

**PEPTIDE-LIPID CONSTRUCTS AND THEIR USE
IN DIAGNOSTIC AND THERAPEUTIC APPLICATIONS**

TECHNICAL FIELD

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The invention relates to methods for effecting qualitative and quantitative changes in the levels of peptide expressed at the surface of cells and multi-cellular structures, and constructs for use in such methods.

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In particular, the invention relates to peptide-lipid constructs for use in diagnostic and therapeutic applications, including serodiagnosis.

15

BACKGROUND ART

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The ability to effect qualitative and quantitative changes in the level of peptides expressed at the surface of cells and multi-cellular structures provides for a range of diagnostic and therapeutic applications.

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Qualitative and quantitative changes in the level of peptides expressed at the surface may modify trans-membrane transport, cell-solute and cell-cell interactions, and thus the functionality of the modified cell or multi-cellular structure.

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Known methods of effecting such changes include gene manipulation, chemical modification of endogenous membrane peptides, and "cell surface painting" using lipid anchors such as GPI.

The specification accompanying international application number PCT/NZ2005/000052 (publication number WO 2005/090368) describes the preparation of water soluble carbohydrate-lipid constructs for use in methods of effecting qualitative and quantitative changes in the level of carbohydrates expressed at the surface of cells and multicellular structures.

The specification accompanying international application number PCT/NZ2006/000245 (publication number WO 2007/035116) describes another method for the preparation of water soluble carbohydrate-lipid constructs where the carbohydrate is the polymer hyaluronic acid. Use of the construct to modify embryos and promote association with endometrial cells is described.

Relatively little work has been performed on the site-directed coupling of peptides to phospholipids as individual components prior to their incorporation in self assembling lipid structures, such as liposomes, or as would be required to provide peptide-lipid constructs for use in methods of effecting qualitative and quantitative changes in the level of peptide expressed at the surface of cells and multicellular structures.

A variety of standard techniques have been described for the covalent coupling of peptides to liposomes surfaces.

Martin *et al* (1990) has reviewed methods of attaching moieties including peptides, to the surface of liposomes.

Blume *et al* (1993) describes the coupling of the water soluble Glu-plasminogen to liposomes by the method described by Kung and Redemann (1986). The chemical ECDI (1-ethyl-(3-

dimethylaminopropyl) carbodiimide hydrochloride) is used to activate the liposomes prior to incubation of the activated liposome suspension with Glu-plasminogen. Proteo-PEG-coated liposomes with Glu-plasminogen covalently attached to the ends
5 of the distearylphosphatidylethanolamine (DSPE)-PEG-COOH are provided.

Haselgrübler *et al* (1995) describes a heterobifunctional crosslinker used to facilitate the preparation of
10 immunoliposomes. The crosslinker is synthesised from a diamine derivative of poly(ethylene glycol) (PEG, average molecular weight 800 dalton (18mer)). The crosslinker has 2-(pyridylthio)propionyl (PDP) and N-hydroxysuccinimide ester (NHS) as functional groups.

15 Ishida *et al* (2001) describes the preparation of liposomes bearing polyethylene glycol-coupled transferrin. Transferrin was conjugated via the terminal carboxyl residue of DSPE-PEG-COOH. The liposomes were proposed as having utility in *in vivo* cytoplasmic targeting of chemotherapeutic agents or
20 plasmid DNAs to target cells.

Massaguer *et al* (2001) describes the incorporation of a peptide sequence (GGRGRS) and hydrophobic derivatives to the
25 surface of chemically activated liposomes. The incorporation was carried out through the carboxyl group of N-glutaryl dipalmitoyl phosphatidyl choline (NGPE).

Massaguer *et al* (2001) noted that considering potential *in vivo* applications, where sterility and simplicity would be
30 some of the most important requirements, processes based on chemical reactions on the surface of liposomes involving extra steps would be more difficult to be scaled up at the

industrial level. A hydrophobic derivative of the peptide sequence was identified as providing optimal properties for incorporation to the surface of liposomes.

- 5 Chung *et al* (2004) describe the antigenic determinant shielding effect of DOPE-PEG incorporated into the membranes of cells and speculated concerning the potential of lipid-PEG(n)(s) to regulate biological cell responses and the extension of this concept to the introduction of functional
10 molecules at the end of the PEG chain.

- Kato *et al* (2004) describe a method for anchoring of macromolecular proteins into the membranes of living mammalian cells. A dioleoylphosphatidylethanolamine (DOPE) derivative
15 coupled with hydrophilic poly(ethylene glycol) (PEG80) was used as the synthetic membrane anchor. Peptides were conjugated at the distal terminal of the PEG moiety via an amino-reactive N-hydroxysuccinimide derivative of the synthetic membrane anchor.

