(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
20 July 2017 (20.07.2017)

WIPO | PCT

(10) International Publication Number
WO 2017/123795 A1

(51) International Patent Classification:
A61K 31/122 (2006.01) *A61K 31/18* (2006.01)
A61K 31/404 (2006.01)

(21) International Application Number:
PCT/US2017/013236

(22) International Filing Date:
12 January 2017 (12.01.2017)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/277,720 12 January 2016 (12.01.2016) US

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

— *of inventorship (Rule 4.17(iv))*

Published:

— *with international search report (Art. 21(3))*

(54) Title: COMPOUNDS INHIBITING NEF-CALNEXIN INTERACTION

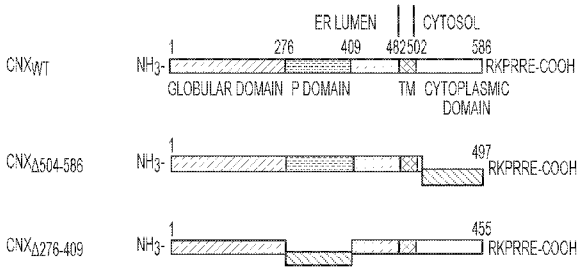


FIG. 1A

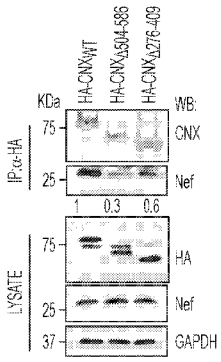


FIG. 1B

(57) Abstract: The invention relates to compounds and methods for restoring or preserving cholesterol efflux in a cell infected with Human Immunodeficiency Virus (HIV) by preventing or decreasing an interaction between Negative Regulatory Factor (Nef) protein and Calnexin protein, and methods for screening for such compounds.

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COMPOUNDS INHIBITING NEF-CALNEXIN INTERACTION

CROSS-REFERENCE OF RELATED APPLICATION

[0001] This application claims priority to U.S. Provisional Application No. 62/277,720 filed January 12, 2016; the entire contents of all of which are hereby incorporated by reference.

BACKGROUND

1. Technical Field

[0002] The field of the currently claimed embodiments of this invention relates to compounds and methods for restoring or preserving cholesterol efflux in a cell infected with Human Immunodeficiency Virus (HIV) by preventing or decreasing an interaction between Negative Regulatory Factor (Nef) protein and Calnexin protein, and methods for screening for such compounds.

2. Discussion of Related Art

[0003] Highly active anti-retroviral therapy (HAART) has transformed treatment of the HIV disease changing prognosis from acutely lethal to chronic illness, and lifespan of HIV-infected subjects approximates that of uninfected individuals. However, HAART does not cure HIV, and chronic HIV infection is associated with a number of co-morbidities, such as premature atherosclerosis and cardio-vascular disease (37). An essential component in pathogenesis of cardio-vascular disease in HIV-infected subjects is HIV-associated dyslipidemia, which is caused both by drugs used to treat HIV infection and by the effects of HIV itself on cholesterol metabolism (38).

[0004] HIV-1 infection, via activity of viral protein Nef, impairs cholesterol efflux mediated by the cholesterol transporter ATP-Binding Cassette A1 (ABCA1) (1). ABCA1 is the main cellular cholesterol transporter regulating delivery of cellular cholesterol to extracellular acceptor, apolipoprotein A-I. Studies in animal models demonstrated that this activity of Nef may be responsible for hypoalphalipoproteinemia and high risk of atherosclerosis observed in HIV-infected subjects (2-4). Recent studies identified calnexin,

an integral endoplasmic reticulum (ER) membrane lectin-like chaperone, as a key player in the mechanism of Nef-mediated inhibition of ABCA1 and cholesterol efflux (5). Calnexin (CNX) and its homologue calreticulin (CRT) regulate folding and maturation of newly synthesized glycoproteins by engaging them in a CNX/CRT cycle (6).

[0005] ABCA1 is a highly glycosylated protein (7). Although no evidence for the role of CNX in ABCA1 biogenesis is available, two well-studied ABC transporters, ABCC7 (also known as cystic fibrosis transmembrane conductance regulator, CFTR) and ABCB1 (also known as multidrug resistance protein 1 or P-glycoprotein 1), interact with CNX, and folding mutants of these transporters are retained within the ER by CNX and eventually degraded (8, 9). Importantly, ABCC7 and ABCB1 mutants that escape CNX binding do not achieve mature glycosylation and these mutations result in reduced transporter function (8, 9). A recently published study demonstrated that ABCA1 interacts with CNX, and reduction of CNX expression by RNAi resulted in a significant decrease in functional activity of ABCA1, evidenced by reduced cholesterol efflux to ABCA1-specific acceptor apoA-I (5). It was also shown that Nef impairs interaction between ABCA1 and CNX, and this effect of Nef is essential for inactivation and downregulation of ABCA1 (5). Importantly, inhibition of ABCA1-calnexin interaction by Nef is specific, as interaction between ABCA1 and two other proteins, dystrophin and serine palmitoyltransferase, shown previously to bind ABCA1 (10), was not affected. Also not affected was the interaction between calnexin and HIV-1 envelope glycoprotein, gp160; in fact this interaction was even enhanced by Nef (5). These findings suggested that Nef modulates activity of calnexin, but the mechanism of this effect and molecular details of Nef/calnexin interaction remained unknown. Moreover, it was unclear whether the interaction between Nef and calnexin is direct, making screen for inhibitory compounds difficult.

[0006] Calnexin is a 592-amino acid Type I transmembrane protein composed of three parts: a lumenal fragment consisting of a globular β-sandwich domain responsible for the interaction with carbohydrates and a proline-rich tandem sequence repeat domain (the P domain) involved in protein-protein interactions, a transmembrane domain, and a cytoplasmic domain of 90 residues (11, 12). The cytoplasmic tail of calnexin can undergo phosphorylation and palmitoylation which regulate calnexin association with a number of proteins and protein complexes that influence functional activity of this chaperone (13-18). For example, palmitoylation of the C-tail of calnexin mediates its association with the ribosome-translocon complex, which is essential for the ability of calnexin to capture its

client proteins as they emerge from the translocon (18). Ribosome association of calnexin is also regulated by phosphorylation on Ser534 and Ser544 by casein kinase 2 and on Ser563 by protein kinase C/proline-directed kinase (11). In addition, phosphorylation at Ser563 has been shown to play essential role in quality control function of calnexin (15). Therefore, the C-tail of calnexin may play a functional role regulating activity of the chaperone both directly, by affecting ER lumenal events involving calnexin, and indirectly, via modification of calnexin localization in the ER.

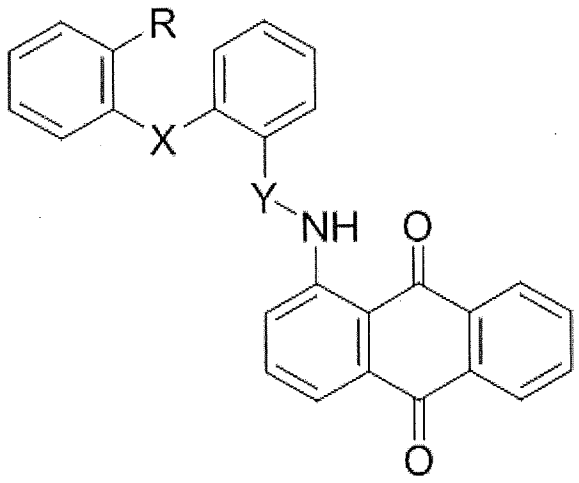
SUMMARY

[0007] An embodiment of the invention relates to a method for restoring or preserving cholesterol efflux in a cell infected with Human Immunodeficiency Virus (HIV) comprising delivering to the cell an effective amount of a composition or formulation comprising a small molecule. The small molecule prevents or decreases an interaction between a Negative Regulatory Factor (Nef) protein and a Calnexin protein.

[0008] Another embodiment of the invention relates to a method for treating or preventing atherosclerosis in a subject infected with HIV comprising administering to said subject an effective amount of a composition or formulation comprising a small molecule. The small molecule prevents or decreases an interaction between a Nef protein and a Calnexin protein.

[0009] Another embodiment of the invention relates to a method for screening for a small molecule that restores or preserves cholesterol efflux in a cell by inhibiting or decreasing an interaction between a Nef protein and a Calnexin protein including: incubating a cell expressing a full-length Nef protein or a segment of the full-length Nef protein and a full-length Calnexin protein or a segment of the full-length Calnexin protein with a small molecule of interest; assaying the incubated cell for cholesterol efflux; and assaying the incubated cell for a level of binding between the full-length Nef protein or the segment of the full-length Nef protein and the full-length Calnexin protein or the segment of the full-length Calnexin protein. In such embodiments, an increase in cholesterol efflux and a decrease in the level of binding as compared to a control is indicative of restoration or preservation of cholesterol efflux by inhibiting or decreasing an interaction between the Nef protein and the Calnexin protein as a result of incubation of the cell with the small molecule of interest.

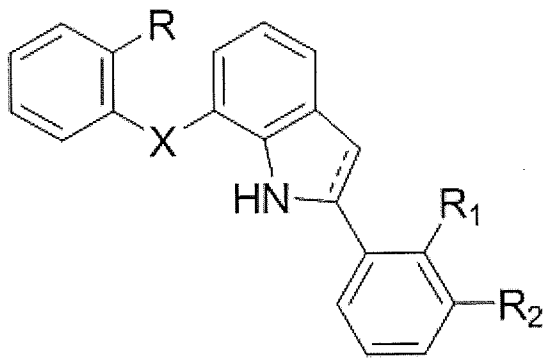
[0010] An embodiment of the invention relates to a small molecule having the structure of Formula (I):



(I),

[0011] Where R is H, CH_2OH, COOH or $COOCH_3$; X is CH_2, NH, O, NCH_3, or SO_2; and Y is a bond, CH_2, CO or SO_2.

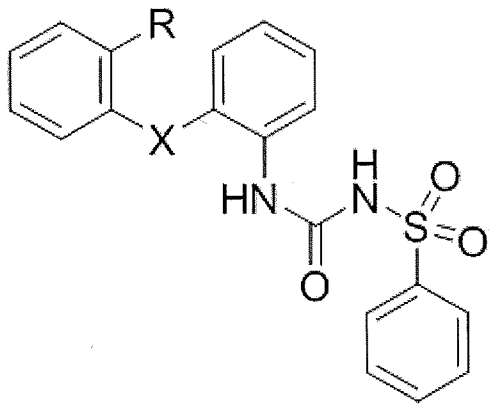
[0012] An embodiment of the invention relates to a small molecule having the structure of Formula (II):



(II),

[0013] Where R, R_1, and R_2 are independently selected from H, CH_2OH, COOH or $COOCH_3$; and X is CH_2, NH, O, NCH_3, or SO_2.

[0014] An embodiment of the invention relates to a small molecule having the structure of Formula (III):



(III),

[0015] Where R is H, CH_2OH, COOH or $COOCH_3$; and X is CH_2, NH, O, NCH_3, or SO_2.

BRIEF DESCRIPTION OF THE DRAWINGS

[0016] Further objectives and advantages will become apparent from a consideration of the description, drawings, and examples.

[0017] **FIG 1** shows a schematic of HA-tagged full-length and mutant calnexin constructs expressed in HEK293T cells and immunoprecipitation results of such constructs;

[0018] **FIG. 2** shows a schematic representation of Nef-CNX binding and the interactions in Nef-CNX docking models mapped on Nef and calnexin sequences;

[0019] **FIG. 3** shows various immunoprecipitation results displaying the interaction between Nef and Calnexin as a result of various conditions;

[0020] **FIG. 4** shows various assays showing the effects of the mutation of certain residues on Nef on regulation of ABCA1 and cholesterol efflux;

[0021] **FIG. 5** shows the results of immunoprecipitation assays showing that Nef directly binds to Calnexin and its cytoplasmic tail;

[0022] **FIG. 6** shows the structures of various small molecules according to some embodiments of the invention, targeting the Nef-Calnexin interaction as well as the effects these molecules have on the Nef-Calnexin; and

[0023] **FIG. 7** shows graphs showing that an embodiment of the invention, compound NSC 13987, prevents impairment of cholesterol efflux by HIV and Nef.

DETAILED DESCRIPTION

[0024] Some embodiments of the current invention are discussed in detail below. In describing embodiments, specific terminology is employed for the sake of clarity. However, the invention is not intended to be limited to the specific terminology so selected. A person skilled in the relevant art will recognize that other equivalent components can be employed and other methods developed without departing from the broad concepts of the current invention. All references cited anywhere in this specification, including the Background and Detailed Description sections, are incorporated by reference as if each had been individually incorporated.

[0025] **Definitions**

[0026] The abbreviations used throughout are: ABCA1, ATP-binding cassette A1; CNX, calnexin; CNX-CT, calnexin cytoplasmic tail; ER, endoplasmic reticulum; HA, hemagglutinin; HIV-1, human immunodeficiency virus type 1; HRP, horseradish peroxidase; PMA, phorbol-12-myristate 13-acetate; RT, reverse transcriptase.

[0027] As used throughout the phrase an "effective amount" of a composition of the invention is measured by the therapeutic effectiveness of a compound of the invention, wherein at least one adverse effect of a disorder is ameliorated or alleviated. More specifically, wherein administering a compound or composition results in restoration or preservation of cholesterol efflux in a cell or mammal infected with Human Immunodeficiency Virus (HIV).

[0028] As used herein and unless otherwise indicated, the term "formulation" refers to a composition comprising a compound of the invention that is described in a particular dosage form (*e.g.*, tablet) or with a particular dosage amount (*e.g.*, 30 mg/kg).

[0029] When administered to a subject (*e.g.*, to an animal for veterinary use or to a human for clinical use), the compounds of the invention can be optionally administered in isolated form. As used herein, "isolated" means that the compounds of the invention are separated from other components of either (a) a natural source, such as a plant or cell, preferably bacterial culture, or (b) a synthetic organic chemical reaction mixture, preferably, via conventional techniques, the compounds of the invention are purified. As used herein, "purified" means that when isolated, the isolate contains at least 80% preferably at least 90%, more preferably at least 95%, and most preferably at least 99% of a compound of the invention by weight of the isolate.

[0030] The phrase "pharmaceutically acceptable salt(s)," as used herein includes but is not limited to salts of acidic or basic groups that may be present in compounds used in the present compositions. Compounds included in the present compositions that are basic in nature are capable of forming a wide variety of salts with various inorganic and organic acids. The acids that may be used to prepare pharmaceutically acceptable acid addition salts of such basic compounds are those that form non-toxic acid addition salts, i.e., salts containing pharmacologically acceptable anions including, but not limited to, sulfuric, citric, maleic, acetic, oxalic, hydrochloride, hydrobromide, hydroiodide, nitrate, sulfate, bisulfate, phosphate, acid phosphate, isonicotinate, acetate, lactate, salicylate, citrate, acid citrate, tartrate, oleate, tannate, pantothenate, bitartrate, ascorbate, succinate, maleate, gentisinate, fumarate, gluconate, glucaronate, saccharate, formate, benzoate, glutamate, methanesulfonate, ethanesulfonate, benzenesulfonate, p-toluenesulfonate and pamoate (*i.e.*, 1,1'-methylene-bis-(2-hydroxy-3-naphthoate)) salts. Compounds included in the present compositions that include an amino moiety may form pharmaceutically acceptable salts with various amino acids, in addition to the acids mentioned above. Compounds, included in the present compositions, that are acidic in nature are capable of forming base salts with various pharmacologically acceptable cations. Examples of such salts include alkali metal or alkaline earth metal salts and, particularly, calcium, magnesium, sodium lithium, zinc, potassium, and iron salts.

