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WEI XIA ET AL: "Folate-Targeted Therapies for Cancer", JOURNAL OF MEDICINAL CHEMISTRY, vol. 53, no. 19, 14 October 2010 (2010-10-14), pages 6811 - 6824, DOI: 10.1021/jm100509v
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(54) **Title:** TARGETED LIGAND-PAYLOAD BASED DRUG DELIVERY FOR CELL THERAPY

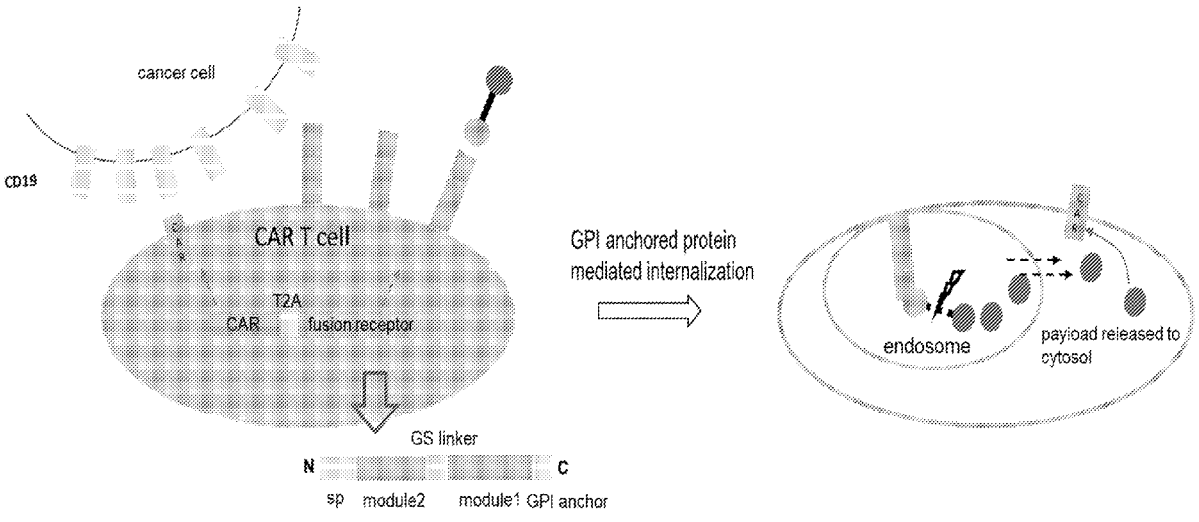

FIG. 1B

(57) **Abstract:** A drug delivery platform providing flexible fine tune of cell therapy is disclosed herein. Particularly, an engineered fusion protein is coupled with a high affinity ligand carrying at least one payload of drug to be internalized by the transplanted cell to observe or regulate transplanted cell therapy effects.

[Continued on next page]

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TARGETED LIGAND-PAYLOAD BASED DRUG DELIVERY FOR CELL THERAPY

CROSS REFERENCE

This application claims the benefit of US provisional application 62/460,118 under 35 U.S.C. §119 (e), filed on February 17, 2017. The content of which is expressly incorporated herein entirely.

FIELD OF INVENTION

This disclosure provides a drug delivery platform for cell therapy. Particularly, an engineered protein is coupled with a high affinity ligand carrying at least one payload of drug to be internalized by the transplanted cell through the engineered protein to regulate transplanted cell therapy effects.

BACKGROUND

In the last few decades, great advances have been made in this field regarding the cell types, delivery methods and suitable diseases models. In terms of cell types, current cell therapies can be roughly categorized as chimeric antigen receptors (CARs), cell for tumor model and stem cell based regenerative medicine.

CAR T also known as chimeric T cell receptors, chimeric immunoreceptors or artificial T cell receptors, enable immune effector cells (usually T cells or NK cells) to recognize target cells with corresponding antigen and exercise their cytotoxic activity. The emergence and development of CAR-T technology provides promises to certain types of cancers, which turns CAR-T into a superstar in the field of both biomedical research and clinical studies.

Regenerative medicine is a game-changing area of medicine with the potential to fully heal damaged tissues and organs, offering solutions and hope for people who have conditions that today are beyond repair. Advances in developmental and cell biology, immunology, and other fields have unlocked new opportunities to refine existing regenerative therapies and develop novel ones.

Stem cells have the ability to develop — through a process called differentiation — into many different types of cells, such as skin cells, brain cells, lung cells and so on. Stem cells are a key component of regenerative medicine, as they open the door to new clinical applications.

A variety of stem cells, including adult and embryonic stem cells may be used in regenerative medicine. In addition, various types of progenitor cells, such as those found in umbilical cord blood, and bioengineered cells called induced pluripotent stem cells are used in regenerative medicine. Each type has unique qualities, with some being more versatile than others.

Many of the regenerative therapies under development begin with the particular patient's own cells. For example, a patient's own skin cells may be collected, reprogrammed in a laboratory to give them certain characteristics, and delivered back to the patient to treat his or her disease.

Although the anti CD19 CAR T has received great success in clinical applications for leukemia treatment, lethal side effects such as the cytokine storm generated from the fast lysis of tumor cells, as well as the killing of normal CD19+ B cells by the fast proliferating anti-CD19 CAR T cell requires finer control of the CAR T cell. In stem cell based regenerative therapy, efforts have been put to better understand the differentiation process and trophic roles of the transplanted cells in the target tissue. Meanwhile, these processes can be potentially altered by some small molecule drugs that specifically delivered to the stem cell to further contribute to the regeneration of the target tissue.

Another long lasting concern about the CAR T cells as well as other stem cell based regenerative therapy is the tumorigenic potential of these transplanted cells. In summary, it will be ideal to have a private doorway to control the activity of the transplanted cell, either CAR T cell or stem cell, after they are being transplanted.

SUMMARY OF THE INVENTION

This disclosure provides a drug delivery platform for fine tuning cell therapy. The drug delivery system comprises:

a. an engineered protein on a target cell for transplant, wherein the fusion protein comprises a first component and a second component, the first component and the second component are connected by a peptide linker, the first component is a non-membrane protein, the second component is a membrane anchored peptide or protein;

b. at least one small ligand conjugated to a linker, wherein the at least one small ligand has intrinsic high affinity to at least one component of the engineered protein; and

c. at least one payload of drug conjugated to the linker, wherein the payload of drug is associated with the target cell when the small ligand binds to at least one component of the engineered protein.

In some embodiment, the aforementioned drug delivery platform has a payload of drug of imaging agent. Such imaging agent may be slected from from the group consisting of fluorescent dye rhodamine, fluorescein, and S0456. Alternatively, such imaging agent is selected from the group consisting of radioisotope chelating imaging moieties, EC 20 chelating head, NOTA and DOTA.

In some embodiment, the aforementioned drug delivery platform has a payload of drug of cytotoxic drug. Such cytoxic drug may be selected from the group consisting of tubulysin, DM1, DM4, and an auristatin.

In some embodiment, the aforementioned drug delivery platform has a payload of drug of a modulator of gene expression.

In some embodiment, the aforementioned drug delivery platform has a payload of drug of modulator of the cell's activity.

In some embodiments, the aforementioned modulator may be selected from the group of Dasatinib, MEK1/2 inhibitor, and PI3K inhibitor; group of HDAC inhibitor, kinase inhibitor and metabolic inhibitor; group of GSK3 beta inhibitor, MAO-B inhibitor and Cdk5 inhibitor.

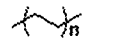
In some embodiments, the aforementioned modulator is a phosphatase inhibitor, an RORγt agonist or an siRNA mi181a1.

In some embodiments the aforementioned payload of drug is a phosphatase inhibitor, including but not limited to inhibitors against SHP1/2, TC-PTP.

In some embodiment, the aforementioned payload of drug in the drug delivery platform is further internalized by the target cell when the small ligand binds to at least one component of the engineered protein.

In some embodiment, the aforementioned drug delivery platform has a releasable linker to connect the small ligand and the payload drug. The linker can be selected from the group

consisting of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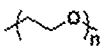
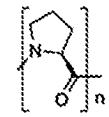
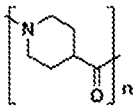
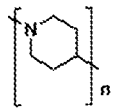
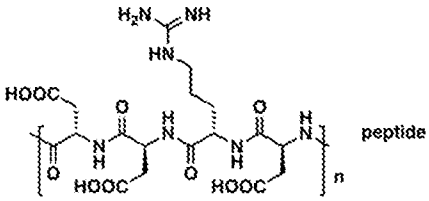
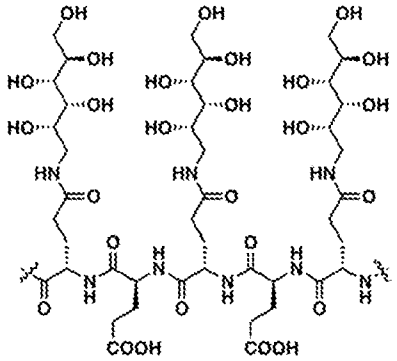

poly ethylene glycol (PEG)


polyproline


oligo-(4-piperidine carboxylic acid)


oligo piperidine


peptide


saccharo-peptide

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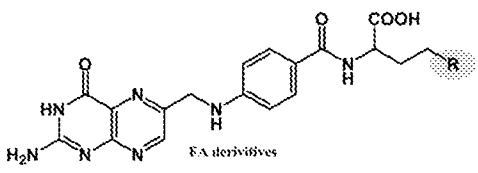
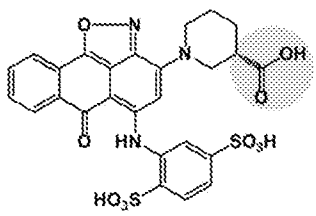
In some embodiment, the aforementioned engineered protein components are are selected from the group consisting of Folate Receptor alpha (FRa), Folate Receptor beta (FRb), Urokinase receptor (uPAR), FK506 binding protein (FKBP), dihydrofolate reductase (DHFR), Single Chain Fragment Variable against Fluorescein isothiocyanate (scFv against FITC), and Single Chain Fragment Variable against dinitrophenol (scFv against DNP).

In some embodiment, the aforementioned small ligand is selected from the group consisting of 
FA derivitives
, 
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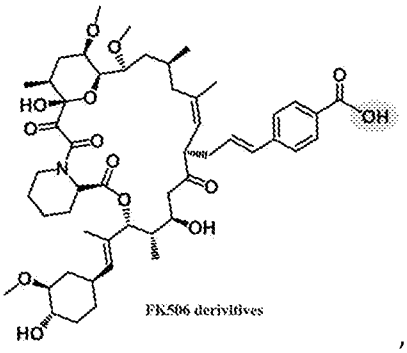

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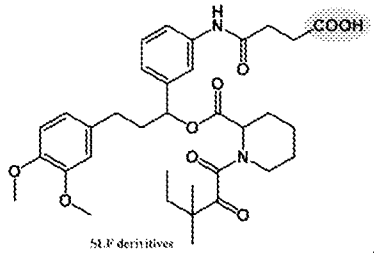

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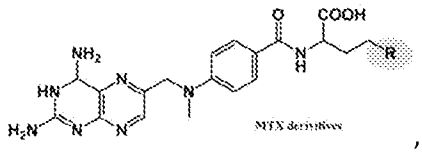

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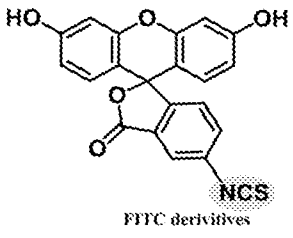

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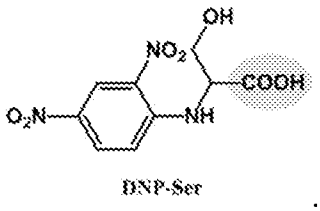

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In some embodiment, the aforementioned drug delivery platform has the first component as FKBP, the second component is a peptide that confers a glycosylphosphatidyl inositol (GPI) anchor on the first component, and the small ligand is FK506 or its derivative. In some embodiment, the FK506 derivative abolishes Calcineurin binding site.

In some embodiment, the aforementioned second component is a full length or truncated Folate Receptor (FR).

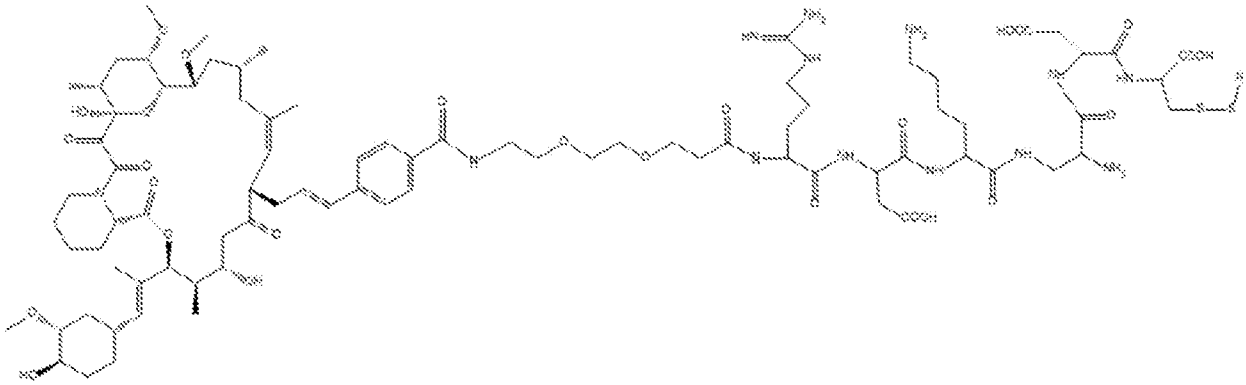
In some embodiment, the aforementioned drug delivery platform has at least one segment of flexible peptide linker SGGGS to connect the first component and the second component of the engineered protein.

In some embodiment the aforementioned drug delivery platform comprises an engineered protein selected from the group consisting of SEQ ID NOS:1-2 (amino acid sequence for mouse FKBP-FRa and amino acid sequence for human FKBP-FRa respectively).

In some embodiment the aforementioned drug delivery platform comprises an engineered protein selected from the group consisting of SEQ ID NOS:12-15.

In some embodiment the aforementioned target cell for transplant is an immune cell. For example, the immune cell can be a NK cell or a Chemeric Antigen Receptor T (CAR T) cell. Such CAR T cell may be expressing amino acid sequence selected from SEQ ID NOS: 3-4.

In some embodiment the aforementioned drug delivery platform has the small ligand conjugate with formula I.



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In some embodiment the aforementioned drug delivery platform has a target cell for transplant as CAR T cell expressing SEQ ID NO:3 (amino acid sequence for mouse antiCD19 CAR T construct) or SEQ ID NO:4 (amino acid sequence for human antiCD19 CAR T construct).

In some embodiment the aforementioned small ligand is further conjugated to a flurorescent dye or radioactive probe for tracking the drug internalization.

In some embodiment the aforementioned drug delivery platform comprises a small ligand that is further conjugated to a regulator of endogenous gene expression of a regulator of a transduced transgene expression.

In some embodiment the aforementioned drug delivery platform, the target cell for transplant is a stem cell, a progenitor cell, or a transplanted cell designed to synthesize a biochemical that is deficient in a patient.

This disclosure further provides a CAR T cell comprising a construct expressing amino acid sequences selected from SEQ ID NOS:12-15.

This disclosure further provides a DNA construct encoding an amino acid sequence selected from the group consisting of SEQ ID NOS:12-15.

This disclosure further provides a DNA construct encoding a FKBP-FRa fusion receptor comprising any of SEQ ID NOS:1-2 operably linked to an EF1a promoter in a expression vector. In some embodiment, such exprssion vector is pWPI having SEQ ID NO:5.

This disclosure further provides a DNA construct comprising any of SEQ ID NOS:6-8.

This disclosure further provides a transplanted cell comprising insert genes hFKBP-FR (SEQ ID NO:7) and human antiCD19 CAR (SEQ ID NO:9).

This disclosure further provides a transpant cell comprising insert genes mFKBP-FR(SEQ ID NO:8) and mouse antiCD19 CAR (SEQ ID NO:10).

This disclosure further provides a method to modulate cell therapy effect. The method comprises:

a. Identifying a target cell for transplant, wherein the transplanted target cell has a cell therapy function;
b. Providing an engineered fusion protein on the surface of the target cell for transplant, the fusion protein comprises a first component and a second component, the first component and the second component are connected by a flexible peptide linker, the first component is a non-membrane protein, the second component is a Glyclosylphosphatidyl inositol (GPI) anchored peptide or protein;
c. Providing a payload of drug conjugate to the target cell, wherein the payload of drug is conjugated to a small ligand through a linker, and optionally conjugated to a fluorescent dye, wherein the small ligand binds to at least one component of the engineered fusion protein with high affinity and is internalized by the target cell together with the payload of drug;
d. releasing the drug within the target cell to modulate the target cell therapy function.

In some embodiment, the aforementioned cell therapy function is to provide optically guided surgery to a subject.

In some embodiment, the aforementioned cell therapy function is to control the target cell proliferation.

In some embodiment, the aforementioned cell therapy function is to execute cytotoxicty to the target cell engaged cancer cell.

In some embodiment, the aforementioned transplanted target cell is an immune cell. For example, the target cell is a CAR T cell.

In some embodiment, the aforementioned transplanted target cell is a stem cell, a progenitor cell or a transplanted cell designed to synthesize a biochemical that is deficient in a patient.

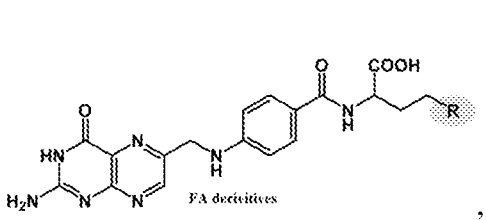
In some embodiment, the aforementioned payload of drug is an imaging agent selected from flurescent dye of Rhodamine and FITC, or a radioisotope imaging agent selected from EC20 chelating head, NOTA and DOTA.

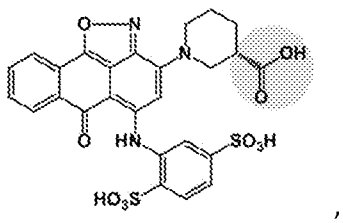
In some embodiment, the aforementioned payload of drug is a cytotoxic drug selected from the group consisting of Tubulysin, DM1, DM4 and auristatin.

In some embodiment, the aforementioned payload of drug is a modulator of gene expression selected from kinase inhibitors consisting of Dasatinib, MEK1/2 inhibitor and PI3 Kinase inhibitor, or an siRNA of mi181a1.

In some embodiment, the aforementioned transplanted target cell comprises a fusion protein selected from the group consisting of SEQ ID NOS: 12-15.

In some embodiment, the aforementioned engineered protein components are selected from the group consisting of FRa, FRb, uPAR, FKBP, DHFR, scFv against FITC, and scFv against DNP.

In some some embodiment, the aforementioned small ligand is selected from the group consisting of 

, 

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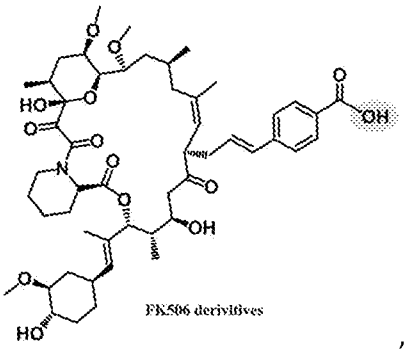

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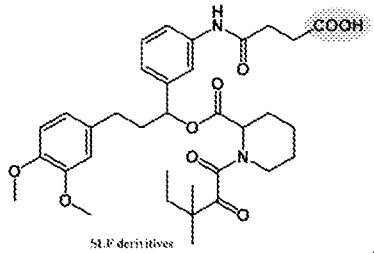

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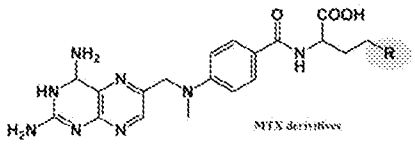

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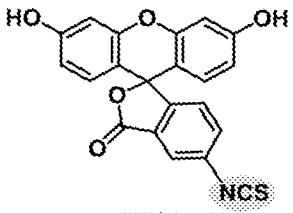

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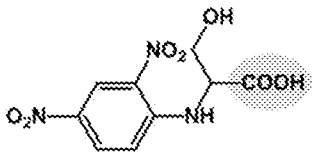

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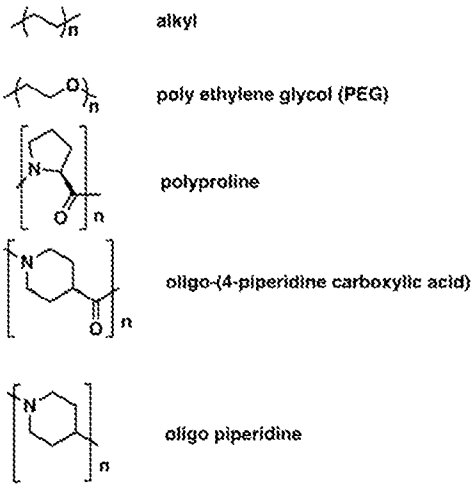
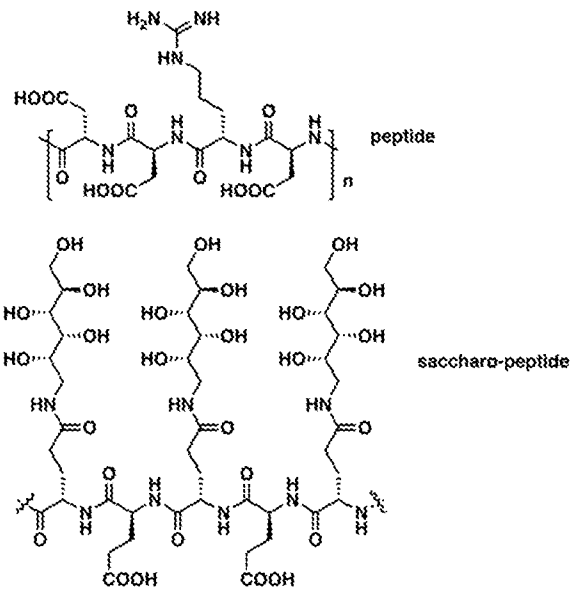
In some embodiment, the aforementioned linker to connect the small ligand and the payload drug is selected from the group consisting of





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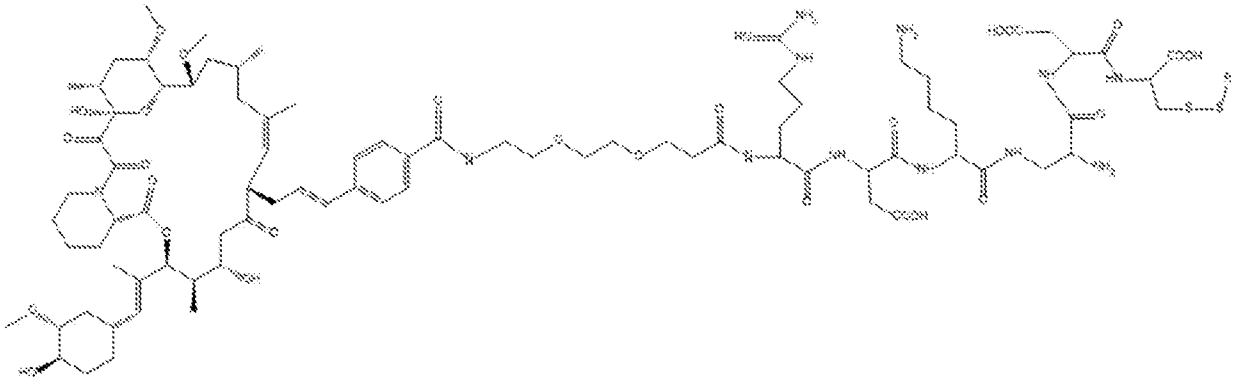
In some embodiment, the aforementioned transplanted target cell comprises an engineered FKBP-LINKER-FRa fusion protein selected from group consisting of SEQ ID NO:1 and SEQ ID NO:2.

In some embodiment, the aforementioned transplanted target cell is CAR T cell comprising an engineered antiCD19 CAR T construct selected from group consisting of SEQ ID NO:3 and SEQ ID NO:4.

In some embodiment, the aforementioned drug conjugate is FK506-releasable linker comprising formula I, wherein the binding domain of FK506 has an affinity to FKBP of about 4pM to about 100pM.



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In some embodiment the aforementioned transplanted target cell is a CAR T cell and the drug conjugate is selected from the group consisting of GSK3b inhibitor, MAPK inhibitor to control excessive cytokine storm of transplanted CAR T cell.

In some embodiment the aforementioned transplanted target cell is a CAR T cell and the drug conjugate is a modulator designed to control unwanted T cell proliferation.

In some embodiment the aforementioned transplanted target cell is a stem cell or progenitor cell and the drug conjugate is GSK3b inhibtor to boost bone fracture repair.

In some embodiment the aforementioned transplanted target cell is a stem cell, a progenitor cell or a transplanted cell designed to synthesize a biochemical that is deficient in a patient; and the drug conjugate is selected from the group consisting of MAO-B inhibitor and cdk5 inhibtior to treat Parkinson disease or other neurodegerative disease.

In some embodiment the aforementioned transplanted target cell is a NK cell and the drug conjugate is a RORγt agonist to control Th17 cell mediated immune responses.

These and other features, aspects and advantages of the present invention will become better understood with reference to the following figures, associated descriptions and claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure1: A. overview of the FKBP-FRa and FK506-payload based drug delivery platform for cell therapy; B. Graphic illustration of the secret pathway platform for CAR T cells delivery of payload.

Figure 2A.left: chemical structure of FK506 with FKBP binding sites (yellow) and derivatized site (red) highlighted. Right: co-crystal structure of ternary complex of a calcineurin A fragment (green), calcineurin B (cyan), FKBP12 (purple) and the FK506 (yellow), PDB: 1TCO

Figure 2B. Various combination options of two modules in an engineered fusion protein and their respective ligand choices, with potential derivatization sites highlighted.

Figure3: left: negative and positive regulation of the CAR T cell activity, adapted from *The quest for spatio-temporal control of CAR T cells, Sun J. etc. 2015.* Right: mechanism of AP1903 (FK506 dimer) induced FKBP-caspase9 mediated apoptosis and the structure of AP1903, adapted *from Inducible Apoptosis as a Safety Switch for Adoptive Cell Therapy, Malcolm K.B. etc. 2011*

Figure 4: **a**. pWPI expression vector map with FKBP-FRa insert (hFRa 1-24: red, FKBP: yellow, hFRa 25-258: red) **b**. FKBP-FRa transduced K562 cells show a higher band around 50kDa (37kDa for FRa plus 12kDa for FKBP) compare to FRa positive KB cells and non-transduced K562 cells. **c.** payload carrier construct and CAR T construct design **d.** The construct design of FKBPFR3GS (noted as FF3). From N terminal to C terminal, it has 1-24 aa of human FRa as the signal peptide, human FKBP protein, three Gly-Ser linker and then 25-258 aa of human FRa. In FKBPFR1GS (noted as FF1), the three Gly-Ser liner of FF3 is substituted with one Gly-Ser linker with other parts unchanged. **e**. The construct design of 4m5.3FR. From N terminal to C terminal, it has hCD8 signal peptide, scFv of 4M5.3 antibody against FITC, GS linker, 25-258aa of human FRa.

Figure 5. Interference between the FR and FKBP in FKBPFR1GS fusion receptor. Binding of Folate acid in FKBPFR1GS fusion protein blocks the binding of FK506-Rhodamine at as low as 0.01nM and totally abolish FK506-Rhodamine binding at 50nM.

