**G, MD-2s was widely expressed in all human tissues analyzed. Furthermore, it was observed that the full length wild-type MD-2 is the predominant form detected, although the ratio between MD-2 and MD-2s varies in different tissues. These findings establish that MD-2s is not a result of tissue-specific alternative splicing, but rather is ubiquitously expressed in all human tissues tested.

[0137] Having established that MD-2s is not expressed in the mouse, it was investigated if MD-2s could be detected in transgenic mice overexpressing the human MD-2 gene. RT-PCR analysis conducted on BMDMs from these mice revealed that MD-2s can be detected irrespective of the presence or absence of human or murine TLR4 (FIG. **1**G, compare lane 3, to lane 1 or 4).

[0138] To determine why the human but not the mouse MD-2 gene alternatively skips exon 2, the gene structures and sequences of the two species were compared (Table 2). Both the human and the murine MD-2 genes are organized into five exons and four introns, and each species encodes a predicted full-length MD-2 protein of 145 amino acids. Alignment of the human and mouse genomic regions revealed that the exons and coding sequences were well conserved. However, analysis of the non-coding regions revealed a number of differences. In particular, it was noted that intron 1 of human

MD-2 is composed of 13239 base pairs, while the mouse has 3067. The longer intron 1 may increase the probability for alternative lariat formation during the splicing process of human MD-2. In addition, after comparing the sequences at the 3' end of intron 1, murine MD-2 was found to have more pyrimidines than human MD-2, which may lead to a more stable lariat formation in murine MD-2, thereby preventing alternative splicing of exon 2 in this species.

TABLE 2

(a)	E-1 coding	Intron 1	Sequences at 3' of Intron 1	E2	E3	E4	E5-coding
Human	112	13241	ttgacattatctttattgcttttag (SEQ ID NO: 14)	90	129	53	99
Mouse	112	3064	ttg-TattTtcttCattCcttttag (SEQ ID NO: 15)	90	129	53	99

(b)
5'-ttgacattatctttattgcttttag**ATAAAATGCAATACCCAATTTCAATTAATGTTAAC**
CCCTGTCTAGAATTGAAAAGATCCAAAGGATTATTGCACATTTTCTACA
TTCCAAgtaagttcaaattttgcttttata-3' (SEQ ID NO: 16)

(a) Comparison of human and mouse MD-2 gene structure.

(b) The intron-exon boundary of exon 2 in the MD-2 gene is depicted, with the intronic sequences in lower case and the excised sequence in upper case.

Example 6

Similar to Wild-Type MD-2, MD-2s is Glycosylated and Secreted

[0139] In order to characterize this newly identified isoform of human MD-2, the smaller RT-PCR fragment was amplified and cloned into an expression vector containing a Myc tag. HEK293 cells were subsequently transiently transfected with MD-2s-Myc. Cellular extracts were later prepared and SDS-PAGE analysis was performed. Similar to wild-type MD-2, multiple forms of MD-2s could be detected upon overexpression (FIG. **2**A, lane 1). The altered electrophorectic mobility of wild-type MD-2 is due to N-linked glycosylations at positions Asn26 and Asn114 (Ohnishi et al. (2001) J Immunol 167, 3354-3359). These residues are still present in MD-2s, but since MD-2s lacks 30 amino acids, the tertiary structure is likely to be different from wild-type MD-2, which could result in occlusion of these known glycosylation sites. To determine if the altered electrophorectic mobility of MD-2s was due to glycosylation, immunoprecipitated MD-2s, isolated from HEK293 cells transiently expressing MD-2s-Myc, was treated with the N-glycosidase, PNGaseF. Samples were then analyzed by SDS-PAGE and immunoblotted with an anti-Myc antibody. It was found that the slowest migrating forms of MD-2s were no longer evident in the PNGaseF-treated sample (FIG. **2**A, lane 2). These results indicate that similar to wild type MD-2, MD-2s is a glycoprotein.

[0140] Next, it was investigated if MD-2s exists as a stably secreted protein. Myc-tagged proteins were immunoprecipitated from culture supernatants obtained from HEK293 cells transiently expressing MD-2s-Myc. Samples were subsequently analyzed by SDS-PAGE and immunoblotted with an anti-Myc antibody. As shown in FIG. **2**B, lane 2, MD-2s is present in a soluble form.

Example 7

MD-2s Fails to Induce NF-κB Activation Following LPS Stimulation

[0141] The requirement for MD-2s in LPS mediated NF-κB activation was assessed. It has been shown that the soluble form of wild-type MD-2 confers LPS responsiveness to cells expressing TLR4; therefore, it was investigated if soluble MD-2s was also bioactive. Culture supernatants were obtained from HEK293 cells transiently expressing control vector, MD-2, or MD-2s, and incubated with HEK293 cells stably transfected with TLR4 and an NF-κB-dependent luciferase reporter gene. As previously shown, soluble MD-2 strongly activated NF-κB following LPS stimulation (FIG. **3**A). However, the secreted form of MD-2s could not confer LPS responsiveness to these cells as measured by NF-κB activation (FIG. **3**A) or IL-8 secretion (FIG. **3**C).