[0031] As used herein and unless otherwise indicated, the term "pharmaceutically acceptable prodrug" means a derivative of a compound that can hydrolyze, oxidize, or otherwise react under biological conditions (in vitro or in vivo) to provide the compound. Examples of prodrugs include, but are not limited to, compounds that comprise biohydrolyzable moieties such as biohydrolyzable amides, biohydrolyzable esters, biohydrolyzable carbamates, biohydrolyzable carbonates, biohydrolyzable ureides, and biohydrolyzable phosphate analogues. Other examples of prodrugs include compounds that comprise oligonucleotides, peptides, lipids, aliphatic and aromatic groups, or NO, NO_2, ONO, and ONO_2 moieties. Prodrugs can typically be prepared using well known methods, such as those described in Burger's Medicinal Chemistry and Drug Discovery, pp. 172, 178, 949, 982 (Manfred E. Wolff ed., 5th ed. 1995), and Design of Prodrugs (H. Bundgaard ed., Elselvier, New York 1985).

[0032] The terms "treating or preventing" are intended to include preventing, eradicating, or inhibiting the resulting increase of undesired physiological activity associated

with a disorder, for example, in the context of the therapeutic or prophylactic methods of the invention. In another embodiment, the term treating or preventing includes antagonistic effects, e.g., diminishment of the activity or production of mediators of a disorder.

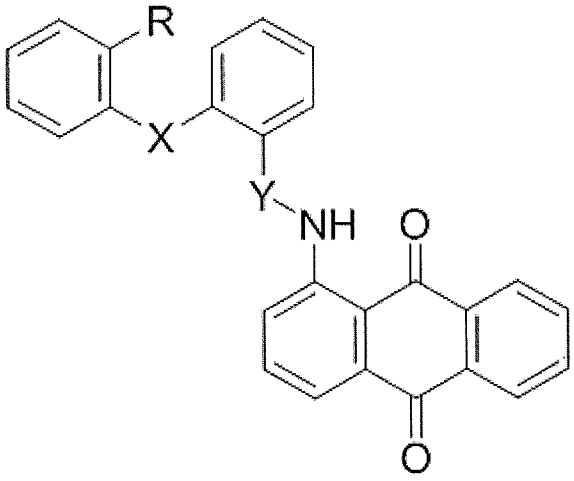
[0033] An embodiment of the invention relates to a method for restoring or preserving cholesterol efflux in a cell infected with Human Immunodeficiency Virus (HIV) comprising delivering to the cell an effective amount of a composition or formulation comprising a small molecule. The small molecule prevents or decreases an interaction between a Negative Regulatory Factor (Nef) protein and a Calnexin protein.

[0034] Some embodiments of the invention relate to the method above, where the small molecule binds to at least one amino acid residue on the Nef protein. The at least one amino acid residue is selected from the group consisting of a lysine at amino acid position 4, a serine at amino acid position 6, a lysine at amino acid position 7, and a tyrosine at amino acid position 124.

[0035] Some embodiments of the invention relate to the method above, where the small molecule binds to at least one amino acid residue on the Calnexin protein. The at least one amino acid residue is selected from the group consisting of an aspartic acid at position 90, a glutamic acid at amino acid position 529, a glutamic acid at amino acid position 532, and a glutamic acid at amino acid position 533.

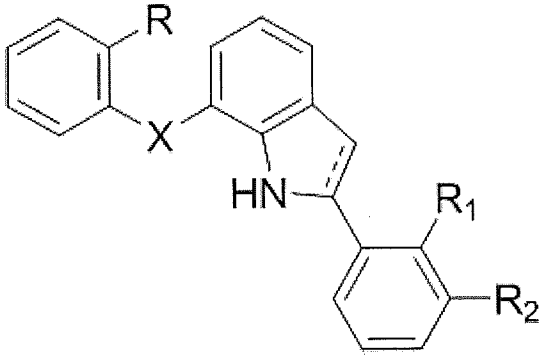
[0036] Some embodiments of the invention relate to the method above, where preventing or decreasing the interaction between the Nef protein and the Calnexin protein results in at least partial restoration of ATP-Binding Cassette A1 (ABCA1) activity.

[0037] Some embodiments of the invention relate to the method above, where the small molecule is a small molecule is selected from the group consisting of Formula (I), Formula (II), Formula (III) or an analog or derivative thereof:



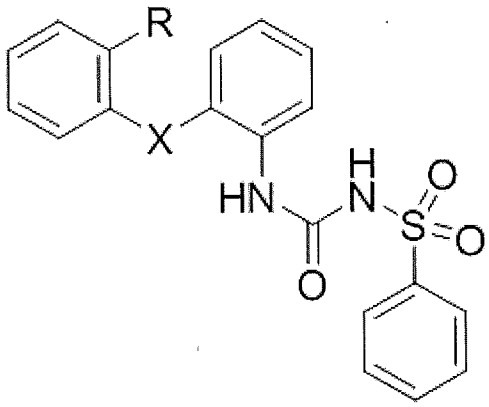
(I),

[0038]



(II),

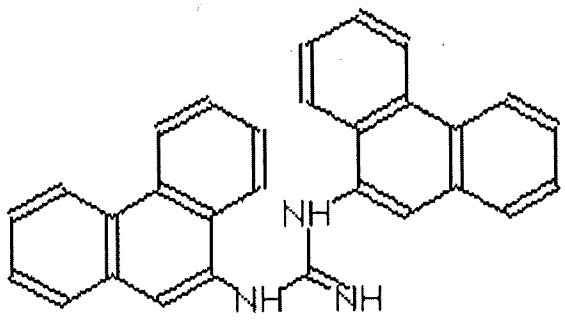
[0039]



(III),

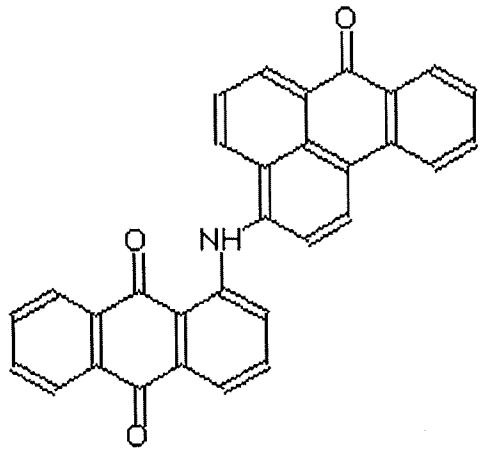
[0040] where R, R_1, and R_2 are independently selected from H, CH_2OH, COOH or $COOCH_3$; X is CH_2, NH, O, NCH_3, or SO_2; and Y is a bond, CH_2, CO or SO_2.

[0041] Some embodiments of the invention relate to the method above, where the small molecule is selected from the group consisting of Formula (IV), Formula (V), Formula (VI) or an analog or derivative thereof:



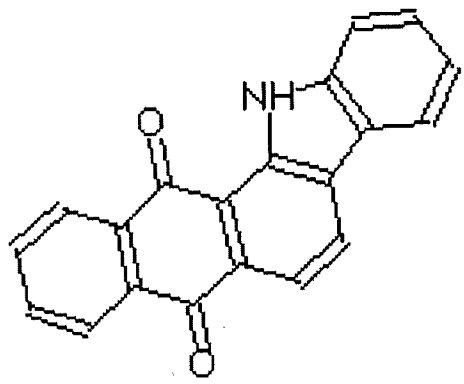
[0042] (IV),

[0043] 1,3-DI-9-Phenanthrylguanidine (NSC 1758),



[0044] (V),

[0045] 1[(7-Oxo-7H-benz[de]anthracene-3-yl)amino] anthraquinone (NSC 13987),



[0046] (VI),

[0047] 5H-Naphtho(2,3-a)carbazole-5,13(12H)-dione (NSC 92938).

[0048] An embodiment of the invention relates to a method for treating or preventing atherosclerosis in a subject infected with HIV comprising administering to said subject an effective amount of a composition or formulation comprising a small molecule. The small molecule prevents or decreases an interaction between a Nef protein and a Calnexin protein.

[0049] Some embodiments of the invention relate to the method above, where the small molecule binds to at least one amino acid residue on the Nef protein. The at least one amino acid residue is selected from the group consisting of a lysine at amino acid position 4, a serine at amino acid position 6, a lysine at amino acid position 7, and a tyrosine at amino acid position 124.

[0050] Some embodiments of the invention relate to the method above, where the small molecule binds to at least one amino acid residue on the Calnexin protein. The at least one amino acid residue is selected from the group consisting of an aspartic acid at position 90, a glutamic acid at amino acid position 529, a glutamic acid at amino acid position 532, and a glutamic acid at amino acid position 533.

[0051] Some embodiments of the invention relate to the method above, where preventing or decreasing the interaction between the Nef protein and the Calnexin protein results in at least partial restoration of ATP-Binding Cassette A1 (ABCA1) activity.

[0052] Some embodiments of the invention relate to the method above, where the small molecule is a small molecule of Formula (I), Formula (II), or Formula (III), or an analog or derivative thereof.

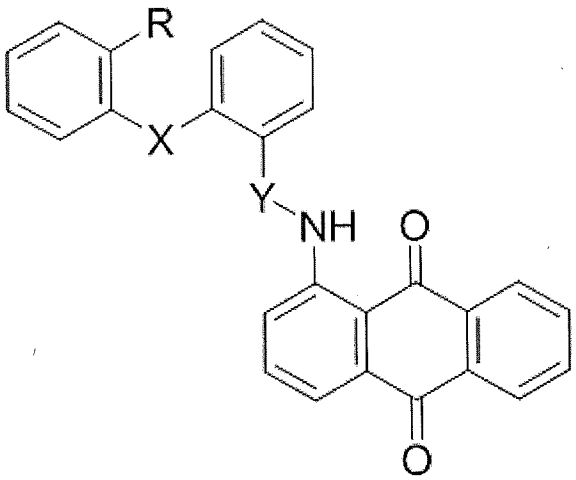
[0053] An embodiment of the invention relates to a method for screening for a small molecule that restores or preserves cholesterol efflux in a cell by inhibiting or decreasing an interaction between a Nef protein and a Calnexin protein including: incubating a cell expressing a full-length Nef protein or a segment of the full-length Nef protein and a full-length Calnexin protein or a segment of the full-length Calnexin protein with a small molecule of interest; assaying the incubated cell for cholesterol efflux; and assaying the incubated cell for a level of binding between the full-length Nef protein or the segment of the full-length Nef protein and the full-length Calnexin protein or the segment of the full-length Calnexin protein. In such embodiments, an increase in cholesterol efflux and a decrease in the level of binding as compared to a control is indicative of restoration or preservation of cholesterol efflux by inhibiting or decreasing an interaction between the Nef protein and the Calnexin protein as a result of incubation of the cell with the small molecule of interest.

[0054] Some embodiments of the invention relate to the method above, further including a step of virtually screening a library of small molecules for a small molecule that is predicted to bind to or interact with at least one of the full-length Nef protein or the segment of the full-length Nef protein and the full-length Calnexin protein or the segment of the full-length Calnexin protein.

[0055] Some embodiments of the invention relate to the method above, where the cells are incubated for at least 1 day.

[0056] Some embodiments of the invention relate to the method above, where the assaying the incubated cell for a level of binding comprises an immunoprecipitation assay. In some embodiments, binding can be assayed with recombinant Nef and calnexin proteins using Surface Plasmon Resonance assay (Biacore) or Isothermal titration calorimetry.

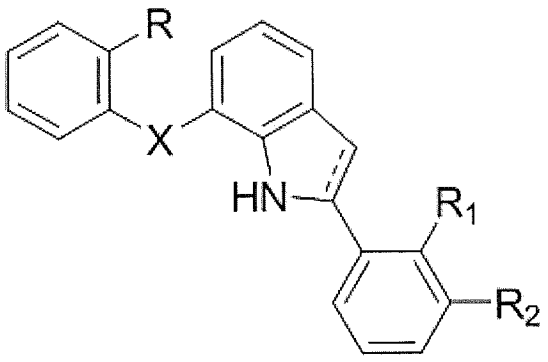
[0057] An embodiment of the invention relates to a small molecule having the structure of Formula (I):



(I),

[0058] Where R is H, CH_2OH, COOH or $COOCH_3$; X is CH_2, NH, O, NCH_3, or SO_2; and Y is a bond, CH_2, CO or SO_2.

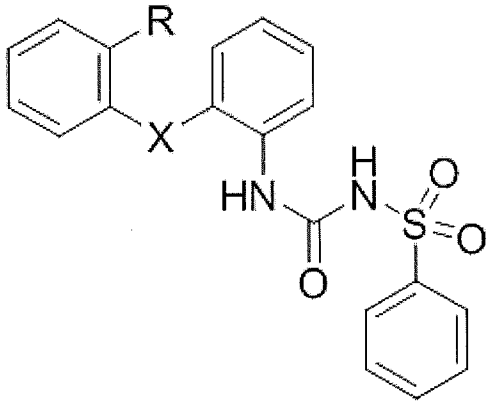
[0059] An embodiment of the invention relates to a small molecule having the structure of Formula (II):



(II),

[0060] Where R, R_1, and R_2 are independently selected from H, CH_2OH, COOH or $COOCH_3$; and X is CH_2, NH, O, NCH_3, or SO_2.

[0061] An embodiment of the invention relates to a small molecule having the structure of Formula (III):



(III),

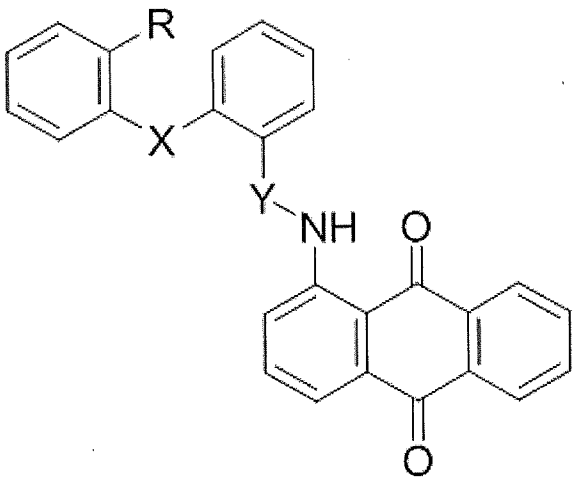
[0062] Where R is H, CH_2OH, COOH or $COOCH_3$; and X is CH_2, NH, O, NCH_3, or SO_2.

[0063] Some embodiments relate to combination therapeutic approaches where any of the methods and/or compounds described are combined with at least one other therapeutic agent or method for treating HIV. Common therapeutic agents include, but are not limited to: Nucleotide reverse transcriptase inhibitors; non-nucleotide RT inhibitors; integrate inhibitors; fusion inhibitors; protease inhibitors; and CCR5 inhibitors.

[0064] Some embodiments are compounds derived from the compounds of Formula (V). Such compounds include the compounds of Formulas (I), (II), and (III), for example. Considerations taken into account when modifying the chemical structure of Formula (V) to reach the chemical scaffolds of Formulas (I), (II) and (III) included the removal of the two aromatic rings and addition of functional groups that would improve the solubility of Formula (V) derivatives in aqueous media. More specifically, in some embodiments, the aromatic rings would be replaced with hydrophilic moieties to promote solubility in aqueous media and promote binding to Nef.

[0065] A first scaffold for Formula (V) derivatives includes changes to the tetracyclic core (Anthraquinone derivatives) as shown in Formula (I):

[0066]

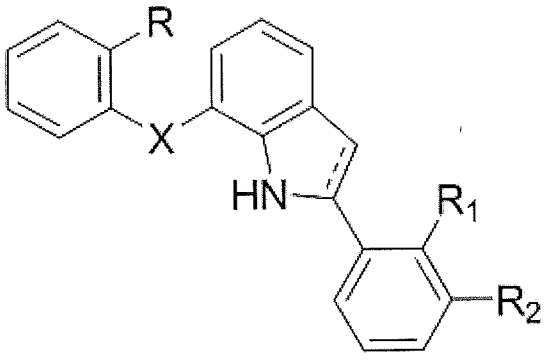


(I),

[0067] Where R is H, CH_2OH, COOH or $COOCH_3$; X is CH_2, NH, O, NCH_3, or SO_2; and Y is a bond, CH_2, CO or SO_2.