20

- The PEG80 moiety facilitated solubilisation of the synthetic membrane anchor in water. As noted by Kato *et al* (2004) if the anchor is insoluble in water, undesirable and complicated processes such as liposome preparation and the fusion of
25 liposomes with the cell membrane may be required to anchor the conjugates into the cell membrane.

- An additional advantage noted by Kato *et al* (2004) was that synthetic membrane anchors with high hydrophile-lipophile
30 balance values (attributable to PEG spacer with a high number of oxyethylene units) were concluded to have no cytolytic activity. However, difficulties arise in the use of synthetic

membrane anchors including a PEG spacer with a high number of oxyethylene units.

5 Firstly, the expression of the conjugative peptide or other endogenous cell surface peptides may be masked by the PEG spacer. Secondly, a PEG spacer with a high number of oxyethylene units may elicit non-specific adherence of protein (including antibodies in certain individuals) and/or the non-specific activation of the complement cascade.

10

Winger et al (1996) describes the conjugation of bromoacetylated DSPE with a thiol terminated decapeptide comprising at its C-terminus the minimal human thrombin-receptor peptide agonist (HS---SerPheLeuLeuArgAsn).

15

Hashimoto et al (1986) describes the conjugation of iodoacetylated DSPE with thiolated compounds.

20 A need exists for peptide-lipid constructs that can be used to effect qualitative and quantitative changes in the level of peptides expressed at the surface of cells and multi-cellular structures.

25 It is an object of this invention to provide peptide-lipid constructs that satisfy this need or at least provide a useful choice.

DISCLOSURE OF INVENTION

30 In a **first** aspect the invention provides a method of detecting reactive antibody in the serum of a subject including the steps of:

- Contacting a sample of the serum with a suspension of cells modified to incorporate a peptide-lipid construct of the structure $(L-S-)_i F(-S-L)_j$ to provide a mixture;
- 5 • Incubating the mixture for a time and at a temperature sufficient to allow agglutination; and
- Determining the degree of agglutination of the cells in the mixture;

10

where:

F is a peptide comprising an epitope for the reactive antibody;

15

S is a spacer covalently linking F to L; and

L is a lipid selected from the group consisting of diacyl- and dialkyl-glycerolipids, including glycerophospholipids; and

i and j are independently 0 or 1,

20

Optionally, the method includes the preliminary step of:

- Adding an amount of the peptide to the sample of the serum;

25

where the amount of the peptide is sufficient to neutralize non-specific agglutination or confirm specificity of the reactive antibody.

Optionally, the method includes the intermediate step of:

- Adding an anti-subject globulin antibody to the mixture prior to determining the degree of agglutination of the cells of the mixture.

Preferably, the subject is a human.

Preferably, the cells are red blood cells.

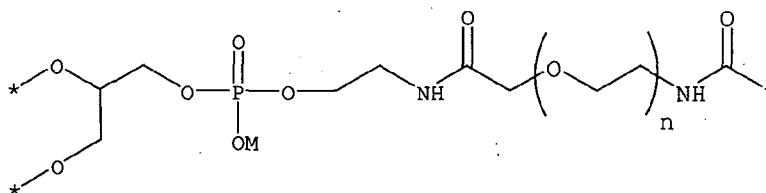
Preferably, the anti-subject globulin antibody is anti-human globulin (AHG) antibody.

Preferably, the reactive antibody is reactive to an antigen selected from the group consisting of: Glycophorin A, Glycophorin B, or mutations thereof (including the MNS blood group system).

The spacer (S) is selected to provide a water soluble peptide-lipid construct.

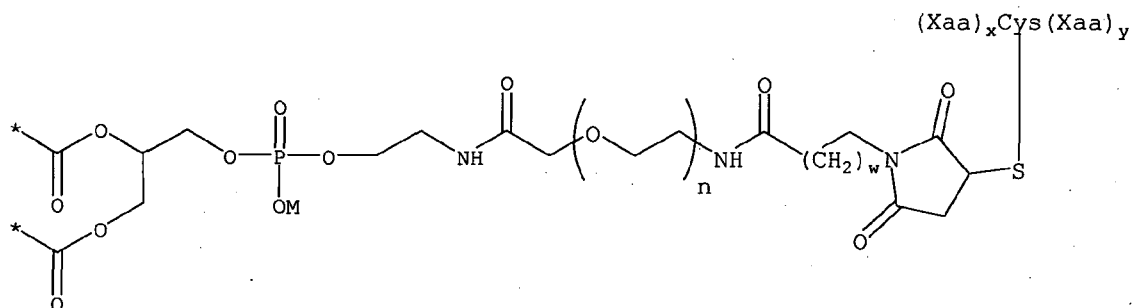
Preferably, S is a spacer covalently linking F to L via an oligomer of ethylene glycol.