[0142] MD-2s was tested to see if it needed to be transiently expressed in TLR4 reporter cells in order to mediate NF-κB activation following LPS stimulation. HEK293 cells stably transfected with TLR4 and an NF-κB-dependent luciferase reporter gene were transiently transfected with plasmids encoding CD14 in combination with either MD-2 or MD-2s, and subsequently treated with LPS. In agreement with published results, wild-type MD-2 activated NF-κB in response to LPS treatment. In contrast, MD-2s was unable to induce LPS-mediated NF-κB activation, even at higher concentrations (FIG. **1**B) or IL-8 secretion (FIG. **1**D). Taken together, these results suggest that the region of human MD-2 encoded by exon 2 plays an important role in mediating LPS-induced signaling.

Example 8

Similar to Wild-Type MD-2, MD-2s Interacts with TLR4

[0143] Given that MD-2s failed to induce LPS-dependent NF-κB activation, the inventors questioned whether this might be due to an inherent inability to interact directly with TLR4. To address this possibility, co-localization studies to examine the cellular distribution of MD-2s with respect to TLR4 were performed. HEK293 cells stably expressing TLR4CFP were subsequently transiently transfected with a plasmid encoding either MD-2 (FIG. **4**A, upper panel) or MD-2s (FIG. **4**A, lower panel) and stained with an anti-Myc antibody. Confocal analysis revealed that both TLR4 and MD-2s exhibited the same cellular distribution (FIG. **4**A, lower right hand side panel). Next whether MD-2s is physically associated with TLR4 was assessed. HEK293 cells were transiently transfected with a plasmid encoding FLAG-tagged TLR4 in combination with either a Myc-tagged MD-2 or a Myc-tagged MD-2s expressing plasmid, and co-immunoprecipitation experiments were performed. It was determined that similar to MD-2, a direct interaction between MD-2s and TLR4 was observed (FIG. **4**B, lane 4), indicating that although MD-2s fails to induce LPS-dependent NF-κB activation, this cannot be attributed to an inability to associate with TLR4.

Example 9

MD-2s Diminishes LPS-Induced NF-κB Activation

[0144] Having determined that MD-2s does not activate NF-κB, we next investigated the effect of MD-2s on MD-2/TLR4-mediated LPS signaling. HEK293 cells were transiently transfected with plasmids encoding CD14, TLR4, and wild-type MD-2 in conjunction with a plasmid encoding the NF-κB-dependent luciferase reporter gene in the presence or absence of a plasmid encoding MD-2s. As shown in FIG. **5**A, MD-2s significantly inhibited LPS-induced NF-κB activation. Furthermore, we assessed the inhibitory role of soluble MD-2s following LPS stimulation. HEK293 cells stably transfected with TLR4 and an NF-κB-dependent luciferase reporter gene were incubated with supernatants obtained from HEK293 cells transiently expressing a constant amount of MD-2 with increasing concentrations of MD-2s. It was determined that soluble MD-2s inhibits NF-κB activation (FIG. **5**B). This suggests that the region encoded by exon 2 is critical for efficient TLR4 signaling.

Example 10

MD-2s Interacts with MD-2 and LPS

[0145] Previous reports indicate that monomeric MD-2 preferentially binds TLR4 and confers LPS responsiveness more efficiently than MD-2 multimers (Re et al. (2002) J Biol Chem 277, 23427-23432). Therefore, it was investigated if MD-2s could interact with wild-type MD-2, which could potentially diminish responsiveness to LPS by reducing the amount of available monomeric MD-2. HEK293 cells were transiently transfected with a plasmid encoding FLAG-tagged MD-2, in combination with either a Myc-tagged MD-2 or a Myc-tagged MD-2s expressing plasmid, and co-immunoprecipitation experiments were performed. Similar to previous reports, it was observed that MD-2 can homodimerise (FIG. **6**A, lane 2). It was also noted that MD-2s associates with wild-type MD-2 (FIG. **11**, lane 3). These results raise the possibility that the mechanism by which MD-2s inhibits LPS-induced TLR4-dependent signaling is by reducing the amount of the active monomeric species of MD-2, and thus increasing the multimeric form of MD-2. Both would be predicted to lead to a reduction in TLR4-dependent signaling during exposure to LPS (Re et al. (2002) J Biol Chem 277, 23427-23432; Teghanemt et al. (2008) J Biol Chem 283, 21881-21889).