[0068] A second scaffold for Formula (V) derivatives includes changes to the tricyclic core (Indole/sulfonylurea derivatives) as shown in Formulas (II) and (III):

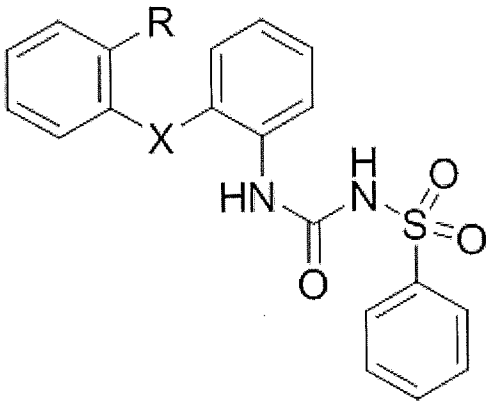
[0069] Formula (II):



(II),

[0070] Where R, R_1, and R_2 are independently selected from H, CH_2OH, COOH or $COOCH_3$; and X is CH_2, NH, O, NCH_3, or SO_2.

[0071] Formula (III):



(III),

[0072] Where R is H, CH_2OH, COOH or $COOCH_3$; and X is CH_2, NH, O, NCH_3, or SO_2.

[0073] *Example*

[0074] In the following example, it is demonstrated that the C-tail of calnexin is targeted by the HIV-1 protein Nef, which uses this interaction to disrupt calnexin-assisted maturation of ABCA1 and impair cholesterol efflux. Important structural features of the Nef/calnexin interaction are characterized and a small molecule compound that blocks this interaction and reverses negative effects of HIV infection on cellular cholesterol metabolism is identified.

[0075] **RESULTS**

[0076] **Cytoplasmic domain of calnexin is necessary for interaction with Nef**

[0077] In a previous study it was shown that HIV-1 Nef interacts with the ER chaperone calnexin (5). To test which region of calnexin is necessary for binding to Nef, calnexin constructs that had deletion of the lumenal repeat segment (aa 276-409) or truncation of the C-terminal cytoplasmic domain (aa 504-586) (Fig. 1A). HEK293T cells were transfected with Nef_{BRU}-expressing vector and HA-tagged variants of wild-type (WT) calnexin or the deletion mutants and performed co-immunoprecipitation. Figure 1B shows that WT calnexin interacted strongly with Nef, whereas calnexin construct with internal repeat motif deletion ($CNX_{\Delta 276-409}$) exhibited binding reduced by 40%. However, binding of Nef to calnexin construct carrying the truncation of the C-terminal cytoplasmic tail ($CNX_{\Delta 504-586}$) was reduced by 70%. This finding highlights the importance of the cytoplasmic region of calnexin in interaction with Nef. The role of calnexin cytoplasmic tail in the interaction with Nef is consistent with Nef's localization to the cytoplasm (19). Of note, the cytoplasmic domain of calnexin is composed mainly of negatively charged amino acids, whereas the N-terminal region of Nef is enriched in positively charged residues. The modest effect that deletions in the lumenal repeat motif of calnexin have on Nef binding may be due to conformational changes, which could affect all domains of calnexin.

[0078] FIG. 1 shows a schematic of HA-tagged full-length and mutant calnexin constructs expressed in HEK293T cells and immunoprecipitation results of such constructs. Specifically, Panel (A) shows HA-tagged full-length and mutant calnexin constructs expressed in HEK293T cells. The various segments represented are the globular domain, tandem repeat motif, TM domain and C-terminal cytoplasmic tail, respectively. Dropped boxes represent deleted fragments. CNX_{WT} represents full length calnexin, $CNX_{\Delta 486-567}$ has 81 out of the 89 cytoplasmic tail residues deleted while maintaining the ER localization sequence RKPRRE; $CNX_{\Delta 257-388}$ construct has 131 residues of the P domain deleted. In panel (B) HEK293T cells were co-transfected with Nef and HA-tagged CNX_{WT}, $CNX_{\Delta 486-567}$ or $CNX_{\Delta 257-388}$ vectors and blotted for HA, Nef and GAPDH (lysate). Calnexin variants were immunoprecipitated 48 h post-transfection using anti-HA coupled agarose beads and resulting immunoprecipitates were immunoblotted for Nef (upper panel). Numbers under the lanes show relative amounts of co-precipitated Nef obtained by gel densitometry.

[0079] **Computational model of Nef-CNX interaction**

[0080] Experimentally solved molecular structure of calnexin is available only for the lumenal domain (12), and to obtain three-dimensional structure of calnexin cytoplasmic domain a modeling with several modeling servers implementing different methods was performed, which produced a number of models ranging from the fully folded structures to structures that included natively disordered regions. The models have been assessed for accuracy and final round of modeling performed with the server QA-RecombineIt. The final model had a loosely folded structure (Fig. 2A, panel *a*). Computational prediction of Nef-CNX complexes showed Nef N-terminal alpha-helix forming the interaction interface with calnexin cytoplasmic domain (Fig. 2A, panels *b* and *c*).

[0081] In comparison with the calnexin cytoplasmic domain model, the model of Nef was based on a number of experimental structures (20-24) and thus had better accuracy. Nef-CNX interaction has been modeled by global docking using four different docking servers, Cluspro, HEX, SwarmDock, and Zdock. Combined set of the best Nef-CNX docking models produced with these servers contained 80 models. The advantage of this approach is that the resulting models represented Nef-CNX interaction modeled by four different, unrelated methods and therefore it was more reliable than using a single server. From these, 49 models have been filtered out as possibly interfering with interaction of Nef with ER membrane. Intermolecular interactions in the remaining subset of 31 models have been identified. There are several distinct clusters of interactions, with sharp maxima for Lys7 and Arg in positions 8, 19, 22, 75 and 109 (Fig. 2B). Notably, similar analysis of interactions carried out on the full initial dataset of 80 docking models showed similar clustering and maxima (not shown). It can therefore be hypothesized that the identified residues represent the overall favorable Nef-CNX interaction sites. All these residues, except Lys7 and Arg8, have been also identified as participating in interactions in the experimental structures of complexes which included Nef. A representative model of Nef-CNX binding is shown in Figure 2A, panels *b* and *c*. Analysis of the conserved residues in Nef performed with ConSurf (25) revealed several such conserved positions in the N-terminal region, including Lys4, Ser6, Lys7 and Arg19. Multiple sequence alignment of the human HIV Nef sequences from Uniprot showed that Lys7 is highly conserved across the spectrum of HIV-1 and HIV-2 sequences. Conserved residues indicate structurally and functionally important positions, including interaction sites. Therefore, Lys7 represents a new interaction site which was not previously identified in Nef interactions with other proteins.

[0082] FIG. 2 shows a schematic representation of Nef-CNX binding and the interactions in Nef-CNX docking models mapped on Nef and calnexin sequences. Specifically, panel (A) shows schematic representation of Nef-CNX binding. (*a*) Schematic representation of the calnexin structure. Lumenal domain is represented by the model structure; the transmembrane region is shown as a helical domain according to the Uniprot (calnexin, P27824) domain classification. Calnexin cytoplasmic domain and Nef are represented by models built as described in Experimental Procedures, and Nef/CNX binding is shown according to the results of docking. (*b*) Docking model of the CNX cytoplasmic domain (green) – Nef (magenta) interaction. The binding interface is formed by the Nef N-terminal alpha-helix, with Lys 7 and Arg 8, 19, and 22 forming interactions with CNX. (*c*) Lys7 in Nef (magenta) displays strong interaction with Glu533 in CNX (green) formed by the hydrogen and ionic bonds. (*d*) Lys4 plays a key role in the N-terminal region of Nef structure model (magenta). It forms a strong intramolecular interaction with Nef Asp90 with hydrogen and ionic bonds, supporting structural rigidity of the Nef N-terminal alpha-helix relative to the rest of Nef structure. Panel (B) shows interactions in Nef-CNX docking models mapped on Nef and calnexin sequences. Bars show the number of interactions, with the numbers for each maximum showing sequence number. In the Nef sequence, there are three distinct interaction clusters centered on residues 7, 22, 75 and 109, with sharp maxima for lysine 7, and arginines in positions 8, 19, 22, 75 and 109. Two interaction clusters in the calnexin sequence are formed by amino acids 528 – 533 and 545 – 557; they include glutamic acid residues in positions 529, 532, 533.

[0083] Lysine residues of Nef in positions 4 and 7 are critical for Nef-CNX interaction

[0084] According to docking modeling and sequence conservation results, Lys7 possibly represents a new binding site in Nef and accordingly it has been selected for mutagenesis experiments. Lys4 has been also selected since it is a Lys7 near neighbor and, as demonstrated in the Nef model, it plays a key structural role for the N-terminus (Fig. 2A, panel *d*). Therefore, mutation of both Lys4 and Lys7 was predicted to invoke structural rearrangement in the Nef N-terminal region thus disrupting the interaction between Nef and calnexin. Alanine substitution of basic residues at the N-terminus of Nef has previously been shown to preserve membrane association and CD4 down-regulation by Nef (26), and intracellular localization of the mutant Nef was indistinguishable from that of Nef WT (27).

[0085] To verify the role of these residues in Nef interaction with calnexin, the mutant HIV-1 NL4-3 clone carrying Nef with Lys4 and Lys7 changed to alanines was used. Calnexin was immunoprecipitated from HEK293T cells transfected with WT or mutant HIV-1 clones and the precipitate was immunoblotted for Nef. As shown in Figure 3A, interaction with calnexin was evident for Nef WT, but not for NefK4,7A. Interaction with the double mutant was reduced by 95%, indicating that the lysine residues in positions 4 and 7 are essential for Nef interaction with calnexin.

[0086] In order to look at the individual contribution of the two lysine residues to the interaction with calnexin, the Nef_{BRU} plasmid was mutagenized to create single and double lysine mutant constructs. HEK293T cells were transfected with WT or mutant Nef constructs and the amount of Nef found to immunoprecipitate with calnexin was analyzed again. Based on densitometric analysis, interaction of CNX with NefK4A was reduced by 50% whereas interaction with NefK7A was reduced by as much as 90% as compared to interaction with WT Nef (Fig. 3B). Interaction of calnexin with NefK4,7A was undetectable. This result was consistent with Figure 3C, where the expression of ABCA1 in the presence of single Nef mutants as compared to the double lysine mutant was evaluated. NefK4A and NefK7A mutants reduced ABCA1 abundance as much as the wild-type Nef, whereas near control level of ABCA1 was observed when both lysine residues were mutated (Fig. 3C). This result highlights the importance of both residues in ABCA1 down-regulation, and suggests that even reduced interaction with calnexin observed for NefK4A and NefK7A mutants is sufficient for ABCA1 downregulation.

[0087] To rule out the possibility that mutation of these residues grossly affected the behavior of the N-terminal domain of Nef, the interaction of the mutant Nef with ABCA1 was tested. Previous studies demonstrated that interaction between Nef and ABCA1 also involves the N-terminal domain (1), although the specific residues involved have not been identified. Co-precipitation analysis revealed about a 30% reduction in NefK4,7A interaction with ABCA1 as compared to ABCA1 interaction with wild-type Nef (Fig. 3D). The reduction, however, remains in stark contrast to the >95% loss of interaction observed in the Nef-CNX interaction studies (Fig. 3A).

[0088] **Functional analysis of Nef mutants**

[0089] In a previous study, it was reported that Nef plays a central role in the down-modulation of ABCA1 expression and function (1). This phenotype was associated with Nef's ability to interact with calnexin and disrupt calnexin interaction with ABCA1 (5).

Identification of Nef residues required for interaction with calnexin provided an opportunity to verify the critical role of this interaction for the effects of Nef on cellular cholesterol metabolism. To assess the functional consequence of losing the Nef/CNX interaction for ABCA1 functionality, HEK293T cells were co-transfected with ABCA1 and HIV-1 NL4-3 infectious clones that express either Nef WT or Nef K4,7A. Lysates were immunoblotted for ABCA1 (Fig. 4A). Consistent with results obtained with Nef-expressing vector (Fig. 3C), total ABCA1 abundance was significantly reduced in the presence of Nef WT, however, expression of ABCA1 in the presence of Nef K4,7A was comparable to that of the control sample, which was transfected with an empty vector. This result is consistent with conclusions of the previous study that identified Nef as the key viral factor responsible for ABCA1 downregulation (1).

[0090] FIG. 3 shows various immunoprecipitation results displaying the interaction between Nef and Calnexin as a result of various conditions. Specifically, Panel A shows HEK293T cells transfected with HIV-1 molecular clones encoding for Nef WT or Nef K4,7A. Panel B shows HEK293T cells transfected with pcDNA plasmids expressing Nef WT or mutants Nef K4A, Nef K7A or NefK4,7A. Cells were lysed 48 h post-transfection. Endogenous calnexin was immunoprecipitated using monoclonal calnexin antibody and immunoprecipitates were blotted for Nef and calnexin (top panels). Whole cell lysates were analyzed for expression of calnexin (CNX), Nef and GAPDH (bottom panels). In panel (C), HEK293T cells were co-transfected with ABCA1-FLAG and Nef WT or mutants Nef K4A, Nef K7A or Nef K4,7A. Cells were lysed 48 h post-transfection and lysates were analyzed for expression of ABCA1, Nef and GAPDH. In panel (D) HEK293T cells were co-transfected with ABCA1-FLAG and Nef WT or NefK4,7A and were lysed 48 h post-transfection. ABCA1 was immunoprecipitated using anti-FLAG beads and precipitates were blotted for ABCA1 and Nef (top panel). Whole cell lysates were analyzed for expression of ABCA1-FLAG, Nef and GAPDH (bottom panel). Numbers under the lanes show relative amounts of co-precipitated Nef obtained by gel densitometry.

[0091] The effect of mutations disrupting Nef/CNX interaction on the ability of Nef to downregulate apoA-1 specific cholesterol efflux was evaluated. Monocyte derived macrophages were infected with HIV-1 expressing either wild-type Nef or Nef K4,7A. Given that the virus carrying the mutation was the X4-tropic strain NL4-3, it was pseudotyped with VSV-G to ensure one-cycle infection. Seven days after infection, cholesterol efflux assay was performed. In agreement with previous reports (1, 5, 28), cells

infected with the wild-type virus had significantly reduced cholesterol efflux relative to mock-infected cells (Fig. 4B). However, infection with the virus carrying Nef K4,7A did not lead to efflux decrease.

[0092] FIG. 4 shows various assays showing the effects of the mutation of certain residues on Nef on regulation of ABCA1 and cholesterol efflux. Specifically, in panel (A) HEK 293T cells were co-transfected with ABCA1 and HIV-1 molecular clones encoding Nef WT or Nef K4,7A (HIV-1 clone with a Nef deletion was used as control). Cells were lysed 48 h post-transfection and immunoblotted for ABCA1, Nef and GAPDH. In panel (B), THP-1 cells were infected with HIV-1 molecular clones pseudotyped with VSV-G consisting of a Nef deletion (ΔNef) or expressing Nef WT or mutant Nef K4,7A. Cholesterol efflux was measured 13 days after infection. Results show apoA-I specific cholesterol efflux as mean ± SEM of quadruplicates. Western blot shows expression of Nef in cell lysates.