Figure 6. FKBPFR1GS jurkat cell shows decreased FK506-Rhodamine intensity after binding to OTL38. FRET from FK506-Rhodamine (donor) to OTL38 (FA-S0456, acceptor, ex/em: 774/794nm) within the fusion receptor indicates the interaction between FR and FKBP.

Figure 7. Increasing the linker length between FKBP and FR significantly lowers the interference between the two parts. Compare to FF1 (1GS between FKBP and FR), FF3 (3GS between FKBP and FR) preserves the binding of FK506-Rhodamine in the presence of 10nM FA, which is comparable to the physiological concentration of FA in human body.

Figure 8. PI-PLC treatment releases the GPI anchored fusion receptor FF3. Jurkat T cell with FF3 fusion receptor shows saturated binding with 20nM FA-FITC (EC17), while after 5mU PI-PLC or 50mU PI-PLC treatment, the FA-FITC loses binding to the cell, which indicates the release of the GPI anchored FF3 fusion receptor.

Figure 9. FA-Rhodamine binding curve in FKBPFR3GS fusion receptor. FKBPFR3GS fusion receptor that stably expressed on human T cell can bind to folate acid derivative (FA-Rhodamine) with high affinity (Kd=0.95nM), which is comparable to the affinity of FA-Rhodamine in FR+ KB cell (Kd around 1nM). Therefore, the binding property of FR in the fusion receptor is preserved.

Figure 10. FK506-Rhodamine binding curve in FKBPFR3GS fusion receptor. FKBPFR3GS fusion receptor that stably expressed on human T cell is able to bind to FK506 derivative (FK506-Rhodamine) with high affinity (Kd=3.93nM), which means the binding property of FKBP in the fusion receptor is preserved.

Figure 11. SLF-FITC binds to FKBPFR3GS fusion receptor with relatively high binding affinity (Kd=62nM), while competition with free SLF (100x, preincubation) blocks this binding. SLF, a mimic of FK506, presents a 10 times lower binding affinity to FKBPFR fusion receptor, compare to the parent ligand FK506, which is consistent with previous report.

Figure 12. FA-Rhodamine binding curve in 4M5.3FR fusion receptor. FA-Rhodamine can binds to 4M5.3FR fusion receptor that stably expressed on human T cell with high affinity (Kd=2.25nM), which is comparable to the affinity of FA-Rhodamine in FR+ KB cell (Kd around 1nM). Therefore, FR binding property is preserved in 4M5.3FR fusion receptor.

Figure 13. FITC-AF647 binding curve in 4M5.3FR fusion receptor. FITC-AF647 can binds to 4M5.3FR fusion receptor that stably expression on human T cell with high affinity (Kd=8.03nM). 100x comp indicates free FITC sodium. The binding property of scFv 4M5.3 with FITC is preserved in 4M5.3FR fusion receptor.

Figure 14. FA-Tubulysin is able to mediate a receptor specific killing effect against FF3+ human T cell. Compensation with FA (100x preincubation with FA) blocks the effect. This implies the successful internalization and release of the free drug Tubulysin through the FF3 fusion receptor system.

Figure 15. FA-Tubulysin specifically kill the hFF3+ population in a mixed human T cell culture. Absolute number of hFF3+ cell decrease as the FA-Tub concentration increases, while hFF3- cells are killed also through released drugs and bystander effect at high concentration.

Figure 16. SLF-Tub specifically kill the hFF3+ Jurkat cells with a IC_{50} = 138nM. This indicates the successful internalization of SLF-Tub by the FKBPFR3GS fusion receptor and the release of the Tubulysin inside the cell.

Figure 17. Both FITC-DM4 and FITC-Tub can specifically kill the 4M5.3FR+ human T cells, while FITC-Tub has a higher IC_{50}. Compensation of free FITC sodium (100x preincubation) blocks the receptor mediated killing effect. This implies the successful internalization and release of FITC-cytotoxic drug into T cell through 4M5.3FR fusion receptor.

Figure 18 FITC-Tubulysin specifically kill the 4M5.3FR+ population in a mixed human T cell culture. Absolute number of 4M5.3FR+ cell decrease as the FITC-Tub concentration increases, while the 4M5.3FR- cells are killed also through released drugs and bystander effect at high concentration.

Figure 19 FITC-DM4 specifically kill the 4M5.3FR+ population in a mixed human T cell culture. Absolute number of 4M5.3FR+ cell decrease as the FITC-DM4 concentration increases, while the 4M5.3FR- cells are killed also through released drugs and bystander effect at high concentration.

Figure 20. Dasatinib (Lck inhibitor) and Ibrutinib (ITK inhibitor) at 10nM concentration decrease the lysis effect of antiCD19 CAR T cell (FMC63 CAR T, Effector) against CD19+ Raji tumor cell (Target). Two Effector: Target ratio (E:T) have been tested. Normal T cell and antiCD19 CAR T with CD19- K562 cell were used as negative control.

Figure 21. FITC-Dasatinib can decrease the lysis effect of FMC63+4M5.3FR+hT cell towards Raji cell. This implies the successful internalization and release of FITC-Dasatinib into T cell through 4M5.3FR fusion receptor and the release of Dasatinib into T cell.

Figure 22. TC-PTP inhibitor at 100nM concentration decrease the co-inhibitor molecule population in exhausted antiCD19 CAR T cell (generated by 7 times of stimulation with CD19+Raji cells, see detailed procedure below). Both PD-1, LAG3 and double positive population decreases upon treatment. This implies that phosphatase inhibitors, like TC-PTP inhibitor may be used as a payload for the secret gateway platform for rejuvenating the exhausted CAR T cell.

TABLE 1. Potential applications of the FKBP-FRa cell therapy platform and the corresponding payload.

SEQUENCE LISTINGS

SEQ ID NO:1 Amino acid sequence for mouse FKBP-FRa

SEQ ID NO:2 Amino acid sequence for human FKBP-FRa

SEQ ID NO:3 Amino acid sequence for mouse antiCD19 CAR T construct

SEQ ID NO:4 Amino acid sequence for human antiCD19 CAR T construct

SEQ ID NO:5 vector pWPI for human T cell transduction

SEQ ID NO:6 pMP71 gb NotIEcoRI mouse antiCD19 for mouse T cell transduction

SEQ ID NO:7 pWPI-FRa 1-24 FKBP FRa

SEQ ID NO:8 pWPI mFKBP-mFRa SGGGS

SEQ ID NO:9 pHR EcorI hAnti cd19 1D3 myc hinge cd28 cd3zeta

SEQ ID NO:10 pWPI pmei mAnti cd19 1D3 myc hinge cd28 cd3zeta

SEQ ID NO:11 FKBP-1SG-FR with GPI anchor amino acid sequence

SEQ ID NO:12 FKBP-3SG-FR with GPI anchor amino acid sequence

SEQ ID NO:13 4M5.3-FR with GPI anchor amino acid sequence

SEQ ID NO:14 FMC63-T2A-FKBP3SGFR

SEQ ID NO:15 FMC63-T2A-4M5.3SGFR

SEQ ID NO:16 FRb with signal peptide

SEQ ID NO:17 uPAR with signal peptide

SEQ ID NO:18 DHFR

SEQ ID NO:19 scFv against FITC: 4M5.3(Kd = 200pM)

SEQ ID NO:20 scFv against FITC 4D5Flu (Kd=10nM)

SEQ ID NO:21 scFv against DNP SPE7

DETAILED DESCRIPTION

While the concepts of the present disclosure are illustrated and described in detail in the figures and the description herein, results in the figures and their description are to be considered as exemplary and not restrictive in character; it being understood that only the illustrative embodiments are shown and described and that all changes and modifications that come within the spirit of the disclosure are desired to be protected.

Unless defined otherwise, the scientific and technology nomenclatures have the same meaning as commonly understood by a person in the ordinary skill in the art pertaining to this disclosure.

This disclosure provides a novel platform for controlling the transplanted cell activity by genetically incorporating a fusion receptor on the transplanted cell surface. These transplanted cells will then be specifically targeted by a small molecule ligand conjugated-drug payload, using the intrinsic high affinity between the small molecule ligand and the fusion receptor on the transplanted cell surface. One part of the fusion receptor is responsible for internalizing the conjugate and the payload will be released through a releasable linker once it is inside of the transplanted cells. Depending on the transplanted cell type and the desired regulation to be imposed on the transplanted cells, the drug payload can be various functions. By changing the payload in the conjugate, for example, as cytotoxic drug or kinase inhibitors, the drug payload may be used to control the multiple aspects of the transplanted cells, such as proliferation, differentiation or cytokine release profile.

The peptidyl-proline isomerase (PPIases) family consists of FK506-binding protein (FKBP), cyclophilins and parvulins. In human, there are 18 FKBPs, 24 cyclophilins and 3 parvulins. Among these, FKBP51 and FKBP52 share high to moderate binding affinity of FK506, $KD^{FK506} \approx 104$ nM and $KD^{FK506} \approx 23$ nM, respectively, comparing to FKBP12 ($KD^{FK506} \approx 0.2$ nM). Additionally, none of these two FKBPs are expressed on the cell membrane, resulting in little cross binding activity in our system. Efforts have also been made to design synthetic ligands that have higher affinity to $FKBP12^{F36V}$ than $FKBP^{WT}$, as well as to $FKBP51^{F67V}$, which preserve the overall structure of the wild type proteins. All the homolog and mutated proteins together with their ligands mentioned above, can be adapted to this disclosure.

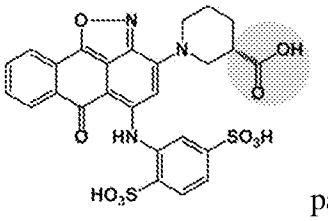
Particularly, in one embodiment, an exemplified pair of small molecule ligand and fusion receptor is chosen as FK506-FKBP. The entire process can be generalized in Figure 1A, where the FK-506-payload binds to the FKBP-FRa engineered cell first; upon this binding, the transmembrane fusion protein will internalize the payload-linker-FK506. Next, the internalized FK506-payload is cleaved at the linker, and the payload got released in the cell. Depending on the cell type and the payload type, the released payload drug can exert its desired function.

In Figure 1B, a specific Chimeric Antigen Receptor T cell mediated cell therapy is illustrated. In this model, a CAR T cell expressing a fusion protein with the structure from N terminus to C terminus comprising a suitable signal peptide, a protein module 2 linked to a protein module 1 of GPI anchor is presented to a cancer cell. In some embodiment, the cancer cell has CD19 surface protein, which will be recognized by the CAR T cell and engaged with the payload associated with the CAR T cell, when a targeting ligand binds to at least one module of the fusion receptor. Typically, with high affinity of the targeting ligand toward any one of these modules, the payload associated with the ligand may be internalized into the target cell and be released to engage the cancer cell through the chimeric antigen receptor.

There can be many different combinations of GPI anchored proteins, represented as Module 1 and its ligands, and Module 2 target cell surface protein and its respective ligands, represented in Figure 2B. It is contemplated that either module 1 protein or module 2 protein, or both can engage a high affinity targeting ligand to facilitate the ligand conjugated payload delivery. For example, it is feasible to have a fusion protein comprising FRa-Linker-FKBP structure, wherein FRa engaging with an FA derivative, at the same time, FKBP engaging a

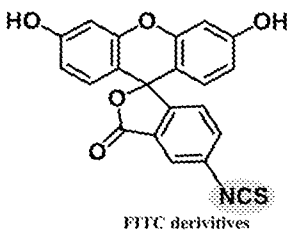
FK506 derivative, either FA derivative or FK 506 derivative or both can be linked to a payload, such as a cytotoxic drug, or an imaging agent, or a modulator. With such flexibility of carrying same or different payload, one can achieve some unexpected, synergy or regulatory effect of different or same payload, or to observe the target cell if the payload is an imaging agent. The advantages of flexibility and diversity of payload delivery of this system will be appreciated with more examples.

Similarly, another embodiment of ligand paired with a GPI anchored protein can be

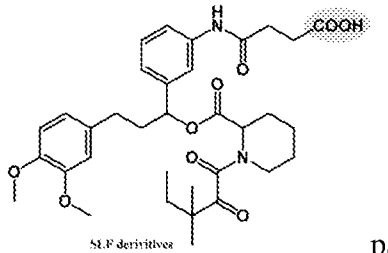


paired with uPAR.

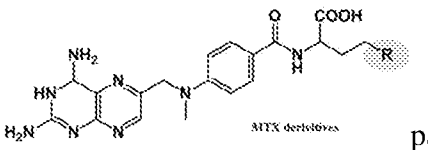
It is also contemplated that FITC or its derivatives may bind to a single chain fragment of variant (scFv) of an antibody against FITC, for example, a ligand structure of



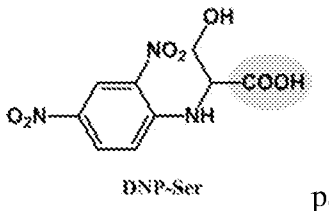
, or a structure of



paired with FKBP, or



paired with DHFR, or



paired with scFV against DNP.

It is worth mentioning a few advantages of choosing FK506-FKBP as an exemplary ligand-protein pair in this delivery system. 1. FKBP is not a membrane protein that naturally present on the mammalian cell membrane, so that the FK506-payload conjugate will specifically bind to the target cell; 2. FKBP protein is a relatively small protein with molecular weight of 12kDa, which makes it easier to be fused with other receptors with minimum perturbation to the

receptors' structure and internalization properties. 3. FK506 is not naturally present inside human being, so that the fusion receptor will not be blocked; 4. The binding affinity between FK506-FKBP is around 4pM so that the payload drug can be delivered with high affinity; 5. The co-crystal structure of FK506-FKBP is available and the well-established derivative site of FK506 preserves the binding of FK506-FKBP while abolishes the unwanted binding between FK506 and calcineurin (See Figure 2A).

It is contemplated that the sequence of FKBP can be modified, and the corresponding FK506 ligand can be modified accordingly to the extent that the modified versions of FKBP and modified version of FK506 still have the desired affinity as exemplified herein or better than the current disclosure.

For the other portion of the fusion protein, folate receptor (FR) is chosen for its well understood internalization process as a monomer. Prior research shows that 'magic carbonate' linked folic acid conjugate can be internalized through FR and cleaved by the reductive environment inside the cell. Using this mechanism, the FK506-FKBP conjugated drug payload is internalized by FR and will then be released to the cytoplasm.

Due to the great potential of CAR T therapy as well as the severe side effects, several controlled CAR T cell designs have been reported. Most of them focused on the ON/OFF switch by incorporating either a Boolean gate or a cascade pathway for the T cell activation (see Figure 3, left, which depicts negative and positive regulation of the CAR T cell activity, adapted from *The quest for spatio-temporal control of CAR T cells, Sun J. etc. 2015*). Malcolm K.B. group designed the FKBP-caspase9 fusion protein and use FK506 dimer to induce the apoptosis of the target cell (see Figure 3, right, which depicts mechanism of AP1903 (FK506 dimer) induced FKBP-caspase9 mediated apoptosis and the structure of AP1903, adapted *from Inducible Apoptosis as a Safety Switch for Adoptive Cell Therapy, Malcolm K.B. etc. 2011*).

The current disclosure has several advantages over these reported methods**:** 1. Instead of a binary ON/OFF switch, our platform can delivery multiple kinds of regulating payloads, modifying many aspects of the target cells, thus it has great flexibility compared to binary ON/OFF switch; 2. the controlling moiety, FK506-payload, is a small molecule, which makes it possible for linear control and dosage optimization compared to pre-engineered cells. 3. The

platform can be utilized in not only CAR T cell, but many other stem cell based regenerative therapies.

The greatest novelty and most important part of this platform is the multifunctional payloads, which can be selected to either address the potential side effects or improve the efficiency of the cell therapy. For instance, cytotoxic drugs can be delivered to the transplanted cells if: 1. the cells over-proliferate and affect the normal organ or system, like anti CD19 CAR T cell. 2. The cells become tumorigenic, which lies in the lentivirus based gene modification and the intrinsic characteristic of stem cells.

On the other hand, some cell therapies receive less success because of the suppressive microenvironment of the target tissue. For instance, in CAR T cell therapy against solid tumor, aside from the low penetration rate, the proliferation and activation of CAR T is highly suppressed by the MDSC and the tumor cells. This can be potentially alleviated by the RORrt agonist or MAP kinase inhibitor induced T cell activation as well as TLR8 agonist induced expression of granzyme B in CAR T cells. Although intracellular targets, like RORrt, may be more suitable for our payload, membrane receptors such as TLR8 may also be accessible due to the proximity on the cell membrane.

In stem cell regenerative therapy, the payload is more diverse according to the disease models. Instead of delivering a pre-fixed gene, which has been developed by using stem cell as a gene delivery platform, the current disclosure provides a fine tune to transplanted cells and their microenvironment, and obtains the desired phenotype through diverse small molecule payloads. Since the small molecule is conjugated to FK506, which specifically target the FKBP-FRa overexpressed transplant cell, the non-specific targeting of normal tissues of the small molecule is also avoided.

One of the many examples is to induce the overexpression of BMP2 in mesenchymal stem cell (MSC) for bone fracture repair in skeletal regenerative therapy. Meanwhile, the expression level of BMP2 and/or VEGF can be increased by introducing GSK3 beta inhibitor to the transplanted cells through this drug payload delivery system. GSK3 beta inhibitor is a desired drug for bone fracture repair. Therefore, GSK3 beta inhibitors is ideal as a potential payload for further modulating the function of the transplanted MSC as well as the microenvironment within the bone fracture sites.

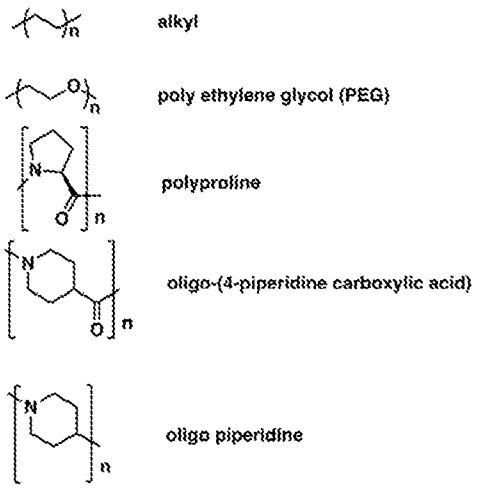
Another example of this drug payload delivery system goes to the neurodegenerative disease, including Alzheimer, Parkinson disease and etc., where MSC based therapy holds a promising future. MSC has been modified to overexpress GDNF, VEGF and many other cytokines to promote the neuronal regeneration. Meanwhile, small molecules like MAO-B inhibitors has been confirmed to increase the expression of GDNF, NGF and BDNF in astrocytes. Several kinase inhibitors have also been proposed for the treatment of Alzheimer disease, such like PI3K inhibitor (BEZ235), Cdk5 inhibitor (roscovitine) and GSK3b inhibitor (NP-12). Using FK506-FKBP pair targeted specific delivery of these small molecules to MSC in neurodegenerative models will improve the regeneration efficacy while avoiding the side effects of these potent inhibitors and agonists in other non-targeted tissues.

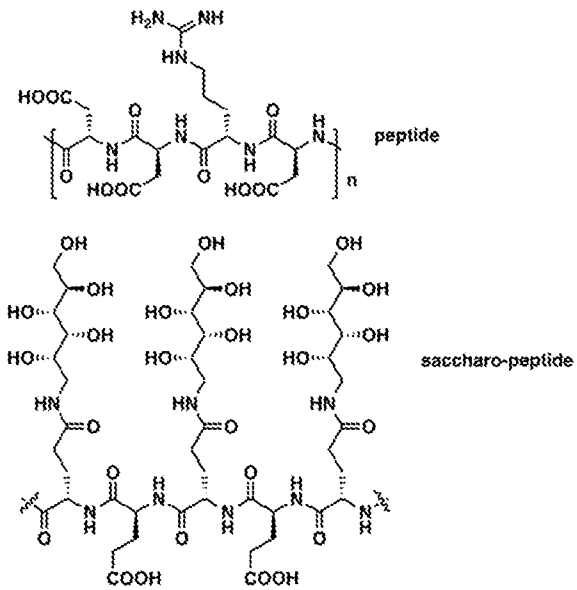
Material and Methods:

Compounds and Synthesis procedure:

Targeting ligand is linked with payload through linkers. The linker optimization options are listed below. payloads are characterized into 3 classes: I imaging, II cytotoxic drug, III regulatory small molecule drug.

Linker optimization:



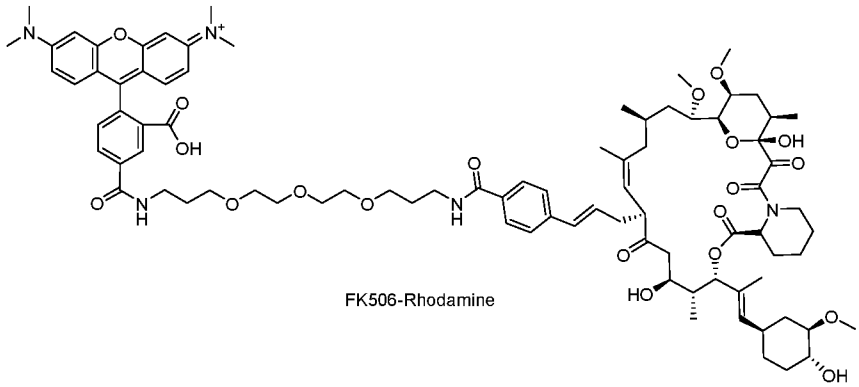


Compounds Classification:

Class	function	example
I	Imaging	Fluorescent dye: Rhodamine, FITC Radioisotope imaging: EC20 chelating head, NOTA, DOTA
II	Cytotoxic drug	Anti-microtubule drug: Tubulysin, DM1, DM4
III	Modulator	Kinase inhibitor: Dasatinib, MEK1/2i, PI3Ki siRNA: mi181a1

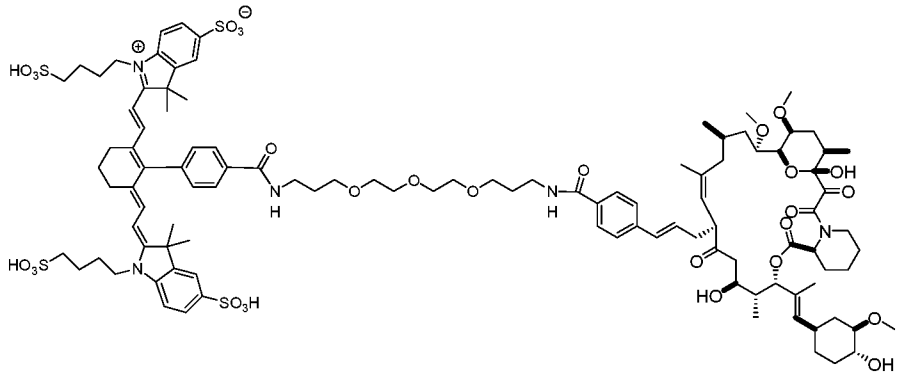
Detailed compound structure and synthesis route

FK506-Rhodamine:



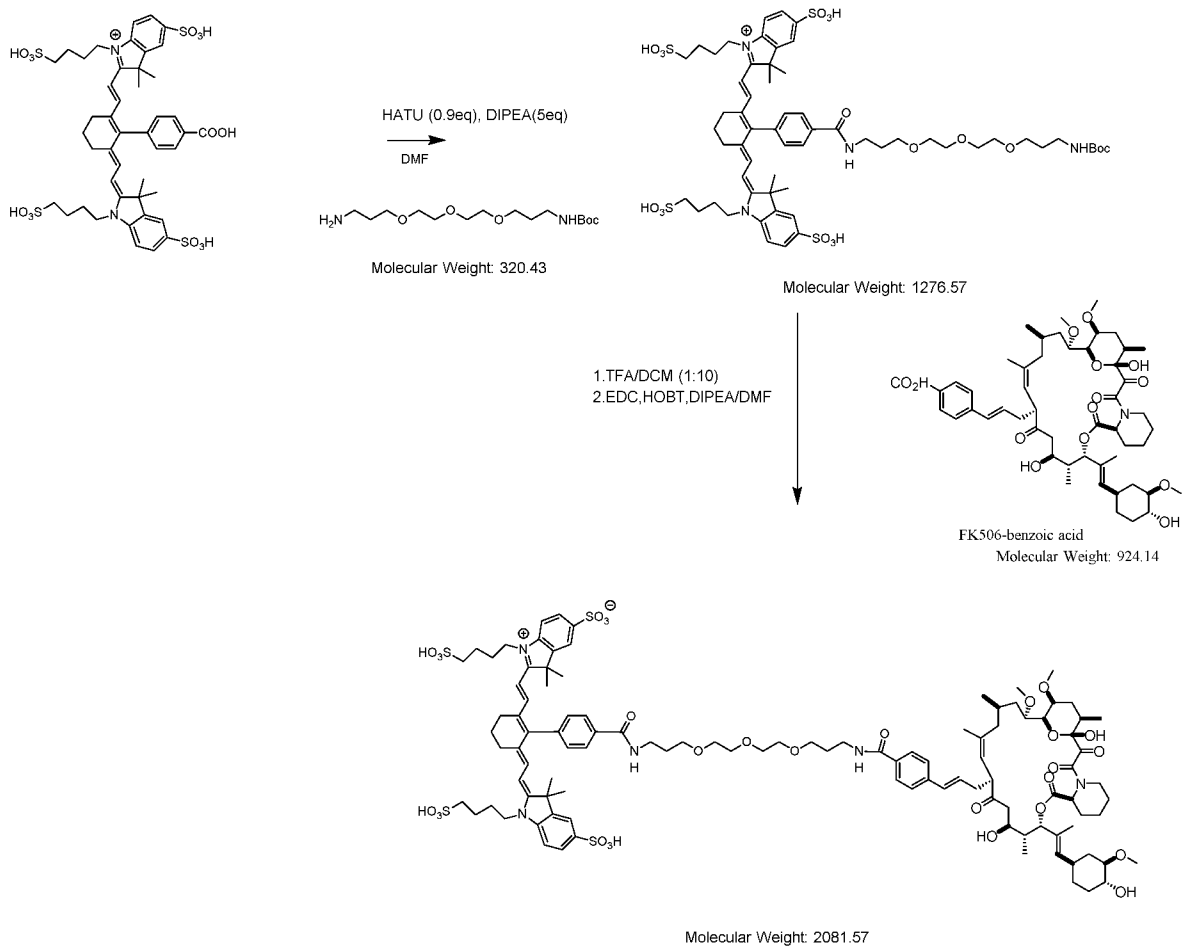
Procedure: Rhodamine-NHS ester (1.0 equiv.) in dimethylformamide was reacted with Boc-NH-PEG_3-NH_2 (1.2 equiv.) and diisopropylethylamine (3.0 equiv.) for 2h at room temperature. The product was purified by preparative reverse-phase HPLC with a UV detector. The purified Rhodamine-PEG_3-NH-Boc conjugate (1.0 equiv.) was subjected to Boc deprotection by stirring in a 1:10 TFA-dichloromethane system for 2h. The crude free amine product was then dissolved in dimethylformamide and activated with EDC (2.0 equiv.), HOBT (2.0 equiv.) in the presence of diisopropylethylamine (3.0 equiv.). After 15 minutes, FK506-CO_2H (1.2 equiv., synthesized using the procedure in the reference: Bioorg. Med. Chem., 17 (2009) 5763-5768) was added and the reaction mixture was stirred overnight. The final FK506-Rhodamine conjugate was isolated after purification on preparative reverse-phase HPLC with a UV detector (monitored at wavelength of 280 nm). The crude product was loaded onto an Xterra RP18 preparative HPLC column (Waters) and eluted with gradient conditions starting with 95% 5 mM sodium phosphate (mobile phase A, pH7.4) and 5% acetonitrile (mobile phase B) and reaching 0% A and 50% B in 35 min at a flow rate of 12mL/min. Retention time of the product peak = 2.5 min during the gradient (0-50%B) in a 7 min analytical HPLC-MS analysis. ESI m/z = 1539.6. Abbreviations: PEG = polyethylene glycol; EDC = 1-Ethyl-3-(3-dimethylaminopropyl)carbodiimide; HOBT = Hydroxybenzotriazole; HPLC = High Performance Liquid Chromatography.