- Preferably, the structure of the peptide-lipid construct includes the substructure:



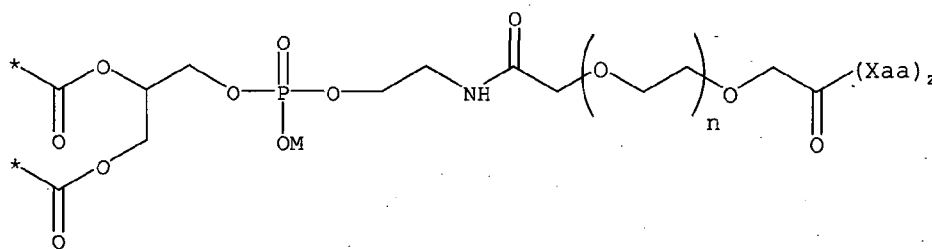
where M is a monovalent cation (M^+), n is 6 to 14 and * is other than H.

More preferably, the structure of the peptide-lipid construct
5 is either:



or

10



where M is a monovalent cation (M^+), n is 6 to 14, w is 1 or 2, the sum of x and y is greater than 5, z is greater than 5,
15 and * is other than H.

Preferably, the sum of i and j is 1.

Optionally, F is a peptide including a proximal terminal
20 sequence (PTS) selected to promote solubility of the peptide.

In a preferment of this option, the PTS of the peptide is selected from the group consisting of:

SerLysLysLysLysGly

AlaAlaAlaAla

GlySerGlySerGly

- 5 Preferably, F is a peptide comprising an epitope of antigens selected from the group consisting of: Glycophorin A, Glycophorin B, or mutations thereof (including the MNS blood group system).
- 10 More preferably, F is a peptide selected from the *List of Peptides*.

Most preferably, F is a peptide selected from the group consisting of:

15

GlnThrAsnAspLysHisLysArgAspThrTyrAlaAlaAlaAlaAlaCys

GlnThrAsnAspLysHisLysArgAspThrTyrGlySerGlySerGlyCys

GlnThrAsnAspMetHisLysArgAspThrTyrGlySerGlySerGlyCys

SerSerGlnThrAsnAspLysHisLysArgAspThrTyrCys

ThrTyrProAlaHisThrAlaAsnGluValCys

ProAlaHisThrAlaAsnGluValCys

SerGlnThrAsnAspLysHisLysArgAspCys

AlaAlaAlaAlaValMetTyrAlaSerSerGly

GlySerGlySerGlyValMetTyrAlaSerSerGly

Preferably, L is a glycerophospholipid. More preferably, L is a glycerophospholipid selected from the group consisting of: 1,2-O-dioleoyl-sn-glycero-3-phosphatidylethanolamine (DOPE)

and 1,2-O-distearyl-*sn*-glycero-3-phosphatidylethanolamine (DSPE).

Preferably, the peptide-lipid construct is an exemplifying
5 embodiment of the second or third aspect of the invention.

In a **second** aspect the invention provides a peptide-lipid construct of the structure:

10 L-S-F

where

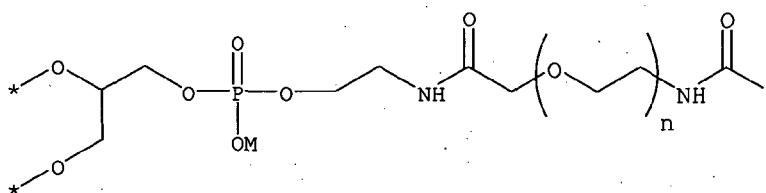
F is a peptide;

15 S is a spacer covalently linking F to L via an oligomer of ethylene glycol; and

L is a lipid selected from the group consisting of diacyl- and dialkyl-glycerolipids, including glycerophospholipids.

20

Preferably, the structure of the peptide-lipid construct includes the substructure:



25

where M is a monovalent cation (M^+), n is 6 to 14 and * is other than H.

Optionally, F is a peptide including a proximal terminal
30 sequence (PTS) selected to promote solubility of the peptide.