[0146] The published structural models of MD-2 were also analyzed to ascertain the structural effect of deleting exon 2. MD-2 consists of a β-cup fold with two anti-parallel β-sheets, the first one composed of six β-strands (numbered 1/2/9/8/5/6) and the other of three (numbered 3/4/7) (Kim et al. (2007) Cell 130, 906-917; Ohto et al. (2007) Science 316, 1632-1634). The missing exon 2 of MD-2s encodes the first two β-strands of the three-stranded β-sheet (β3 and β4 strands) (FIG. **6**B). The hinges connecting β-strands 2 to 3 and 4 to 5 are also partially lost. Furthermore, the disulphide bond between Cys25 and Cys51, which assists in closing the MD-2 cavity and stabilizing the cup-like structure, is disrupted. The β6 and β7 strands that line the entrance to the deep hydrophobic cavity are still encoded by MD-2s mRNA.

[0147] Previous mutational studies have demonstrated that the LPS-binding region of MD-2 depends on Lys89, Arg90, Lys91, Phe119, Phe121, Lys122, Lys125, Lys128, and Lys132. Several of these residues have also been shown to be directly involved in the binding of Eritoran and Lipid IVa to MD-2 (Kim et al. (2007) Cell 130, 906-917; Ohto et al. (2007) Science 316, 1632-1634). Although all of the aforementioned residues are present in MD-2s, structural analysis of this protein implied that the ligand-binding pocket may be severely disrupted, suggesting that MD-2s may be unable to bind LPS efficiently. To address this possibility, HEK293 cells were transiently transfected with plasmids encoding either MD-2 or MD-2s. Culture supernatants were then incubated with biotin-LPS and Myc-tagged proteins were immunoprecipitated. In agreement with previous studies, secreted MD-2 bound readily to LPS (FIG. **6**C, lane 4) (Visintin et al. (2003) J Biol Chem 278, 48313-48320). Interestingly, under similar conditions, an interaction between secreted MD-2s and LPS was also detected (FIG. **6**C, lane 6), suggesting that exogenous MD-2s may actively sequester LPS from MD-2. Hence, these results suggest a second way that MD-2s could suppress LPS-induced activation of TLR4 is by directly binding LPS, thereby reducing the availability of LPS to bind with monomeric MD-2 and thus diminishing TLR4 signal transduction.

Example 11

[0148] Real-time polymerase chain reaction analysis for MD-2s expression was performed on epithelial cells. The primers/probes for MD-2s are as shown in Table 3. Results are shown in FIG. **9***b*.

TABLE 3

Sense	5'-ATTGGGTCTGCAACTCATCC-3' (SEQ ID NO: 7)
Antisense	5'-CGCTTTGGAAGATTCATGGT-3' (SEQ ID NO: 8)
Probe	5'-CCTACTGTGGGAGAGATTTAAAG-3' (SEQ ID NO: 9)

Example 12

Flow-Cytometric Analysis of MD-2 and MD-2S Expression

[0149] HEK293T cells were retrovirally transduced to generate a cell line stably expressing TLR4-mCitrine. TLR4-mCitrine cells in 12-well dishes were transfected with 300 ng of plasmid encoding myc-tagged MD2 or MD2S using GeneJuice lipofection reagent (Novagen) and cultured overnight. Cells were dislodged by scraping, washed once with cold PBS and incubated with a 1:50 dilution of anti-myc Alexa 647-conjugated antibody (AbD Serotec) at 4° C. for 30 minutes. Cells were washed four times with PBS for and fluorescence was assessed with an LSR II flow cytometer (BD Biosciences) running FACS Diva software (BD Biosciences). Data was processed using FlowJo software v8.6.3 (Tree Star).

Example 13

Confocal Imaging of MD-2 and MD-2s Transfected Cells

[0150] TLR4-mCitrine cells were cultured on glass-bottom confocal dishes (MatTek) coated with collagen. After 24-hours of culture, cells were transfected with up to 300 ng of plasmid encoding myc-tagged MD-2 or MD-2S using GeneJuice lipofection reagent (Novagen) and cultured for approximately 24 hours. Cells were stained with anti-myc Alexa-647 antibody (AbD Serotec) in culture medium at 4° C. for 20 minutes. Cells were gently washed 3 times with PBS and culture medium was replaced. Cells were imaged at room temperature using an SP2 AOBS confocal laser scanning microscope (Leica Microsystems) running LCS software (Leica Microsystems).