FK506-NIR dye:

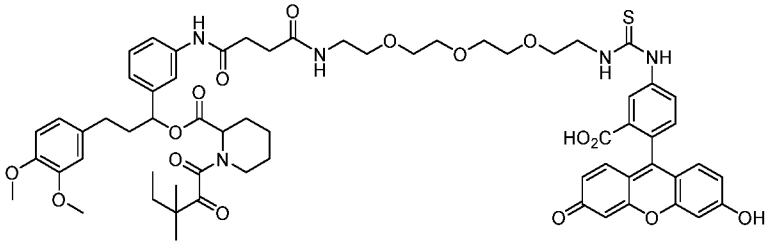


Molecular Weight: 2081.57

Synthesis procedure:

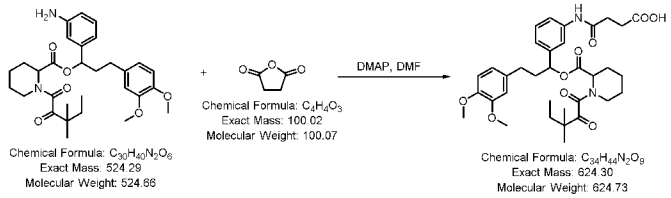


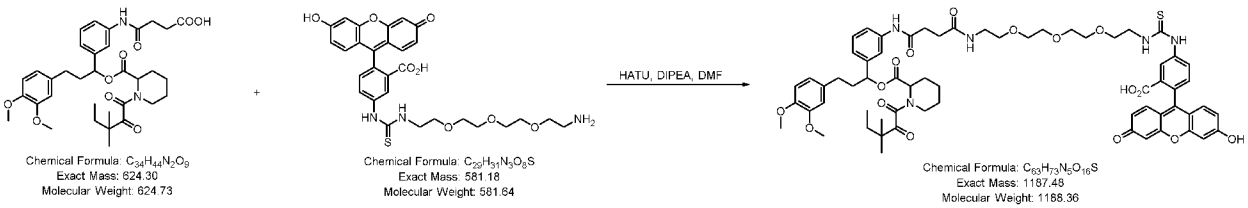
SLF-FITC:



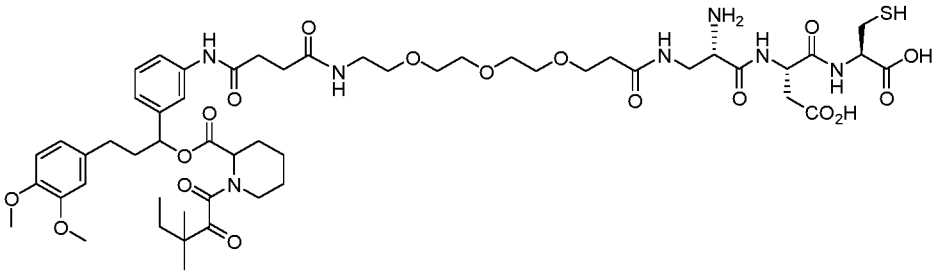
Chemical Formula: $C_{63}H_{73}N_5O_{16}S$
Exact Mass: 1187.48
Molecular Weight: 1188.36

Synthesis procedure:





SLF-EC20:



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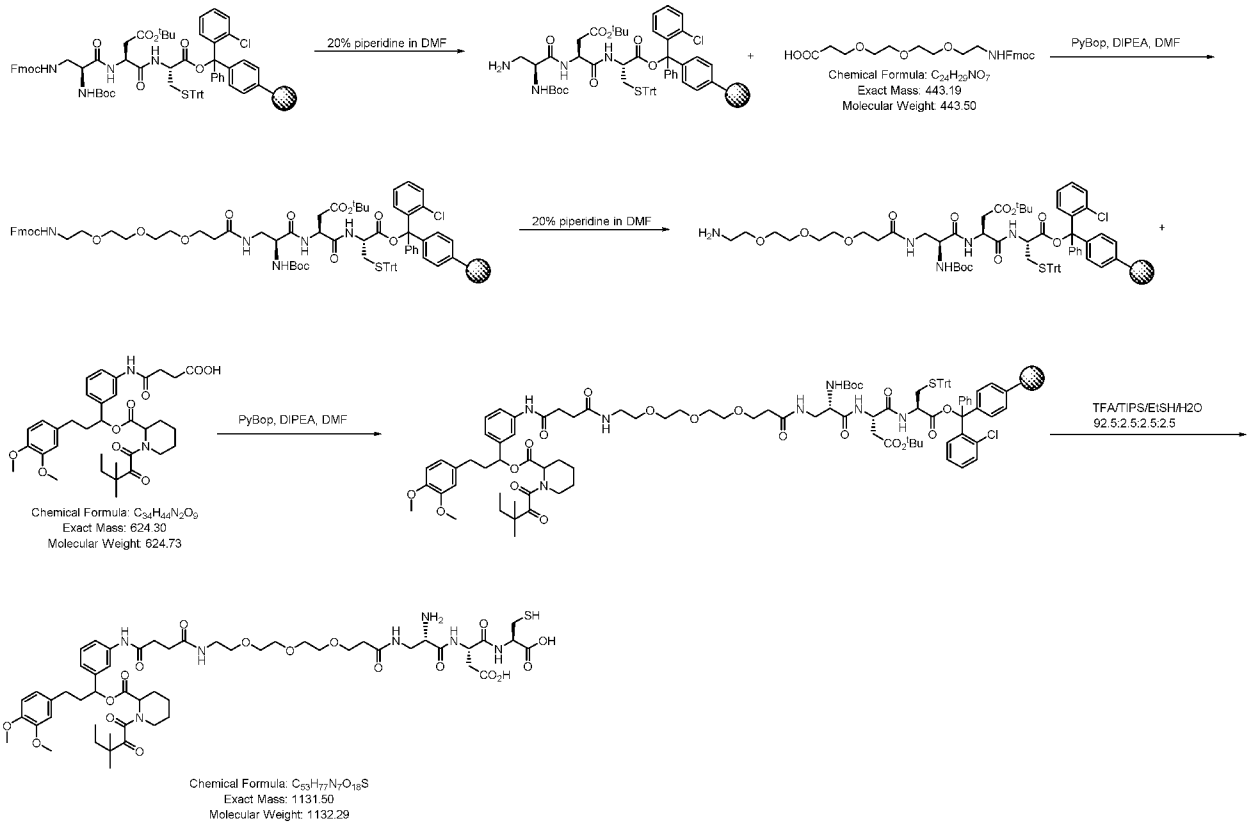
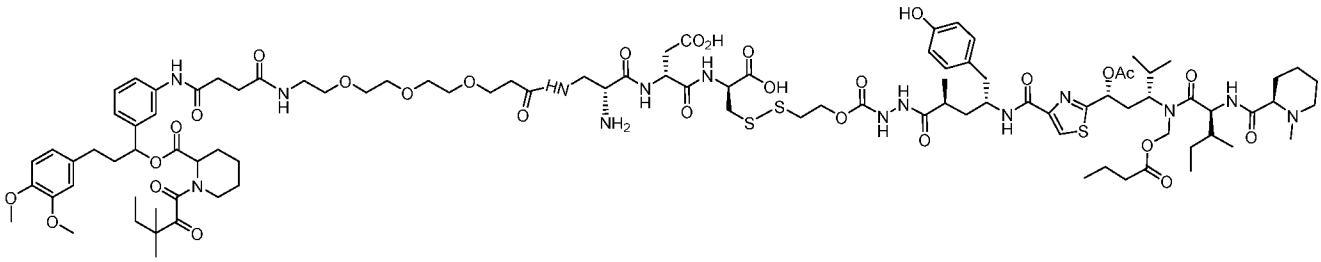
Exact Mass: 1131.50
Molecular Weight: 1132.29

Synthesis procedure:

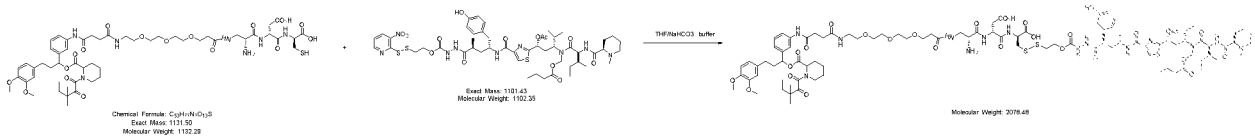


SLF-Tubulysin:

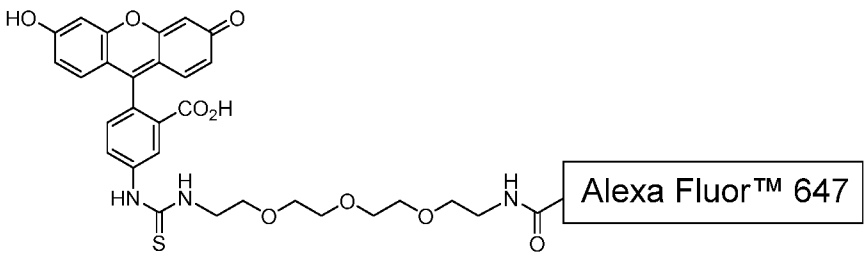


Molecular Weight: 2078.48

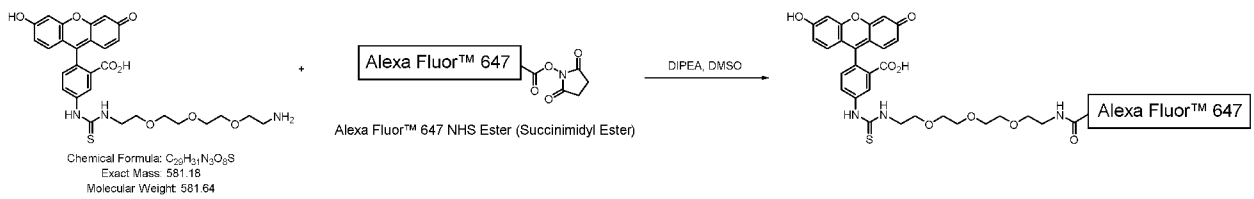
Synthesis procedure:



FITC-AF647:



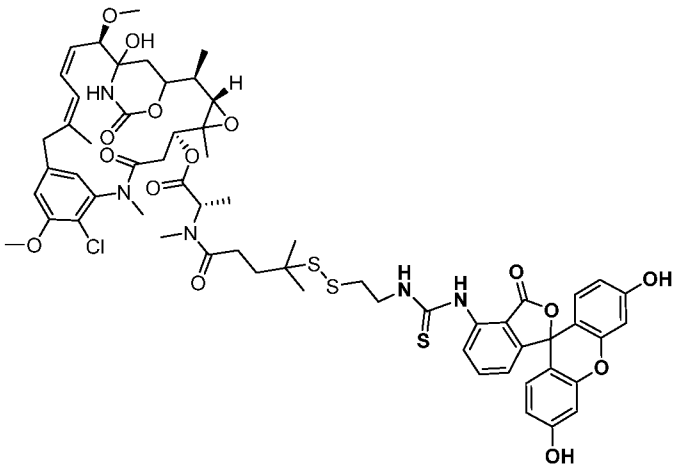
Synthesis procedure:



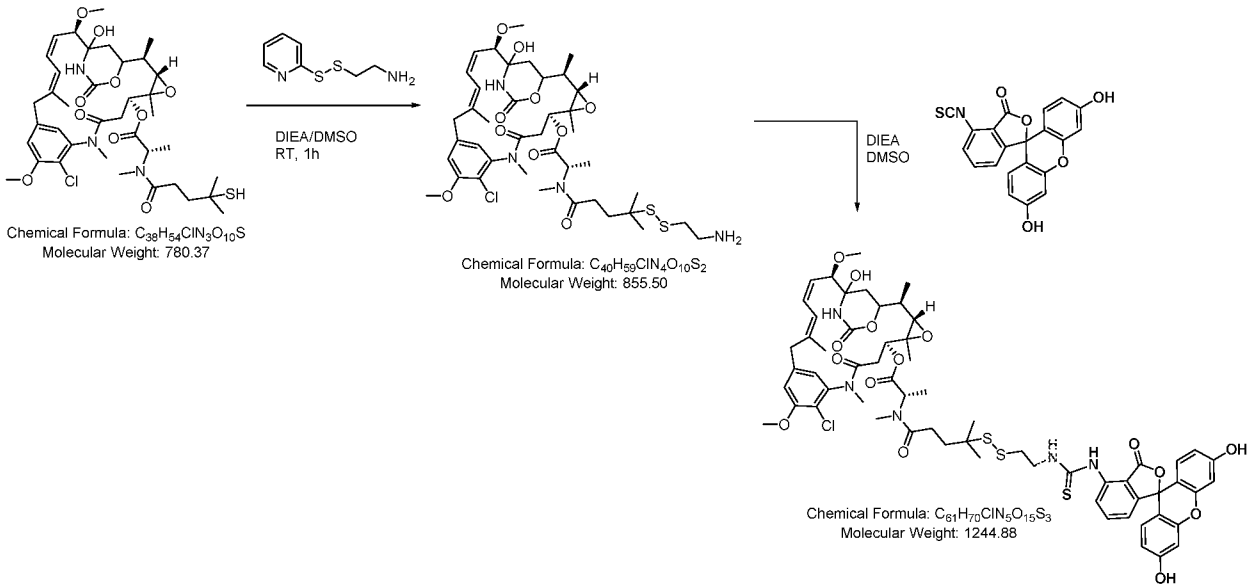
Chemical Formula: $C_{29}H_{31}N_3O_8S$
Exact Mass: 581.18
Molecular Weight: 581.64

Alexa Fluor™ 647 NHS Ester (Succinimidyl Ester)

FITC-DM4:



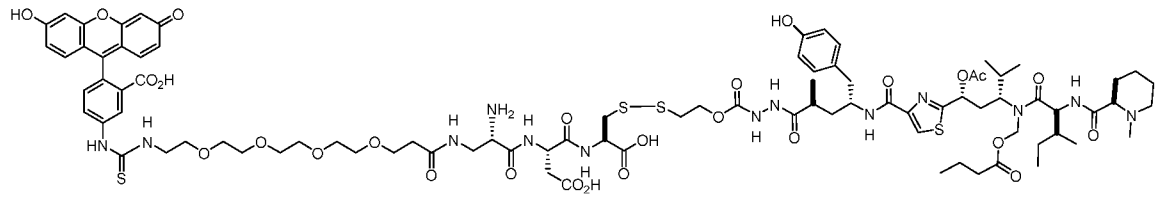
Synthesis procedure:



Procedure: DM4 (1.0 equiv.) in dimethylsulfoxide was reacted with 2-(pyridin-2-yldisulfaneyl)ethan-1-amine (1.0 equiv.) and diisopropylethylamine (3.0 equiv.) for 1h at room temperature. The resulting crude product was then reacted with FITC (1.0 equiv.) and the reaction mixture was stirred for 1h. The final FITC-DM4 conjugate was isolated after purification on preparative reverse-phase HPLC with a UV detector (monitored at wavelength of 280 nm). The crude product was loaded onto an Xterra RP18 preparative HPLC column (Waters) and eluted with gradient conditions starting with 95% 5 mM sodium phosphate (mobile phase A, pH7.4) and 5% acetonitrile (mobile phase B) and reaching 0% A and 100% B in 10 min at a flow rate of 12mL/min. Retention time of the product peak = 4.23 min during the gradient (0-100%B) in a 7

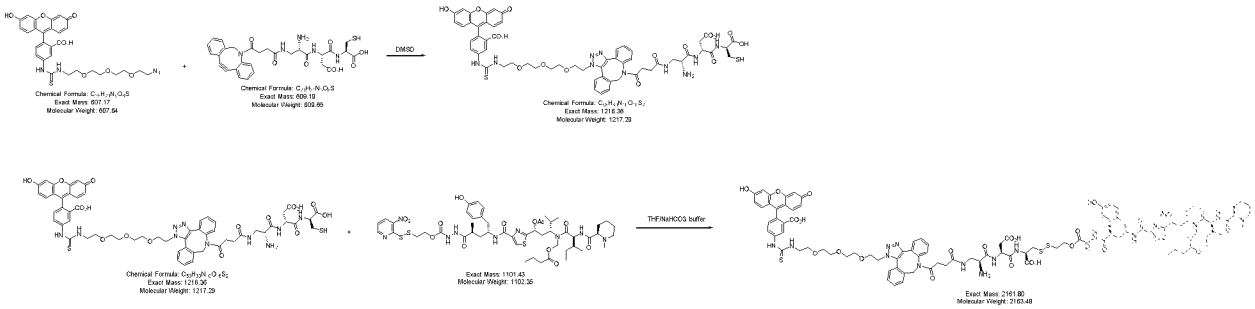
min analytical HPLC-MS analysis. ESI m/z = 1244.8. Abbreviations: FITC = fluorescein isothiocyanate; HPLC = High Performance Liquid Chromatography.

FITC-Tub

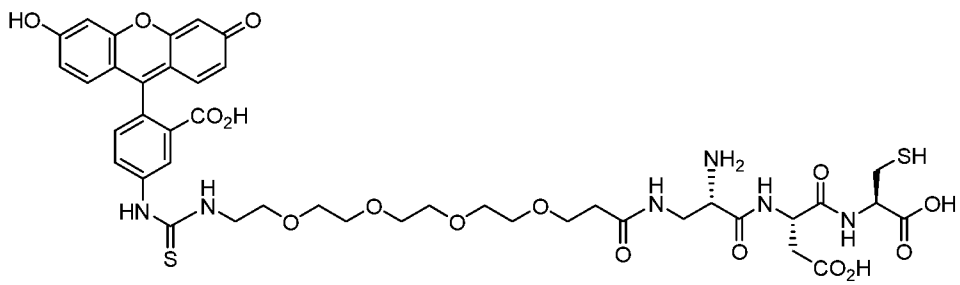


Chemical Formula: $C_{87}H_{117}N_{13}O_{27}S_4$
Exact Mass: 1903.71
Molecular Weight: 1905.20

Synthesis procedure:



FITC-EC20



Chemical Formula: $C_{42}H_{50}N_6O_{16}S_2$
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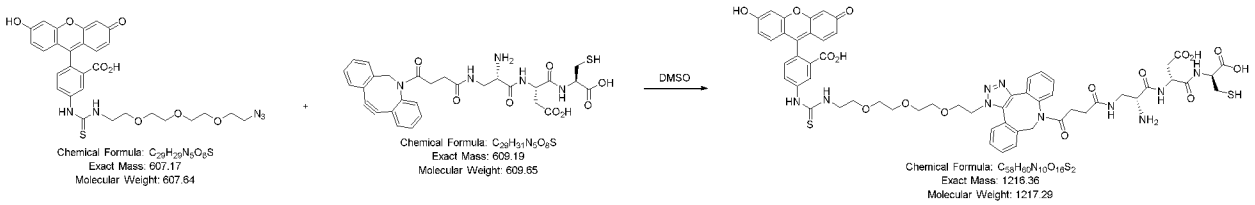
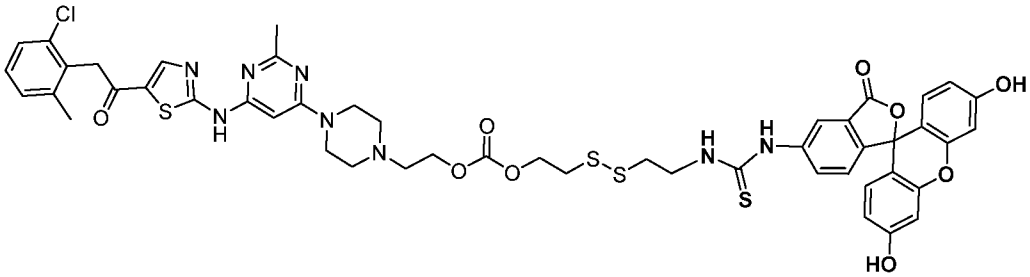
Synthesis procedure:

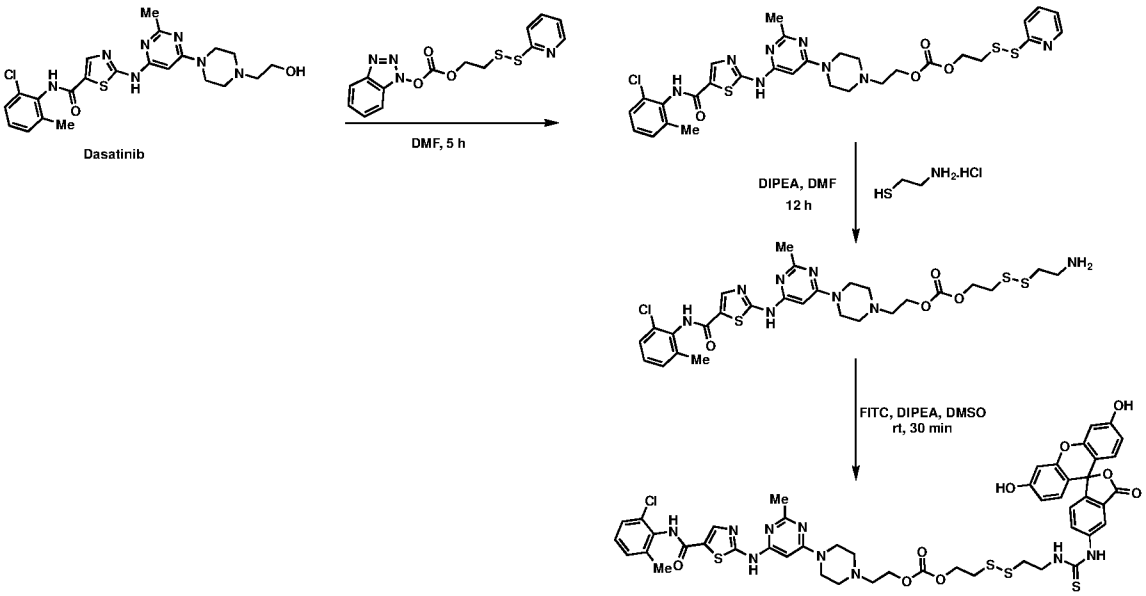


FITC-Dasatinib



Molecular Weight: 1055.65

Synthesis procedure:



The experiment procedure:

Cell culture

293TN cells were cultured in DMEM with 10% FBS, no antibiotic for lentivirus packaging. Raji and Jurkat cells were cultured in RPMI-1640 with 10% FBS, 10% Penicillin/Streptomycin. Primary human T cells were isolated from hPBMC using ficoll, enriched by negative selection with EasySep™ Human T Cell Enrichment Kit (19051, Stemcell Tech), activated by Dynabeads CD3/CD28 (11161D, Thermo Fisher) for 1 days, cultured with TexMACS medium supplemented with 30IU hIL2 (130-097-745, Miltenyi Biotec Inc.). T cells were cryopreserved in RPMI-1640 with 20% human AB serum (HP1022, Valley Biomedical) and 10% DMSO.

Lentivirus packaging

Pantropic VSV-G pseudotyped lentivirus was produced via transfection of 293TN cell with the transgene expression vector and packaging plasmid mix (CPCP-K2A, Cellecta) using Lipofectamine 2000. At 24h, viral supernatant was harvested, concentrated and then added to certain cell lines or the primary T cells that were thawed the same day. For T cell transduction, cells were centrifuged at 2500rpm for 90 mins, 37 degree after adding the virus supernatant and 8ug/ml polybrene.

Binding assay

For binding assay, cells were incubated with ligand-dye alone or with ligand-dye and free ligands (100x, preincubated for 30 min) for 30min, at 4 degree. Cells were washed 3 times after incubation, and re-suspended in 2% FBS PBS, 7-AAD were added to gate out the dead cells. FRET imaging of FK506-Rhodamine and FA-S0456: To understand the occupation of the fusion receptor, FKBP-FRa+ jurkat cells are incubated with FA/FA-S0456, FK506/FK506-Rhodamine at the indicated sequence and concentration. FRET is visualized by the loss of intensity of FA-Rhodamine as its energy transferred to FA-OTL38 on the same or nearby receptor, detected by BD Fortessa flow cytometer. Results were analyzed using FlowJo software.

PI-PLC treatment to release the GPI anchored protein

$1x10^5$ cells were incubated with 5mU or 50mU PI-PLC (P5542-5UN, Sigma) in digestion buffer (2% BSA) at 37 degree for 30 min; after incubation, cells were washed three times by PBS and then incubated with ligand-dye for 30min on ice.

Cell viability assay

Cells were seeded to 96 well plate and incubated with different concentration of certain ligand-cytotoxic drug for 2h, with or without 100x preincubation of the free ligand competition. After 2h incubation, cells were washed by warm medium 3 times and replenished with fresh medium. After 72h, cell number were tested by CellTiter-Glo® assay (G7570, Promega) or quantified by ligand-dye staining of receptor positive cell.

CAR T cell lysis effect

$1x10^5$ CAR T and certain number of Raji cell were co-incubated in 96 well plate, according to the E:T ratio, with or without the treatment drug. After 24h, 100ul supernatant were taken out for LDH assay. Lysis percentage were calculated as (treatment group – CAR T only)/(maximum lysis-CAR T only)%

Exhaustion of CAR T cell

$1x10^6$ Raji cell were repeated added to $1x10^6$ CAR T cell in 24 well plate every 12h, without changing the medium. Exhaustion status were characterized by lower lysis effect and higher expression of co-inhibitory molecules: PD-1, LAG-3 and Tim-3.

In vivo ablation of the fusion receptor positive CAR T by ligand-cytotoxic drug

$4x10^5$ luc+Raji cells were iv injected into the NSG mice. After 6 days, $1x10^7$ fusion receptor positive CAR T cells were iv injected. On Day 8, ligand-cytotoxic drug (0.5umole/kg, 1umole/kg) were iv injected once. IL2, INFr were measured by ELISA using serum sample taken every 3 days after the CAR T injection. CAR T cell in peripheral blood were counted by flow cytometry.

In vivo modulation of fusion receptor positive CAR T by ligand-drug

$4x10^5$ luc+Raji cells were iv injected into the NSG mice. After 6 days, $1x10^7$ fusion receptor positive CAR T cells were iv injected. On Day 7, ligand-drug drug (0.5umole/kg, 1umole/kg) were iv injected once. In the case of CAR T exhaustion model, $1x10^5$ CAR T were iv injection on Day 6, once the CAR T population were shown in peripheral blood and tumor burden is not stabilized and continue to increase, ligand-drug (0.5umole/kg, 1umole/kg) were iv injected.

In vivo imaging and tracking of fusion receptor positive CAR T

$2x10^6$ Raji were subcutaneously injected to the right should of NSG mice. 14 days later, $1x10^7$ fusion receptor positive CAR T were iv injected. On Day 16, animals were administrated 99mTc-bound conjugates (10 nmol, 150 μCi) by iv injection and imaged by SPECT imaging machine.

EXAMPLES

1. Design of fusion protein and its expression

1.1 Design of FKBP-FR fusion receptor (SEQ ID NO:2)

Synthesis of FK506 derivatives: FK506-Rhodamine and FK506-tubulysin Synthesis was described in materials and methods section.

hFRa is a GPI anchored membrane protein, which has 24 amino acids on the N terminal as a signal peptide. In order to preserve the membrane presentation and internalization property, we choose to use the full length of FRa, and incorporate the hFKBP sequence as well as a flexible peptide linker (SGGGS) between T24 and R25 of hFRa (Figure 4a). The flexible linker is chosen to be resistant to common enzyme digestions in human body. The whole sequence is then inserted into a pWPI lentivirus expression vector, with EF1a as the desired promoter for protein expression in transduced T cell.