In a preferment of this option, the PTS of the peptide is selected from the group consisting of:

SerLysLysLysLysGly

AlaAlaAlaAla

GlySerGlySerGly

5

Preferably, the terminal sequence of the peptide is selected from the group consisting of:

GlyLysLysLysLysSerCys

AlaAlaAlaAlaCys

GlySerGlySerGlyCys

CysSerLysLysLysLysGly

CysAlaAlaAlaAla

CysGlySerGlySerGly

- 10 Preferably, S is covalently linked to F via a sulphide bond formed with the Cys residue of the peptide.

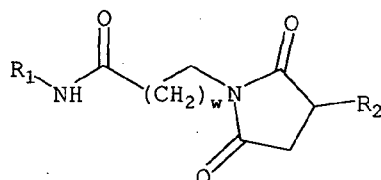
- More preferably, S is covalently linked to F via a sulphide bond formed with a Cys residue of the peptide at or proximal
15 to a terminus of the peptide.

Most preferably, S is linked to F via a sulphide bond formed with a Cys residue of the peptide at the carboxy-terminus of the peptide.

20

The spacer (S) is of the structure $S_1-S_2-S_3$ and selected to provide a water soluble peptide-lipid construct. S_1 is an oligomer of ethylene glycol.

Preferably, S_2-S_3 is selected from the group consisting of:

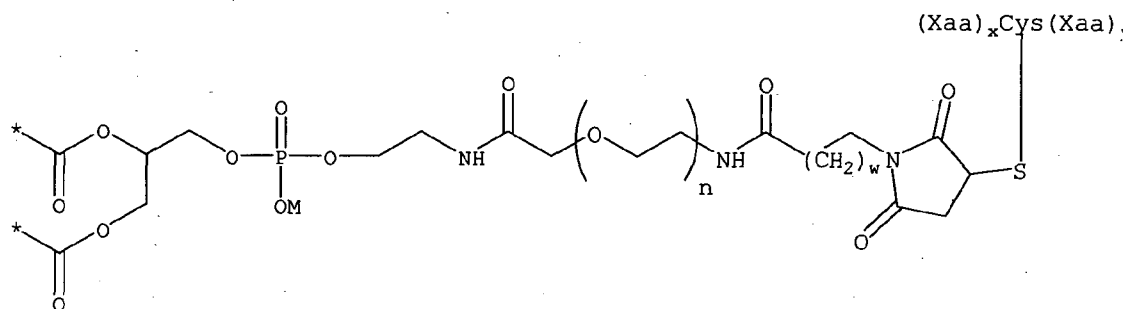


5

where R_1 is a terminal carbon of S_1 , R_2 is the sulphur of the Cys residue and w is 1 or 2.

Preferably, the structure of the peptide-lipid construct is:

10



where M is a monovalent cation (M^+), n is 6 to 14, w is 1 or 2, the sum of x and y is greater than 5, and $*$ is other than H. More preferably, n is 6. Most preferably, y is 0.

15

Preferably, F is a peptide comprising an epitope of antigens selected from the group consisting of: Glycophorin A, Glycophorin B, or mutations thereof (including the MNS blood group system).

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More preferably, F is a peptide selected from the *List of Peptides*.

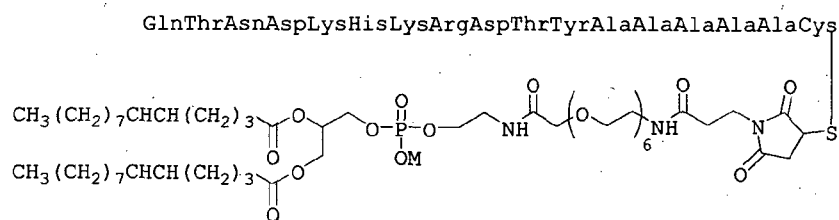
Most preferably, F is a peptide selected from the group consisting of:

GlnThrAsnAspLysHisLysArgAspThrTyrAlaAlaAlaAlaAlaCys
 GlnThrAsnAspLysHisLysArgAspThrTyrGlySerGlySerGlyCys
 GlnThrAsnAspMetHisLysArgAspThrTyrGlySerGlySerGlyCys
 SerSerGlnThrAsnAspLysHisLysArgAspThrTyrCys
 ThrTyrProAlaHisThrAlaAsnGluValCys
 ProAlaHisThrAlaAsnGluValCys
 SerGlnThrAsnAspLysHisLysArgAspCys

- 5 Preferably, L is a glycerophospholipid. More preferably, L is a glycerophospholipid selected from the group consisting of: 1,2-O-dioleoyl-*sn*-glycero-3-phosphatidylethanolamine (DOPE) and 1,2-O-distearyl-*sn*-glycero-3-phosphatidylethanolamine (DSPE).