Example 14

MD-2 was Found to be Tyrosine Phosphorylated Upon Stimulation with LPS

[0151] Tyrosine phosphorylation of numerous proteins is induced upon stimulation with LPS and indeed the LPS receptor, TLR4, is itself tyrosine phosphorylated. Given the important role of MD-2 following LPS stimulation, the inventors investigated whether MD-2 is post-translationally modified as well. HEK293 cells were transiently transfected with plasmids expressing Flag-TLR4, Flag-MD-2 and CD14 or mock transfected. 24 hrs later, cells were left untreated or stimulated with LPS for various time points. Proteins were immunoprecipitated from cell extracts with an anti-Flag Ab and analyzed by immunoblotting with an Ab that detects proteins phosphorylated on phosphotyrosine residues. Upon stimulation with LPS, MD-2 was found to be tyrosine phosphorylated (FIG. **13**A). The presence of 5 mM phosphotyrosine, a competitive inhibitor, completely abrogated the immunoreactivity detected by the anti-phosphotyrosine Ab, in contrast, phosphoserine or phosphothreonine had no effect on MD-2 tyrosine phosphorylation (data not shown), which confirms the specificity of this result. In addition, MD-2 tyrosine phosphorylation was not observed after stimulation with IL-1β or TNFα or RsDPLA, a biologically inactive analogue of lipid A (data not shown). To further confirm that MD-2 is posttranslationally modified, the inventors pre-treated HEK 293 cells, overexpressing TLR4 and MD-2, with the tyrosine kinase inhibitor herbimycin A for two hours prior to LPS stimulation and observed that herbimycin A significantly inhibited LPS-induced MD-2 tyrosine phosphorylation in a dose dependent manner (FIG. **13**B, compare lanes 3 and 4 to lane 2).

[0152] Next, the inventors investigated whether MD-2 phosphorylation occurred during trafficking, instead of on the cell surface. More specifically, the inventors examined the role of receptor or ligand internalization and endocytosis on the phosphorylation status of MD-2. Since cytochalasins effectively block LPS internalization and signaling for cytokine release (Poussin et al. (2006) J Biol Chem 273, 20285-20291), HEK293 cells, overexpressing TLR4 and MD-2, were pre-treated with Cytochalasin-D for one hour prior to LPS stimulation. The inventors observed that LPS-induced MD-2 tyrosine phosphorylation was significantly inhibited following pretreatment with cytochalasin D (FIG. **13**B, lane 5). Thus according to certain embodiments MD-2 tyrosine phosphorylation occurs intracellularly during trafficking and not on the cell surface.

Example 15

Identification of Tyr-22 and Tyr-131 as Possible Phospho-Acceptors

[0153] Human MD-2 contains nine tyrosine residues (FIG. **14**A). The inventors mutated all nine tyrosine residues conservatively to phenylalanine and tested their ability to respond to LPS. HEK293 cells stably transfected with a NF-κB reporter gene and TLR4 were transiently transfected with plasmids encoding wild-type MD-2, MD-2-Y22F, MD-2-Y34F, MD-2-Y36F, MD-2-Y42F, MD-2-Y65F, MD-2-Y75F, MD-2-Y79F, MD-2-Y102F, or MD-2-Y131F. 24 hrs later, cells were stimulated with LPS. As can be seen in FIG. **14**B, upon LPS stimulation the mutant proteins MD-2-Y22F and MD-2-Y131F are significantly less potent in their ability to activate NF-κB compared to wild-type MD-2. Analysis of a double mutant protein, MD-2-Y22F and Y131F, further confirmed that these residues are important for MD-2 to signal NF-κB activation in response to LPS (FIG. **14**C). It was also determined that the mutant proteins lacking tyrosine residues located at positions 22 and 131 had a diminished ability to activate IL-8 (FIG. **14**D). The inventors further characterized these mutant MD-2 proteins by analyzing their phosphorylation status after LPS stimulation. Supporting the prediction that the sites mutagenized were phosphorylation sites, the mutant proteins were indeed less phosphorylated compared to normal MD-2 (FIG. **14**E). Additionally, the amount of phosphorylated p38 after LPS stimulation was measured. Cells transfected with the mutant MD-2 proteins had less phosphor-p38 compared to the normal MD-2 transfected cells, indicating dysfunctional signaling in these cells (FIG. **14**E). In addition, it was confirmed that these mutant proteins were secreted (data not shown), and that they displayed a similar glycosylation pattern as wild-type MD-2 upon SDS-PAGE analysis, and that they were expressed at similar levels (FIG. **14**E).

[0154] Given that it has been shown that Tyr 22 and Tyr 131 are possible phospho-accepting residues, the inventors next determined the location of these residues with respect to the published crystal structure of MD-2. As shown in FIGS. **15** A and C, the hydroxyl-groups of both residues appear to be surface exposed, thereby allowing phosphorylation of these tyrosine residues to occur. Although Tyr 131 is located at the hydrophobic pocket of MD-2, neither Tyr 22 nor 131 are involved in the main dimerization interface of the TLR4-MD-2-LPS complex (FIGS. **15**, B and D).