1.2 Expression of FKBP-FR fusion receptor in transduced cells

Expression of FKBP-FRa is confirmed by western blot in lentivirus transduced K562. Transduced K562 cell lysis shows specific band around 50kDa compared to non-transduced cells against hFRa antibody (Figure 4b).

1.3 Construction of fusion protein of FKBPFR3GS (noted as FF3)

See Figure 4d (SEQ ID NO:12) . From N terminal to C terminal it has 1-24 aa of human FRa as the signal peptide, human FKBP protein, three Gly-Ser linker and then 2-258 aa of human FRa. In a construct design of FKBPFR1GS (noted as FF1), the three Gly-Ser linker of FF3 is substituted with one Gly-Ser linker with other parts unchanged. As will be shown in the binding assays, increasing linker length reduces the interference between the two components in the fusion protein.

1.4 Construction of fusion protein of FITC-svFv-FR with GS linker.

See Figure 4e. The construct is also named as 4M5.3 FR (SEQ ID NO:13). From N-terminal to C-terminal, it has hCD8 signal peptide, svFv of 4M5.3 (against FITC), GS linker, 25-258 aa of human FRa.

1.5. In vivo noninvasive tracking of FKBP-FRa/FKBPtFRa positive cells by FK506-99mTc

PET imaging

For CAR T cell model, $1x10^6$ KB cells are subcutaneously implanted in NSG (Jackson laboratory). After the tumor reaches $100mm^3$, 15 million anti-FITC CAR+ FKBP-FRa+ or anti-FITC CAR+ FKBP-FRa- human T cells are intravenously injected to the mice. FITC-FA is injected at the indicated days to induce the proliferation of the CAR T. Mice are imaged every two days after the CAR T implantation by the following procedure. At the day of imaging, FK506-EC20 head is formulated with 99mTc according to previous report. 200uCi 99mTc in 100ul solution is i.v. injected to each mouse and whole body image is taken by MiLab PET/CT, focusing on the tumor area, spleen and lymph nodes. 3D images are reconstructed by PMOD software. After the last imaging at around day 10 after CAR T implantation, mice are euthanized and 99mTc distribution in each organ are counted by gamma counter.

For Hematopoietic Stem Cell transplantation model, humanized NSG mice are generated as reported before. 10 million CD34+ FKBP-FRa+ hHSC are i.v infused into the humanized NSG mice. 4 months later, whole body image is taken using FK506-99mTc as mentioned above, focusing on the bone marrow and spine.

2. FKBP-FRa fusion receptor specifically binds and internalizes FK506-payload

2.1 FKBP-FRa fusion receptor specifically binds FK506-Rhodamine

For binding assay, cells were incubated with ligand-dye alone or with ligand-dye and free ligands (100x, preincubated for 30 min) for 30min, at 4 degree. Cells were washed 3 times after incubation, and re-suspended in 2% FBS PBS, 7-AAD were added to gate out the dead cells. BD Fortessa flow cytometer were used. Results were analyzed using FlowJo software.

2.2. Binding of FK506-Rhodamine by FKBP-FRa fusion receptor (FRET imaging of FK506-Rhodamine and FA-S0456)

To understand the occupation of the fusion receptor, FKBP-FRa+ jurkat cells are incubated with FA/FA-S0456, FK506/FK506-Rhodamine at the indicated sequence and concentration. FRET is visualized by the loss of intensity of FA-Rhodamine as its energy transferred to FA-OTL38 on the same or nearby receptor, detected by BD Fortessa flow cytometer.

Figure 5 shows binding of Folate acid in FKBPFR1GS fusion protein blocks the binding of FK506-Rhodamine at as low as 0.01nM and totally abolishes FK506 Rhodamine binding at 50nM.

Figure 6 shows FKBPFR1GS jurkat cells have decreased FK506-Rhodamine intensity after

binding to OTL38, a folate receptor targeted dye. FRET from FK506-Rhodamine (donor) to OTL38 (FA-S0456, acceptor, ex/em:774/794nm) indicates the interaction between FR and FKBP within the fusion receptor.

Figure 7 shows increasing the linker length between FKBP and FR significantly lowers the interference between the two components of the fusion protein. Compare to FF1 (1GS between FKBP and FR), FF3 (3GS between FKBP and FR) preserves the binding of FK506-Rhodamine in the presence of 10nM FA, which is comparable to the physiological concentration of FA in human body.

2.3. Release of GPI anchored FF3 fusion receptor

Using PI-PLC treat T cells having FF3 fusion protein resulted the release of GPI anchored receptor FF3. Jurkat T cell with FF3 fusion receptor shows saturated binding with 20nM FA-FITC (EC17), while after 5mU PI-PLC or 50mU PI-PLC treatment, the FA-FITC loses binding to the cell, which indicates the release of the GPI anchored FF3 fusion receptor. See Figure 8.

2.4 Fusion protein FKBPFR3GS in human T cell retains FR binding property

FA-Rhodamine binding curve is shown in FKBPFR3GS fusion receptor. FKBPFR3GS fusion receptor that stably expressed on human T cell can bind to folate acid derivative (FA-Rhodamine) with high affinity (Kd=0.95nM), which is comparable to the affinity of FA-Rhodamine in FR+ KB cell (Kd around 1nM). Therefore, the binding property of FR in the fusion receptor is preserved. See Figure 9.

2.5 Fusion protein FKBPFR3GS in human T cell retains FKBP binding property

FK506-Rhodamine binding curve in FKBPFR3GS fusion receptor. FKBPFR3GS fusion receptor that stably expressed on human T cell is able to bind to FK506 derivative (FK506-Rhodamine) with high affinity (Kd=3.93nM), which means the binding property of FKBP in the fusion receptor is preserved. See Figure 10.

2.6 SLF-FITC binds to FKBPFR3GS fusion receptor with relative high binding affinity (Kd=62nM)

Competition of free SLF (100, preincubation) blocks SLF-FITC binding. SLF, a mimic of FK506, presents a 10 times lower binding affinity to FKBPFR fusion receptor, compared to the parent ligand FK506. See Figure 11 and compare with Figure 10.

2.7 Binding curve of FA-Rhodamine in 4M5.3FR fusion receptor.

FA-Rhodamine can bind to 4M5.3FR fusion receptor that stably expressed on human T cell with high affinity (Kd=2.25nM), which is comparable to the affinity of FA-Rhodamine in FR+ KB cell (Kd around 1nM). Therefore, FR binding property is preserved in 4M5.3FR fusion receptor. See Figure 12.

2.8 FITC-AF647 binding curve in 4M5.3FR fusion receptor.

FITC-AF647 can bind to 4M5.3FR fusion receptor that stably expression on human T cell with high affinity (Kd=8.03nM). 100x comp indicates free FITC sodium. The binding property of scFv 4M5.3 with FITC is preserved in 4M5.3FR fusion receptor. See Figure 13.

3.1. FA-Tubulysin killing effect against FF3+ human T cell

FA-Tubulysin is able to mediate a receptor specific killing effect against FF3+ human T cell. Compensation with FA (100x preincubation with FA) blocks the effect. This implies the successful internalization and release of the free drug Tubulysin through the FF3 fusion receptor system. See Figure 14.

3.2 FA-Tubulysin killing effect against hFF3 + population in a mixed human T cell culture.

FA-Tubulysin specifically kills the hFF3+ population in a mixed human T cell culture. Percentage of hFF3+ cell decrease as the FA-Tub concentration increases. See Figure 15.

3.3 SLF-Tub specifically kill the hFF3+ Jurkat cells with a IC_{50} = 138nM.

2h incubation of SLF-Tub with hFF3 Jurkat cells is able to kill the receptor positive cells.This indicates the successful internalization of SLF-Tub by the FKBPFR3GS fusion receptor and the release of the Tubulysin inside the cell. See Figure 16.

3.4. FITC-DM4 and FITC-Tub killing effects against 4M5.3FR+ human T cells

Both FITC-DM4 and FITC-Tub can specifically kill the 4M5.3FR+ human T cells, while FITC-Tub has a higher IC_{50}. Compensation of free FITC sodium (100x preincubation) blocks the receptor mediated killing effect. This implies the successful internalization and release of FITC-cytotoxic drug into T cell through 4M5.3FR fusion receptor. See Figure 17.

3.5. FITC-Tubulysin specifically kill the 4M5.3FR+ population in a mixed human T cell culture.

Absolute number of 4M5.3FR+ cell decrease as the FITC-Tub concentration increases, while 4M5.3FR- cells are killed also through released drugs and bystander effect at high concentration. See Figure 18.

3.6. FITC-DM4 specifically kill the 4M5.3FR+ population in a mixed human T cell culture.

Absolute number of 4M5.3FR+ cell decrease as the FITC-DM4 concentration increases, while 4M5.3FR- cells are killed also through released drugs and bystander effect at high concentration. See Figure 19.

3.7 Kinase inhibitors modulation effect on anti CD19 CAR T cells against CD19+ Raji

Dasatinib (Lck inhibitor) and Ibrutinib (ITK inhibitor) at 10nM concentration decrease the lysis effect of antiCD19 CAR T cell (FMC63 CAR T, Effector) against CD19+ Raji tumor cell (Target). Two Effector: Target ratio (E:T) have been tested. Normal T cell and antiCD19 CAR T with CD19- K562 cell were used as negative control. See Figure 20.

3.8. FITC-Dasatinib can decrease the lysis effect of FMC63+4MFR+hT cell towards Raji cell.

This implies the successful internalization and release of FITC-Dasatinib into T cell through 4M5.3FR fusion receptor and the release of Dasatinib into T cell. See Figure 21.

3.9 TC-PTP inhibitor at 100nM concentration decrease the co-inhibitor molecule population in exhausted antiCD19 CAR T cell

Exhausted antiCD19 CAR T cells are generated by 7 times of stimulation with CD19+Raji cells, see detailed procedure in material and methods section). PD-1 positive, LAG3 positive and double positive population decreases upon treatment. See Figure 22.

4. Other FK506-payload to control the activity of cell therapy

The technical advantageous feature of this drug payload delivery system is to have multi-functionality. The potential payloads and corresponding effects are listed below (Table 1). The small molecule payloads are selected based on the following parameters**:** 1. the functionality assay of the free drug, both in vitro and in vivo, has been confirmed by either published literature or work in our lab. 2. The chemical structure of the drug has relatively more accessible free amine for derivatization. 3. Any of the following will be preferable: FDA proved drug; commercially available for reasonable price. The FK506-payload will be tested first for in vitro

experiments, T cell activation and stem cell cytokine release will be monitored by multiplex immunoassays. For in vivo disease models, we have well established CAR T therapy and bone fracture mouse models in our lab, and several potential collaborators for the neurodegenerative mouse models.

Disease model	Subtype	Cell type	Cell source	Payload type
stem cell therapy	HSC transplant	BMSC	Murine BM	GSK3b inhibitor
Tumor	tumor microenviroment	CAR T	hPBMC T cell	GSK3b inhibitor, HDAC inhibitor, MAPK inhibitor

Reference to any prior art in the specification is not an acknowledgement or suggestion that this prior art forms part of the common general knowledge in any jurisdiction or that this prior art could reasonably be expected to be combined with any other piece of prior art by a skilled person in the art.

By way of clarification and for avoidance of doubt, as used herein and except where the context requires otherwise, the term "comprise" and variations of the term, such as "comprising", "comprises" and "comprised", are not intended to exclude further additions, components, integers or steps.

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CLAIMS

1. A drug delivery platform for cell therapy, comprising:
   a. an engineered protein on a target cell for transplant, wherein the engineered protein comprises a first component and a second component, the first component and the second component are connected by a peptide linker, the first component is a non-membrane protein, the second component is a membrane anchored peptide or protein;
   b. at least one small ligand conjugated to a linker, wherein the at least one small ligand has intrinsic high affinity to at least one component of the engineered protein; and
   c. at least one payload of drug conjugated to the linker, wherein the payload of drug is associated with the target cell when the small ligand binds to at least one component of the engineered protein.

2. The drug delivery platform according to claim 1, wherein the payload of drug is any one of: an imaging agent, a cytotoxic drug, a modulator of gene expression, or a modulator of the cell's activity.

3. The drug delivery platform according to claim 2, wherein the imaging agent is selected from the group consisting of fluorescent dye rhodamine, fluorescein, and S0456, radioisotope chelating imaging moieties, EC 20 chelating head, NOTA and DOTA.

4. The drug delivery platform according to claim 2, wherein the cytotoxic drug is selected from the group consisting of tubulysin, DM1, DM4, and an auristatin.

5. The drug delivery platform according to claim 2, wherein the modulator of gene expression is selected from the group consisting of Dasatinib, MEK1/2 inhibitor, PI3K inhibitor, HDAC inhibitor, kinase inhibitor, metabolic inhibitor, GSK3 beta inhibitor, MAO-B inhibitor, Cdk5 inhibitor, or an RORγt agonist.

6. The drug delivery platform according to any one of claims 1-5, wherein the payload of drug is a siRNA mi181a1, a phosphatase inhibitor including but not limited to inhibitors against SHP1/2 or TC-PTP and/or wherein the payload of drug is further

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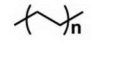
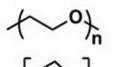
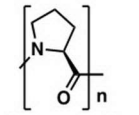
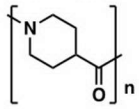
internalized by the target cell when the small ligand binds to at least one component of the engineered protein.

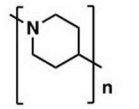
7. The drug delivery platform according to any one of claims 1-6, wherein the linker to connect the small ligand and the payload drug is selected from the group consisting of

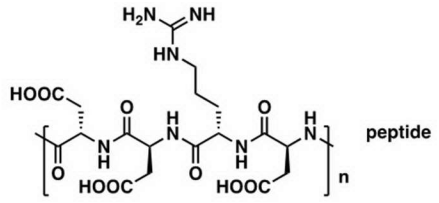


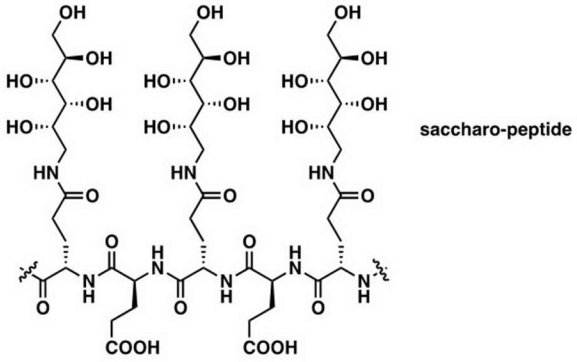












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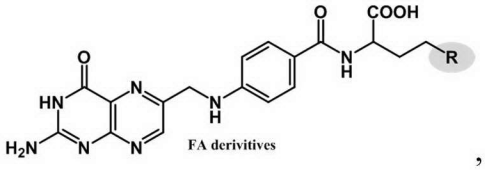
8. The drug delivery platform according to any one of claims 1-7, wherein the engineered protein components are selected from the group consisting of Folate Receptor alpha (FRa), Folate Receptor beta (FRb), Urokinase receptor (uPAR), FK506 binding protein (FKBP), dihydrofolate reductase (DHFR), Single Chain Fragment Variable against Fluorescein isothiocyanate (scFv against FITC), and Single Chain Fragment Variable against dinitrophenol (scFv against DNP).
9. The drug delivery platform according to any one of claims 1-8, wherein the small ligand is selected from the group consisting of 

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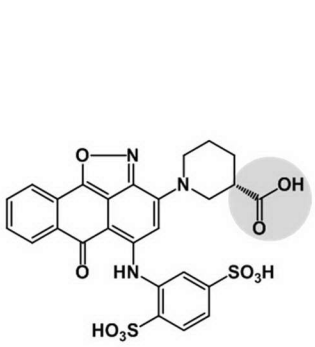

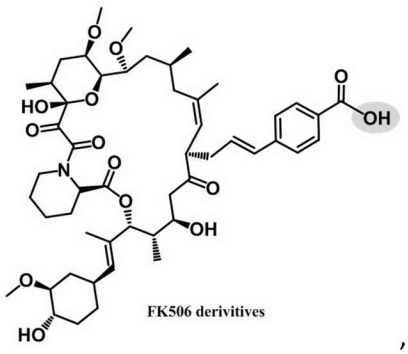

FK506 derivitives

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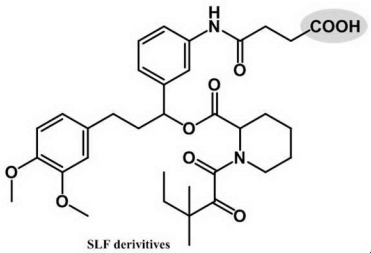

SLF derivitives

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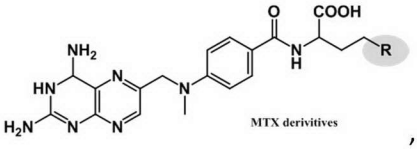

MTX derivitives

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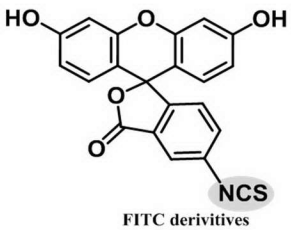
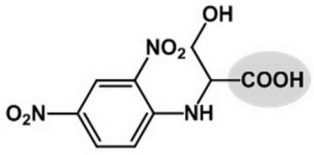


FITC derivitives



DNP-Ser

and .

10. The drug delivery platform according to any one of claims 1-9, wherein the first component is FKBP, and the second component is a peptide that confers a glycosylphosphatidyl inositol (GPI) anchor on the first component, and the small ligand is FK506 or its derivative.
11. The drug delivery platform according to claim 10, wherein the second component is a full length or truncated Folate Receptor (FR).
12. The drug delivery platform according to any one of claims 1-11, wherein the peptide linker is at least one segment of SGGGS.
13. The drug delivery platform according to any one of claims 1-12, wherein the engineered protein is selected from the group consisting of SEQ ID NOS:1 -2 or SEQ ID NOS:12-15.

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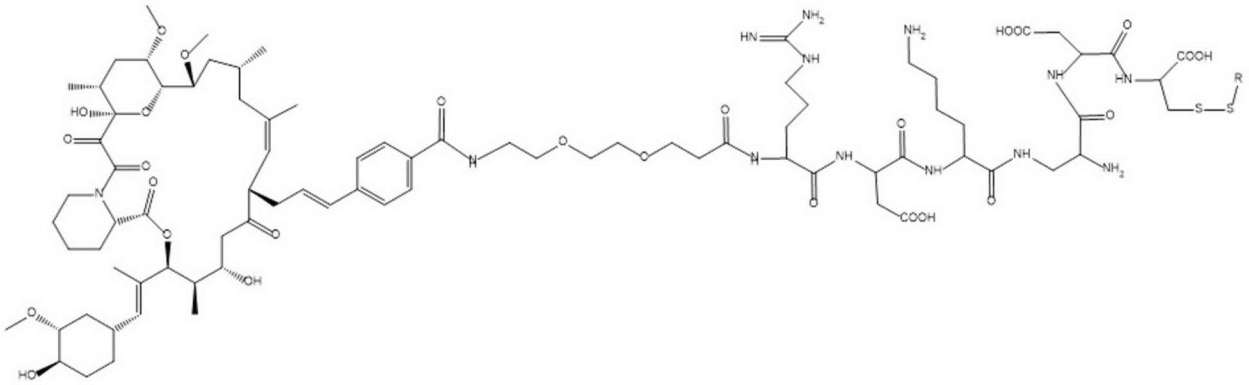
14. The drug delivery platform according to any one of claims 1-13, wherein the target cell for transplant is (i) an immune cell or (ii) a stem cell, a progenitor cell or a transplanted cell designed to synthesize a biochemical that is deficient in a patient.
15. The drug delivery platform according to claim 14, wherein the immune cell is a chimeric antigen receptor (CAR) T cell.
16. The drug delivery platform according to claim 15, wherein the CAR T cell expresses an amino acid sequence selected from SEQ ID NOS: 3-4.
17. The drug delivery platform according to any one of claims 1-16, wherein the small ligand conjugate has formula I.



I

18. The drug delivery platform according to any one of claims 1-17, wherein the small ligand is further conjugated to a fluorescent dye or radioactive probe, a regulator of endogenous gene expression, or to a regulator of a transduced transgene expression.
19. Use of the drug delivery platform according to any one of claims 1-18 in the manufacture of a medicament for modulating cell therapy effect, wherein:
    a. a target cell identified for transplant is to be contacted with the drug delivery platform;
    b. the transplanted target cell has a cell therapy function; and
    c. the payload drug is released within the target cell and modulates the target cell therapy function.
20. A method to modulate cell therapy effect, comprising:
    a. Identifying a target cell for transplant, wherein the transplanted target cell has a cell therapy function;

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b. Providing an engineered protein on the surface of the target cell for transplant, the engineered protein comprises a first component and a second component, the first component and the second component are connected by a peptide linker, the first component is a non-membrane protein, the second component is a membrane anchored peptide or protein;

c. Providing a payload of drug conjugate to the target cell, wherein the payload of drug is conjugated to a small ligand through a linker, and optionally conjugated to a fluorescent dye, wherein the small ligand binds to at least one component of the engineered protein with high affinity and is internalized by the target cell together with the payload of drug;

d. releasing the payload drug within the target cell to modulate the target cell therapy function.

21. The method or use according to claim 19 or 20, wherein the cell therapy function is (i) to provide optically guided surgery to a subject, (ii) to control the target cell proliferation, or (iii) to execute cytotoxicity to the target cell engaged cancer cell.

22. The method or use according to any one of claims 19-21, wherein the payload of drug is: (i) an imaging agent selected from flurescent dye of Rhodamine and FITC, (ii) a radioisotope imaging agent selected from EC20 chelating head, NOTA and DOTA, (iii) a cytotoxic drug selected from the group consisting of Tubulysin, DM1, DM4 and auristatin, (iv) a modulator of gene expression selected from kinase inhibitors consisting of Dasatinib, MEK1/2 inhibitor and PI3 Kinase inhibitor, or an siRNA of mi181a1 or (v) a phosphatase inhibitor, including but not limited to inhibitors against SHP1/2, TC-PTP.

23. The method or use according to any one of claims 19-22, wherein the transplanted target cell comprises an engineered protein selected from the group consisting of SEQ ID NOS: 12-15.

24. The method or use according to any one of claims 19-23, wherein the the engineered protein components are selected from the group consisting of FRa, FRb, uPAR, FKBP, DHFR, scFv against FITC, and scFv against DNP.

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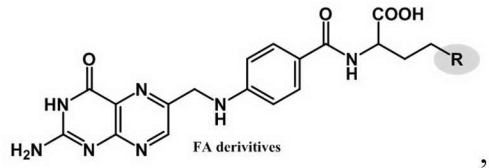
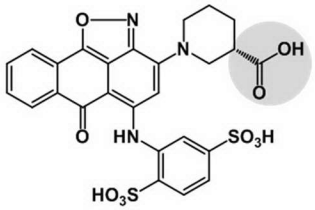
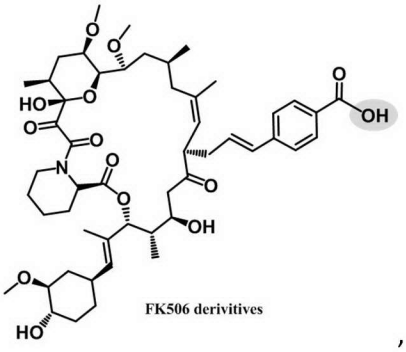
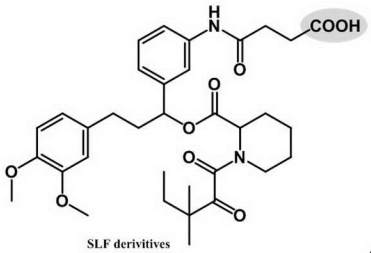
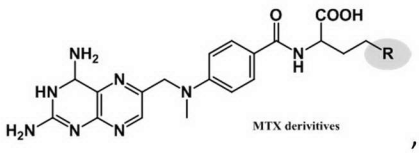
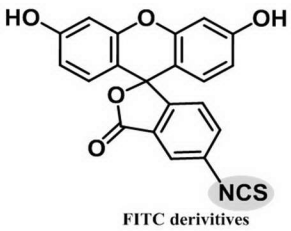
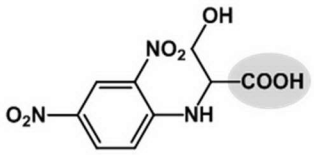
25. The method or use according to any one of claims 19-24, wherein the small ligand is selected from the group consisting of 

, 
, 

, 

, 

, 



and .

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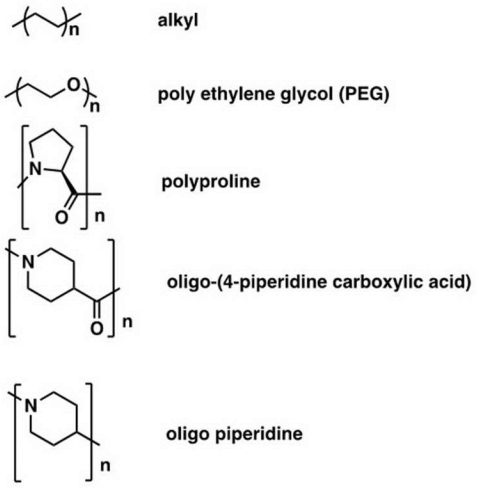
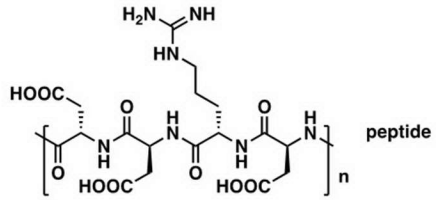
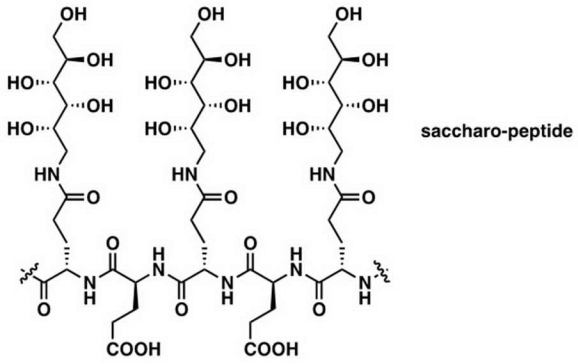
26. The method or use according to any one of claims 19-25, wherein the linker to connect the small ligand and the payload drug is selected from the group consisting of

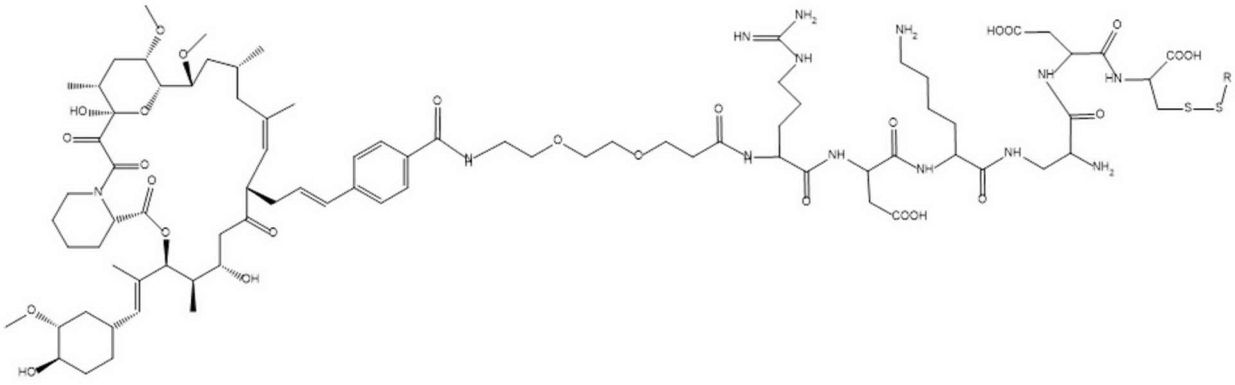






27. The method or use according to any one of claims 19-26, wherein the transplanted target cell comprises an engineered FKBP-LINKER-FRa fusion protein selected from the group consisting of SEQ ID NO: 1 and SEQ ID NO: 2.