[0093] **Interaction between Nef and calnexin is direct**

[0094] To test whether Nef and calnexin interact directly with each other, CNX and the cytoplasmic tail of CNX (CNX-CT) was expressed in *E coli* and purified recombinant proteins by column chromatography. For purification of full-length calnexin, a novel purification system based on the ultra-high affinity ($K_d \sim 10^{-14}$-10^{-17}M) small protein complex of genetically inactivated colicin 7 DNAse (CL7) and its inhibitor, immunity protein 7 (Im7) (29-32) was developed and implemented. A CL7 variant, which possesses no DNAse activity but retains full Im7 affinity, was attached as a C-terminal tag on His-tagged calnexin construct (Fig. 5A, left side). A cleavage site for the pre-scission protease (PSC) inserted between CNX and CL7 allowed for elution of CNX from the Im7 column through cleavage by PSC. A single purification step provided an excellent yield of ~90% pure protein (Fig. 5A), in which major contamination represented CNX molecules (confirmed by mass-spec), most likely, truncated from the N-terminus. The CNX-CT construct was designed with a single N-terminal His-tag and was purified using the standard procedure (Fig. 5A, right side).

[0095] Binding of myristoylated Nef_{SF2} (33) to CNX and its cytoplasmic domain was analyzed using surface plasmon resonance (Figs. 5B,C). CNX and CNX-CT were immobilized on microchip surfaces and myristoylated Nef was injected over the surface. Nef_{SF2} directly bound to calnexin with an affinity (K_D) of 89.1 nM (k_a = 1.338E5 $M^{-1}s^{-1}$, k_d = 0.01192 s^{-1}, Chi^2 = 2.77 RU) (Fig. 5B). Binding to CNX-CT was observed to have higher affinity of K_D=9.4 nM (k_a = 9.083E5 $M^{-1}s^{-1}$, k_d = 0.008569 s^{-1}, Chi^2 = 0.474 RU) (Fig. 5C).

Taken together, these experiments demonstrate that Nef/CNX interaction is direct and involves the cytoplasmic domain of calnexin.

[0096] FIG. 5 shows the results of immunoprecipitation assays showing that Nef directly binds to Calnexin and its cytoplasmic tail. Specifically, panel (A) shows purification of CNX and CNX-CT. Steps of full-length CL7-tagged calnexin (CNX-CL7) purification are shown in detail. Whole cell lysate (WCL) was centrifuged to remove cell debris, the supernatant (SN) was treated with 0.07% polyethylene-emine (PE) to precipitate DNA, the pellet (PL), which contained most of CNX protein, was washed with detergent-containing buffer to release CNX into solution, centrifuged and the resulting supernatant was loaded on Immunity protein 7 (Im7) column. Bound proteins were eluted by treating the column with pre-scission protease (PSC) (EL lane), whereas flow-through (FT) lane shows unbound proteins. ΔCNX – truncated CNX fragment; SUMO – SUMO domain; P(PSC), P(SUMOP) – cleavage sites for the PSC and SUMO proteases, respectively; H8 – 8-Histidine tag. In panels (B) and (C), surface plasmon resonance experiments were done in a Biacore T-200 by using a CM5 chip. Panel (B) shows CNX and Panel (C) shows CNX-CT proteins captured by amine coupling and myristoylated Nef_{SF2} protein injected over the chip surface at 6 different concentrations (6.25 nM - 200 nM range) in triplicates. Lines representing actual data and a curve fit to a monovalent analyte binding model in BiaEvaluation software are shown.

[0097] **Virtual screening for compounds interfering with Nef/CNX interaction**

[0098] Docking-based virtual screening has been performed on compounds from the Zinc NCI Plated 2007 dataset with docking program Vina (34). Nef model described in Figure 2 has been used, with the interaction site for ligand docking selected to cover amino acid residues Lys4 and Lys7. The dataset consisted of 139,735 compounds. Ten putative ligands were identified and prioritized according to the Vina ranking, and structural alignment of these compounds to the Nef-CNX complex is shown in Figure 6A (panel a). The model shows that these compounds can block Nef/CNX interaction at the CNX residues Glu529, Glu532 and Glu533. Docking of NSC 13987, which turned out in the later studies to be the most effective inhibitor of the Nef-CNX interaction, is shown in panel b (Fig. 6A). Interactions of the compound with Nef include two hydrogen bonds with Nef amino acid residues Ser6 and Tyr124. Three of the 10 compounds, NSC 1758, NSC 13987, and NSC 92938 have been submitted for experimental testing. The chemical names and molecular structures of these compounds are shown in Figure 6B.

[0099] **Testing the compounds' activity**

[00100] To test whether the compounds identified in the virtual screen can interfere with Nef/CNX interaction, a co-immunoprecipitation assay was performed. HEK293T cells were transfected with plasmid encoding for Nef_{BRU} and 6 h post-transfection were treated with NSC 1758 (4 μM), NSC 13987 (5 μM), or NSC 92938 (5 μM). These concentrations of the compounds were determined by the MTT assay to reduce cell metabolism by less than 10% during 5-day incubation (Fig. 6C). Among the 3 compounds tested, one compound, NSC 13987, inhibited co-immunoprecipitation of Nef and calnexin by over 50%, whereas the effect of NSC 1758 and NSC 92938 showed a trend towards inhibiting Nef/CNX binding but did not reach statistical significance (Fig. 6D). It was previously shown that membrane localization of Nef is important for interaction of Nef with calnexin (5). In order to rule out the possibility that the compound interferes with membrane localization of Nef, it was tested whether NSC 13987 affects interaction between Nef and ABCA1, as ABCA1/Nef interaction also requires membrane localization of Nef (1). As shown in Fig. 6E, ABCA1/Nef interaction remained unaffected in the presence of compound indicating that the inhibition was specific to the molecular interaction of Nef and CNX.

[00101] FIG. 6 shows the structures of various small molecules targeting the Nef-Calnexin interaction as well as the effects these molecules have on the Nef-Calnexin. Specifically, panel (A) *a*, shows the results of ten compounds with the best score (grey) from virtual screening performed on the Zinc NCI Plated 2007 dataset. Their overall location in the structural alignment with the model of Nef - CNX complex is shown as translucent molecular surface. The model shows that these compounds can block the Nef/CNX interaction at calnexin residues Glu529, Glu532 and Glu533. The set of compounds includes NSC 1758, NSC 13987, and NSC 92938 selected for experimental testing. ***b***, Compound NSC 13987 docked to Nef binding site, which is centered on Lys4 and Lys7. Interactions of the compound with Nef include two hydrogen bonds with Nef amino acid residues Ser6 and Tyr124. Panel (B) shows the chemical structure and name of compounds NSC 1758, NSC 13987, and NSC 92938. Panel (C) shows the dose-response effect of NSC 1758, NSC 13987 and NSC 92938 on viability of THP-1 cells. THP-1 cells were treated with indicated compounds for 5 days and cytotoxicity was measured using MTT assay. In panel (D), HEK 293T cells were transfected with HA-tagged Nef, treated with compounds NSC 1758, NSC 13987 or NSC 92938, and lysed. Nef was immunoprecipitated using anti-HA agarose beads and bound complexes were immunoblotted for Nef and calnexin (left panels labeled IP: αHA). Densitometric quantification of calnexin co-immunoprecipitation with Nef is

presented in the right panel. Error bars indicate +/- SD of 3 independent experiments, and p values are shown above the bars. Whole cell lysates were analyzed for amount of calnexin, Nef and GAPDH (left panels labeled Lysate). In panel (E), HEK293T cells were co-transfected with ABCA1-FLAG and Nef_{BRU} and treated with compound NSC 13987. Cells were lysed 48 h post-transfection and ABCA1-FLAG was immunoprecipitated using anti-FLAG beads. Precipitated complexes were blotted for ABCA1 and Nef (top panels). Input amount was analyzed from whole cell lysates by immunoblotting for ABCA1, Nef and GAPDH (bottom panels).

[00102] Next, it was tested whether the three compounds could prevent impairment of cholesterol efflux by Nef. THP-1 cells were transfected with a Nef encoding plasmid and drug treatment was started 6 h after transfection. The following day cells were activated with PMA after which cholesterol efflux assay was performed. Drug treatment was continued throughout the duration of the experiment. Figure 7A shows cholesterol efflux measured in untreated cells or cells treated with DMSO or each of the 3 compounds. Cholesterol efflux in Nef-transfected untreated or DMSO-treated cells was reduced by over 2-fold relative to mock-transfected cells. NSC 13987, which showed inhibition of Nef/CNX interaction (Fig. 6D), significantly increased cholesterol efflux as compared to DMSO-treated Nef expressing cells, although the rescue was not complete. Two other compounds did not significantly rescue Nef-suppressed cholesterol efflux.

[00103] To test the effect of NSC 13987 in the context of natural infection, monocyte-derived macrophages (MDM) were infected with HIV-1 ADA, treated with NSC 13987 and cholesterol efflux was measured. Viral replication in the presence of the compound was reduced (Fig. 7B), consistent with demonstrated rescue by the compound of Nef-inhibited cholesterol efflux (Fig. 7A) and previous studies demonstrating anti-HIV activity of ABCA1 and ABCA1-stimulated cholesterol efflux (28, 35, 36). Consistent with previous studies (1, 5, 36), cholesterol efflux from HIV-infected cells was decreased by 60%, whereas HIV-infected cells treated with NSC 13987 showed cholesterol efflux not significantly different from that of mock-infected cells (Fig. 7C). Taken together, these results provide a proof of concept for the idea that HIV-induced impairment of cholesterol efflux can be reversed pharmacologically by blocking the Nef/CNX interaction.

[00104] FIG. 7 shows graphs showing that an embodiment of the invention, compound NSC 13987, prevents impairment of cholesterol efflux by HIV and Nef. Specifically, in panel (A) THP-1 cells were transfected with Nef and incubated with compounds NSC 1758,

NSC 13987 and NSC 92938 or DMSO, and cholesterol efflux was measured 5 days post-transfection. Error bars show SEM. In panel (B) primary macrophages were infected in triplicate with HIV-1 ADA. Compound NSC 13987 (5 μM) or DMSO was added 3 days after infection and maintained thereafter, and virus replication was monitored by measuring RT-activity in the supernatant over a 14-day period. Results of 3 measurements are shown as mean ± SEM. *, $p<0.005$; **, $p<0.007$. In panel (C) primary macrophages were infected with HIV-1 ADA or mock-infected and treated with DMSO or NSC13987 as in panel B. Cholesterol efflux was measured 14 days post-infection. Error bars show SEM.

[00105] DISCUSSION

[00106] In this example, a small-molecule compound that blocks HIV-mediated impairment of cellular cholesterol metabolism was identified. Excitingly, this compound also inhibited replication of HIV, suggesting that, if developed into a drug, it can target both HIV infection and virus-induced metabolic co-morbidities.

[00107] Previous studies demonstrated that HIV critically depends on interaction with host cholesterol metabolism and modifies it for optimization of viral replication (1, 2, 28, 35, 36). Specifically, HIV, through viral protein Nef, reduces abundance and impairs functional activity of ABCA1, a key transporter in cholesterol efflux pathway (1). As a result, host cells accumulate excessive cholesterol promoting formation of plasma membrane lipid rafts, which are sites of HIV entry, assembly and budding (39). Recently, it was demonstrated that an important mechanism of down-regulation and/or functional impairment of ABCA1 by HIV is Nef-mediated inhibition of the interaction between ABCA1 and the ER chaperone, calnexin (5). The current study provides the first characterization of the exact molecular structures involved in Nef-CNX interaction.

[00108] First, it was established that interaction between Nef and calnexin involves the cytoplasmic domain of calnexin. While this finding is consistent with demonstrated localization of Nef to the cytoplasmic side of membranes (27) and lack of evidence for Nef localization to ER, it is surprising given that the C-tail of calnexin is not involved in the interaction between calnexin and ABCA1, which is disrupted by Nef (5). Indeed, calnexin interactions with glycosylated proteins are mediated by its lumenal domains (12). Therefore, Nef interaction with the C-tail alters activity of the lumenal domains of calnexin. How Nef is doing it is unknown and several possibilities can be considered. Binding of Nef may prevent post-translational modifications of the C-tail of calnexin, such as phosphorylation on Ser563

that has been shown to regulate calnexin interaction with α1-antitrypsin and a number of other glycoproteins (15). However, docking analysis did not reveal Ser563 as a likely site for interaction with Nef (Fig. 5B). The same argument can be applied to SUMOylation at Lys506, which has been shown to regulate calnexin interaction with another ER protein, protein tyrosine phosphatase 1B (40): Lys506 is not among the preferred sites for Nef binding. It is possible that Nef binding itself induces a conformational change in calnexin extending to its lumenal domains, but mechanistic details of such an effect await careful structural analysis. Regardless of the mechanism, this finding provides the first example of a pathogen utilizing the calnexin C-tail to regulate functional activity of this chaperone.

[00109] Second, the Nef residues critical for interaction with calnexin were identified: mutation of lysine residues in positions 4 and 7 of Nef abrogated Nef/CNX binding, prevented ABCA1 downregulation, and restored cholesterol efflux in cells infected with HIV-1. The finding that Nef/CNX interaction involves the flexible N-terminal region of Nef was surprising, as this region has not been implicated before in protein-protein interactions. However, molecular modeling (Fig. 2) suggests that Lys4 of Nef forms a hydrogen bond with Asp90 located in an alpha-helix, thus contributing to stabilization of the structure of the N-terminal region, and therefore acts as a structural anchor for the Nef Lys7 interaction with calnexin. Nef Lys7 is predicted to form a strong interaction with Glu533 in calnexin through the hydrogen and ionic bonds. Thus, mutation of both lysine residues destabilizes the structure of Nef, and cancels the strong interaction with calnexin provided by Lys7, which explains the dramatic effect of these mutations on Nef/CNX interaction. The N-terminal region of Nef has not been involved in protein-protein interactions, but its basic and hydrophobic residues were shown to be essential for membrane association of Nef (41). Interestingly, lysine residues at positions 4 and 7, which participate in interaction with calnexin, were not essential for the membrane association of Nef (42). Therefore, this study a novel epitope on Nef involved in the interaction with the cytoplasmic tail of calnexin was identified.

[00110] Using this information, a virtual screening for compounds that can potentially disrupt Nef-CNX interaction was performed, and a number of candidates were identified. One of these compounds, 1[(7-Oxo-7H-benz[de]anthracene-3-yl)amino]anthraquinone (NSC 13987), prevented co-precipitation of CNX with Nef, reversed Nef-mediated effect on ABCA1 abundance, and restored cholesterol efflux impaired by Nef, thus effectively reversing the effects of Nef on host cholesterol metabolism. In addition, the compound

resulted in a near 2-fold inhibition of viral replication (Fig. 7B). This latter effect may have two main explanations. First, the compound prevents ABCA1 downregulation by Nef, and ABCA1 has been shown to inhibit HIV-1 replication by reducing lipid rafts abundance on the plasma membrane and affecting production and infectivity of nascent virions (3, 28, 35, 36). Second, previous reports presented evidence that anthraquinone derivatives inhibit the ribonuclease H function of HIV-1 reverse transcriptase (43, 44). These findings provide basis for using NSC 13987 as a foundation for development of novel treatment approaches based on targeting the interaction of HIV with host cholesterol metabolism. Based on the known effects of LXR agonists, it is unlikely that this approach would generate a stand-alone treatment for HIV. However, it may effectively supplement current treatment regimens significantly increasing their efficiency and/or allowing for reduction of doses. Furthermore, the effects of Nef secreted from HIV-infected cells may be responsible for many lipid-related complications of HIV disease, such as atherosclerosis, diabetes, lipodistrophy and neurodegeneration. The approach proposed in this study will also reverse HIV-induced impairment of cholesterol metabolism in uninfected cells mitigating lipid-related complications of HIV infection in addition to contributing to the treatment of HIV itself.