[0155] In conclusion, two of the substitutions, MD-2-Y22F and MD-2-Y131F, resulted in a 50% decrease in NF-κB activity upon LPS stimulation, indicating that these residues were critical for maximal NF-κB activation and can be phospho-accepting residues. In addition, by analyzing the published crystal structure of MD-2, the inventors determined that the hydroxyl groups of both MD2 tyrosine residues, located at positions 22 and 131, are surface exposed thereby permitting phosphorylation of the aforementioned residues to occur.

TABLE 4

Y to F sequences of human MD-2.

Y22F	MLPFLFFSTLFSSIFTEAQKQFWVCNSSDASISYTYCDKMQYPISINVNPCIE LKRSKGLLHIFYIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFC RALKGETVNTTISFSFKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVILHQPN SN (SEQ ID NO: 17)
Y34F	MLPFLFFSTLFSSIFTEAQKQYWVCNSSDASISFTYCDKMQYPISINVNPCIE LKRSKGLLHIFYIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFC RALKGETVNTTISFSFKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVILHQPN SN (SEQ ID NO: 18)
Y36F	MLPFLFFSTLFSSIFTEAQKQYWVCNSSDASISYTFCDKMQYPISINVNPCIE LKRSKGLLHIFYIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFC RALKGETVNTTISFSFKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVILHQPN SN (SEQ ID NO: 19)
Y42F	MLPFLFFSTLFSSIFTEAQKQYWVCNSSDASISYTYCDKMQFPISINVNPCIE LKRSKGLLHIFYIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFC RALKGETVNTTISFSFKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVILHQPN SN (SEQ ID NO: 20)
Y65F	MLPFLFFSTLFSSIFTEAQKQYWVCNSSDASISYTYCDKMQYPISINVNPCIE LKRSKGLLHIFFIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFC RALKGETVNTTISFSFKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVILHQPN SN (SEQ ID NO: 21)
Y75F	MLPFLFFSTLFSSIFTEAQKQYWVCNSSDASISYTYCDKMQYPISINVNPCIE LKRSKGLLHIFYIPRRDLKQLFFNLYITVNTMNLPKRKEVICRGSDDDYSFC RALKGETVNTTISFSFKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVILHQPN SN (SEQ ID NO: 22)
Y79F	MLPFLFFSTLFSSIFTEAQKQYWVCNSSDASISYTYCDKMQYPISINVNPCIE LKRSKGLLHIFYIPRRDLKQLYFNLFITVNTMNLPKRKEVICRGSDDDYSFC RALKGETVNTTISFSFKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVILHQPN SN (SEQ ID NO: 23)
Y102F	MLPFLFFSTLFSSIFTEAQKQYWVCNSSDASISYTYCDKMQYPISINVNPCIE LKRSKGLLHIFYIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDFSFC RALKGETVNTTISFSFKGIKFSKGKYKCVVEAISGSPEEMLFCLEFVILHQPN SN (SEQ ID NO: 24)
Y131F	MLPFLFFSTLFSSIFTEAQKQYWVCNSSDASISYTYCDKMQYPISINVNPCIE LKRSKGLLHIFYIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFC RALKGETVNTTISFSFKGIKFSKGKFKCVVEAISGSPEEMLFCLEFVILHQPN SN (SEQ ID NO: 25)
Y22F + Y131F	MLPFLFFSTLFSSIFTEAQKQFWVCNSSDASISYTYCDKMQYPISINVNPCIE LKRSKGLLHIFYIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFC RALKGETVNTTISFSFKGIKFSKGKFKCVVEAISGSPEEMLFCLEFVILHQPN SN (SEQ ID NO: 26)

Example 16

MD-2 was Shown to Interact with Lyn

[0156] Prior studies have shown that the Src kinase, Lyn, is recruited to TLR4 (Medvedev et al. (2007) J Biol Chem 282, 16042-16053) as well as to CD14 (Stefanova et al. (1993) J Biol Chem 268, 20725-20728). Furthermore it has been suggested that Lyn may be involved in TLR4 tyrosine phosphorylation. Similar to previous results, the inventors found that TLR4 immunoprecipitated with Lyn upon LPS stimulation (FIG. **16**A). Given that MD-2 tyrosine phosphorylation was abolished following pretreatment with herbimycin A (FIG. **13**B), a potent Src kinase inhibitor, which has been shown to inhibit Lyn activity (June et al. (2006) Proc Natl Acad Sci USA 87, 7722-7726), Lyn involvement in the phosphorylation of MD-2 was investigated. HEK293 cells were transiently transfected with Myc-TLR4, HA-MD-2, Flag-Lyn and CD14 constructs. HA-tagged proteins were immunoprecipitated from cell lysates with an anti-HA antibody and immunoblotted with an anti-Flag antibody. The inventors observed that Lyn immunoprecipitated with MD-2 (FIG. **16**B). However, given that Lyn also immunoprecipitates with TLR4, the inventors examined whether the interaction between MD2 and Lyn was due to a direct interaction. HEK293 cells were transiently transfected with plasmids expressing HA-MD-2 and Flag-Lyn. HA-tagged proteins were then immunoprecipitated and subsequently immunoblotted with an anti-Flag antibody. The inventors discovered that even without the presence of TLR4, MD-2 immunoprecipitated with Lyn, thus confirming that Lyn and MD-2 could directly interact (FIG. **16**C). This result thus suggested that Lyn is the most likely kinase that phosphorylates MD2.