28. The method or use according to any one of claims 19-27, wherein the drug conjugate FK506-releasable linker comprises formula I, wherein the binding domain of FK506 has an affinity to FKBP of about 100pM.



I

29. The method or use according to any one of claims 19-28, wherein the target cell for transplant is (i) an immune cell, (ii) a CAR T cell, (iii) or a stem cell, a progenitor cell, or a transplanted cell designed to synthesize a biochemical that is deficient in a patient.

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30. The method or use according to claim 29, wherein the CAR T cell comprises an engineered anti-CD19 CAR T construct selected from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 4.
31. The method or use according to claim 29 or 30, wherein the target cell for transplant is a CAR T cell, and the drug conjugate is (i) designed to control a cytokine storm induced by the transplanted CAR T cellor (ii) contains a modulator designed to control unwanted T cell proliferation.
32. The method or use according to claim 29, wherein the immune cell is a NK cell and the drug conjugate is a RORγt agonist to control Th17 cell mediated immune responses.
33. An isolated cell comprising the drug delivery platform according to any one of claims 1-18, wherein the cell is an immune cell.
34. An isolated cell according to claim 33, wherein the immune cell is a CAR-T cell.
35. Use of an isolated cell according to claim 33 or 34 in the manufacture of a medicament for treating cancer.

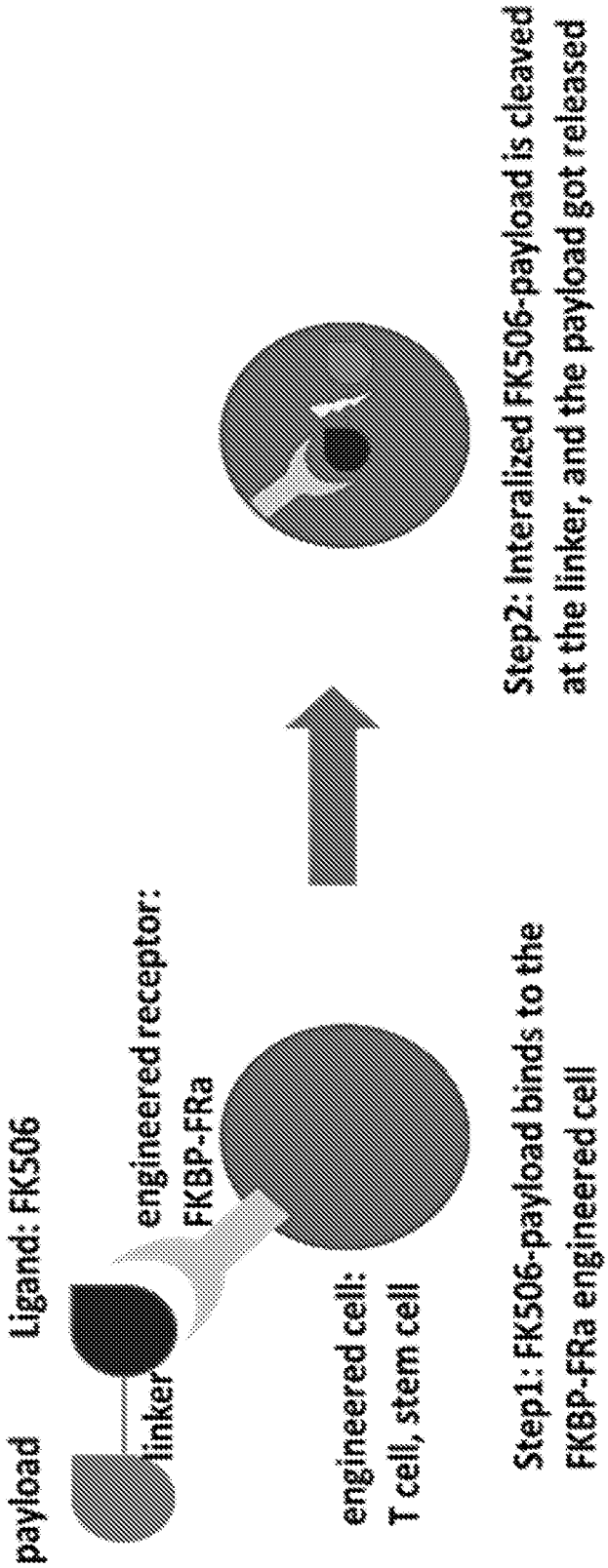

payload
linker
Ligand: FK506
engineered receptor:
FKBP-FRa
engineered cell:
T cell, stem cell
Step1: FK506-payload binds to the
FKBP-FRa engineered cell
Step2: Interalized FK506-payload is cleaved
at the linker, and the payload got released

FIG. 1A

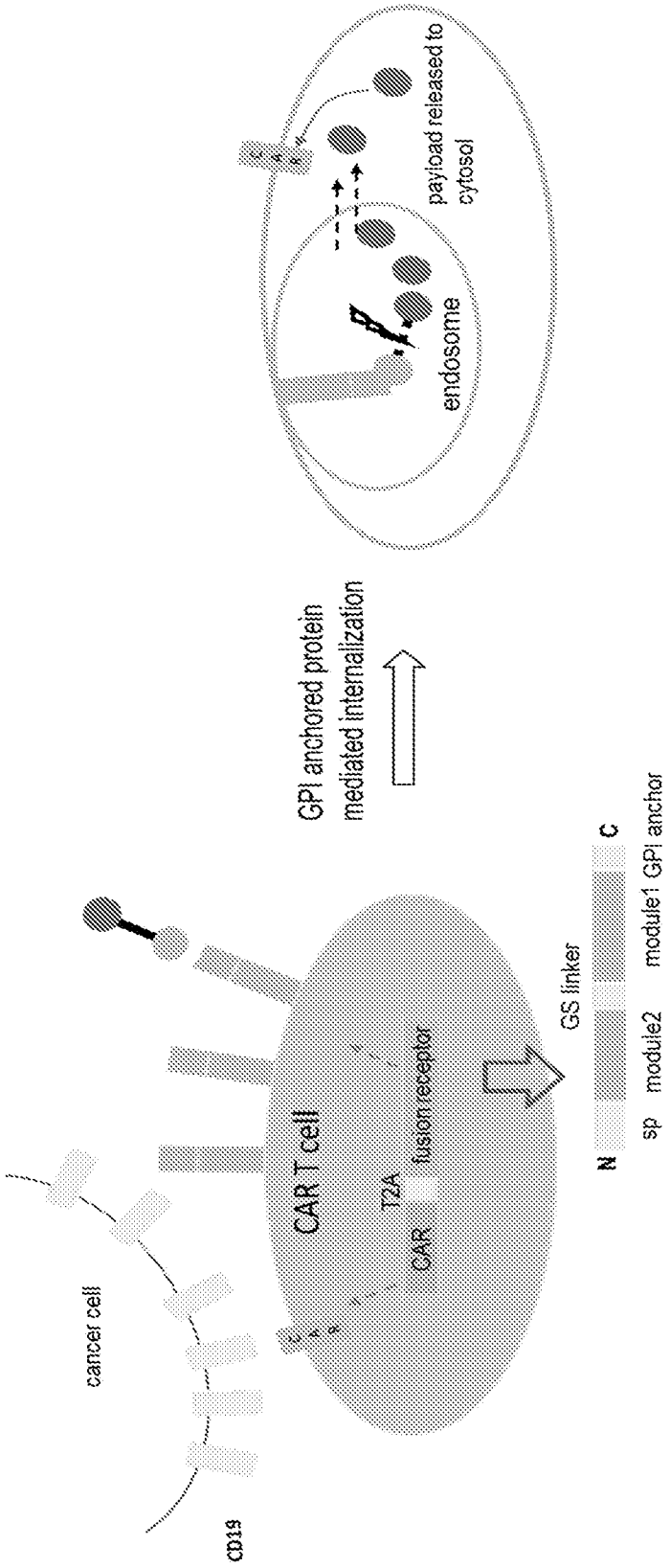

payload released to cytosol
endosome
GPI anchored protein mediated internalization
CAR T cell
T2A
CAR
fusion receptor
GS linker
N
C
sp
module2
module1
GPI anchor
cancer cell
CD19

FIG. 1B

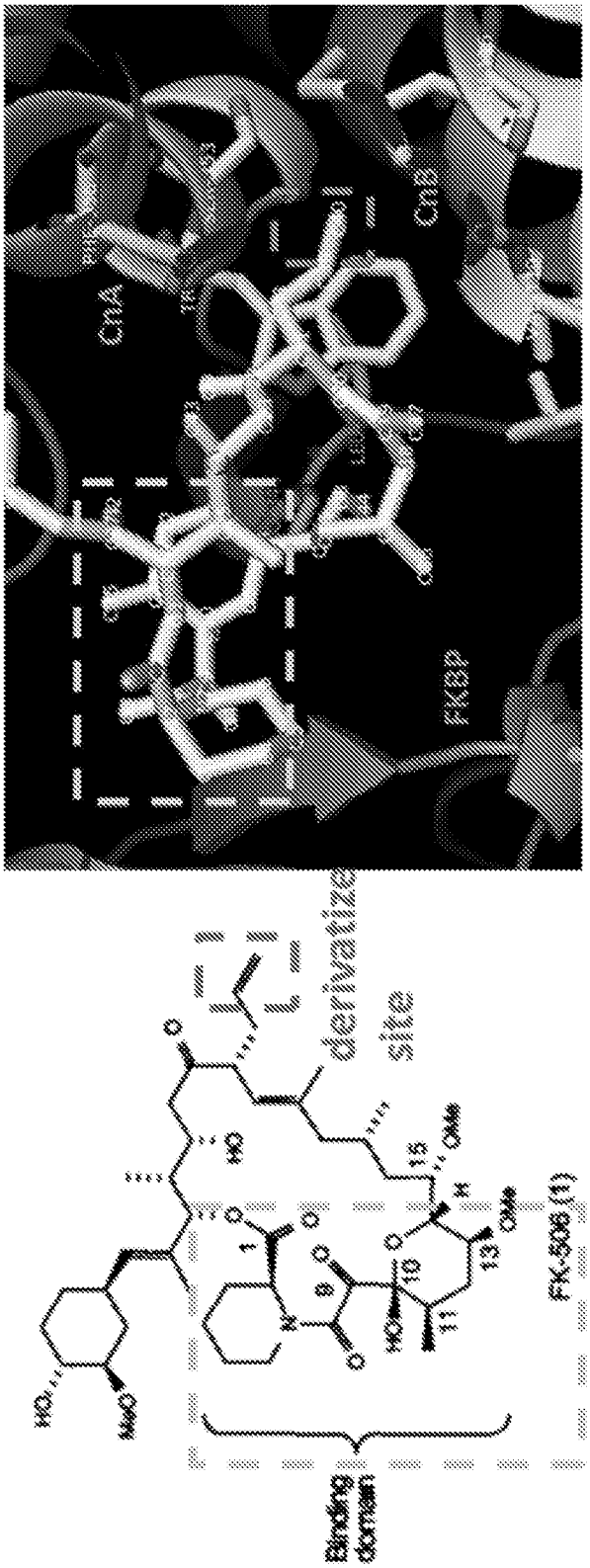


FIG. 2A

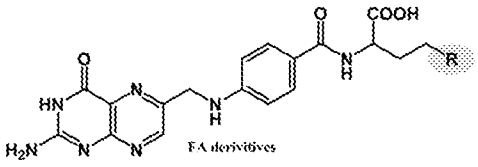
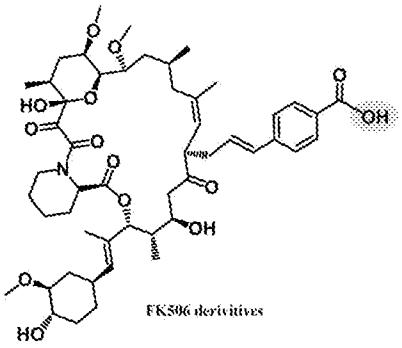
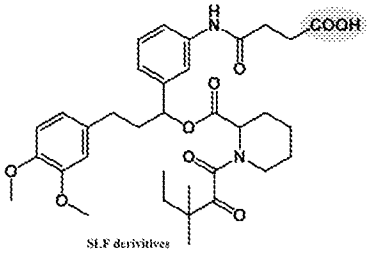
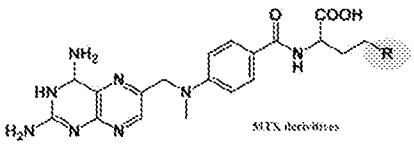
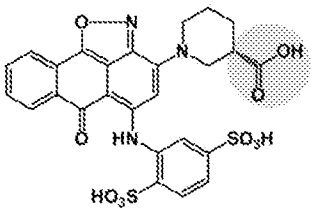
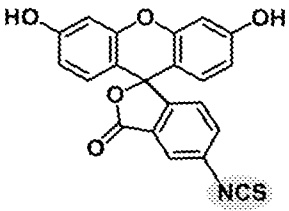
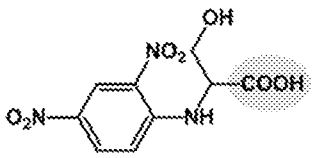
Module1: GPI anchored protein		Module 2	
Protein	Ligand	Protein	Ligand
FRa	 FA derivitives	FKBP	 FK506 derivitives
			 SLF derivitives
FRb		DHFR	 MTX derivitives
uPAR		scFv against FITC	 FITC derivitives
		scFV against DNP	 DNP-Ser

FIG. 2B

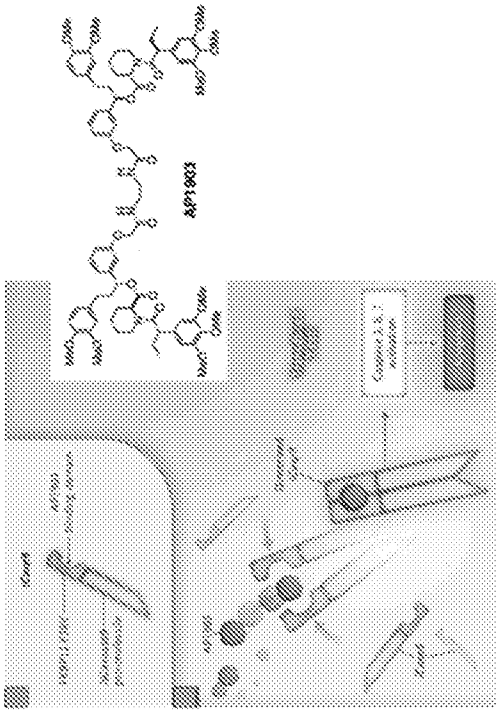
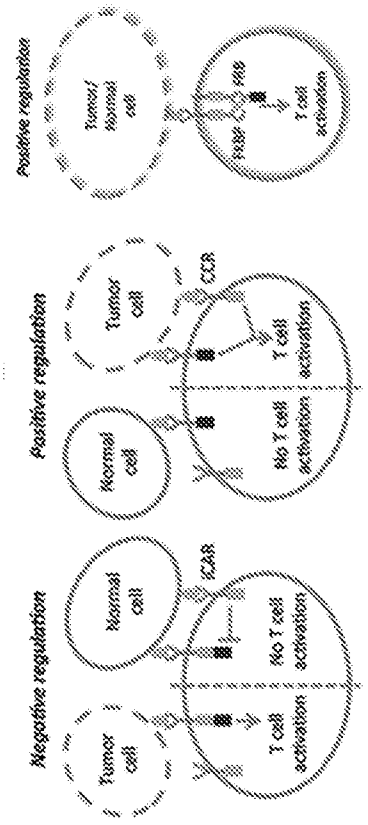


FIG. 3


Positive regulation
Tumor/ Normal cell
T cell activation
Positive regulation
Tumor cell
CCR
Normal cell
T cell activation
No T cell activation
Negative regulation
Normal cell
ICAR
Tumor cell
T cell activation
No T cell activation

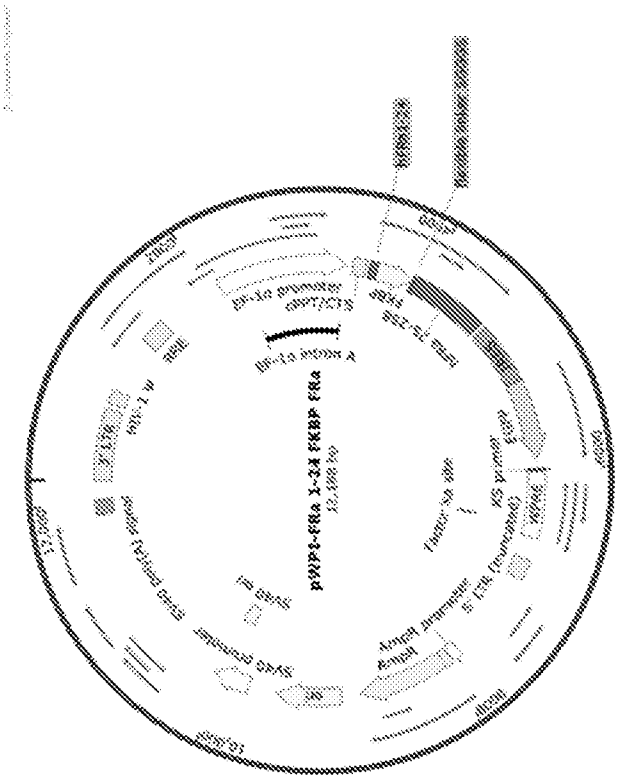

pWPI-FRa 1-34 FKBP FRa
10,189 bp

FIG. 4A

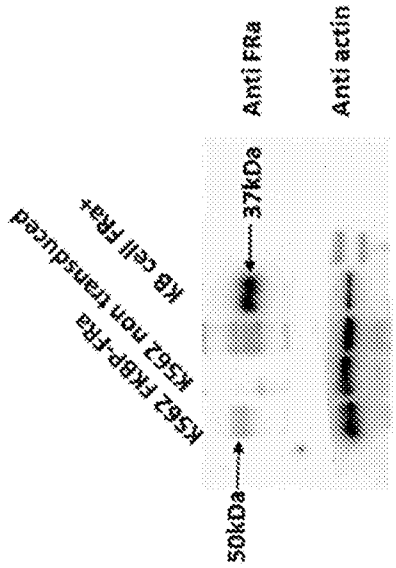

Anti FRa
Anti actin
37kDa
50kDa
K562 FKBP-FRa
K562 non transduced
KB cell FRa+

FIG. 4B

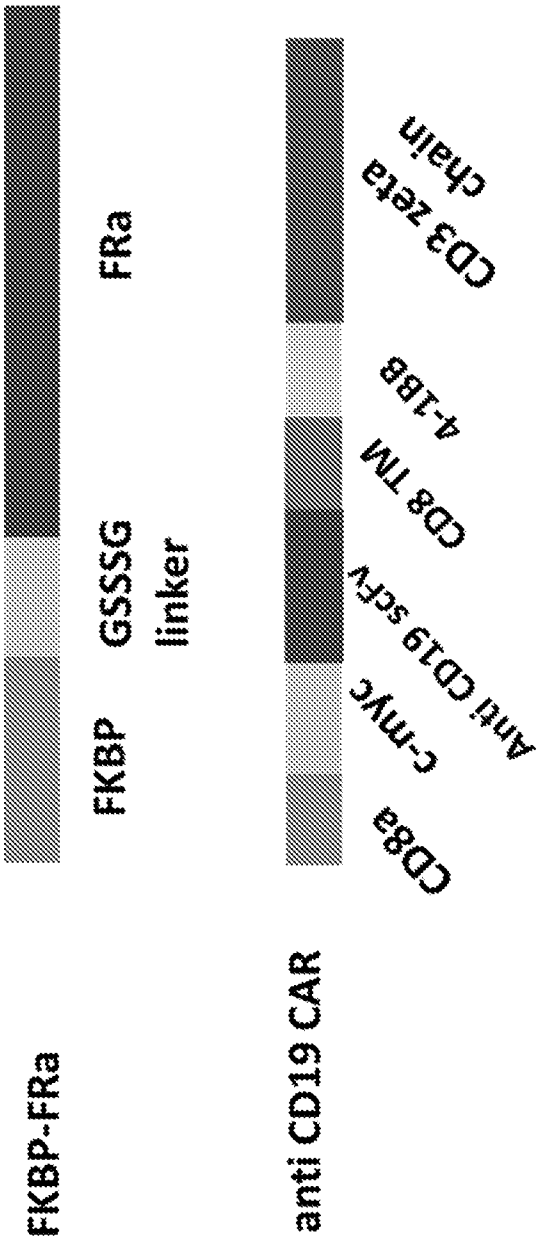

FKBP-FRa
FKBP
GSSSG linker
FRa
anti CD19 CAR
CD8a
c-myc
Anti CD19 scFv
CD8 TM
4-1BB
CD3 zeta chain

FIG. 4C

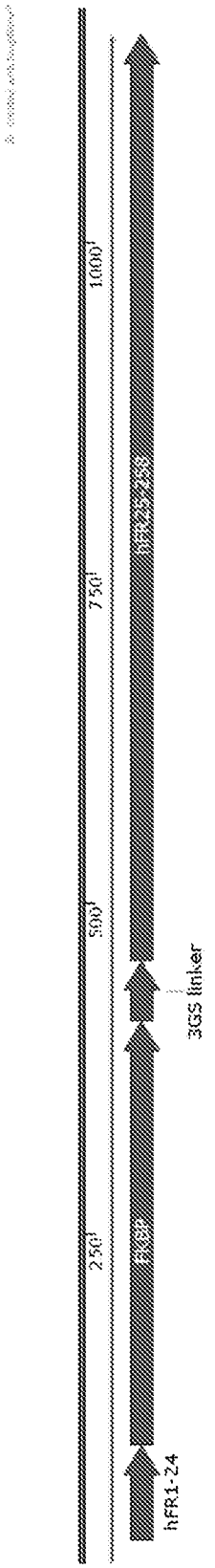

250
500
750
1000
hFR1-24
3GS linker

FIG. 4D

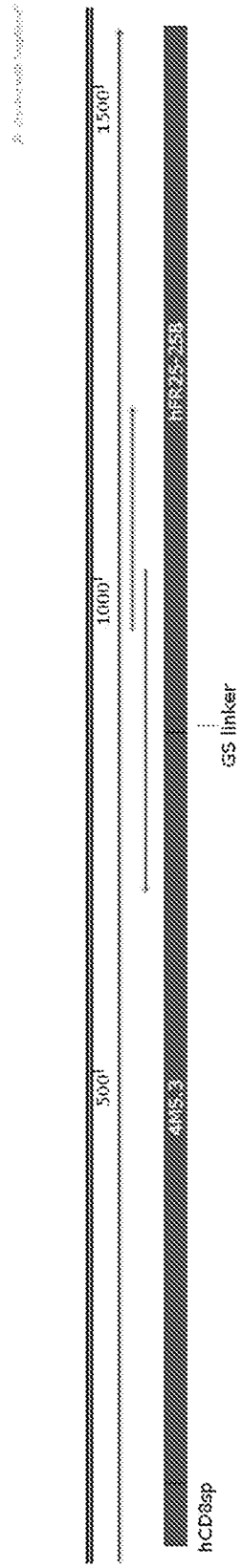

500
1000
1500
GS linker
hCD8sp

FIG. 4E

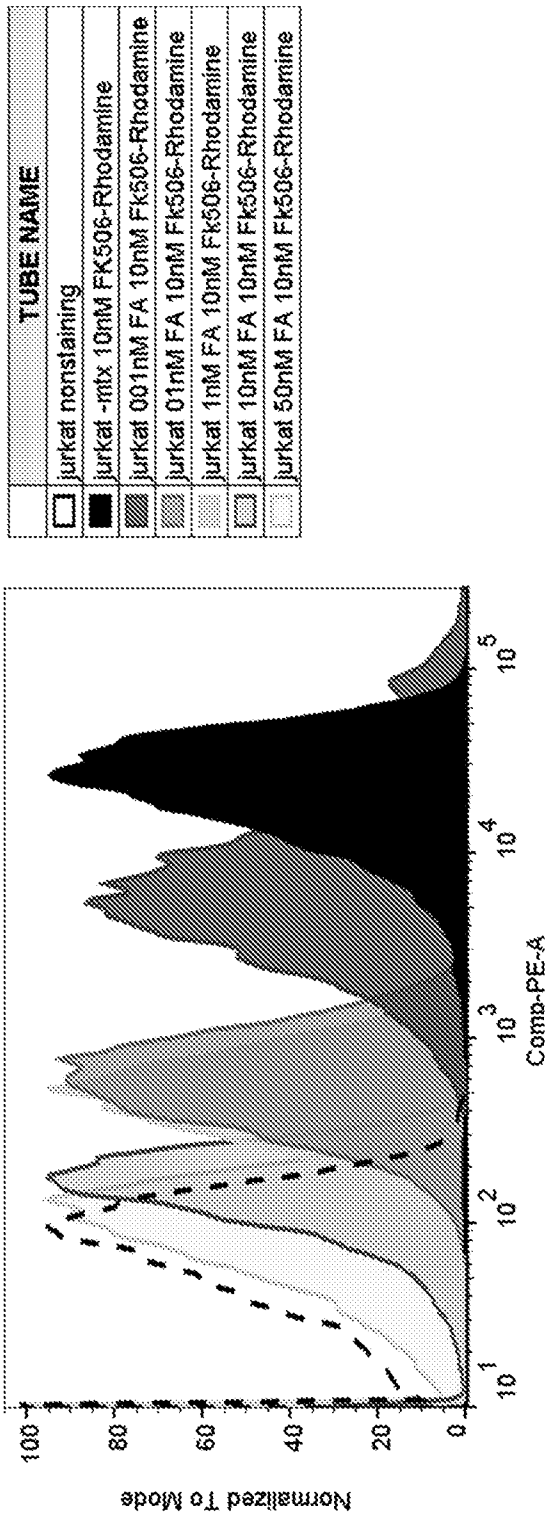

TUBE NAME
jurkat nonstaining
jurkat -mtx 10nM FK506-Rhodamine
jurkat 001nM FA 10nM Fk506-Rhodamine
jurkat 01nM FA 10nM Fk506-Rhodamine
jurkat 1nM FA 10nM Fk506-Rhodamine
jurkat 10nM FA 10nM Fk506-Rhodamine
jurkat 50nM FA 10nM Fk506-Rhodamine
Normalized To Mode
100
80
60
40
20
0
10^1
10^2
10^3
10^4
10^5
Comb-PE-A