[00111] Calnexin is an ER-integral membrane protein and is responsible for the folding of several glycoproteins. Depletion of calnexin has been shown to result in the elevation of several other ER-folding factors minimizing aberrant protein folding and expression (45). This is mainly true for glycoproteins which are common substrates of other soluble ER chaperones like calreticulin. However, solubility and oligosaccharide variability impose a limit on this commonality making calnexin vital for expression and function of proteins like ABCA1 and several others (5, 46, 47). Nef's ability to target several host factors, such as CD4, MHC I, CXCR4, may in part be due to the limitation it imposes on their access to chaperone proteins like calnexin. Therefore, the positive effect of compound NSC13987 may well extend to restoring the expression and function of other proteins targeted by Nef.

[00112] In conclusion, in this study the molecular mechanisms and exact structures involved in interaction between HIV Nef and host canexin were identified and a compound capable of reversing the effects of Nef was characterized, thus presenting potential utility in treatment of HIV infection and its metabolic side effects.

[00113] **EXPERIMENTAL PROCEDURES**

[00114] *Reagents* - The following reagents were purchased from the indicated suppliers: mouse monoclonal anti-calnexin (ab31290, Abcam); anti-HA Epitope tag Antibody (NB600-363, Novus Biologicals); anti-Nef serum (NIH AIDS Reagent Program); anti-ABCA1 (NB400-105, Novus Biologicals); polyclonal rabbit anti-calnexin (H-70, Santa Cruz Biotech); anti-GAPDH (G9545, Sigma Aldrich); HRP conjugated donkey anti-rabbit and Goat anti-mouse (Jackson Immuno Research); anti-HA Agarose (26181, Thermo Scientific); EZview Red Protein A Affinity Gel (P6486, Sigma-Aldrich). Metafectene® (Biontex; IGEPAL (CA-630, SigmaAldrich); Triton™ (X-100, Sigma Aldrich); 10% SDS (Corning).

[00115] *Nef and Calnexin Mutagenesis* – Nef expression plasmid pcDNA3.1 Nef was obtained through the NIH AIDS Reagent Program (Cat#11431) from Dr. J. Victor Garcia. The Nef insert was cloned by PCR using primers as previously described (48) and was mutagenized. Nef mutants K4A, K7A and K4,7A were generated from the pcDNA3.1 Nef_{BRU} plasmid using site-directed mutagenesis with Pfu Ultra High-Fidelity DNA Polymerase (Agilent Technologies). Forward and reverse primer sequences used were as follows: Nef K4A Fwd, 5'-TTTGCTATAAGATGGGTGGCGCGTGGTCAAAAAGTAGTGTGG-3', Rev 5'-CCACACTACTTTTTGACCACGCGCCACCCATCTTATAGCAAA-3'; Nef K7A Fwd, 5'GATGGGTGGCAAGTGGTCAGCAAGTAGTGTGGTTGGATGG-3', Rev 5'-CCATCCAACCACACTACTTGCTGACCACTTGCCACCCATC-3 and NefK4,7A FWD 5'-GGGTGGCGCGTGGTCAGCAAGTAGTGTGGTTGGA-3', Rev 5'-TCCAACCACACTACTTGCTGACCACGCGCCACCC-3'. Resulting cDNA was transformed into XL10-Gold Ultracompetent Cells and final plasmid preps were sequenced to confirm mutations. The plasmid pCG-NL4-3-IRES-GFP was kindly provided by the lab of Dr. Marc Harris (27).

[00116] Human CNX cDNA construct with a C-terminal HA tag was prepared by standard PCR method from CNX cDNA clone (Open Biosystems) in the pHCMV3 vector (Gelantis). Truncated CNX construct was generated similarly by using primers described previously (49). The HA-tagged $CNX_{\Delta 504\text{-}586}$ construct lacks the 87 residues of the cytoplasmic tail. Deletion of the repeated sequence motifs referred to as $CNX_{\Delta 276\text{-}409}$ was made by restriction digest of full length HA-tagged pHCMV3-CNX and re-ligation (46).

[00117] *Expression and Purification of Calnexin* – A CNX expression vector with a His-tag at the N-terminus and the CL7-tag was designed, which can be cleaved by the PSC protease, at the CNX C-terminus (Fig. 5A). The CNX-CT construct was designed with a

single N-terminal His-tag followed by the SUMO-domain (to allow His-tag cleavage by the SUMO-protease, SUMO-P). CNX and CNX-CT were expressed in *E. coli* BL21 DE. Cells were grown at 37°C to OD ~ 0.8-0.9, then temperature was decreased to 18-20°C and expression was induced with 0.1 mM IPTG overnight. Cells were frozen at -80^{0}C until protein purification.

[00118] A novel purification system based on the natural ultra-high affinity complex ($K_m \sim 10^{-14}$-10^{-17} M) between the colicin E7 DNAse domain (CL7) and its inhibitor, immunity protein 7 (Im7) (29-32) was developed and implemented. The proteins have been modified to remove DNAse activity of CL7 and allow for efficient immobilization of the Im7 unit on the activated agarose beads (DGV, unpublished results). The CNX construct tagged at the C-terminus with CL7 was expressed in *E. coli*, the cells were lysed, centrifuged to remove cell debris, and the supernatant was treated with 0.07% polyethylene-emine (PE) to precipitate CNX (Fig. 5A). The pellet was washed with 20 mM Tris-HCl, pH 8.0, 600 mM NaCl, 1.5% dodecyl-maltopyranoside to release CNX into solution, centrifuged again, and the resulting supernatant was loaded on the Im7 column. CNX protein was eluted from the column upon treatment by PSC protease. This single purification step provided an excellent yield of ~90-95% pure protein, in which major contamination represents truncated CNX molecules (confirmed by mass-spectroscopy). Given that these molecules are retained on the column and that affinity tag is localized at the C-terminus of CNX, truncation occurred most likely from the N-terminus (proteolytic sensitivity of CNX at the N-end was reported previously (50)). CNX-CT was purified in standard procedure using the commercial His-Trap column. All procedures were carried out at 4°C.

[00119] *Surface Plasmon Resonance Experiments* - Direct binding between purified recombinant proteins was evaluated by surface plasmon resonance technology utilizing a Biacore T-200 instrument at the Biacore Molecular Interaction Shared Resource of Georgetown University. Full length CNX and the C-terminal (cytoplasmic) domain of CNX (CNX-CT) were captured on CM5 chips by amine coupling. Three surfaces of CM5 chip were activated by NHS/CDC (N-hydroxysuccinimide/1-ethyl-3-(3-dimethylaminopropyl)carbodiimide hydrochloride) for 720 sec. Flow cell 1 was left empty as a reference surface. Full length CNX and CNX-CT were diluted in 10 mM sodium acetate (pH 4.0) buffer at 1.8 μM and 10.6 μM, respectively, and captured on flow cell 3 and flow cell 2, at 3200 RU and 16600 RU, respectively. After protein capture, all 3 flow cells were inactivated by 720 sec injection of 1 M ethanolamine. Myristoylated Nef_{SF2} protein was

injected over the chip surface at 6 different concentrations (6.25 nM, 12.5 nM, 25 nM, 50 nM, 100 nM, 200 nM) in triplicates. All binding studies were done at 25°C. Flow rate for protein capture was 10 µl/min, and kinetics experiment was at 50 µl/min. HPS-P (10 mM HEPES pH 7.4, 150 mM NaCl, 0.005% surfactant P-20) + 2 mM $CaCl_2$ was used as the running buffer. The data was analyzed by BiaEvaluation software using the bivalent analyte model.

[00120] *Cells and Transfection* - HEK293T and THP-1 cells were cultured in RPMI supplemented with 10% fetal bovine serum and antibiotics. For transfection, 293T cells were passaged and cultured overnight in 6-well plates and transfected with plasmid DNA using Metafectene according to the manufacturer's (Biontex) instructions.

[00121] *Compounds* – Three out of 10 compounds obtained from NCI drug database were tested for blocking Nef/CNX interaction. Tested compounds were 1,3-DI-9-Phenanthrylguanidine (NSC 1758), 1[(7-Oxo-7H-benz[de]anthracene-3-yl)amino]anthraquinone (NSC 13987) and 5H-Naphtho(2,3-a)carbazole-5,13(12H)-dione (NSC 92938). All compounds were dissolved in DMSO and diluted in cell culture medium (RPMI 1640 with 10% fetal bovine serum and antibiotics) to ensure the final concentration of the solvent to be <1%.

[00122] *MTT Assay* – THP-1 cells were seeded in 96 well plates (30,000 cells/well) and incubated at 37°C, 5% CO_2 in the presence of compounds for 5 days. The MTT assay for cytotoxicity was done in quadruplicates according to manufacturer's instructions (Sigma-Aldrich). The concentrations selected for experimental testing - 4 µM for NSC 1758, and 5 µM for NSC 13987 and NSC 92938 – reduced MTT metabolism by less than 10% relative to untreated cultures.

[00123] *Immunoprecipitation* - For calnexin mutant/Nef interaction analysis, HEK293T cells were transfected with HA-tagged calnexin mutants and Nef_{BRU} expression plasmid. Cells were lysed 48 h post-transfection with 1% IGEPAL and 0.1% SDS lysis buffer on ice for 30 min. Lysates were incubated with anti-HA agarose beads for 2 h at 4°C with rotation. Respective immunoprecipitates were washed three times with TBS (150 mM NaCl, 30 mM Tris-HCl, 5 mM EDTA, pH 7.5). Bound complexes were eluted by boiling in sample buffer for 5 min. Supernatants were separated by SDS-PAGE for immunoblotting. Immunoprecipitation of calnexin from cells transfected with pCG-NL4-3-IRES-GFP or mutant variant was performed similarly with the following modifications. Cell lysates were incubated with monoclonal anti-calnexin antibody for 2 h with rotation at 4°C. EZView

protein A agarose beads were then added and the mix was further incubated for 1 h at 4°C with roation. Bound complexes were recovered as described above. For studies of Nef/CNX interactions in the presence of compounds, HEK293T cells were first transfected with HA-tagged Nef and compounds were added after 6 h. Cells were lysed 48 h post-transfection and immunoprecipitation was carried out using anti-HA agarose beads as described above.

[00124] *Molecular Modeling and Docking* – Structure modeling of the calnexin cytoplasmic domain was performed using servers Hhpred (51), iTasser (52), ModWeb (53), Phyre2 (54), and RaptorX (55), with subsequent quality assessment of the obtained models and building of the final model by the QA-RecombineIt server (56). The Modbase (53) GI 66933005 model based on PDB 1JHN (96% sequence identity) was used for the lumenal domain structure. Nef structure has been modeled using as templates the crystallographic and solution NMR experimental structures covering different parts of Nef sequence, available from the PDB (57): 4EN2, 3TB8, 4EMZ, 3REB, 3RBB, 3REA, 1EFN. These structures are based on the HIV-1 sequences P03404, P03406, P03407, Q90VU7 (Uniprot (58)). Modeling was performed for the target sequence P03407 (HIV-1 group M subtype B isolate ARV2/BRU) with servers Hhpred, iTasser, M4T (59), ModWeb, Phyre2, Swiss-Model (60). The resulting models have been then submitted to the QA-RecombineIt server, producing the final model used for interactions prediction.

[00125] In order to obtain indications as to which regions of Nef can represent interactions interfaces, location of possible interactions sites has been estimated with a sequence-based method ConSurf (25). Sequence conservation for Nef has been assessed by constructing multiple alignments using T-Coffee (61). We have subsequently carried out docking of the structure models of calnexin cytoplasmic domain and Nef to identify the sites in Nef interacting with calnexin. Docking was performed using servers Cluspro (62), HEX (63), SwarmDock (64), Zdock (65), each run producing 10 best models. To obtain a representative array of docking models, docking has been carried out for calnexin and Nef submitted to docking runs alternatively as receptor and ligand. Since both calnexin cytoplasmic domain and Nef bind to ER membrane, the resulting docking models that were able to disrupt this binding have been filtered out from the final data.

[00126] To assess average number of interactions for each residue position in Nef and CNX sequences in the set of docking models of binding between CNX cytoplasmic domain and Nef, the overall number of Nef-CNX interactions for all models, for each residue in Nef and CNX involved in intermolecular interaction has been calculated. Number of interactions

for each amino acid residue in Nef and CNX is the total number of interactions for this residue in docking models where such interaction was identified.

[00127] *Virtual screening* – structure-based virtual screening (docking-based) was carried out on the NCI Plated 2007 dataset (http://zinc.docking.org/catalogs/ncip) from Zinc database (http://zinc.docking.org/) (66). Locally installed docking program AutoDock Vina (34) has been used for screening.

[00128] *HIV Infection* – HIV particles pseudotyped with VSV-G were produced from HEK293T cells by transfecting with pCG-NL4-3-IRES-GFP or Nef mutant derivative. Monocyte-derived macrophages were infected with the respective wild-type or mutant virus particles normalized by RT activity. Infection was allowed to proceed for 10 days and the level of infection was monitored by RT assay.

[00129] *Cholesterol Efflux* - Infected cells were seeded in a 24-well plate and labeled with [^{3}H] cholesterol for 48 h. Following this step, cells were washed with PBS to remove any free cholesterol and efflux was initiated by adding apoA-I (20 μg/mL) and incubating for 3 h in serum free medium. The media from the wells was then carefully collected and any cell debris was removed by centrifuging at 5,000 rpm for 5 min. Cell monolayers were lysed with 1% Triton X-100. Level of radioactivity in the media as well as in the cells was determined by scintillation counting. Cholesterol efflux was calculated as the percentage of radioactivity in the media divided by the total amount measured in the cells and media. Cholesterol efflux in the presence of compounds was performed similarly with the following modifications. THP-1 cells were first transfected with BRU Nef using Lipofectamine™ LTX reagent (ThermoFisher Scientific). Compounds were added to cells 6 h post transfection and incubated overnight. The following day cells were washed with PBS and treatment with compounds was continued for 48 h with the addition of [^{3}H] cholesterol and Phorbol 12-myristate 13-acetate (PMA). Efflux measurements were then performed as described above.

[00130] *Nef sequence(s)* - HIV-1 group M is the most is the most common type of HIV accounting for more than 90% of the AIDS epidemic. Within this group are several subtypes, the most common of which are Subtypes A- H. In the example above, a consensus Nef sequence (Nef consB).

[00131] The nucleotide sequence of this consensus sequence is:

atgggtggcaagtggtcaaaacgtagtgtggttggatggcctgctgtaagggaaagaatgagacgagctgagccagcagcagatgg
ggtgggagcagtatctcgagacctggaaaaacatggagcaatcacaagtagcaatacagcagctaacaatgctgattgtgcctggcta
gaagcacaagaggaggaggaggtgggttttccagtcagacctcaggtacctttaagaccaatgacttacaaggcagctgtagatctta

gccacttttaaaagaaaaggggggactggaagggctaatttactcccaaaaaagacaagatatccttgatctgtgggtctaccacaca caaggctacttccctgattggcagaactacacaccagggccagggatcagatatccactgacctttggatggtgcttcaagctagtacc agttgagccagagaaggtagaagaggccaatgaaggagagaacaacagcttgttacaccctatgagcctgcatgggatggatgacc cggagaaagaagtgttagtgtggaagtttgacagccgcctagcatttcatcacatggcccgagagctgcatccggagtactacaagga ctgctga

[00132] The amino acid sequence of the consenus sequence is:

MGGKWSKRSVVGWPAVRERMRRAEPAADGVGAVSRDLEKHGAITSSNTAANNAD CAWLEAQEEEEVGFPVRPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIYSQKRQDILD LWVYHTQGYFPDWQNYTPGPGIRYPLTFGWCFKLVPVEPEKVEEANEGENNSLLHP MSLHGMDDPEKEVLVWKFDSRLAFHHMARELHPEYYKDC.