Example 17

Lyn Peptide Inhibitor Diminished MD-2 Tyrosine Phosphorylation

[0157] Given that MD-2 tyrosine phosphorylation was abolished following pretreatment with herbimycin A, and that

MD-2 and Lyn were found to be in a complex together, the inventors confirmed that Lyn was required for MD-2 tyrosine phosphorylation. A Lyn specific peptide inhibitor (Adachi et al. (1999) J Immunol 163, 939-946) was used to examine the effect of inhibiting Lyn activation on MD-2 phosphorylation. HEK 293 cells, overexpressing TLR4, Myc-MD-2 and CD14 were pretreated with the Lyn peptide inhibitor for two hours prior to LPS stimulation. As can be seen in FIG. **17**A, the Lyn peptide inhibitor significantly abolished LPS-induced MD-2 tyrosine phosphorylation in a dose dependent manner (FIG. **17**A, compare lanes 4-6 to lane 3). Furthermore, following pretreatment with the Lyn peptide inhibitor, LPS-induced activation of IL-8 and NF-kB was abolished in HEK293 cells overexpressing TLR4, CD14 and MD2 (FIG. **17**B), thus confirming the important role for Lyn kinase in mediating the signaling of the LPS-MD-2-TLR4-complex.

[0158] Various embodiments of the invention are described above in the Detailed Description. While these descriptions directly describe the above embodiments, it is understood that those skilled in the art may conceive modifications and/or variations to the specific embodiments shown and described herein. Any such modifications or variations that fall within the purview of this description are intended to be included therein as well. Unless specifically noted, it is the intention of the inventors that the words and phrases in the specification and claims be given the ordinary and accustomed meanings to those of ordinary skill in the applicable art(s).

[0159] The foregoing description of various embodiments of the invention known to the applicant at this time of filing the application has been presented and is intended for the purposes of illustration and description. The present description is not intended to be exhaustive nor limit the invention to the precise form disclosed and many modifications and variations are possible in the light of the above teachings. The embodiments described serve to explain the principles of the invention and its practical application and to enable others skilled in the art to utilize the invention in various embodiments and with various modifications as are suited to the particular use contemplated. Therefore, it is intended that the invention not be limited to the particular embodiments disclosed for carrying out the invention.

[0160] While particular embodiments of the present invention have been shown and described, it will be obvious to those skilled in the art that, based upon the teachings herein, changes and modifications may be made without departing from this invention and its broader aspects and, therefore, the appended claims are to encompass within their scope all such changes and modifications as are within the true spirit and scope of this invention. It will be understood by those within the art that, in general, terms used herein are generally intended as "open" terms (e.g., the term "including" should be interpreted as "including but not limited to," the term "having" should be interpreted as "having at least," the term "includes" should be interpreted as "includes but is not limited to," etc.).

SEQUENCE LISTING

```
<160> NUMBER OF SEQ ID NOS: 28

<210> SEQ ID NO 1
<211> LENGTH: 130
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Gly Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu
        35                  40                  45

Tyr Ile Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile
    50                  55                  60

Cys Arg Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly
65                  70                  75                  80

Glu Thr Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe
                85                  90                  95

Ser Lys Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro
            100                 105                 110

Glu Glu Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn
        115                 120                 125

Ser Asn
    130


<210> SEQ ID NO 2
```