FIG. 5

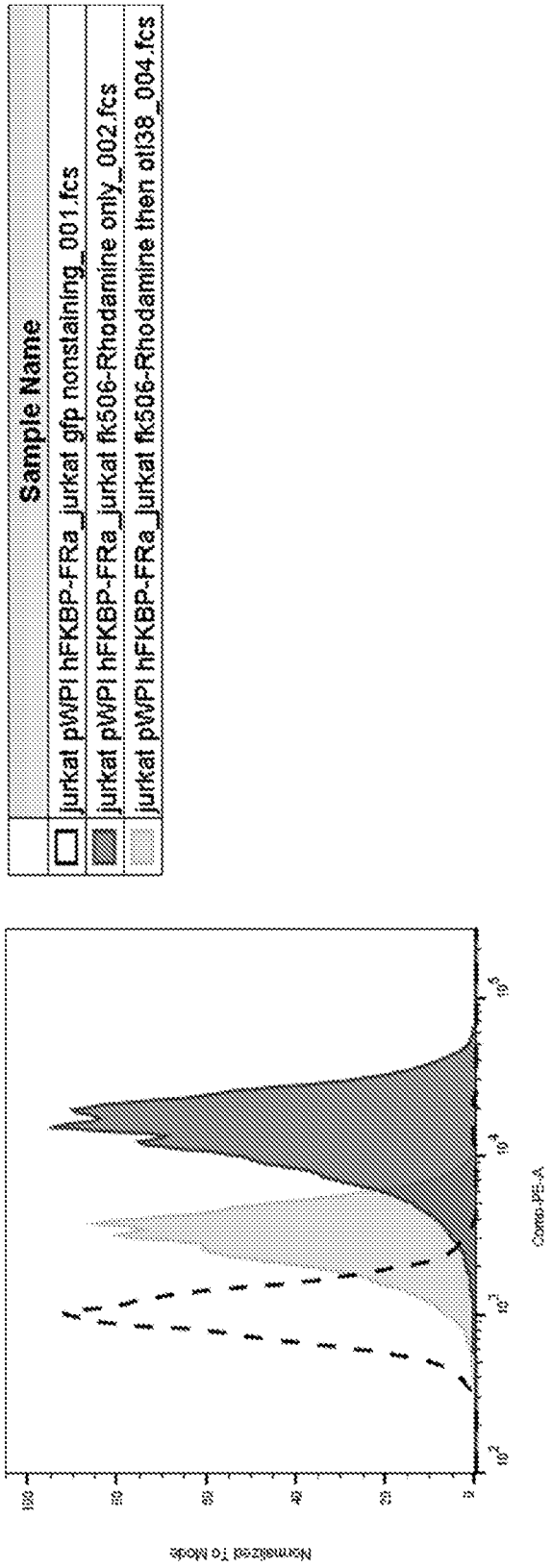

Sample Name
jurkat pWPI hFKBP-FRa_jurkat gfp nonstaining_001.fcs
jurkat pWPI hFKBP-FRa_jurkat fk506-Rhodamine only_002.fcs
jurkat pWPI hFKBP-FRa_jurkat fk506-Rhodamine then otl38_004.fcs
Normalized To Mode
Comp-PE-A

FIG. 6

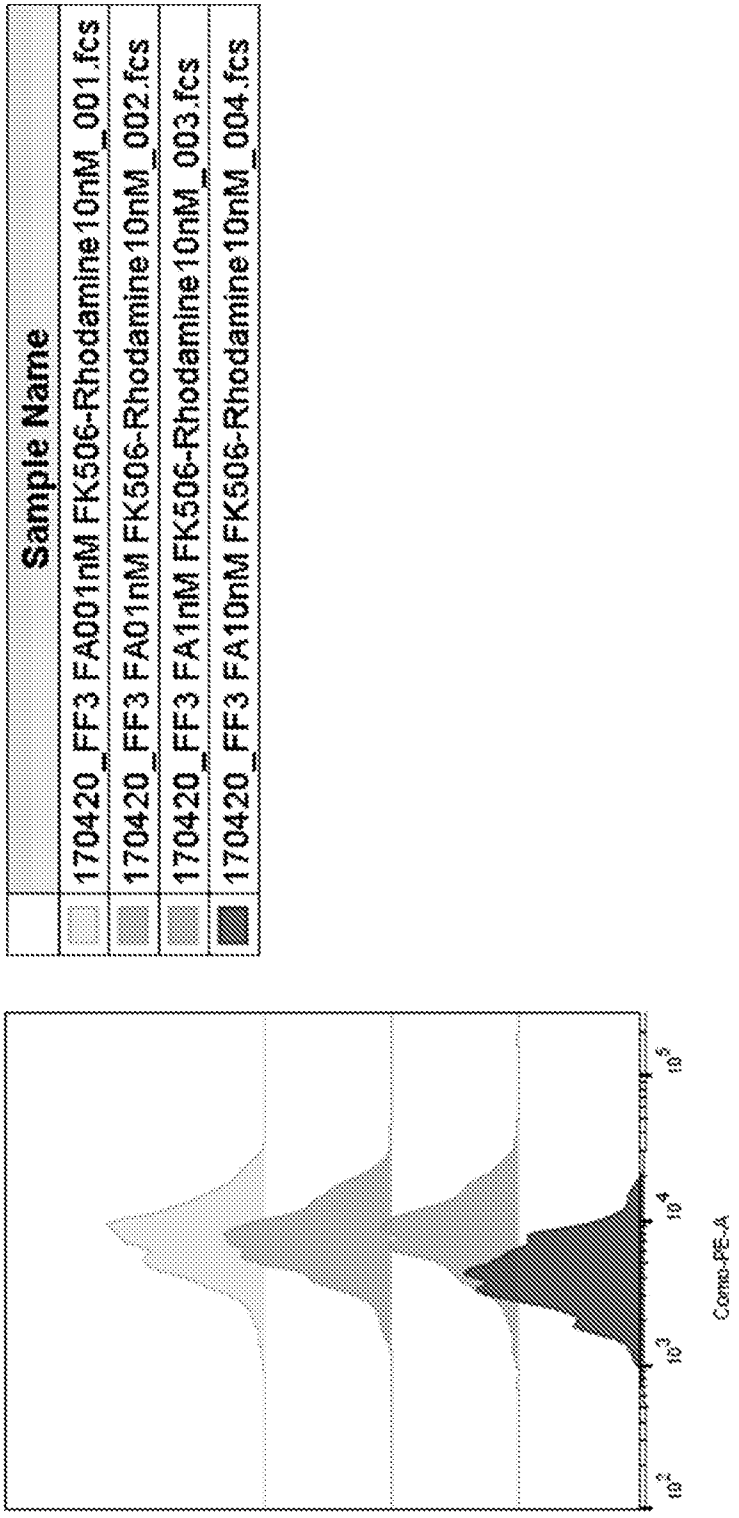

Sample Name
170420_FF3 FA001nM FK506-Rhodamine10nM_001.fcs
170420_FF3 FA01nM FK506-Rhodamine10nM_002.fcs
170420_FF3 FA1nM FK506-Rhodamine10nM_003.fcs
170420_FF3 FA10nM FK506-Rhodamine10nM_004.fcs
Comp-PE-A
10^2
10^3
10^4
10^5

FIG. 7

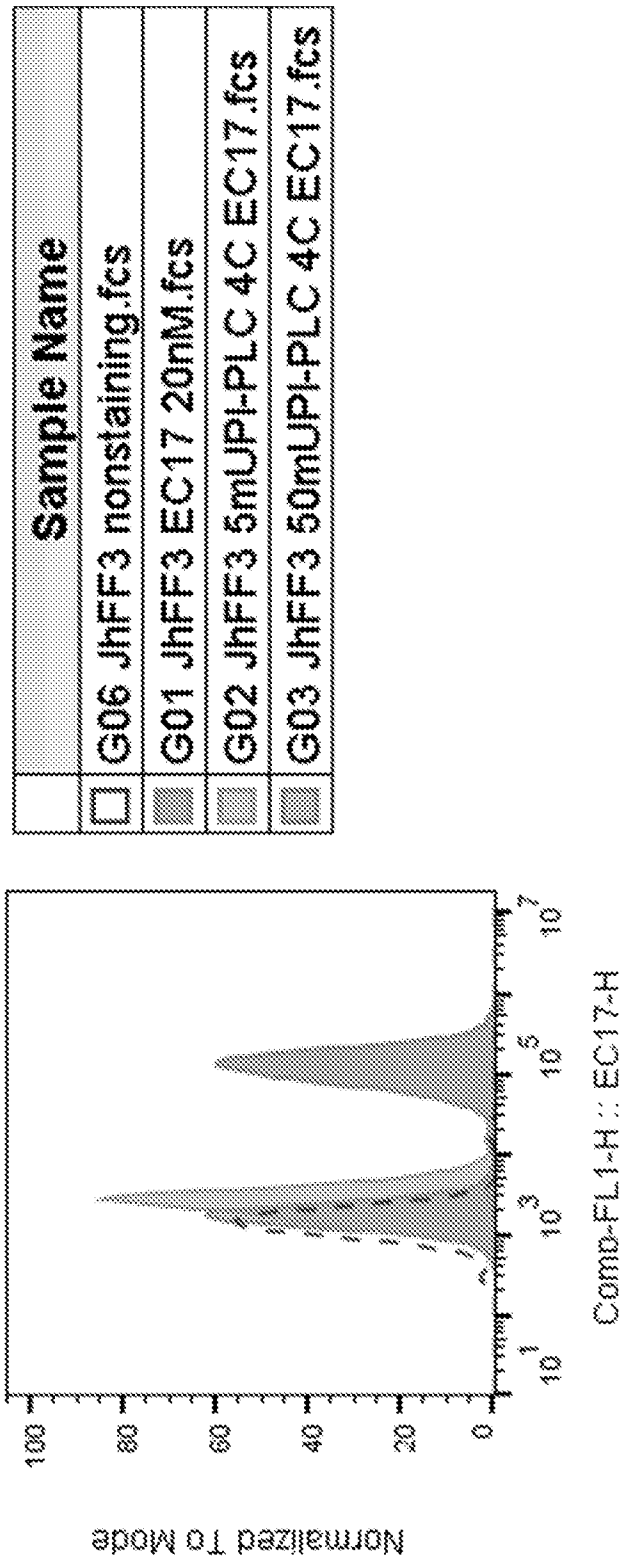

Sample Name
G06 JhFF3 nonstaining.fcs
G01 JhFF3 EC17 20nM.fcs
G02 JhFF3 5mUPI-PLC 4C EC17.fcs
G03 JhFF3 50mUPI-PLC 4C EC17.fcs
Normalized To Mode
100
80
60
40
20
0
Comp-FL1-H :: EC17-H
10^1
10^3
10^5
10^7

FIG. 8

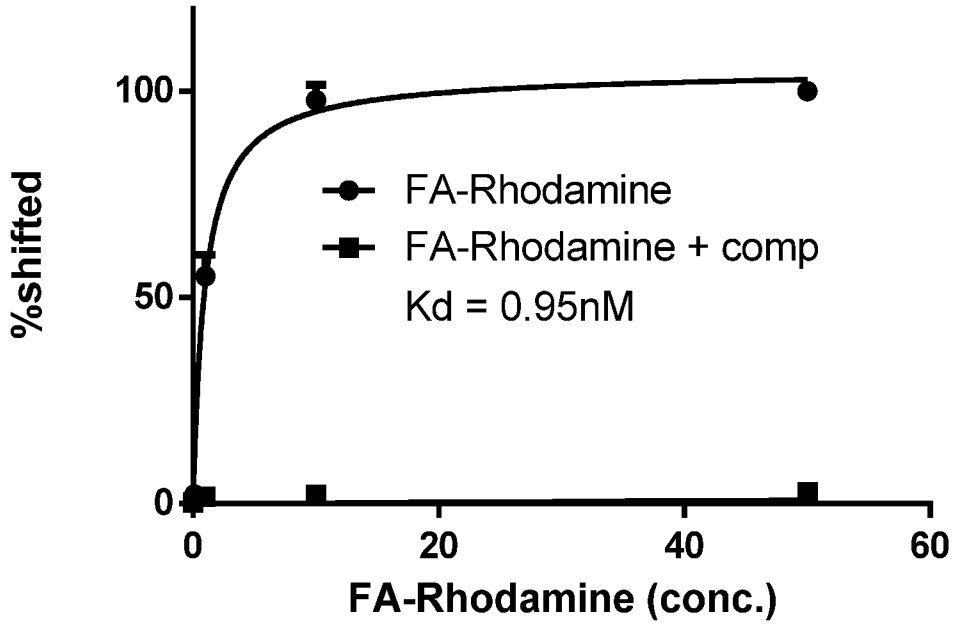

100
50
0
%shifted
FA-Rhodamine
FA-Rhodamine + comp
Kd = 0.95nM
0
20
40
60
FA-Rhodamine (conc.)

FIG. 9

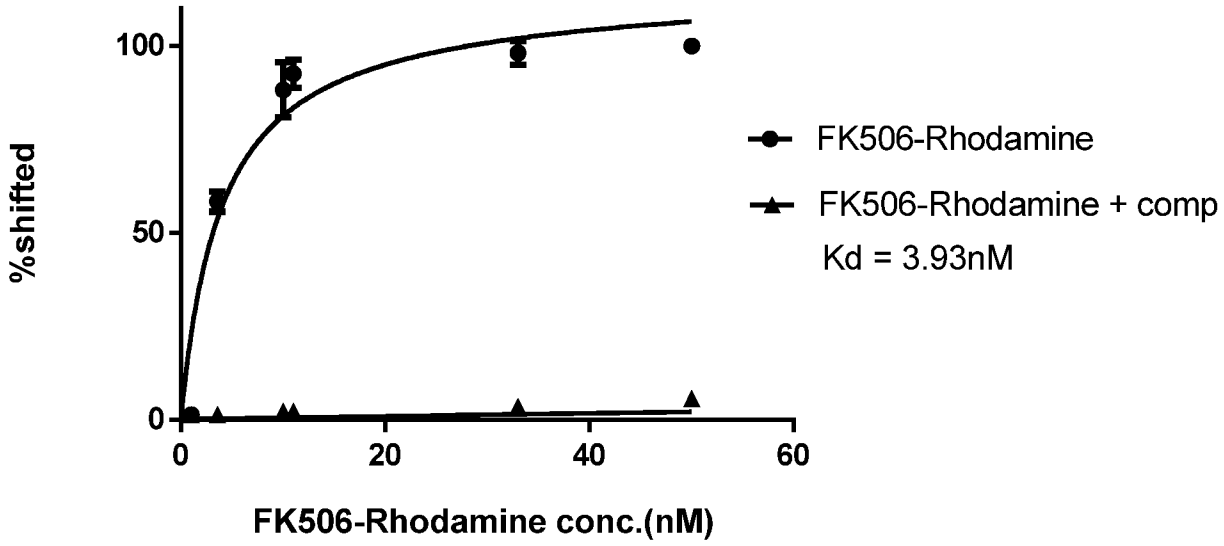

100
50
0
%shifted
0
20
40
60
FK506-Rhodamine conc.(nM)
FK506-Rhodamine
FK506-Rhodamine + comp
Kd = 3.93nM

FIG. 10

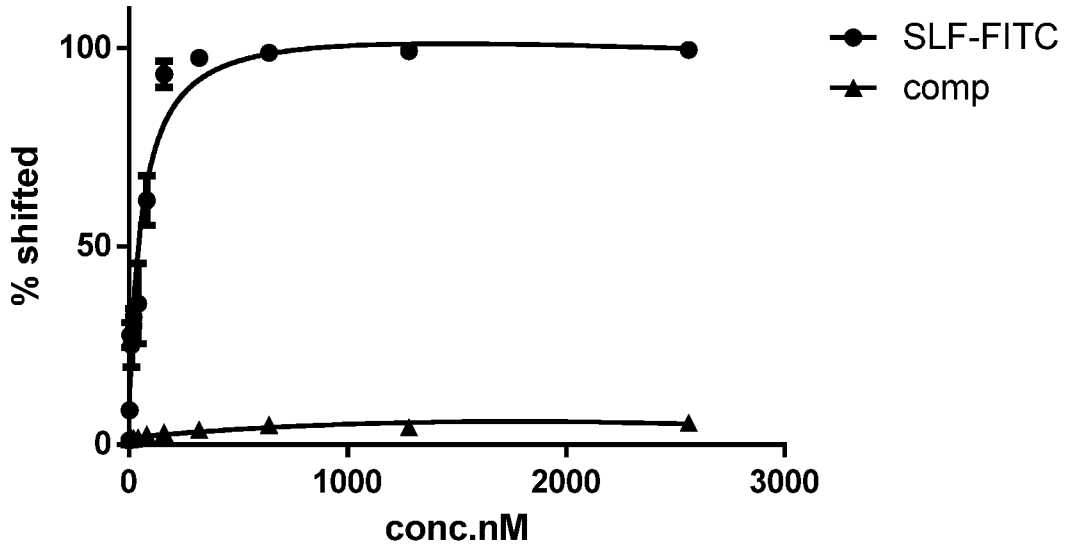


FIG. 11

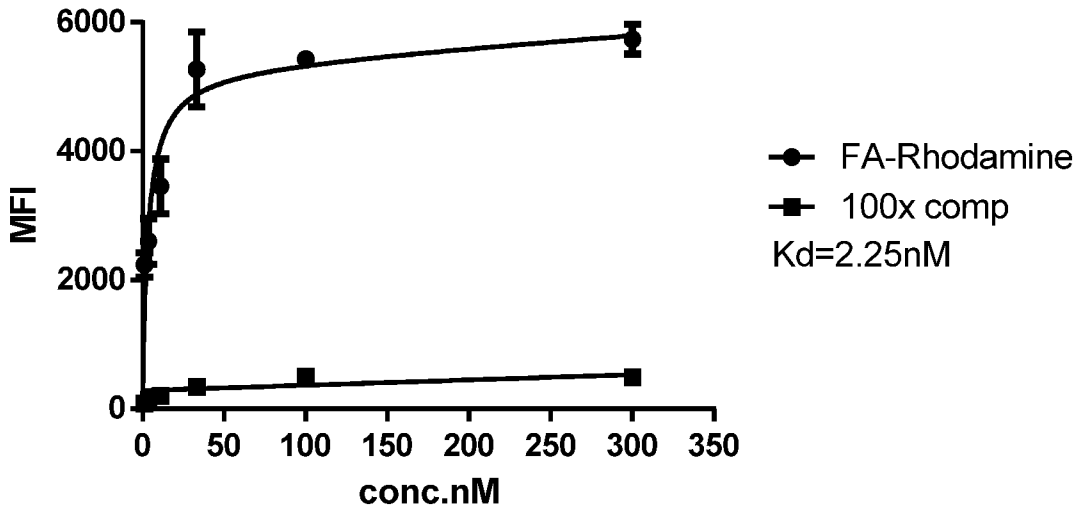

6000
4000
2000
0
MFI
0
50
100
150
200
250
300
350
conc.nM
FA-Rhodamine
100x comp
Kd=2.25nM

FIG. 12

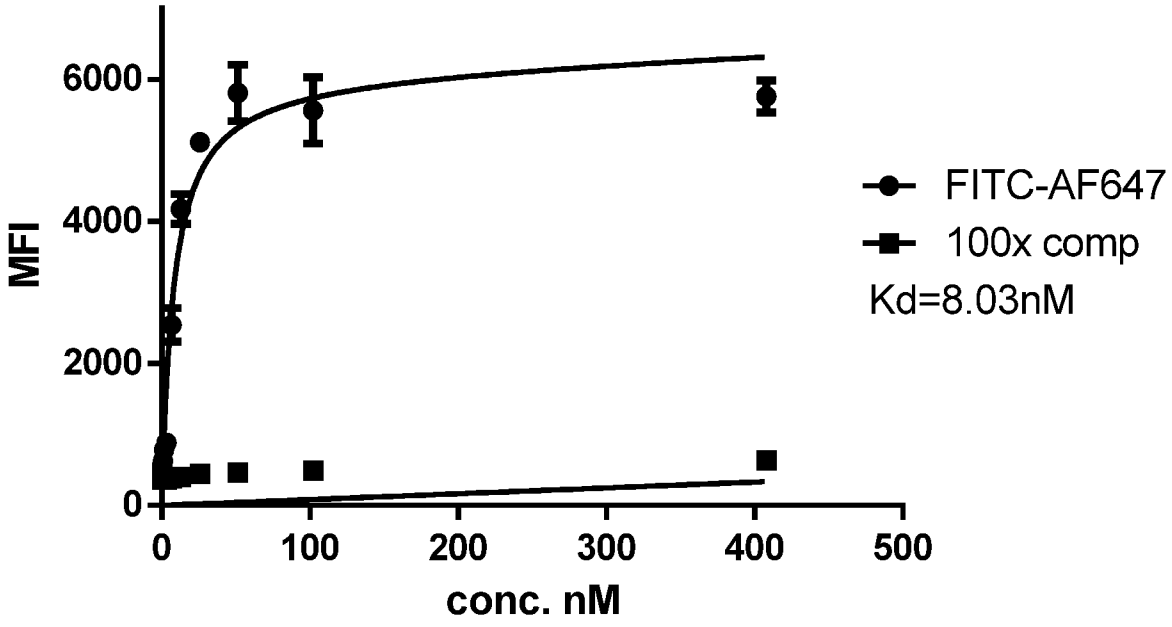

6000
4000
2000
0
MFI
0
100
200
300
400
500
conc. nM
FITC-AF647
100x comp
Kd=8.03nM

FIG. 13

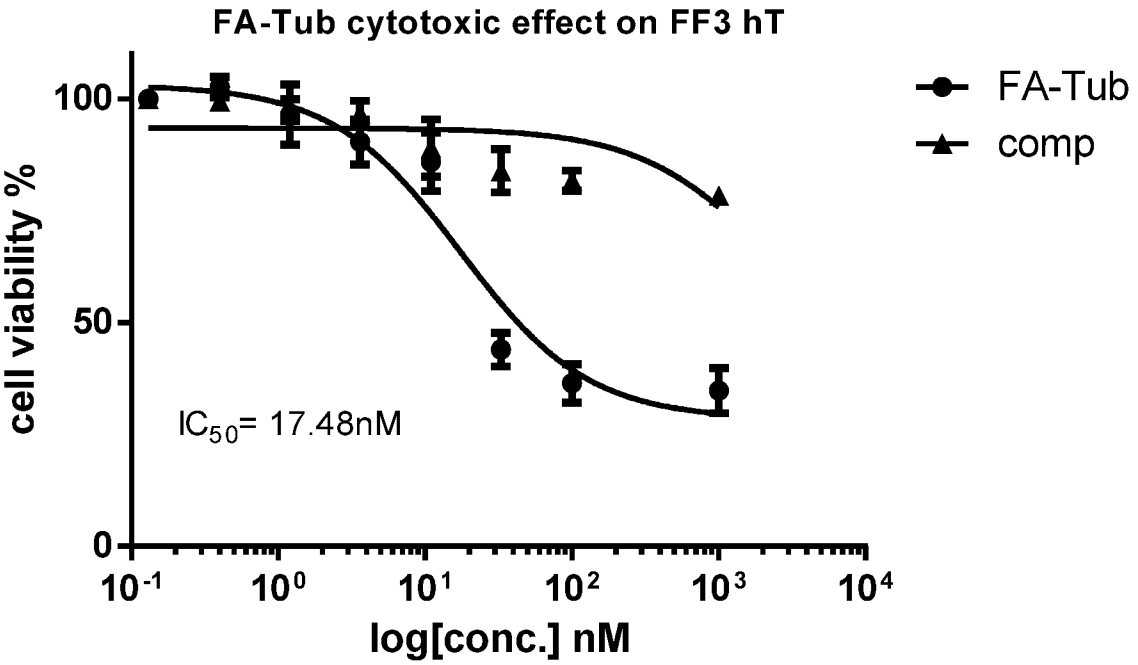

FA-Tub cytotoxic effect on FF3 hT
cell viability %
100
50
0
IC_{50}= 17.48nM
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}
log[conc.] nM
FA-Tub
comp

FIG. 14

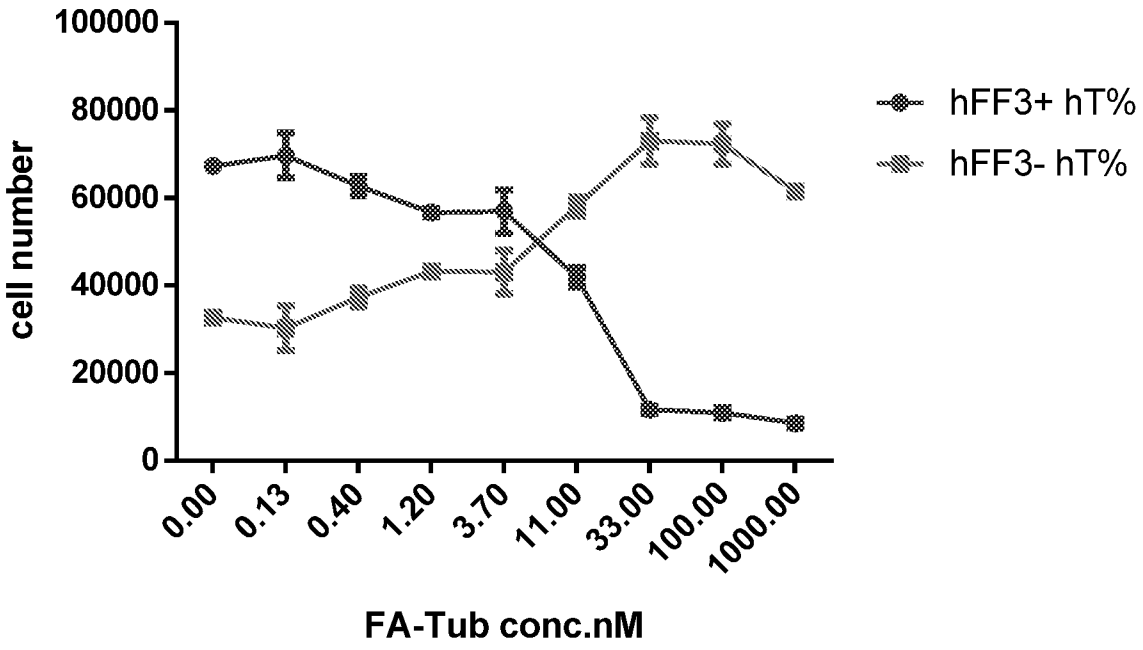

100000
80000
60000
40000
20000
0
cell number
0.00
0.13
0.40
1.20
3.70
11.00
33.00
100.00
1000.00
FA-Tub conc.nM
hFF3+ hT%
hFF3- hT%