[00133] This consensus sequence was previously developed by comparing the Nef sequences of the HIV Subtypes A- H (67). All Nef sequences of these HIV Subtypes have a conserved lysine at the 4th and 7th positions. The consensus sequence described in the example was specifically derived from HIV subtype B.

[00134] *Calnexin sequence* - In the example above, the nucleotide sequence of Calnexin is:

ATGGAAGGGAAGTGGTTGCTGTGTATGTTACTGGTGCTTGGAACTGCTATTGTTG AGGCTCATGATGGACATGATGATGATGTGATTGATATTGAGGATGACCTTGACGA TGTCATTGAAGAGGTAGAAGACTCAAAACCAGATACCACTGCTCCTCCTTCATCT CCCAAGGTTACTTACAAAGCTCCAGTTCCAACAGGGGAAGTATATTTTGCTGATT CTTTTGACAGAGGAACTCTGTCAGGGTGGATTTTATCCAAAGCCAAGAAAGACG ATACCGATGATGAAATTGCCAAATATGATGGAAAGTGGGAGGTAGAGGAAATGA AGGAGTCAAAGCTTCCAGGTGATAAAGGACTTGTGTTGATGTCTCGGGCCAAGC ATCATGCCATCTCTGCTAAACTGAACAAGCCCTTCCTGTTTGACACCAAGCCTCT CATTGTTCAGTATGAGGTTAATTTCCAAAATGGAATAGAATGTGGTGGTGCCTAT GTGAAACTGCTTTCTAAAACACCAGAACTCAACCTGGATCAGTTCCATGACAAGA CCCCTTATACGATTATGTTTGGTCCAGATAAATGTGGAGAGGACTATAAACTGCA CTTCATCTTCCGACACAAAAACCCCAAAACGGGTATCTATGAAGAAAAACATGC TAAGAGGCCAGATGCAGATCTGAAGACCTATTTTACTGATAAGAAAACACATCTT TACACACTAATCTTGAATCCAGATAATAGTTTTGAAATACTGGTTGACCAATCTG TGGTGAATAGTGGAAATCTGCTCAATGACATGACTCCTCCTGTAAATCCTTCACG TGAAATTGAGGACCCAGAAGACCGGAAGCCCGAGGATTGGGATGAAAGACCAA AAATCCCAGATCCAGAAGCTGTCAAGCCAGATGACTGGGATGAAGATGCCCCTG

CTAAGATTCCAGATGAAGAGGCCACAAAACCCGAAGGCTGGTTAGATGATGAGC
CTGAGTACGTACCTGATCCAGACGCAGAGAAACCTGAGGATTGGGATGAAGACA
TGGATGGAGAATGGGAGGCTCCTCAGATTGCCAACCCTAGATGTGAGTCAGCTC
CTGGATGTGGTGTCTGGCAGCGACCTGTGATTGACAACCCCAATTATAAAGGCAA
ATGGAAGCCTCCTATGATTGACAATCCCAGTTACCAGGGAATCTGGAAACCCAG
GAAAATACCAAATCCAGATTTCTTTGAAGATCTGGAACCTTTCAGAATGACTCCT
TTTAGTGCTATTGGTTTGGAGCTGTGGTCCATGACCTCTGACATTTTTTTTGACAA
CTTTATCATTTGTGCTGATCGAAGAATAGTTGATGATTGGGCCAATGATGGATGG
GGCCTGAAGAAAGCTGCTGATGGGGCTGCTGAGCCAGGCGTTGTGGGGCAGATG
ATCGAGGCAGCTGAAGAGCGCCCGTGGCTGTGGGTAGTCTATATTCTAACTGTAG
CCCTTCCTGTGTTCCTGGTTATCCTCTTCTGCTGTTCTGGAAAGAAACAGACCAGT
GGTATGGAGTATAAGAAAACTGATGCACCTCAACCGGATGTGAAGGAAGAGGAA
GAAGAGAAGGAAGAGGAAAAGGACAAGGGAGATGAGGAGGAGGAAGGAGAAG
AGAAACTTGAAGAGAAACAGAAAAGTGATGCTGAAGAAGATGGTGGCACTGTC
AGTCAAGAGGAGGAAGACAGAAAACCTAAAGCAGAGGAGGATGAAATTTTGAA
CAGATCACCAAGAAACAGAAAGCCACGAAGAGAGTGA

[00135] The amino acid sequence is:

[00136] MEGKWLLCMLLVLGTAIVEAHDGHDDDVIDIEDDLDDVIEEVEDSKP
DTTAPPSSPKVTYKAPVPTGEVYFADSFDRGTLSGWILSKAKKDDTDDEIAKYDGK
WEVEEMKESKLPGDKGLVLMSRAKHHAISAKLNKPFLFDTKPLIVQYEVNFQNGIEC
GGAYVKLLSKTPELNLDQFHDKTPYTIMFGPDKCGEDYKLHFIFRHKNPKTGIYEEK
HAKRPDADLKTYFTDKKTHLYTLILNPDNSFEILVDQSVVNSGNLLNDMTPPVNPSR
EIEDPEDRKPEDWDERPKIPDPEAVKPDDWDEDAPAKIPDEEATKPEGWLDDEPEYV
PDPDAEKPEDWDEDMDGEWEAPQIANPRCESAPGCGVWQRPVIDNPNYKGKWKPP
MIDNPSYQGIWKPRKIPNPDFFEDLEPFRMTPFSAIGLELWSMTSDIFFDNFIICADRRI
VDDWANDGWGLKKAADGAAEPGVVGQMIEAAEERPWLWVVYILTVALPVFLVILF
CCSGKKQTSGMEYKKTDAPQPDVKEEEEEKEEEKDKGDEEEEGEEKLEEKQKSDAE
EDGGTVSQEEEDRKPKAEEDEILNRSPRNRKPRRE.

[00137] It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the scope of the invention, methods and structures within the scope of the invention includes equivalents.

[00138] The embodiments illustrated and discussed in this specification are intended only to teach those skilled in the art how to make and use the invention. In describing embodiments of the invention, specific terminology is employed for the sake of clarity. However, the invention is not intended to be limited to the specific terminology so selected. The above-described embodiments of the invention may be modified or varied, without departing from the invention, as appreciated by those skilled in the art in light of the above teachings. It is therefore to be understood that, within the scope of the claims and their equivalents, the invention may be practiced otherwise than as specifically described.

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WE CLAIM:

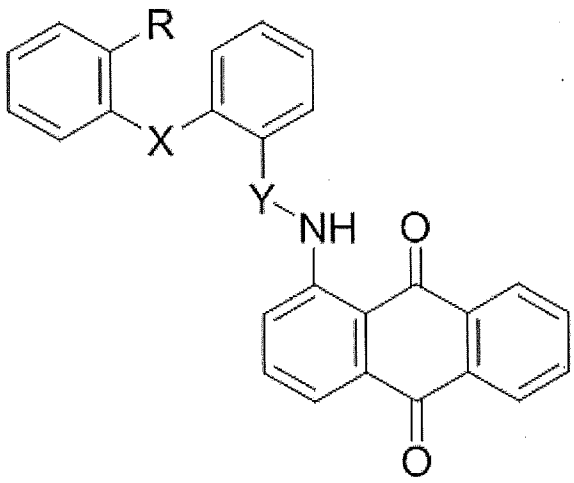
1. A method for restoring or preserving cholesterol efflux in a cell infected with Human Immunodeficiency Virus (HIV) comprising delivering to the cell an effective amount of a composition or formulation comprising a small molecule, wherein the small molecule prevents or decreases an interaction between a Negative Regulatory Factor (Nef) protein and a Calnexin protein.

2. The method of claim 1, wherein the small molecule binds to at least one amino acid residue on the Nef protein, wherein the at least one amino acid residue is selected from the group consisting of a lysine at amino acid position 4, a serine at amino acid position 6, a lysine at amino acid position 7, and a tyrosine at amino acid position 124.

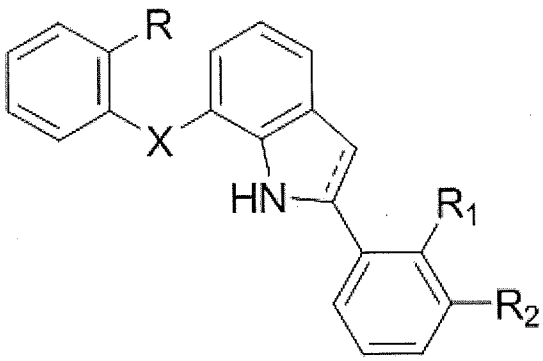
3. The method of claim 1, wherein the small molecule binds to at least one amino acid residue on the Calnexin protein, wherein the at least one amino acid residue is selected from the group consisting of an aspartic acid at position 90, a glutamic acid at amino acid position 529, a glutamic acid at amino acid position 532, and a glutamic acid at amino acid position 533.

4. The method of claim 1, wherein preventing or decreasing the interaction between the Nef protein and the Calnexin protein results in at least partial restoration of ATP-Binding Cassette A1 (ABCA1) activity.

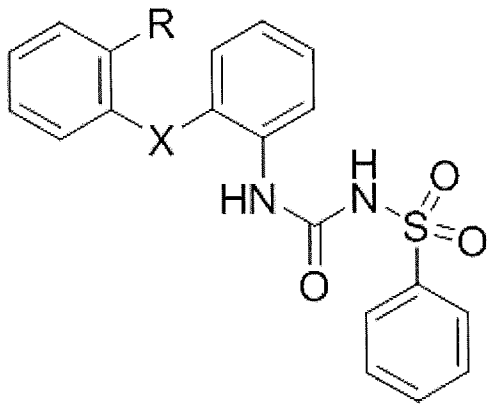
5. The method of claim 1, wherein the small molecule is a small molecule is selected from the group consisting of Formula (I), Formula (II), Formula (III) or an analog or derivative thereof:



(I),



(II),



(III),

wherein:

R, R_1, and R_2 are independently selected from H, CH_2OH, COOH or $COOCH_3$;

X is CH_2, NH, O, NCH_3, or SO_2; and

Y is a bond, CH_2, CO or SO_2.

6. A method for treating or preventing atherosclerosis in a subject infected with HIV comprising administering to said subject an effective amount of a composition or formulation comprising a small molecule, wherein the small molecule prevents or decreases an interaction between a Nef protein and a Calnexin protein.

7. The method of claim 6, wherein the small molecule binds to at least one amino acid residue on the Nef protein, wherein the at least one amino acid residue is selected from the group consisting of a lysine at amino acid position 4, a serine at amino acid position 6, a lysine at amino acid position 7, and a tyrosine at amino acid position 124.

8. The method of claim 6, wherein the small molecule binds to at least one amino acid residue on the Calnexin protein, wherein the at least one amino acid residue is selected from the group consisting of an aspartic acid at position 90, a glutamic acid at amino acid position 529, a glutamic acid at amino acid position 532, and a glutamic acid at amino acid position 533.

9. The method of claim 6, wherein preventing or decreasing the interaction between the Nef protein and the Calnexin protein results in at least partial restoration of ATP-Binding Cassette A1 (ABCA1) activity.

10. The method of claim 6, wherein the small molecule is a small molecule of Formula (I), Formula (II), or Formula (III), or an analog or derivative thereof.

11. A method for screening for a small molecule that restores or preserves cholesterol efflux in a cell by inhibiting or decreasing an interaction between a Nef protein and a Calnexin protein comprising:

incubating a cell expressing a full-length Nef protein or a segment of the full-length Nef protein and a full-length Calnexin protein or a segment of the full-length Calnexin protein with a small molecule of interest;

assaying the incubated cell for cholesterol efflux; and

assaying the incubated cell for a level of binding between the full-length Nef protein or the segment of the full-length Nef protein and the full-length Calnexin protein or the segment of the full-length Calnexin protein,

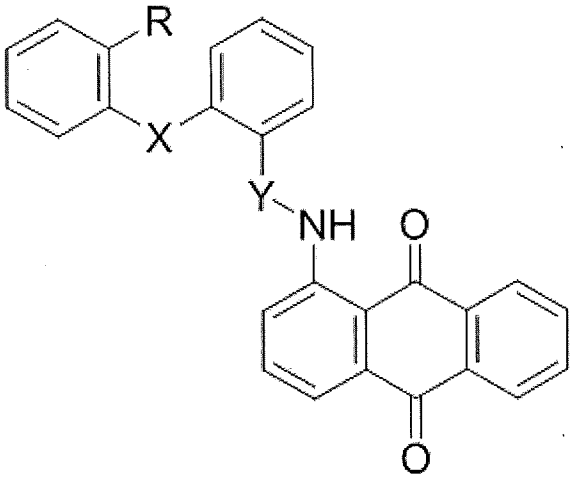
wherein an increase in cholesterol efflux and a decrease in the level of binding as compared to a control is indicative of restoration or preservation of cholesterol efflux by inhibiting or decreasing an interaction between the Nef protein and the Calnexin protein as a result of incubation of the cell with the small molecule of interest.

12. The method of claim 11, further comprising virtually screening a library of small molecules for a small molecule that is predicted to bind to or interact with at least one of the full-length Nef protein or the segment of the full-length Nef protein and the full-length Calnexin protein or the segment of the full-length Calnexin protein.

13. The method of claim 11, wherein the cells are incubated for at least 1 day.

14. The method of claim 11, wherein the assaying the incubated cell for a level of binding comprises an immunoprecipitation assay, surface plasmon resonance (SPR) assay, or isothermal titration calorimetry (ITC) assay.

15. A small molecule having the structure of Formula (I):



(I),

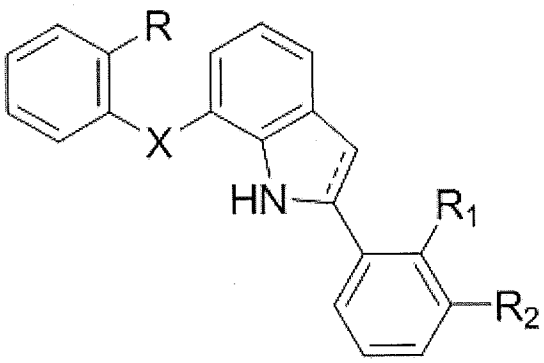
wherein:

R is H, CH_2OH, COOH or $COOCH_3$;

X is CH_2, NH, O, NCH_3, or SO_2; and

Y is a bond, CH_2, CO or SO_2.

16. A small molecule having the structure of Formula (II):



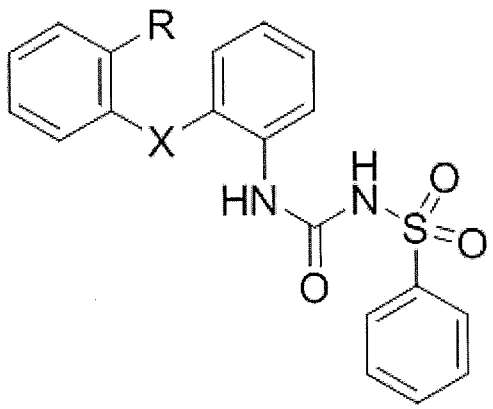
(II),

wherein:

R, R_1, and R_2 are independently selected from H, CH_2OH, COOH or $COOCH_3$; and

X is CH_2, NH, O, NCH_3, or SO_2.

17. A small molecule having the structure of Formula (III):



(III),

wherein:

R is H, CH_2OH, COOH or $COOCH_3$; and

X is CH_2, NH, O, NCH_3, or SO_2.