-continued

```
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
1               5                   10                  15

Ser Tyr Thr Tyr Cys Gly Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu
            20                  25                  30

Tyr Ile Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile
        35                  40                  45

Cys Arg Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly
    50                  55                  60

Glu Thr Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe
65                  70                  75                  80

Ser Lys Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro
                85                  90                  95

Glu Glu Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn
            100                 105                 110

Ser Asn


<210> SEQ ID NO 3
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Lys Met Gln Tyr Pro Ile Ser Ile Asn Val Asn Pro Cys Ile Glu Leu
1               5                   10                  15

Lys Gly Ser Lys Gly Leu Leu His Ile Phe Tyr Ile Pro
            20                  25


<210> SEQ ID NO 4
<211> LENGTH: 393
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

atgttaccat ttctgttttt ttccaccctg ttttcttcca tatttactga agctcagaag      60

cagtattggg tctgcaactc atccgatgca agtatttcat acacctactg tgggagagat     120

ttaaagcaat tatatttcaa tctctatata actgtcaaca ccatgaatct tccaaagcgc     180

aaagaagtta tttgccgagg atctgatgac gattactctt tttgcagagc tctgaaggga     240

gagactgtga atacaacaat atcattctcc ttcaagggaa taaaattttc taagggaaaa     300

tacaaatgtg ttgttgaagc tatttctggg agcccagaag aaatgctctt ttgcttggag     360

tttgtcatcc tacaccaacc taattcaaat tag                                  393


<210> SEQ ID NO 5
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

gaagctcaga agcagtattg ggtctgcaac tcatccgatg caagtatttc atacacctac      60

tgtgggagag atttaaagca attatatttc aatctctata taactgtcaa caccatgaat     120
```

-continued

```
cttccaaagc gcaaagaagt tatttgccga ggatctgatg acgattactc tttttgcaga    180

gctctgaagg gagagactgt gaatacaaca atatcattct ccttcaaggg aataaaattt    240

tctaagggaa aatacaaatg tgttgttgaa gctatttctg ggagcccaga agaaatgctc    300

ttttgcttgg agtttgtcat cctacaccaa cctaattcaa attag                   345


<210> SEQ ID NO 6
<211> LENGTH: 90
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

ataaaatgca atacccaatt tcaattaatg ttaacccctg tctagaattg aaaagatcca     60

aaggattatt gcacattttc tacattccaa                                      90


<210> SEQ ID NO 7
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 7

attgggtctg caactcatcc                                                 20


<210> SEQ ID NO 8
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 8

cgctttggaa gattcatggt                                                 20


<210> SEQ ID NO 9
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct

<400> SEQUENCE: 9

cctactgtgg gagagattta aag                                             23


<210> SEQ ID NO 10
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

atgttaccat ttctgttt                                                   18


<210> SEQ ID NO 11
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

ctaatttgaa ttaggttg                                                   18
```

-continued

```
<210> SEQ ID NO 12
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Mus

<400> SEQUENCE: 12

tctgcaactc ctccgatg                                                   18


<210> SEQ ID NO 13
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Mus

<400> SEQUENCE: 13

ggcggtgaat gatggtga                                                   18


<210> SEQ ID NO 14
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

ttgacattat ctttattgct tttag                                           25


<210> SEQ ID NO 15
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Mus

<400> SEQUENCE: 15

ttgtattttc ttcattcctt ttag                                            24


<210> SEQ ID NO 16
<211> LENGTH: 140
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

ttgacattat ctttattgct tttagataaa atgcaatacc caatttcaat taatgttaac     60

ccctgtctag aattgaaaag atccaaagga ttattgcaca ttttctacat tccaagtaag    120

ttcaaatttt tgcttttata                                                140


<210> SEQ ID NO 17
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Tyrosine to phenylalanine mutation at position
      22

<400> SEQUENCE: 17

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Phe Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
        35                  40                  45

Asn Pro Cys Ile Glu Leu Lys Arg Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
```

-continued

```
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160


<210> SEQ ID NO 18
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Tyrosine to phenylalanine mutation at position
      34

<400> SEQUENCE: 18

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Phe Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
        35                  40                  45

Asn Pro Cys Ile Glu Leu Lys Arg Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160


<210> SEQ ID NO 19
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Tyrosine to phenylalanine mutation at position
      36

<400> SEQUENCE: 19

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Phe Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
        35                  40                  45
```

-continued

```
Asn Pro Cys Ile Glu Leu Lys Arg Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160


<210> SEQ ID NO 20
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Tyrosine to phenylalanine mutation at position
      42

<400> SEQUENCE: 20

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Phe Pro Ile Ser Ile Asn Val
        35                  40                  45

Asn Pro Cys Ile Glu Leu Lys Arg Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160


<210> SEQ ID NO 21
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Tyrosine to phenylalanine mutation at position
      65

<400> SEQUENCE: 21

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15
```

-continued

```
Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
        35                  40                  45

Asn Pro Cys Ile Glu Leu Lys Arg Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Phe Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160


<210> SEQ ID NO 22
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Tyrosine to phenylalanine mutation at position
      75

<400> SEQUENCE: 22

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
        35                  40                  45

Asn Pro Cys Ile Glu Leu Lys Arg Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Phe Phe Asn Leu Tyr Ile
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160


<210> SEQ ID NO 23
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Tyrosine to phenylalanine mutation at position
      79
```

-continued

```
<400> SEQUENCE: 23

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
        35                  40                  45

Asn Pro Cys Ile Glu Leu Lys Arg Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Phe Ile
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160


<210> SEQ ID NO 24
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Tyrosine to phenylalanine mutation at position
      102

<400> SEQUENCE: 24

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
        35                  40                  45

Asn Pro Cys Ile Glu Leu Lys Arg Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Phe Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160


<210> SEQ ID NO 25
<211> LENGTH: 160
<212> TYPE: PRT
```