FIG. 15

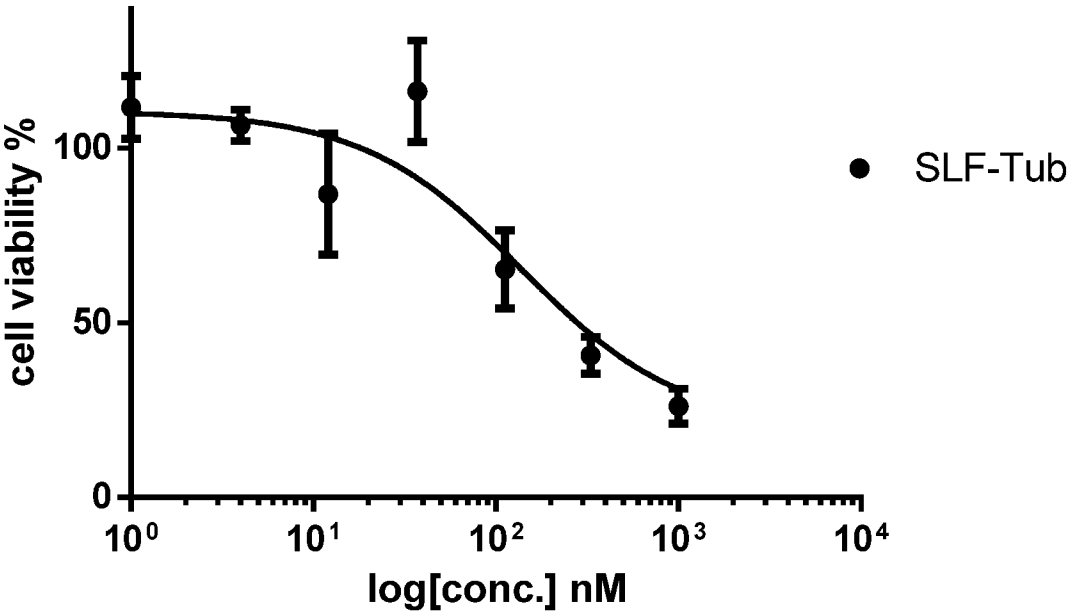


FIG. 16

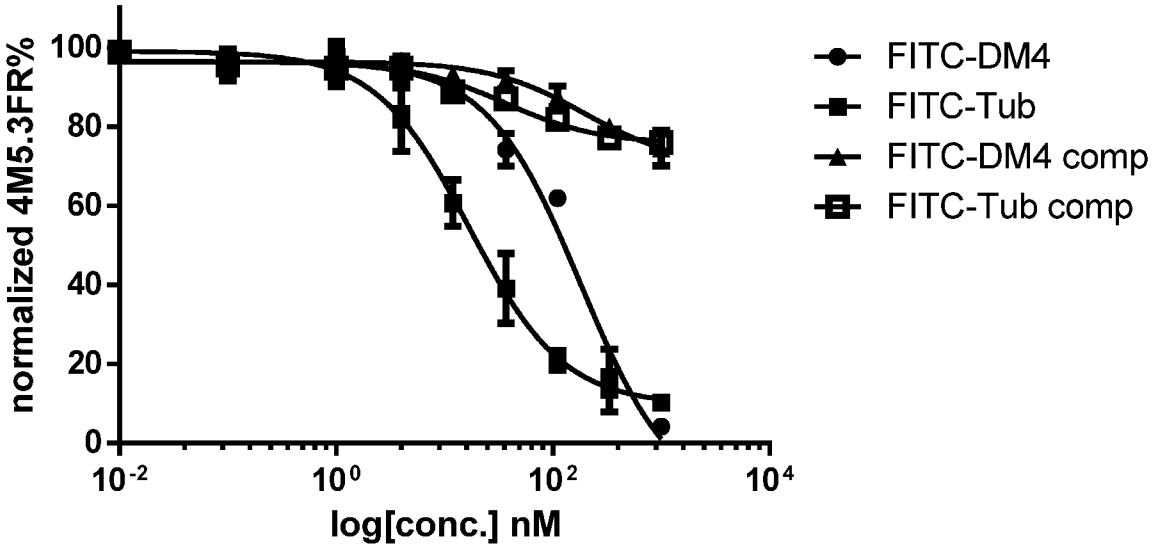

normalized 4M5.3FR%
100
80
60
40
20
0
10-2
100
102
104
log[conc.] nM
FITC-DM4
FITC-Tub
FITC-DM4 comp
FITC-Tub comp

FIG. 17

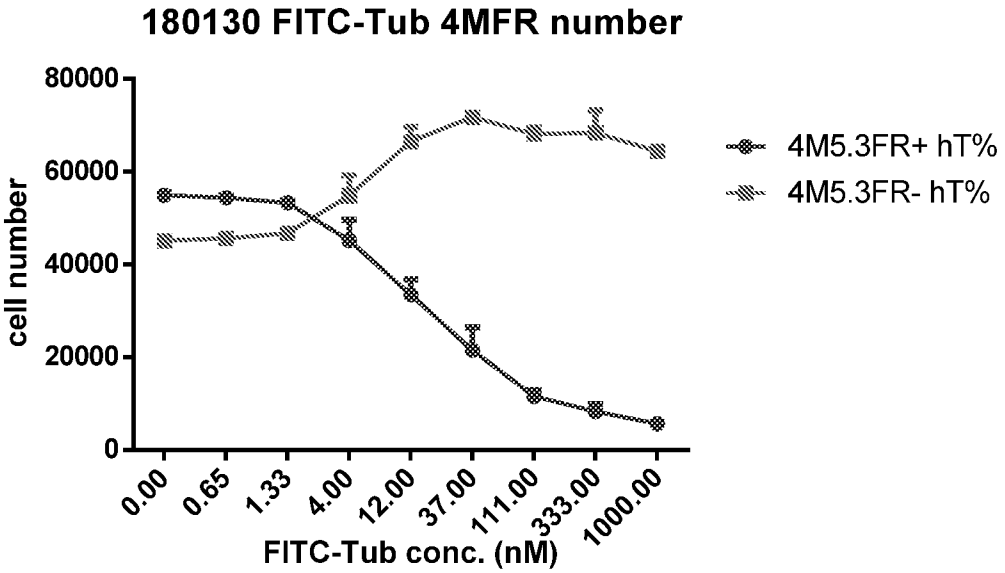

180130 FITC-Tub 4MFR number
cell number
80000
60000
40000
20000
0
0.00
0.65
1.33
4.00
12.00
37.00
111.00
333.00
1000.00
FITC-Tub conc. (nM)
4M5.3FR+ hT%
4M5.3FR- hT%

FIG. 18

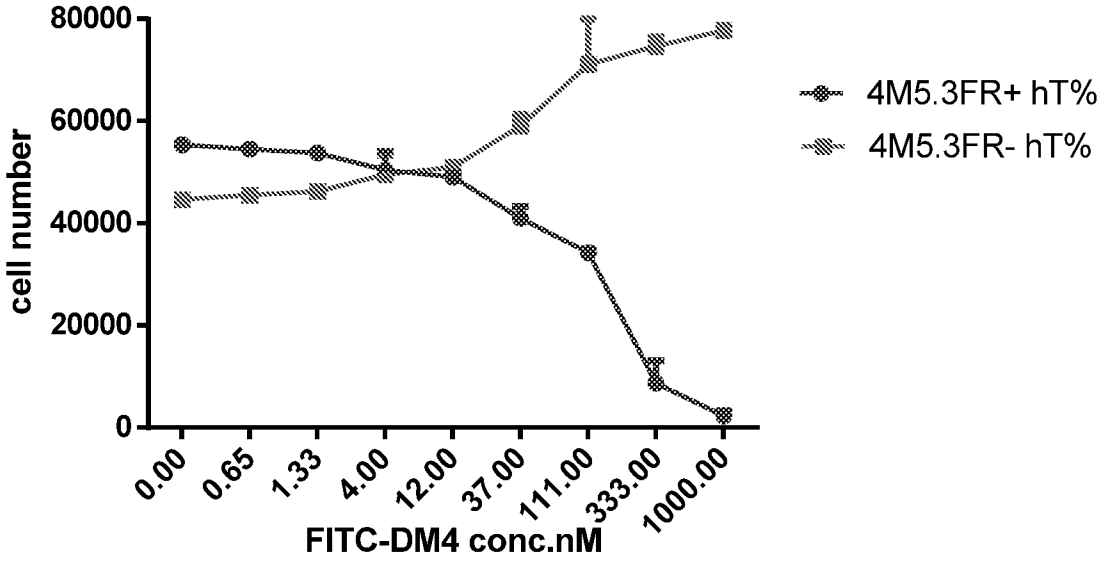

80000
60000
40000
20000
0
cell number
0.00
0.65
1.33
4.00
12.00
37.00
111.00
333.00
1000.00
FITC-DM4 conc.nM
4M5.3FR+ hT%
4M5.3FR- hT%

FIG. 19

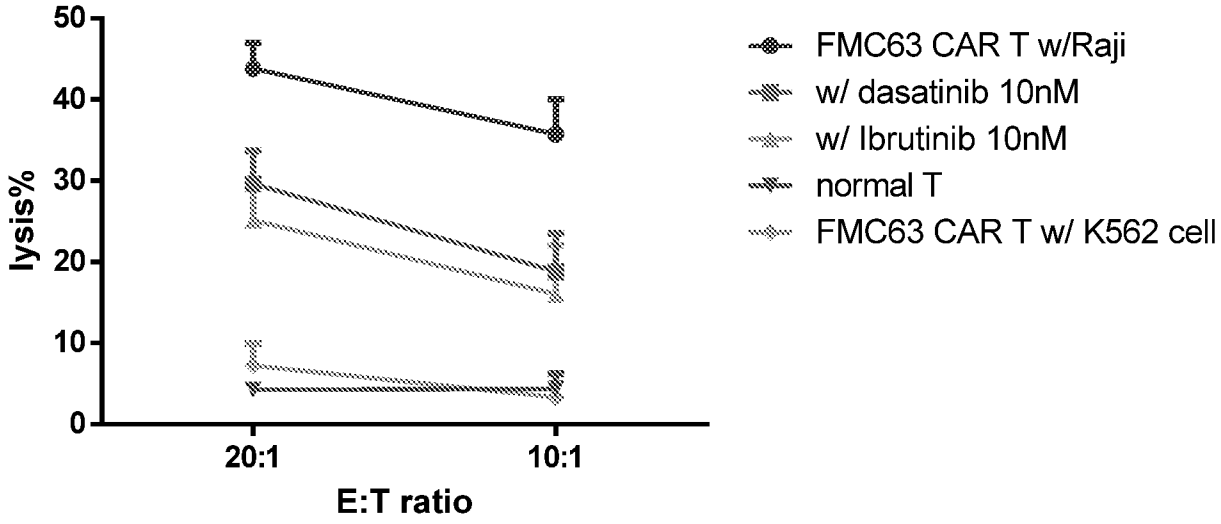

50
40
30
20
10
0
lysis%
20:1
10:1
E:T ratio
FMC63 CAR T w/Raji
w/ dasatinib 10nM
w/ Ibrutinib 10nM
normal T
FMC63 CAR T w/ K562 cell

FIG. 20

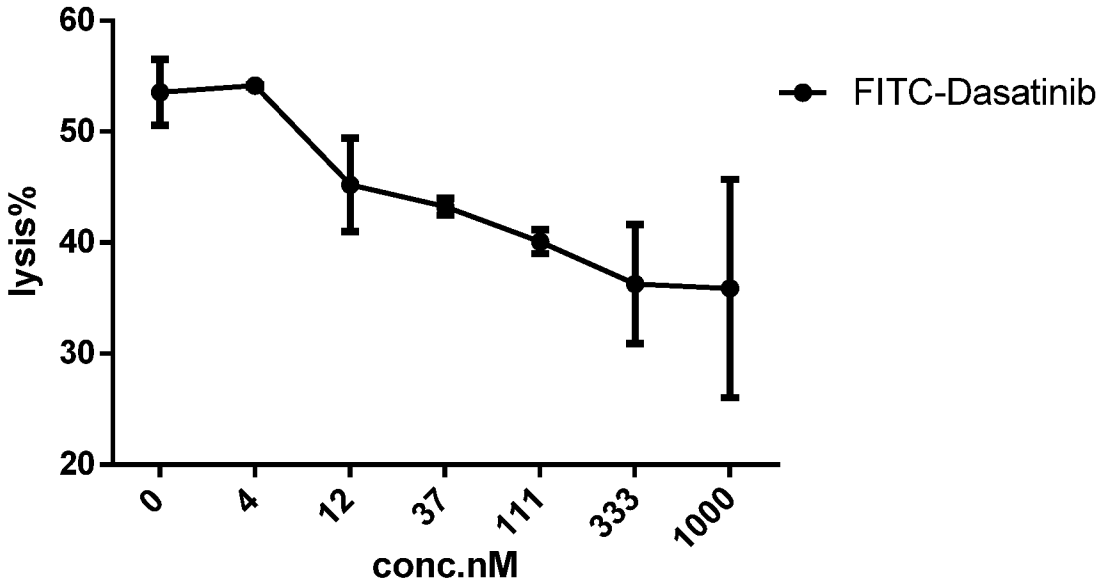

60
50
40
30
20
lysis%
0
4
12
37
111
333
1000
conc.nM
FITC-Dasatinib

FIG. 21

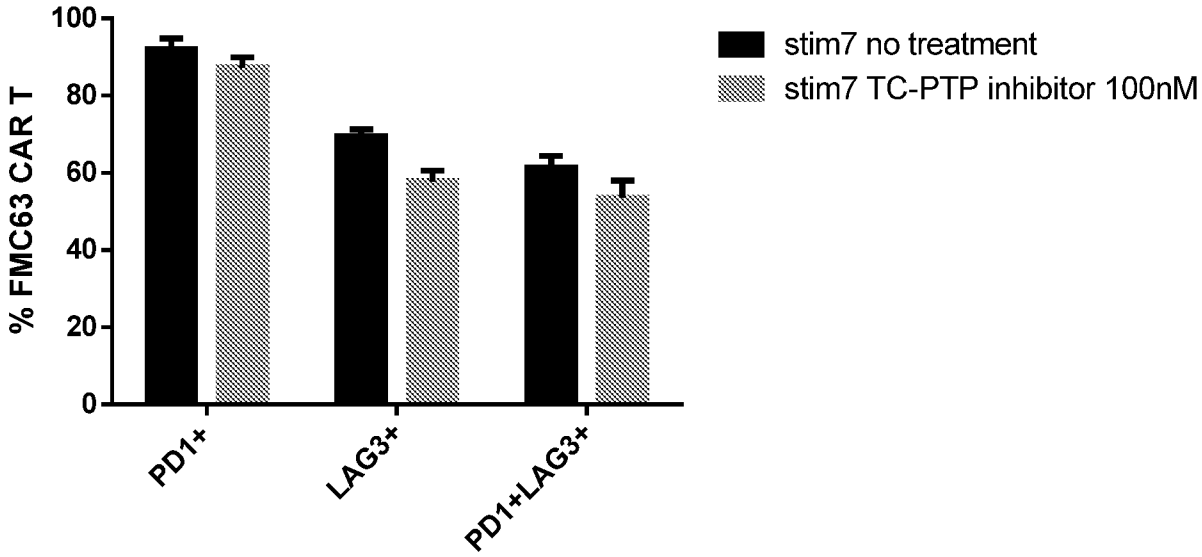

100
80
60
40
20
0
% FMC63 CAR T
PD1+
LAG3+
PD1+LAG3+
stim7 no treatment
stim7 TC-PTP inhibitor 100nM

FIG. 22

SEQUENCE LISTING

<110> Purdue Research Foundation

<120> FUSION PROTEIN AND LIGAND-PAYLOAD BASED DRUG DELIVERY FOR CELL THERAPY

<130> 67762-02

<150> 62/460,118
<151> 2017-02-17

<160> 21

<170> PatentIn version 3.5

<210> 1
<211> 367
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence for mouse FKBP-FRa with linker peptide

<400> 1

Met Ala His Leu Met Thr Val Gln Leu Leu Leu Leu Val Met Trp Met
1 5 10 15

Ala Glu Cys Ala Gln Ser Arg Ala Gly Val Gln Val Glu Thr Ile Ser
20 25 30

Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val
35 40 45

His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg
50 55 60

Asp Arg Asn Lys Pro Phe Lys Phe Thr Leu Gly Lys Gln Glu Val Ile
65 70 75 80

Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala
85 90 95

Lys Leu Ile Ile Ser Ser Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro
100 105 110

```
Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu
        115                 120                 125

Lys Leu Glu Ser Gly Gly Gly Ser Thr Arg Ala Arg Thr Glu Leu Leu
    130                 135                 140

Asn Val Cys Met Asp Ala Lys His His Lys Glu Lys Pro Gly Pro Glu
145                 150                 155                 160

Asp Asn Leu His Asp Gln Cys Ser Pro Trp Lys Thr Asn Ser Cys Cys
                165                 170                 175

Ser Thr Asn Thr Ser Gln Glu Ala His Lys Asp Ile Ser Tyr Leu Tyr
            180                 185                 190

Arg Phe Asn Trp Asn His Cys Gly Thr Met Thr Ser Glu Cys Lys Arg
        195                 200                 205

His Phe Ile Gln Asp Thr Cys Leu Tyr Glu Cys Ser Pro Asn Leu Gly
    210                 215                 220

Pro Trp Ile Gln Gln Val Asp Gln Ser Trp Arg Lys Glu Arg Ile Leu
225                 230                 235                 240

Asp Val Pro Leu Cys Lys Glu Asp Cys Gln Gln Trp Trp Glu Asp Cys
                245                 250                 255

Gln Ser Ser Phe Thr Cys Lys Ser Asn Trp His Lys Gly Trp Asn Trp
            260                 265                 270

Ser Ser Gly His Asn Glu Cys Pro Val Gly Ala Ser Cys His Pro Phe
        275                 280                 285

Thr Phe Tyr Phe Pro Thr Ser Ala Ala Leu Cys Glu Glu Ile Trp Ser
    290                 295                 300

His Ser Tyr Lys Leu Ser Asn Tyr Ser Arg Gly Ser Gly Arg Cys Ile
305                 310                 315                 320
```

```
Gln Met Trp Phe Asp Pro Ala Gln Gly Asn Pro Asn Glu Glu Val Ala
                325                 330                 335


Arg Phe Tyr Ala Glu Ala Met Ser Gly Ala Gly Phe His Gly Thr Trp
            340                 345                 350


Pro Leu Leu Cys Ser Leu Ser Leu Val Leu Leu Trp Val Ile Ser
        355                 360                 365


<210>  2
<211>  369
<212>  PRT
<213>  artificial

<220>
<223>  Amino acid sequence for human FKBP-FRa with linker peptide

<400>  2

Met Ala Gln Arg Met Thr Thr Gln Leu Leu Leu Leu Leu Val Trp Val
1               5                   10                  15


Ala Val Val Gly Glu Ala Gln Thr Gly Val Gln Val Glu Thr Ile Ser
            20                  25                  30


Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val
        35                  40                  45


His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg
    50                  55                  60


Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile
65                  70                  75                  80


Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala
                85                  90                  95


Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro
            100                 105                 110
```

```
Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu
        115                 120                 125


Lys Leu Glu Ser Gly Gly Gly Ser Arg Ile Ala Trp Ala Arg Thr Glu
    130                 135                 140


Leu Leu Asn Val Cys Met Asn Ala Lys His His Lys Glu Lys Pro Gly
145                 150                 155                 160


Pro Glu Asp Lys Leu His Glu Gln Cys Arg Pro Trp Arg Lys Asn Ala
                165                 170                 175


Cys Cys Ser Thr Asn Thr Ser Gln Glu Ala His Lys Asp Val Ser Tyr
            180                 185                 190


Leu Tyr Arg Phe Asn Trp Asn His Cys Gly Glu Met Ala Pro Ala Cys
        195                 200                 205


Lys Arg His Phe Ile Gln Asp Thr Cys Leu Tyr Glu Cys Ser Pro Asn
    210                 215                 220


Leu Gly Pro Trp Ile Gln Gln Val Asp Gln Ser Trp Arg Lys Glu Arg
225                 230                 235                 240


Val Leu Asn Val Pro Leu Cys Lys Glu Asp Cys Glu Gln Trp Trp Glu
                245                 250                 255


Asp Cys Arg Thr Ser Tyr Thr Cys Lys Ser Asn Trp His Lys Gly Trp
            260                 265                 270


Asn Trp Thr Ser Gly Phe Asn Lys Cys Ala Val Gly Ala Ala Cys Gln
        275                 280                 285


Pro Phe His Phe Tyr Phe Pro Thr Pro Thr Val Leu Cys Asn Glu Ile
    290                 295                 300


Trp Thr His Ser Tyr Lys Val Ser Asn Tyr Ser Arg Gly Ser Gly Arg
305                 310                 315                 320
```

```
Cys Ile Gln Met Trp Phe Asp Pro Ala Gln Gly Asn Pro Asn Glu Glu
                325                 330                 335

Val Ala Arg Phe Tyr Ala Ala Ala Met Ser Gly Ala Gly Pro Trp Ala
            340                 345                 350

Ala Trp Pro Phe Leu Leu Ser Leu Ala Leu Met Leu Leu Trp Leu Leu
        355                 360                 365

Ser
```

<210> 3
<211> 485
<212> PRT
<213> artificial

<220>
<223> Amino acid sequence for mouse antiCD19 CAR T construct

<400> 3

```
Met Gly Val Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp Ile Thr
1               5                   10                  15

Asp Ala Ile Cys Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp Ile
            20                  25                  30

Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Thr Ser Leu Gly Glu Thr
        35                  40                  45

Val Thr Ile Gln Cys Gln Ala Ser Glu Asp Ile Tyr Ser Gly Leu Ala
    50                  55                  60

Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile Tyr Gly
65                  70                  75                  80

Ala Ser Asp Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
                85                  90                  95

Ser Gly Thr Gln Tyr Ser Leu Lys Ile Thr Ser Met Gln Thr Glu Asp
            100                 105                 110
```

```
Glu Gly Val Tyr Phe Cys Gln Gln Gly Leu Thr Tyr Pro Arg Thr Phe
        115                 120                 125

Gly Gly Gly Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly
145                 150                 155                 160

Ala Glu Leu Val Arg Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Val
                165                 170                 175

Ser Gly Asp Thr Ile Thr Phe Tyr Tyr Met His Phe Val Lys Gln Arg
            180                 185                 190

Pro Gly Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Glu Asp Glu
        195                 200                 205

Ser Thr Lys Tyr Ser Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Ala
    210                 215                 220

Asp Thr Ser Ser Asn Thr Ala Tyr Leu Lys Leu Ser Ser Leu Thr Ser
225                 230                 235                 240

Glu Asp Thr Ala Thr Tyr Phe Cys Ile Tyr Gly Gly Tyr Tyr Phe Asp
                245                 250                 255

Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser Ser Ile Glu Phe Met
            260                 265                 270

Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg Ser Asn Gly Thr Ile Ile
        275                 280                 285

His Ile Lys Glu Lys His Leu Cys His Thr Gln Ser Ser Pro Lys Leu
    290                 295                 300

Phe Trp Ala Leu Val Val Val Ala Gly Val Leu Phe Cys Tyr Gly Leu
305                 310                 315                 320
```

```
Leu Val Thr Val Ala Leu Cys Val Ile Trp Thr Asn Ser Arg Arg Asn
                325                 330                 335

Arg Gly Gly Gln Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
            340                 345                 350

Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala
        355                 360                 365

Ala Tyr Arg Pro Arg Ala Lys Phe Ser Arg Ser Ala Glu Thr Ala Ala
    370                 375                 380

Asn Leu Gln Asp Pro Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
385                 390                 395                 400

Arg Glu Glu Tyr Asp Val Leu Glu Lys Lys Arg Ala Arg Asp Pro Glu
                405                 410                 415

Met Gly Gly Lys Gln Gln Arg Arg Arg Asn Pro Gln Glu Gly Val Tyr
            420                 425                 430

Asn Ala Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
        435                 440                 445

Thr Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
    450                 455                 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
465                 470                 475                 480

Thr Leu Ala Pro Arg
                485
```

<210> 4
<211> 496
<212> PRT
<213> artificial

<220>

<223> Amino acid sequence for human antiCD19 CAR T construct

<400> 4

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
            20                  25                  30


Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
        35                  40                  45


Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
    50                  55                  60


Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr
65                  70                  75                  80


His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
                85                  90                  95


Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
            100                 105                 110


Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
        115                 120                 125


Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
    130                 135                 140


Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
145                 150                 155                 160


Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
                165                 170                 175


Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
            180                 185                 190
```

```
Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu
        195                 200                 205

Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys
    210                 215                 220

Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr
225                 230                 235                 240

Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
                245                 250                 255

Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
            260                 265                 270

Ser Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn
        275                 280                 285

Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys
    290                 295                 300

Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
305                 310                 315                 320

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
                325                 330                 335

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
            340                 345                 350

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
        355                 360                 365

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
    370                 375                 380

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
385                 390                 395                 400
```

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
405 410 415

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
420 425 430

Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
435 440 445

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
450 455 460

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
465 470 475 480

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
485 490 495

<210> 5
<211> 12182
<212> DNA
<213> artificial

<220>
<223> Vector sequence for pWPI for human T cell transduction

<400> 5
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ctgacctttg gatggtgcta caagctagta ccagttgagc cagataaggt agaagaggcc 180

aataaaggag agaacaccag cttgttacac cctgtgagcc tgcatgggat ggatgacccg 240

gagagagaag tgttagagtg gaggtttgac agccgcctag catttcatca cgtggcccga 300

gagctgcatc cggagtactt caagaactgc tgatatcgag cttgctacaa gggactttcc 360

gctggggact ttccagggag gcgtggcctg ggcgggactg gggagtggcg agccctcaga 420

tcctgcatat aagcagctgc tttttgcctg tactgggtct ctctggttag accagatctg 480

agcctgggag ctctctggct aactagggaa cccactgctt aagcctcaat aaagcttgcc 540

ttgagtgctt caagtagtgt gtgcccgtct gttgtgtgac tctggtaact agagatccct 600

cagacccttt tagtcagtgt ggaaaatctc tagcagtggc gcccgaacag ggacttgaaa 660

gcgaaaggga aaccagagga gctctctcga cgcaggactc ggcttgctga agcgcgcacg 720

gcaagaggcg aggggcggcg actggtgagt acgccaaaaa ttttgactag cggaggctag 780

aaggagagag atgggtgcga gagcgtcagt attaagcggg ggagaattag atcgcgatgg 840

gaaaaaattc ggttaaggcc agggggaaag aaaaaatata aattaaaaca tatagtatgg 900

gcaagcaggg agctagaacg attcgcagtt aatcctggcc tgttagaaac atcagaaggc 960

tgtagacaaa tactgggaca gctacaacca tcccttcaga caggatcaga agaacttaga 1020

tcattatata atacagtagc aaccctctat tgtgtgcatc aaaggataga gataaaagac 1080

accaaggaag ctttagacaa gatagaggaa gagcaaaaca aaagtaagac caccgcacag 1140

caagcggccg ctgatcttca gacctggagg aggagatatg agggacaatt ggagaagtga 1200

attatataaa tataaagtag taaaaattga accattagga gtagcaccca ccaaggcaaa 1260

gagaagagtg gtgcagagag aaaaaagagc agtgggaata ggagctttgt tccttgggtt 1320

cttgggagca gcaggaagca ctatgggcgc agcgtcaatg acgctgacgg tacaggccag 1380

acaattattg tctggtatag tgcagcagca gaacaatttg ctgagggcta ttgaggcgca 1440

acagcatctg ttgcaactca cagtctgggg catcaagcag ctccaggcaa gaatcctggc 1500

tgtggaaaga tacctaaagg atcaacagct cctggggatt tggggttgct ctggaaaact 1560

catttgcacc actgctgtgc cttggaatgc tagttggagt aataaatctc tggaacagat 1620

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ttctatagtg aatagagtta ggcagggata ttcaccatta tcgtttcaga cccacctccc 1920

aaccccgagg ggacccgaca ggcccgaagg aatagaagaa gaaggtggag agagagacag 1980

agacagatcc attcgattag tgaacggatc tcgacggtat cgatgtcgac gataagcttt 2040

gcaaagatgg ataaagtttt aaacagagag gaatctttgc agctaatgga ccttctaggt 2100

cttgaaagga gtgggaattg gctccggtgc ccgtcagtgg gcagagcgca catcgcccac 2160

agtccccgag aagttggggg gaggggtcgg caattgaacc ggtgcctaga gaaggtggcg 2220

cggggtaaac tgggaaagtg atgtcgtgta ctggctccgc ctttttcccg agggtggggg 2280

agaaccgtat ataagtgcag tagtcgccgt gaacgttctt tttcgcaacg ggtttgccgc 2340

cagaacacag gtaagtgccg tgtgtggttc ccgcgggcct ggcctcttta cgggttatgg 2400

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cgggttggaa gtgggtggga gagttcgagg ccttgcgctt aaggagcccc ttcgcctcgt 2520

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ccgtccaggc acctcgatta gttctcgagc ttttggagta cgtcgtcttt aggttggggg 3120

gaggggtttt atgcgatgga gtttccccac actgagtggg tggagactga agttaggcca 3180

gcttggcact tgatgtaatt ctccttggaa tttgcccttt ttgagtttgg atcttggttc 3240

attctcaagc ctcagacagt ggttcaaagt ttttttcttc catttcaggt gtcgtgagga 3300

atttcgacat ttaaatttaa ttaatctcga cggtatcggt taacttttaa aagaaaaggg 3360

gggattgggg ggtacagtgc aggggaaaga atagtagaca taatagcaac agacatacaa 3420

actaaagaat tacaaaaaca aattacaaaa attcaaaatt ttatcgatca cgagactagc 3480

ctcgaggttt atggctcacc tgatgactgt gcagttgttg ctcctggtga tgtggatggc 3540

cgaatgtgct cagtccagag ctggagtgca ggtggagacc atctctcctg gagacgggcg 3600

caccttccca aagcgcggcc agacctgcgt ggtgcactac acggggatgc ttgaagatgg 3660

aaagaaattt gattcctctc gggacagaaa caagcctttt aagtttacac taggcaagca 3720

ggaggtgatc cgaggctggg aggaaggggt agcccagatg agtgtgggtc agagagccaa 3780

actgataatc tcctcagact atgcctatgg agccaccggg cacccaggca tcatcccacc 3840

acatgccact cttgtttttg atgtggagct tctaaaactg gaaagcggcg gcggcagcac 3900

tcgggccagg actgaacttc tcaatgtctg catggatgcc aaacaccaca aagaaaaacc 3960

gggccctgag gacaatttac acgaccagtg cagcccctgg aagacgaatt cctgctgttc 4020

cacgaacaca agccaggaag cacataagga catttcctac ctgtaccggt tcaactggaa 4080

ccactgcgga actatgacat cggaatgcaa acggcacttt atccaagaca cctgcctcta 4140

tgagtgttcc ccgaacttgg gaccctggat ccagcaggtg gaccagagct ggcgcaaaga 4200

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<213> artificial

<220>
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Met Thr Thr Gln Leu Leu Leu Leu Leu Val Trp Val Ala Val Val Gly
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Glu Ala Gln Thr Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly
20 25 30

Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly
35 40 45

Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys
50 55 60

Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu
65 70 75 80

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