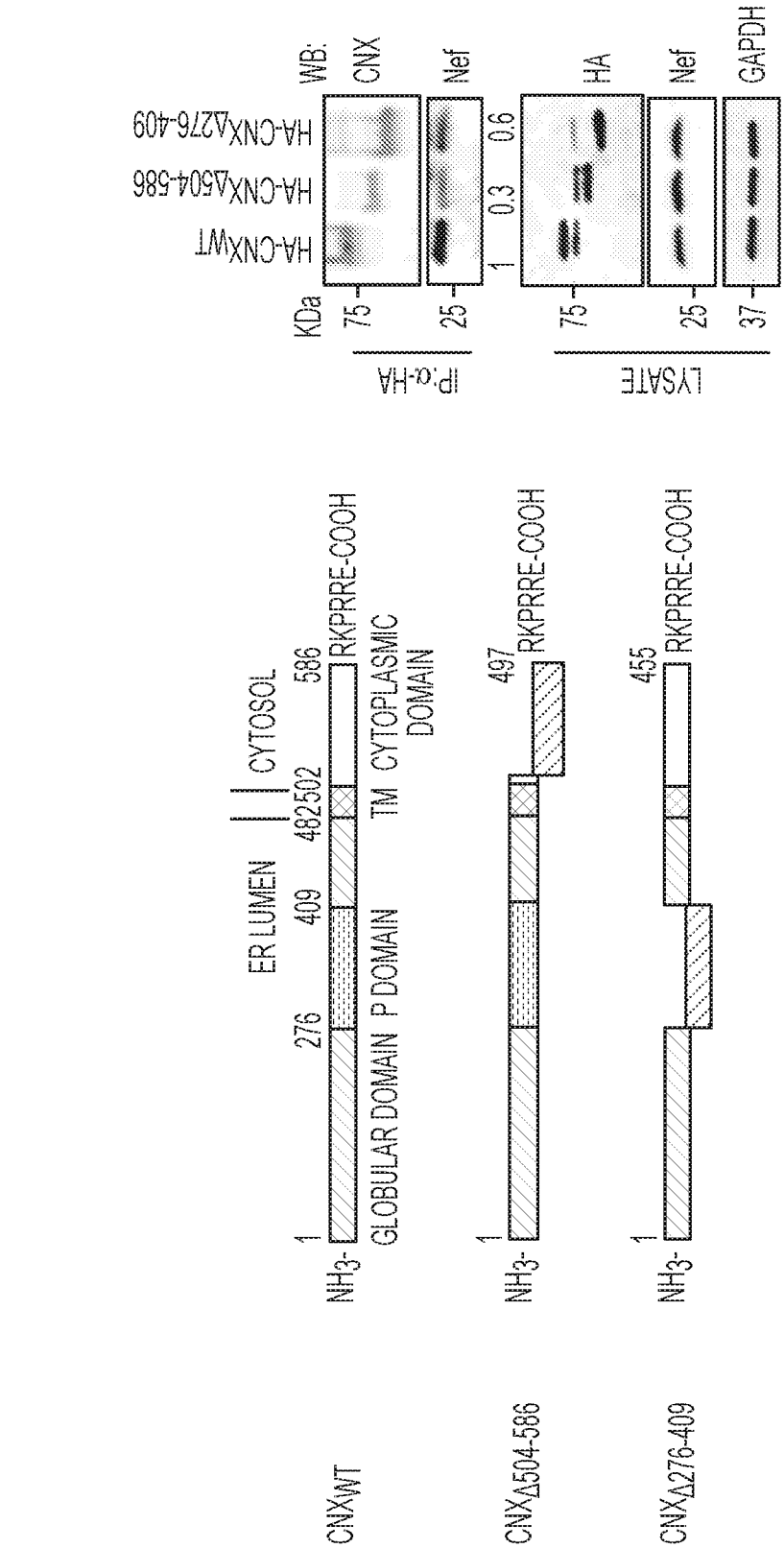

CNXWT
CNXΔ504-586
CNXΔ276-409
NH3-
1
276
409
482
502
586
497
455
ER LUMEN
CYTOSOL
GLOBULAR DOMAIN
P DOMAIN
TM
CYTOPLASMIC DOMAIN
RKPRRE-COOH

FIG. 1A

HA-CNXWT
HA-CNXΔ504-586
HA-CNXΔ276-409
KDa
WB:
CNX
Nef
HA
GAPDH
IP:α-HA
LYSATE
75
25
37
1
0.3
0.6

FIG. 1B

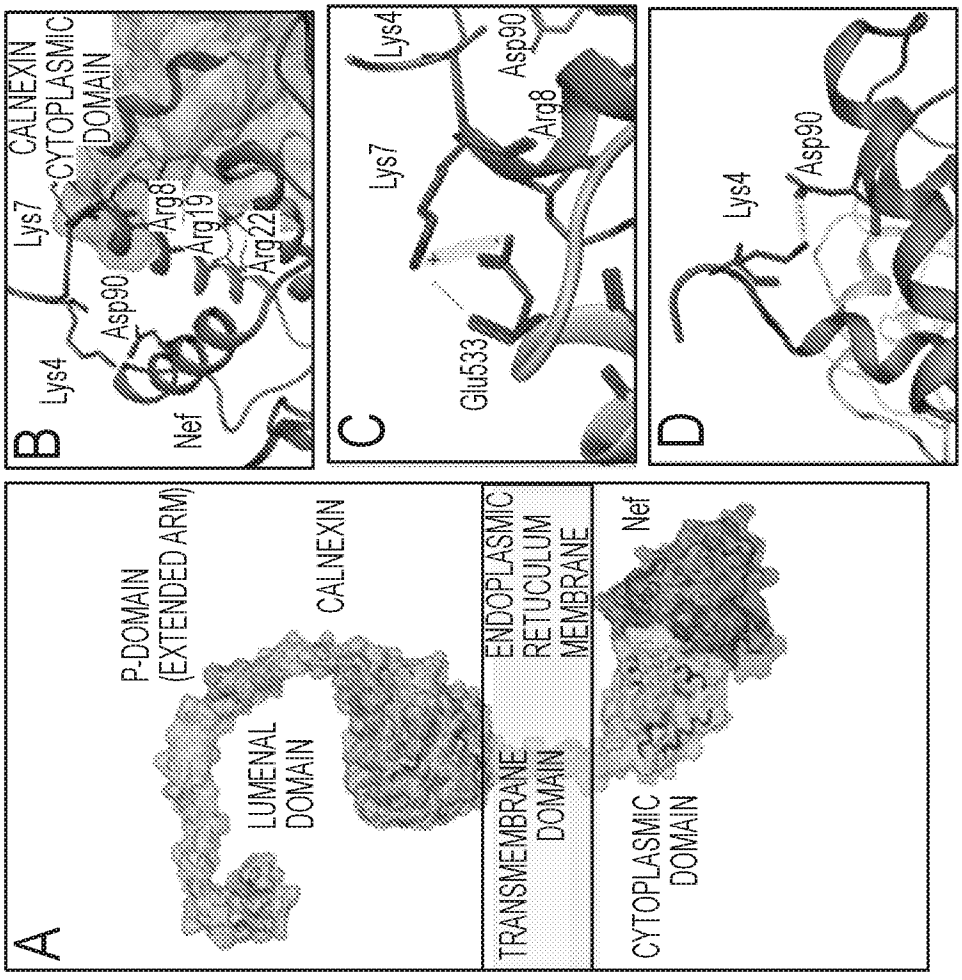

A
P-DOMAIN (EXTENDED ARM)
LUMENAL DOMAIN
CALNEXIN
TRANSMEMBRANE DOMAIN
ENDOPLASMIC RETICULUM MEMBRANE
CYTOPLASMIC DOMAIN
Nef
B
Lys4
Lys7
CALNEXIN CYTOPLASMIC DOMAIN
Asp90
Arg8
Arg19
Arg22
Nef
C
Lys7
Lys4
Asp90
Arg8
Glu533
D
Lys4
Asp90

FIG. 2A

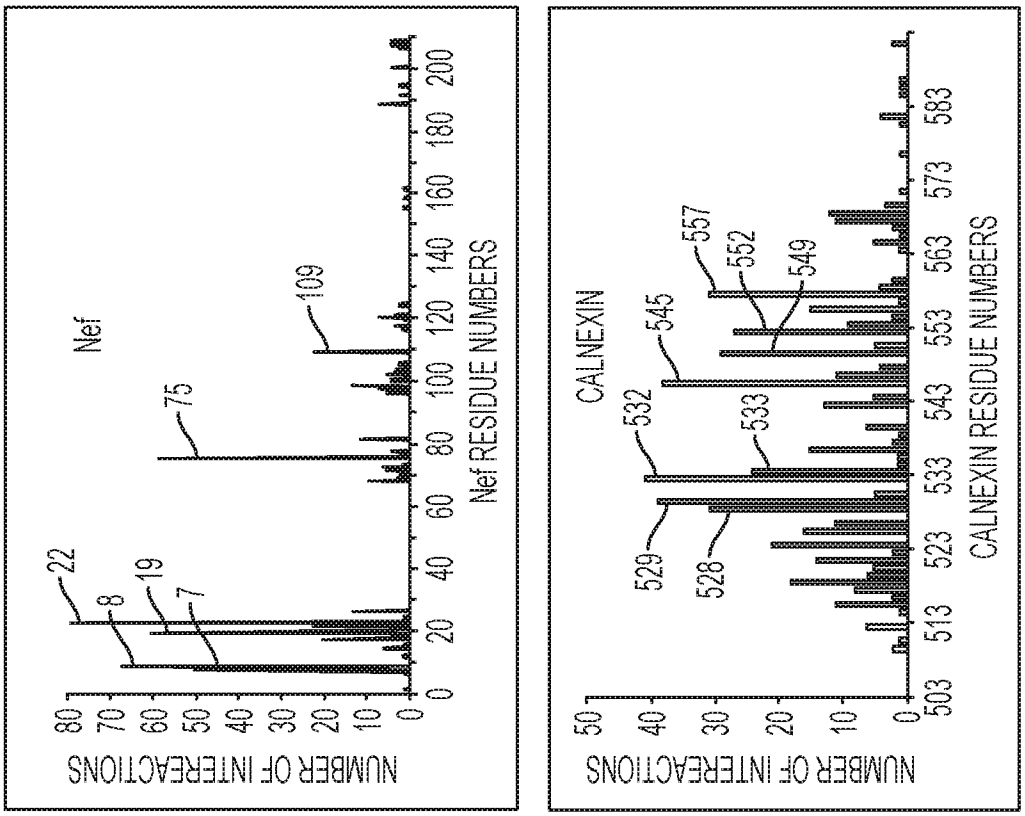

Nef
NUMBER OF INTERACTIONS
Nef RESIDUE NUMBERS
22
8
19
7
75
109
CALNEXIN
NUMBER OF INTERACTIONS
CALNEXIN RESIDUE NUMBERS
529
528
532
533
545
557
552
549

FIG. 2B

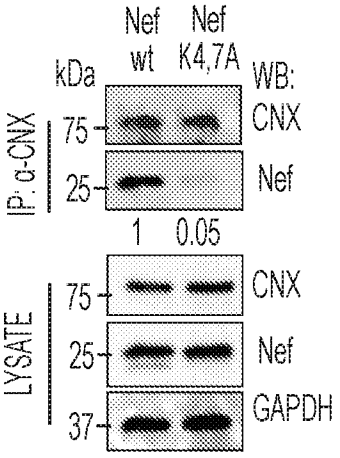


FIG. 3A

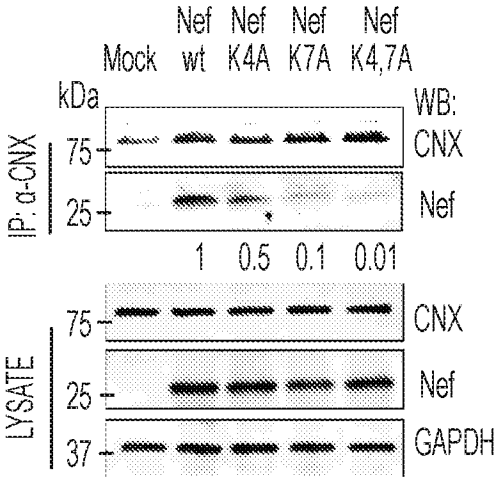


FIG. 3B

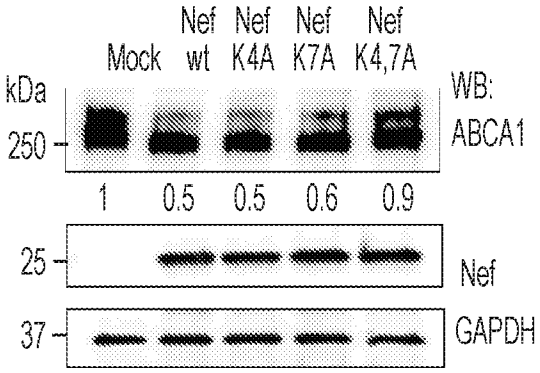


FIG. 3C

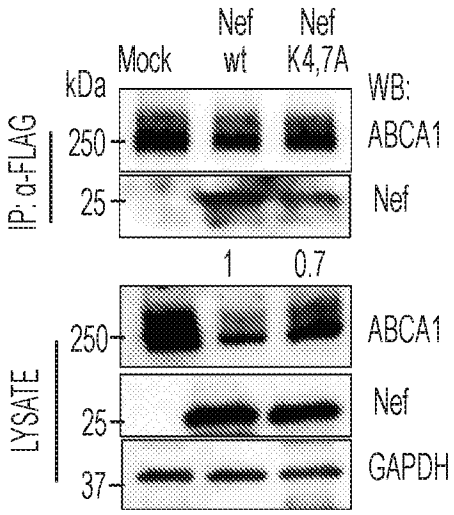


FIG. 3D

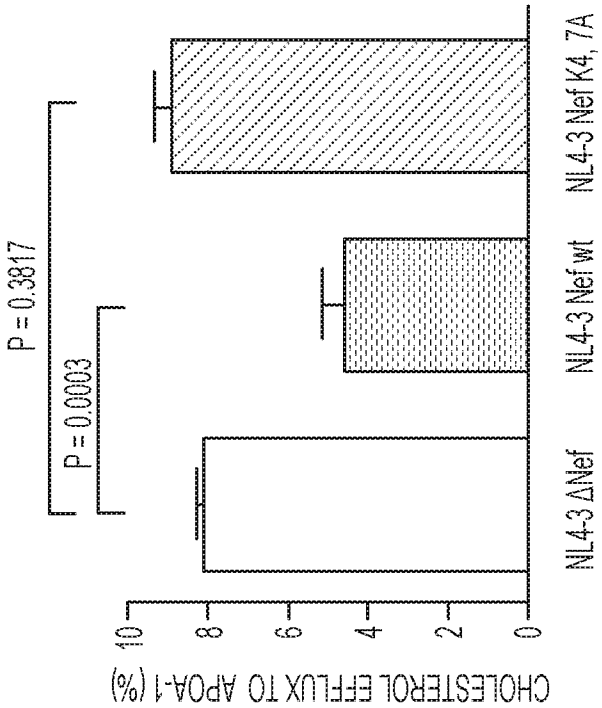

CHOLESTEROL EFFLUX TO APOA-1 (%)
0
2
4
6
8
10
P = 0.0003
P = 0.3817
NL4-3 ΔNef
NL4-3 Nef wt
NL4-3 Nef K4, 7A

FIG. 4B

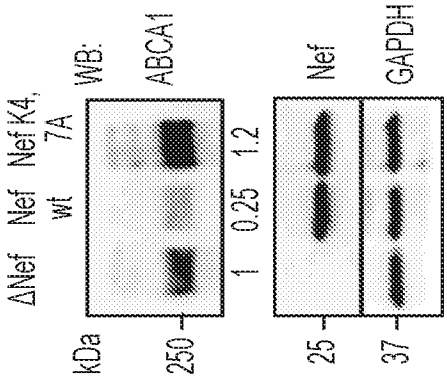
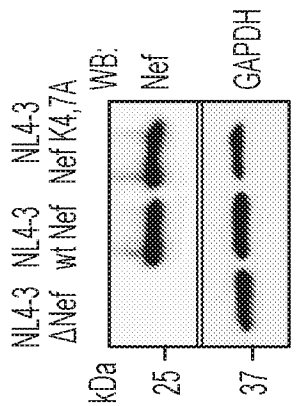