-continued

```
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Tyrosine to phenylalanine mutation at position
      131

<400> SEQUENCE: 25

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
        35                  40                  45

Asn Pro Cys Ile Glu Leu Lys Arg Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Phe Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160


<210> SEQ ID NO 26
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Tyrosine to phenylalanine mutation at position
      22 and 131

<400> SEQUENCE: 26

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Phe Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
        35                  40                  45

Asn Pro Cys Ile Glu Leu Lys Arg Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Phe Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160
```

-continued

```
<210> SEQ ID NO 27
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
        35                  40                  45

Asn Pro Cys Ile Glu Leu Lys Gly Ser Lys Gly Leu Leu His Ile Phe
    50                  55                  60

Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
65                  70                  75                  80

Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
                85                  90                  95

Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
            100                 105                 110

Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
        115                 120                 125

Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
    130                 135                 140

Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser Asn
145                 150                 155                 160


<210> SEQ ID NO 28
<211> LENGTH: 129
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Consensus

<400> SEQUENCE: 28

Met Leu Pro Phe Leu Phe Phe Ser Thr Leu Phe Ser Ser Ile Phe Thr
1               5                   10                  15

Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn Ser Ser Asp Ala Ser Ile
            20                  25                  30

Ser Tyr Thr Tyr Cys Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr
        35                  40                  45

Ile Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys
    50                  55                  60

Arg Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu
65                  70                  75                  80

Thr Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser
                85                  90                  95

Lys Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu
            100                 105                 110

Glu Met Leu Phe Cys Leu Glu Phe Val Ile Leu His Gln Pro Asn Ser
        115                 120                 125

Asn
```

1-6. (canceled)

7. A method of inhibiting toll-like receptor 4 signaling ("TLR4"), inhibiting lipopolysaccharide ("LPS") signaling, treating a condition mediated by TLR4 signaling, or reducing a likelihood of developing a condition mediated by TLR4 signaling in a subject in need thereof, comprising:

providing a purified polypeptide comprising an amino acid sequence that is at least 80% identical to SEQ ID NO:1 or SEQ ID NO:2; and

administering the polypeptide to the subject to inhibit TLR4 signaling, inhibit LPS signaling, treat the condition mediated by TLR4 signaling, or reduce the likelihood of developing the condition mediated by TLR4 signaling.

8. The method of claim **7**, wherein the condition mediated by TLR signaling is selected from the group consisting of sepsis, septic shock, inflammation, gram negative bacterial infection, gram negative bacterial lung infection, immune response, atherosclerosis and combinations thereof.

9-40. (canceled)

41. The method of claim **7**, wherein the polypeptide comprises the amino acid sequence as disclosed by SEQ ID NO:1 or SEQ ID NO:2.

42. The method of claim **7**, wherein the polypeptide is glycosylated.

43. The method of claim **7**, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2 and 1-20 conservative amino acid substitutions.

44. The method of claim **7**, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2 and 1-20 amino acid insertions, deletions and/or substitutions.

45. A method of inhibiting Lipopolysaccharide ("LPS") induced lung inflammation in a subject in need thereof, comprising:

providing a purified polypeptide comprising an amino acid sequence that is at least 85% identical to SEQ ID NO:1 or SEQ ID NO:2; and

administering the polypeptide to the subject to inhibit LPS induced lung inflammation.

46. The method of claim **45**, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO: 1.

47. The method of claim **46**, wherein the polypeptide is glycosylated.

48. The method of claim **45**, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:2.

49. The method of claim **48**, wherein the polypeptide is glycosylated.

50. The method of claim **45**, wherein the purified polypeptide comprising an amino acid sequence that is at least 90% identical to SEQ ID NO:1 or SEQ ID NO:2.

51. The method of claim **45**, wherein the purified polypeptide comprising an amino acid sequence that is at least 95% identical to SEQ ID NO:1 or SEQ ID NO:2.

52. The method of claim **45**, wherein the purified polypeptide comprising an amino acid sequence that is at least 96% identical to SEQ ID NO:1 or SEQ ID NO:2.

53. The method of claim **45**, wherein the purified polypeptide comprising an amino acid sequence that is at least 97% identical to SEQ ID NO:1 or SEQ ID NO:2.

54. The method of claim **45**, wherein the purified polypeptide comprising an amino acid sequence that is at least 98% identical to SEQ ID NO:1 or SEQ ID NO:2.

55. The method of claim **45**, wherein the purified polypeptide comprising an amino acid sequence that is at least 99% identical to SEQ ID NO:1 or SEQ ID NO:2.

* * * * *