```
Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro
            100                 105                 110

Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Ser
        115                 120                 125

Gly Gly Gly Ser Arg Ile Ala Trp Ala Arg Thr Glu Leu Leu Asn Val
    130                 135                 140

Cys Met Asn Ala Lys His His Lys Glu Lys Pro Gly Pro Glu Asp Lys
145                 150                 155                 160

Leu His Glu Gln Cys Arg Pro Trp Arg Lys Asn Ala Cys Cys Ser Thr
                165                 170                 175

Asn Thr Ser Gln Glu Ala His Lys Asp Val Ser Tyr Leu Tyr Arg Phe
            180                 185                 190

Asn Trp Asn His Cys Gly Glu Met Ala Pro Ala Cys Lys Arg His Phe
        195                 200                 205

Ile Gln Asp Thr Cys Leu Tyr Glu Cys Ser Pro Asn Leu Gly Pro Trp
    210                 215                 220

Ile Gln Gln Val Asp Gln Ser Trp Arg Lys Glu Arg Val Leu Asn Val
225                 230                 235                 240

Pro Leu Cys Lys Glu Asp Cys Glu Gln Trp Trp Glu Asp Cys Arg Thr
                245                 250                 255

Ser Tyr Thr Cys Lys Ser Asn Trp His Lys Gly Trp Asn Trp Thr Ser
            260                 265                 270

Gly Phe Asn Lys Cys Ala Val Gly Ala Ala Cys Gln Pro Phe His Phe
        275                 280                 285

Tyr Phe Pro Thr Pro Thr Val Leu Cys Asn Glu Ile Trp Thr His Ser
    290                 295                 300
```

```
Tyr Lys Val Ser Asn Tyr Ser Arg Gly Ser Gly Arg Cys Ile Gln Met
305                 310                 315                 320


Trp Phe Asp Pro Ala Gln Gly Asn Pro Asn Glu Glu Val Ala Arg Phe
                325                 330                 335


Tyr Ala Ala Ala Met Ser Gly Ala Gly Pro Trp Ala Ala Trp Pro Phe
            340                 345                 350


Leu Leu Ser Leu Ala Leu Met Leu Leu Trp Leu Leu Ser
        355                 360                 365


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<211>  375
<212>  PRT
<213>  artificial

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Glu Ala Gln Thr Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly
            20                  25                  30


Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly
        35                  40                  45


Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys
    50                  55                  60


Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu
65                  70                  75                  80


Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile
                85                  90                  95
```

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Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro
            100                 105                 110

Pro His Ala Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Ile
    130                 135                 140

Ala Trp Ala Arg Thr Glu Leu Leu Asn Val Cys Met Asn Ala Lys His
145                 150                 155                 160

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

Pro Trp Arg Lys Asn Ala Cys Cys Ser Thr Asn Thr Ser Gln Glu Ala
            180                 185                 190

His Lys Asp Val Ser Tyr Leu Tyr Arg Phe Asn Trp Asn His Cys Gly
        195                 200                 205

Glu Met Ala Pro Ala Cys Lys Arg His Phe Ile Gln Asp Thr Cys Leu
    210                 215                 220

Tyr Glu Cys Ser Pro Asn Leu Gly Pro Trp Ile Gln Gln Val Asp Gln
225                 230                 235                 240

Ser Trp Arg Lys Glu Arg Val Leu Asn Val Pro Leu Cys Lys Glu Asp
                245                 250                 255

Cys Glu Gln Trp Trp Glu Asp Cys Arg Thr Ser Tyr Thr Cys Lys Ser
            260                 265                 270

Asn Trp His Lys Gly Trp Asn Trp Thr Ser Gly Phe Asn Lys Cys Ala
        275                 280                 285

Val Gly Ala Ala Cys Gln Pro Phe His Phe Tyr Phe Pro Thr Pro Thr
    290                 295                 300
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Val Leu Cys Asn Glu Ile Trp Thr His Ser Tyr Lys Val Ser Asn Tyr
305                 310                 315                 320


Ser Arg Gly Ser Gly Arg Cys Ile Gln Met Trp Phe Asp Pro Ala Gln
                325                 330                 335


Gly Asn Pro Asn Glu Glu Val Ala Arg Phe Tyr Ala Ala Ala Met Ser
            340                 345                 350


Gly Ala Gly Pro Trp Ala Ala Trp Pro Phe Leu Leu Ser Leu Ala Leu
        355                 360                 365


Met Leu Leu Trp Leu Leu Ser
    370                 375


<210>  13
<211>  513
<212>  PRT
<213>  artificial

<220>
<223>  4M5.3-FR with GPI anchor amino acid sequence

<400>  13

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
            20                  25                  30


Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
        35                  40                  45


Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Arg Trp Tyr Leu Gln
    50                  55                  60


Lys Pro Gly Gln Ser Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg
65                  70                  75                  80


Val Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95
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Phe Thr Leu Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
            100                 105                 110

Phe Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr
        115                 120                 125

Lys Leu Glu Ile Lys Ser Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala
    130                 135                 140

Lys Lys Asp Asp Ala Lys Lys Asp Asp Ala Lys Lys Asp Gly Gly Val
145                 150                 155                 160

Lys Leu Asp Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly Ala Met
                165                 170                 175

Lys Leu Ser Cys Val Thr Ser Gly Phe Thr Phe Gly His Tyr Trp Met
            180                 185                 190

Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Gln
        195                 200                 205

Phe Arg Asn Lys Pro Tyr Asn Tyr Glu Thr Tyr Tyr Ser Asp Ser Val
    210                 215                 220

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser Val Tyr
225                 230                 235                 240

Leu Gln Met Asn Asn Leu Arg Val Glu Asp Thr Gly Ile Tyr Tyr Cys
                245                 250                 255

Thr Gly Ala Ser Tyr Gly Met Glu Tyr Leu Gly Gln Gly Thr Ser Val
            260                 265                 270

Thr Val Ser Ser Gly Gly Gly Ser Arg Ile Ala Trp Ala Arg Thr Glu
        275                 280                 285

Leu Leu Asn Val Cys Met Asn Ala Lys His His Lys Glu Lys Pro Gly
    290                 295                 300
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Pro Glu Asp Lys Leu His Glu Gln Cys Arg Pro Trp Arg Lys Asn Ala
305                 310                 315                 320

Cys Cys Ser Thr Asn Thr Ser Gln Glu Ala His Lys Asp Val Ser Tyr
                325                 330                 335

Leu Tyr Arg Phe Asn Trp Asn His Cys Gly Glu Met Ala Pro Ala Cys
            340                 345                 350

Lys Arg His Phe Ile Gln Asp Thr Cys Leu Tyr Glu Cys Ser Pro Asn
        355                 360                 365

Leu Gly Pro Trp Ile Gln Gln Val Asp Gln Ser Trp Arg Lys Glu Arg
    370                 375                 380

Val Leu Asn Val Pro Leu Cys Lys Glu Asp Cys Glu Gln Trp Trp Glu
385                 390                 395                 400

Asp Cys Arg Thr Ser Tyr Thr Cys Lys Ser Asn Trp His Lys Gly Trp
                405                 410                 415

Asn Trp Thr Ser Gly Phe Asn Lys Cys Ala Val Gly Ala Ala Cys Gln
            420                 425                 430

Pro Phe His Phe Tyr Phe Pro Thr Pro Thr Val Leu Cys Asn Glu Ile
        435                 440                 445

Trp Thr His Ser Tyr Lys Val Ser Asn Tyr Ser Arg Gly Ser Gly Arg
    450                 455                 460

Cys Ile Gln Met Trp Phe Asp Pro Ala Gln Gly Asn Pro Asn Glu Glu
465                 470                 475                 480

Val Ala Arg Phe Tyr Ala Ala Ala Met Ser Gly Ala Gly Pro Trp Ala
                485                 490                 495

Ala Trp Pro Phe Leu Leu Ser Leu Ala Leu Met Leu Leu Trp Leu Leu
            500                 505                 510
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Ser

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<400> 14

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His Ala Ala Arg Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
            20                  25                  30


Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
        35                  40                  45


Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
    50                  55                  60


Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr
65                  70                  75                  80


His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
                85                  90                  95


Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
            100                 105                 110


Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
        115                 120                 125


Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
    130                 135                 140
```

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
145                 150                 155                 160


Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
                165                 170                 175


Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
            180                 185                 190


Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu
        195                 200                 205


Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys
    210                 215                 220


Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr
225                 230                 235                 240


Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
                245                 250                 255


Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
            260                 265                 270


Ser Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn
        275                 280                 285


Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys
    290                 295                 300


Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
305                 310                 315                 320


Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
                325                 330                 335


Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
            340                 345                 350
```

```
Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
        355                 360                 365

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
    370                 375                 380

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
385                 390                 395                 400

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
                405                 410                 415

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
            420                 425                 430

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
        435                 440                 445

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
    450                 455                 460

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
465                 470                 475                 480

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly
                485                 490                 495

Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
            500                 505                 510

Asn Pro Gly Pro Met Ala Gln Arg Met Thr Thr Gln Leu Leu Leu Leu
        515                 520                 525

Leu Val Trp Val Ala Val Val Gly Glu Ala Gln Thr Gly Val Gln Val
    530                 535                 540

Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln
545                 550                 555                 560
```

```
Thr Cys Val Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe
                565                 570                 575

Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys
            580                 585                 590

Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val
        595                 600                 605

Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala
    610                 615                 620

Thr Gly His Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp
625                 630                 635                 640

Val Glu Leu Leu Lys Leu Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly
                645                 650                 655

Ser Gly Gly Gly Gly Ser Arg Ile Ala Trp Ala Arg Thr Glu Leu Leu
            660                 665                 670

Asn Val Cys Met Asn Ala Lys His His Lys Glu Lys Pro Gly Pro Glu
        675                 680                 685

Asp Lys Leu His Glu Gln Cys Arg Pro Trp Arg Lys Asn Ala Cys Cys
    690                 695                 700

Ser Thr Asn Thr Ser Gln Glu Ala His Lys Asp Val Ser Tyr Leu Tyr
705                 710                 715                 720

Arg Phe Asn Trp Asn His Cys Gly Glu Met Ala Pro Ala Cys Lys Arg
                725                 730                 735

His Phe Ile Gln Asp Thr Cys Leu Tyr Glu Cys Ser Pro Asn Leu Gly
            740                 745                 750

Pro Trp Ile Gln Gln Val Asp Gln Ser Trp Arg Lys Glu Arg Val Leu
        755                 760                 765
```

```
Asn Val Pro Leu Cys Lys Glu Asp Cys Glu Gln Trp Trp Glu Asp Cys
    770                 775                 780

Arg Thr Ser Tyr Thr Cys Lys Ser Asn Trp His Lys Gly Trp Asn Trp
785                 790                 795                 800

Thr Ser Gly Phe Asn Lys Cys Ala Val Gly Ala Ala Cys Gln Pro Phe
                805                 810                 815

His Phe Tyr Phe Pro Thr Pro Thr Val Leu Cys Asn Glu Ile Trp Thr
            820                 825                 830

His Ser Tyr Lys Val Ser Asn Tyr Ser Arg Gly Ser Gly Arg Cys Ile
        835                 840                 845

Gln Met Trp Phe Asp Pro Ala Gln Gly Asn Pro Asn Glu Glu Val Ala
    850                 855                 860

Arg Phe Tyr Ala Ala Ala Met Ser Gly Ala Gly Pro Trp Ala Ala Trp
865                 870                 875                 880

Pro Phe Leu Leu Ser Leu Ala Leu Met Leu Leu Trp Leu Leu Ser
                885                 890                 895
```

<210> 15
<211> 1029
<212> PRT
<213> artificial

<220>
<223> FMC63-T2A-4M5.3SGFR

<400> 15

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asp
            20                  25                  30

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
        35                  40                  45
```

```
Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
    50                  55                  60

Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr
65                  70                  75                  80

His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
                85                  90                  95

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
            100                 105                 110

Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
        115                 120                 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu Ser
145                 150                 155                 160

Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys Thr
                165                 170                 175

Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln
            180                 185                 190

Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser Glu
        195                 200                 205

Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys
    210                 215                 220

Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr
225                 230                 235                 240

Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly
                245                 250                 255
```

```
Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
            260                 265                 270

Ser Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn
        275                 280                 285

Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys
    290                 295                 300

Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
305                 310                 315                 320

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
                325                 330                 335

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
            340                 345                 350

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
        355                 360                 365

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
    370                 375                 380

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
385                 390                 395                 400

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
                405                 410                 415

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
            420                 425                 430

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
        435                 440                 445

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
    450                 455                 460
```

```
Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
465                 470                 475                 480

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly
                485                 490                 495

Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
            500                 505                 510

Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu
        515                 520                 525

Ala Leu Leu Leu His Ala Ala Arg Pro Asp Val Val Met Thr Gln Thr
    530                 535                 540

Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
545                 550                 555                 560

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Arg
                565                 570                 575

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Val Leu Ile Tyr Lys
            580                 585                 590

Val Ser Asn Arg Val Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
        595                 600                 605

Ser Gly Thr Asp Phe Thr Leu Lys Ile Asn Arg Val Glu Ala Glu Asp
    610                 615                 620

Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe
625                 630                 635                 640

Gly Gly Gly Thr Lys Leu Glu Ile Lys Ser Ser Ala Asp Asp Ala Lys
                645                 650                 655

Lys Asp Ala Ala Lys Lys Asp Asp Ala Lys Lys Asp Asp Ala Lys Lys
            660                 665                 670
```

```
Asp Gly Gly Val Lys Leu Asp Glu Thr Gly Gly Gly Leu Val Gln Pro
        675                 680                 685

Gly Gly Ala Met Lys Leu Ser Cys Val Thr Ser Gly Phe Thr Phe Gly
    690                 695                 700

His Tyr Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu
705                 710                 715                 720

Trp Val Ala Gln Phe Arg Asn Lys Pro Tyr Asn Tyr Glu Thr Tyr Tyr
                725                 730                 735

Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
            740                 745                 750

Ser Ser Val Tyr Leu Gln Met Asn Asn Leu Arg Val Glu Asp Thr Gly
        755                 760                 765

Ile Tyr Tyr Cys Thr Gly Ala Ser Tyr Gly Met Glu Tyr Leu Gly Gln
    770                 775                 780

Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Ser Arg Ile Ala Trp
785                 790                 795                 800

Ala Arg Thr Glu Leu Leu Asn Val Cys Met Asn Ala Lys His His Lys
                805                 810                 815

Glu Lys Pro Gly Pro Glu Asp Lys Leu His Glu Gln Cys Arg Pro Trp
            820                 825                 830

Arg Lys Asn Ala Cys Cys Ser Thr Asn Thr Ser Gln Glu Ala His Lys
        835                 840                 845

Asp Val Ser Tyr Leu Tyr Arg Phe Asn Trp Asn His Cys Gly Glu Met
    850                 855                 860

Ala Pro Ala Cys Lys Arg His Phe Ile Gln Asp Thr Cys Leu Tyr Glu
865                 870                 875                 880
```

```
Cys Ser Pro Asn Leu Gly Pro Trp Ile Gln Gln Val Asp Gln Ser Trp
                885                 890                 895


Arg Lys Glu Arg Val Leu Asn Val Pro Leu Cys Lys Glu Asp Cys Glu
            900                 905                 910


Gln Trp Trp Glu Asp Cys Arg Thr Ser Tyr Thr Cys Lys Ser Asn Trp
        915                 920                 925


His Lys Gly Trp Asn Trp Thr Ser Gly Phe Asn Lys Cys Ala Val Gly
    930                 935                 940


Ala Ala Cys Gln Pro Phe His Phe Tyr Phe Pro Thr Pro Thr Val Leu
945                 950                 955                 960


Cys Asn Glu Ile Trp Thr His Ser Tyr Lys Val Ser Asn Tyr Ser Arg
                965                 970                 975


Gly Ser Gly Arg Cys Ile Gln Met Trp Phe Asp Pro Ala Gln Gly Asn
            980                 985                 990


Pro Asn Glu Glu Val Ala Arg Phe  Tyr Ala Ala Ala Met  Ser Gly Ala
        995                 1000                1005


Gly Pro  Trp Ala Ala Trp Pro  Phe Leu Leu Ser Leu  Ala Leu Met
    1010                1015                1020


Leu Leu  Trp Leu Leu Ser
    1025


<210>  16
<211>  255
<212>  PRT
<213>  artificial

<220>
<223>  FRb with signal peptide

<400>  16
```

```
Met Val Trp Lys Trp Met Pro Leu Leu Leu Leu Leu Val Cys Val Ala
1               5                  10                  15

Thr Met Cys Ser Ala Gln Asp Arg Thr Asp Leu Leu Asn Val Cys Met
            20                  25                  30

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

Asp Gln Cys Ser Pro Trp Lys Lys Asn Ala Cys Cys Thr Ala Ser Thr
    50                  55                  60

Ser Gln Glu Leu His Lys Asp Thr Ser Arg Leu Tyr Asn Phe Asn Trp
65                  70                  75                  80

Asp His Cys Gly Lys Met Glu Pro Ala Cys Lys Arg His Phe Ile Gln
                85                  90                  95

Asp Thr Cys Leu Tyr Glu Cys Ser Pro Asn Leu Gly Pro Trp Ile Gln
            100                 105                 110

Gln Val Asn Gln Ser Trp Arg Lys Glu Arg Phe Leu Asp Val Pro Leu
        115                 120                 125

Cys Lys Glu Asp Cys Gln Arg Trp Trp Glu Asp Cys His Thr Ser His
    130                 135                 140

Thr Cys Lys Ser Asn Trp His Arg Gly Trp Asp Trp Thr Ser Gly Val
145                 150                 155                 160

Asn Lys Cys Pro Ala Gly Ala Leu Cys Arg Thr Phe Glu Ser Tyr Phe
                165                 170                 175

Pro Thr Pro Ala Ala Leu Cys Glu Gly Leu Trp Ser His Ser Tyr Lys
            180                 185                 190

Val Ser Asn Tyr Ser Arg Gly Ser Gly Arg Cys Ile Gln Met Trp Phe
        195                 200                 205
```

```
Asp Ser Ala Gln Gly Asn Pro Asn Glu Glu Val Ala Arg Phe Tyr Ala
    210                 215                 220


Ala Ala Met His Val Asn Ala Gly Glu Met Leu His Gly Thr Gly Gly
225                 230                 235                 240


Leu Leu Leu Ser Leu Ala Leu Met Leu Gln Leu Trp Leu Leu Gly
                245                 250                 255


<210>  17
<211>  335
<212>  PRT
<213>  artificial

<220>
<223>  uPAR with signal peptide

<400>  17

Met Gly His Pro Pro Leu Leu Pro Leu Leu Leu Leu Leu His Thr Cys
1               5                   10                  15


Val Pro Ala Ser Trp Gly Leu Arg Cys Met Gln Cys Lys Thr Asn Gly
            20                  25                  30


Asp Cys Arg Val Glu Glu Cys Ala Leu Gly Gln Asp Leu Cys Arg Thr
        35                  40                  45


Thr Ile Val Arg Leu Trp Glu Glu Gly Glu Glu Leu Glu Leu Val Glu
    50                  55                  60


Lys Ser Cys Thr His Ser Glu Lys Thr Asn Arg Thr Leu Ser Tyr Arg
65                  70                  75                  80


Thr Gly Leu Lys Ile Thr Ser Leu Thr Glu Val Val Cys Gly Leu Asp
                85                  90                  95


Leu Cys Asn Gln Gly Asn Ser Gly Arg Ala Val Thr Tyr Ser Arg Ser
            100                 105                 110


Arg Tyr Leu Glu Cys Ile Ser Cys Gly Ser Ser Asp Met Ser Cys Glu
        115                 120                 125
```

```
Arg Gly Arg His Gln Ser Leu Gln Cys Arg Ser Pro Glu Glu Gln Cys
    130                 135                 140

Leu Asp Val Val Thr His Trp Ile Gln Glu Gly Glu Glu Gly Arg Pro
145                 150                 155                 160

Lys Asp Asp Arg His Leu Arg Gly Cys Gly Tyr Leu Pro Gly Cys Pro
                165                 170                 175

Gly Ser Asn Gly Phe His Asn Asn Asp Thr Phe His Phe Leu Lys Cys
            180                 185                 190

Cys Asn Thr Thr Lys Cys Asn Glu Gly Pro Ile Leu Glu Leu Glu Asn
        195                 200                 205

Leu Pro Gln Asn Gly Arg Gln Cys Tyr Ser Cys Lys Gly Asn Ser Thr
    210                 215                 220

His Gly Cys Ser Ser Glu Glu Thr Phe Leu Ile Asp Cys Arg Gly Pro
225                 230                 235                 240

Met Asn Gln Cys Leu Val Ala Thr Gly Thr His Glu Pro Lys Asn Gln
                245                 250                 255

Ser Tyr Met Val Arg Gly Cys Ala Thr Ala Ser Met Cys Gln His Ala
            260                 265                 270

His Leu Gly Asp Ala Phe Ser Met Asn His Ile Asp Val Ser Cys Cys
        275                 280                 285

Thr Lys Ser Gly Cys Asn His Pro Asp Leu Asp Val Gln Tyr Arg Ser
    290                 295                 300

Gly Ala Ala Pro Gln Pro Gly Pro Ala His Leu Ser Leu Thr Ile Thr
305                 310                 315                 320

Leu Leu Met Thr Ala Arg Leu Trp Gly Gly Thr Leu Leu Trp Thr
                325                 330                 335
```

<210> 18
<211> 187
<212> PRT
<213> artificial

<220>
<223> DHFR

<400> 18

```
Met Val Gly Ser Leu Asn Cys Ile Val Ala Val Ser Gln Asn Met Gly
1               5                  10                  15


Ile Gly Lys Asn Gly Asp Leu Pro Trp Pro Pro Leu Arg Asn Glu Phe
            20                  25                  30


Arg Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu Gly Lys Gln
        35                  40                  45


Asn Leu Val Ile Met Gly Lys Lys Thr Trp Phe Ser Ile Pro Glu Lys
    50                  55                  60


Asn Arg Pro Leu Lys Gly Arg Ile Asn Leu Val Leu Ser Arg Glu Leu
65                  70                  75                  80


Lys Glu Pro Pro Gln Gly Ala His Phe Leu Ser Arg Ser Leu Asp Asp
                85                  90                  95


Ala Leu Lys Leu Thr Glu Gln Pro Glu Leu Ala Asn Lys Val Asp Met
            100                 105                 110


Val Trp Ile Val Gly Gly Ser Ser Val Tyr Lys Glu Ala Met Asn His
        115                 120                 125


Pro Gly His Leu Lys Leu Phe Val Thr Arg Ile Met Gln Asp Phe Glu
    130                 135                 140


Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Glu Lys Tyr Lys Leu Leu
145                 150                 155                 160
```

Pro Glu Tyr Pro Gly Val Leu Ser Asp Val Gln Glu Glu Lys Gly Ile
165 170 175

Lys Tyr Lys Phe Glu Val Tyr Glu Lys Asn Asp
180 185

<210> 19
<211> 255
<212> PRT
<213> artificial

<220>
<223> scFv against FITC: 4M5.3(Kd = 200pM)

<400> 19

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Arg Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Val Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Ser Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala
115 120 125

Lys Lys Asp Asp Ala Lys Lys Asp Gly Gly Val Lys Leu Asp Glu Thr
130 135 140

```
Gly Gly Gly Leu Val Gln Pro Gly Gly Ala Met Lys Leu Ser Cys Val
145                 150                 155                 160


Thr Ser Gly Phe Thr Phe Gly His Tyr Trp Met Asn Trp Val Arg Gln
                165                 170                 175


Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Gln Phe Arg Asn Lys Pro
            180                 185                 190


Tyr Asn Tyr Glu Thr Tyr Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr
        195                 200                 205


Ile Ser Arg Asp Asp Ser Lys Ser Ser Val Tyr Leu Gln Met Asn Asn
    210                 215                 220


Leu Arg Val Glu Asp Thr Gly Ile Tyr Tyr Cys Thr Gly Ala Ser Tyr
225                 230                 235                 240


Gly Met Glu Tyr Leu Gly Gln Gly Thr Ser Val Thr Val Ser Ser
                245                 250                 255


<210>  20
<211>  244
<212>  PRT
<213>  artificial

<220>
<223>  scFv against FITC 4D5Flu (Kd=10nM)

<400>  20

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
            20                  25                  30


Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

```
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Gly Gly Gly
            100                 105                 110

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
        115                 120                 125

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
    130                 135                 140

Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp
145                 150                 155                 160

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr
                165                 170                 175

Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe
            180                 185                 190

Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn
        195                 200                 205

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly
    210                 215                 220

Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val
225                 230                 235                 240

Thr Val Ser Ser
```

<210> 21
<211> 244
<212> PRT
<213> artificial

<220>
<223> scFv against DNP SPE7

<400> 21

```
Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu
1               5                  10                  15


Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe
    50                  55                  60


Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
                85                  90                  95


His Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
            100                 105                 110


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
        115                 120                 125


Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu
    130                 135                 140


Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met His Trp
145                 150                 155                 160


Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile Gly Arg Ile Asp
                165                 170                 175
```

```
Pro Asn Gly Gly Gly Thr Lys Tyr Asn Glu Lys Phe Lys Ser Lys Ala
            180                 185                 190


Thr Leu Thr Val Asp Lys Pro Ser Ser Thr Ala Tyr Met Gln Leu Ser
        195                 200                 205


Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Met Trp
    210                 215                 220


Tyr Tyr Gly Thr Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
225                 230                 235                 240


Thr Val Ser Ser
```