kDa
250
25
37
ΔNef
Nef wt
Nef K4, 7A
1
0.25
1.2
WB:
ABCA1
Nef
GAPDH

FIG. 4A


kDa
25
37
NL4-3 ΔNef
NL4-3 Nef wt
NL4-3 Nef K4,7A
WB:
Nef
GAPDH

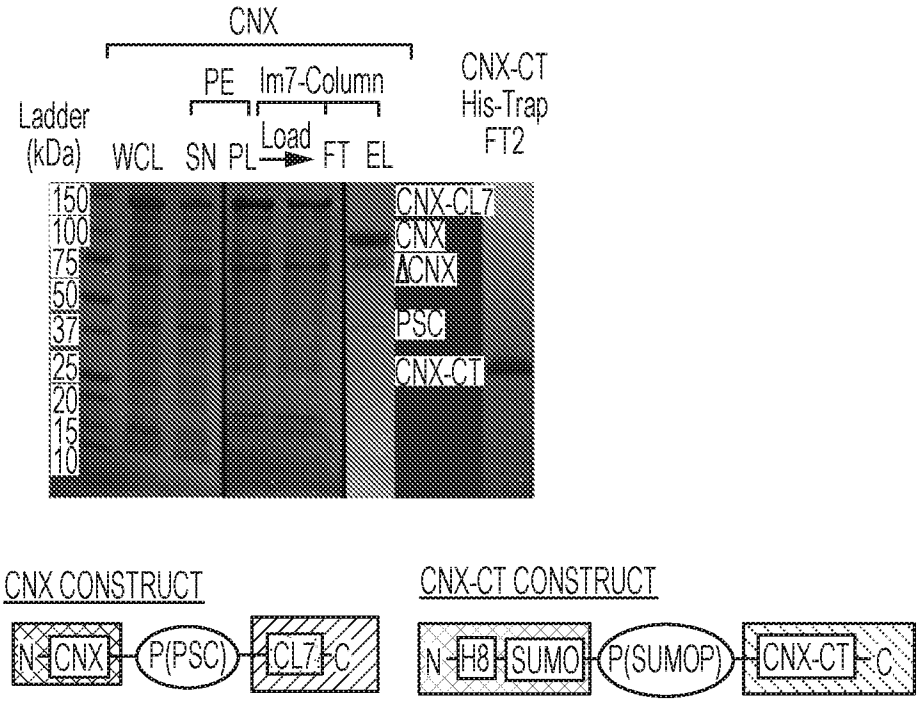

CNX
PE
Im7-Column
CNX-CT
His-Trap
FT2
Ladder
(kDa)
WCL
SN
PL
Load
FT
EL
150
100
75
50
37
25
20
15
10
CNX-CL7
CNX
ΔCNX
PSC
CNX-CT
CNX CONSTRUCT
N
CNX
P(PSC)
CL7
C
CNX-CT CONSTRUCT
N
H8
SUMO
P(SUMOP)
CNX-CT
C

FIG. 5A

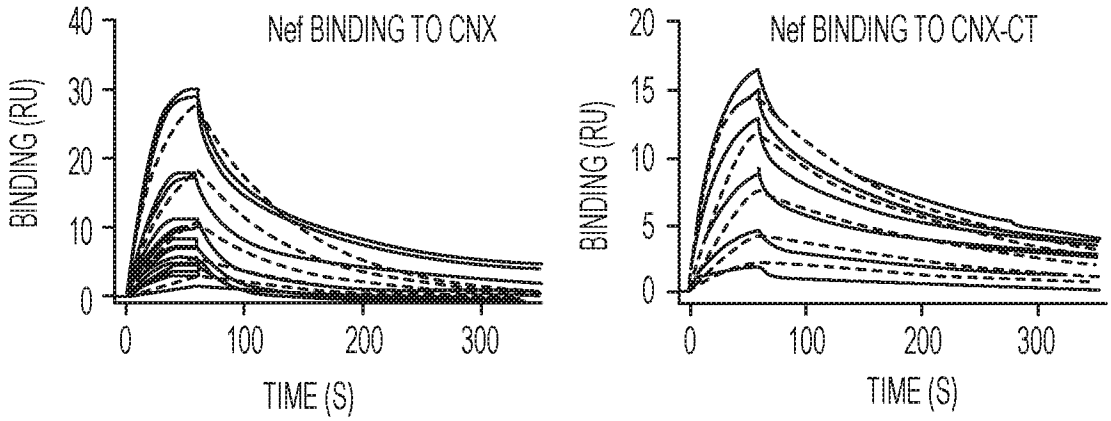

Nef BINDING TO CNX
BINDING (RU)
40
30
20
10
0
0
100
200
300
TIME (S)
Nef BINDING TO CNX-CT
BINDING (RU)
20
15
10
5
0
0
100
200
300
TIME (S)

FIG. 5B

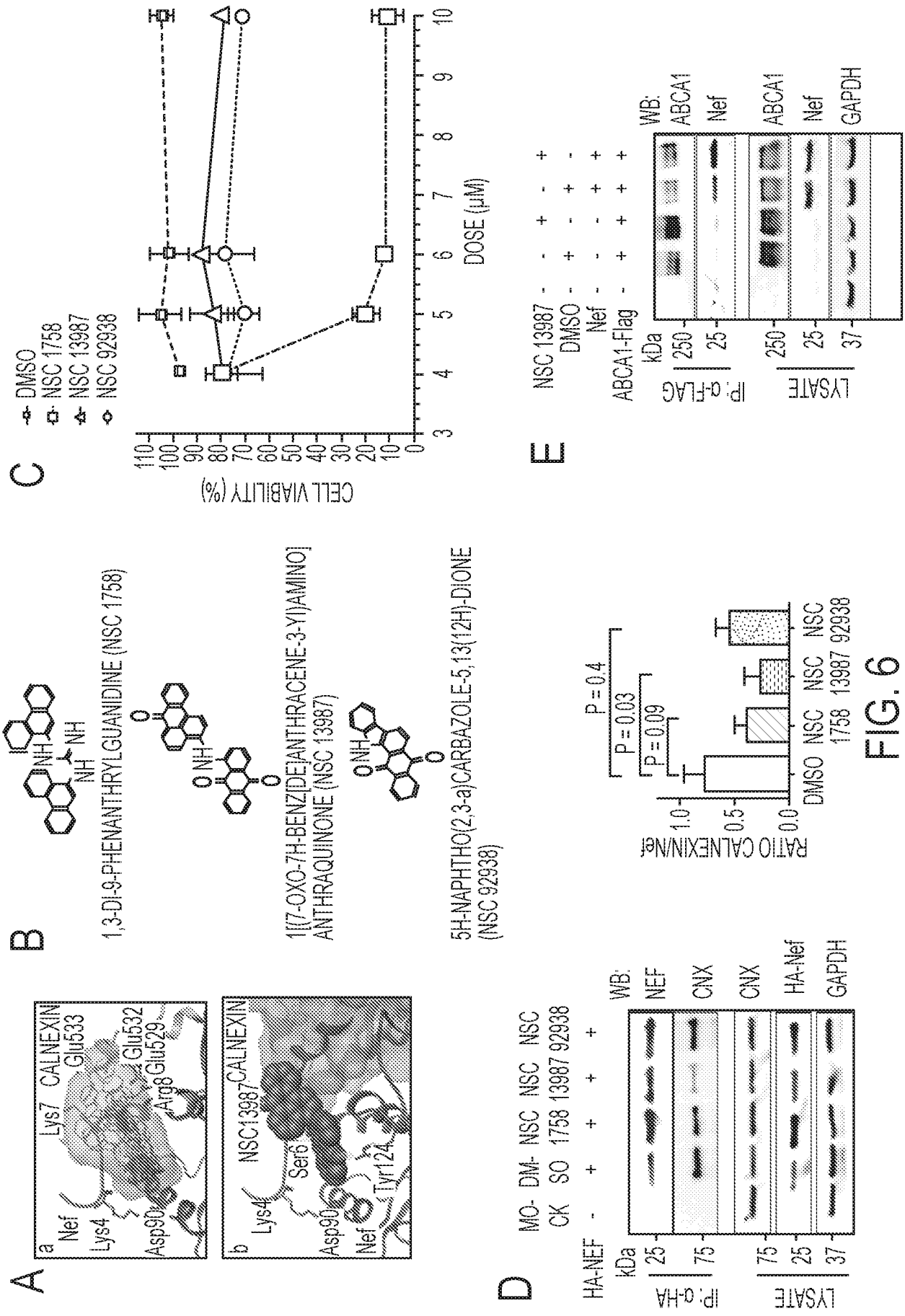

A
a
Nef
Lys4
Asp90
Lys7
CALNEXIN
Glu533
Glu532
Glu529
Arg8
b
NSC13987
CALNEXIN
Lys4
Ser6
Asp90
Nef
Tyr124
B
1,3-DI-9-PHENANTHRYLGUANIDINE (NSC 1758)
1[(7-OXO-7H-BENZ[DE]ANTHRACENE-3-YI)AMINO]
ANTHRAQUINONE (NSC 13987)
5H-NAPHTHO(2,3-a)CARBAZOLE-5,13(12H)-DIONE
(NSC 92938)
C
DMSO
NSC 1758
NSC 13987
NSC 92938
CELL VIABILITY (%)
DOSE (μM)
D
MO- DM- NSC NSC NSC
CK SO 1758 13987 92938
HA-NEF - + + + + +
kDa
IP: α-HA
LYSATE
WB:
NEF
CNX
CNX
HA-Nef
GAPDH
RATIO CALNEXIN/Nef
P = 0.4
P = 0.03
P = 0.09
DMSO NSC NSC NSC
1758 13987 92938
E
NSC 13987 - - + - +
DMSO - + - + +
Nef - - + + +
ABCA1-Flag - + + + +
kDa
IP: α-FLAG
LYSATE
WB:
ABCA1
Nef
ABCA1
Nef
GAPDH

FIG. 6

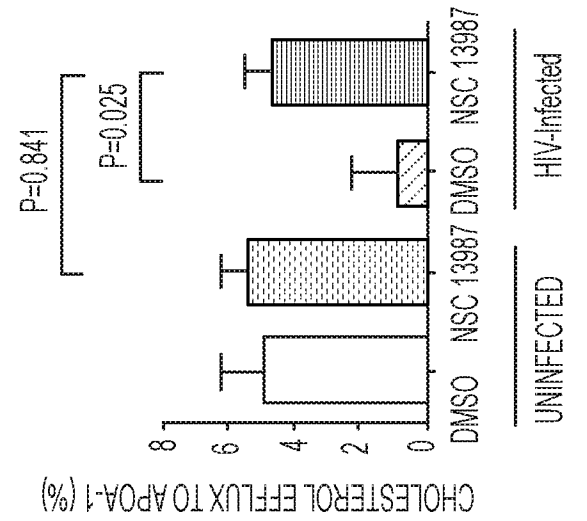


FIG. 7C

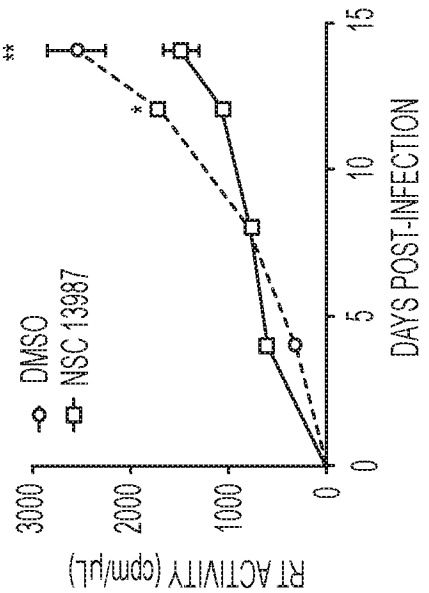


FIG. 7B

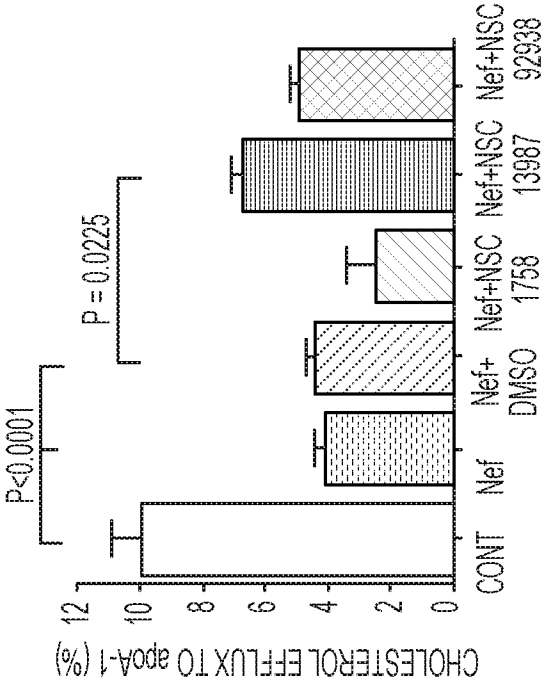


FIG. 7A

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2017/013236

A. CLASSIFICATION OF SUBJECT MATTER

A61K 31/122(2006.01)i, A61K 31/404(2006.01)i, A61K 31/18(2006.01)i

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61K 31/122; C07C 275/28; A61K 31/17; C12Q 1/68; A61K 31/404; A61K 31/18

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
Korean utility models and applications for utility models
Japanese utility models and applications for utility models

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
eKOMPASS(KIPO internal), STN Express(Registry, Caplus), Google & Keywords:Nef, calnexin, Negative Regulatory Factor, cholesterol, screen, assay, analyze

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Chemical Abstract compound, STN express. See RN 35106-31-1 (Entered STN: 16 November 1984).	15
A		11-14,16,17
X	Chemical Abstract compound, STN express. See RN 162331-05-7 (Entered STN: 20 April 1995).	16
A		11-15,17
A	JENNELLE, L. et al., "HIV-1 protein Nef inhibits activity of ATP-binding cassette transporter A1 by targeting endoplasmic reticulum chaperone calnexin", Journal of Biological Chemistry, 17 October 2014, Vol. 289, No. 42, pp. 28870-28884 See page 28879, left column.	11-17
A	US 6750253 B1 (OTTOSEN, E. R.) 15 June 2004 See column 15, lines 25-42.	11-17
A	US 2008-0227099 A1 (LAWN, R. M. et al.) 18 September 2008 See the whole document.	11-17

☐ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents,such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
25 April 2017 (25.04.2017)	**26 April 2017 (26.04.2017)**

Name and mailing address of the ISA/KR
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Korean Intellectual Property Office
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2017/013236

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 1-10
because they relate to subject matter not required to be searched by this Authority, namely:
Claims 1-10 pertain to methods for treatment of the human body by surgery or therapy, and thus relate to a subject matter which this International Searching Authority is not required, under PCT Article 17(2)(a)(i) and PCT Rule 39.1(iv), to search.

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required addtional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of any additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.

PCT/US2017/013236

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 6750253 B1	15/06/2004	AT 278663 T	15/10/2004
		AU 5807000 A	05/02/2001
		AU 768878 B2	08/01/2004
		CA 2379293 A1	25/01/2001
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		EP 1210325 B1	06/10/2004
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		HU 0201913 A2	28/10/2002
		HU 0201913 A3	28/11/2002
		JP 2003-505363 A	12/02/2003
		PL 353644 A1	01/12/2003
		PT 1210325 E	31/01/2005
		RU 2247719 C2	10/03/2005
		WO 01-05751 A1	25/01/2001
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		US 6821774 B1	23/11/2004
		US 7351535 B2	01/04/2008