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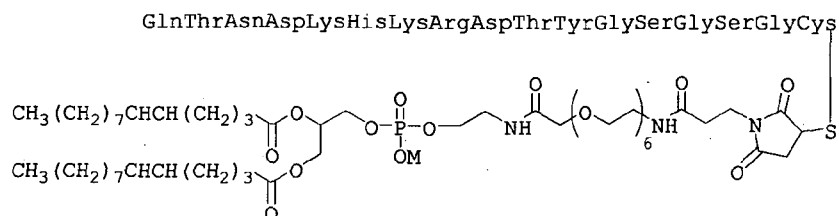
In an exemplifying **first** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:



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where M is a monovalent cation (M^+) and designated DOPE-PEG₆-βAla-Mal-PTS-1MUTK) (**M1**).

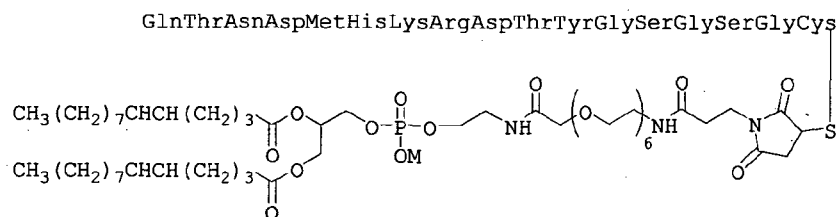
In an exemplifying **second** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:



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where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-PTS-2MUTK (**M2**).

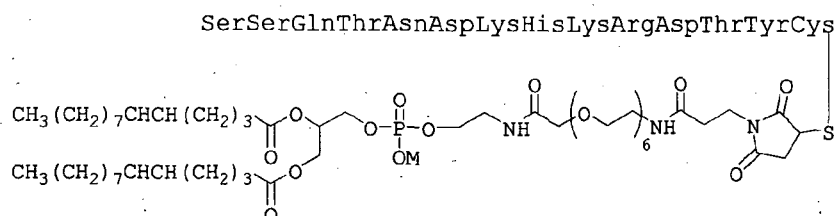
In an exemplifying **third** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:



where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-PTS-3MUTM (**M3**).

15

In an exemplifying **fourth** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:

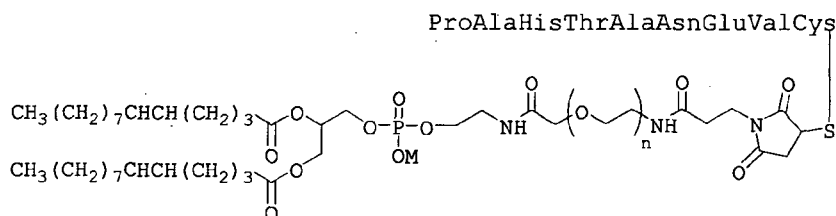


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where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-13MUTK (**M13**).

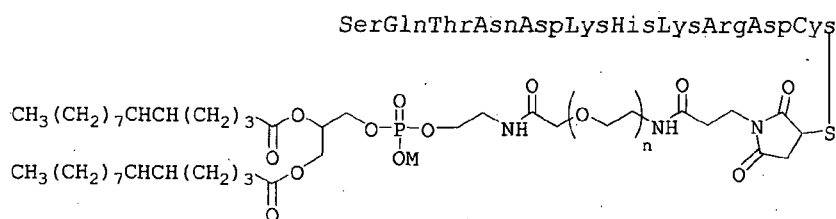
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In an exemplifying **fifth** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:



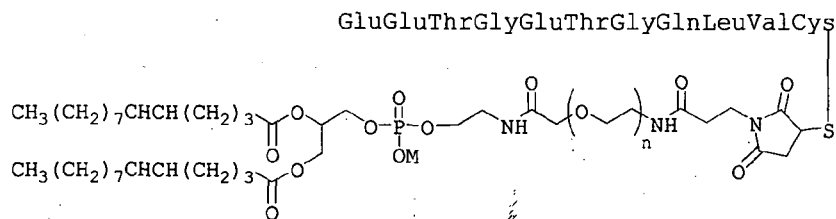
where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-18Mur (**M18**) (n=6).

10 In an exemplifying **sixth** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:



15 where M is a monovalent cation (M^+) and designated DOPE-PEG₆-
βAla-Mal-21MUTK(**M21**) (n=6).

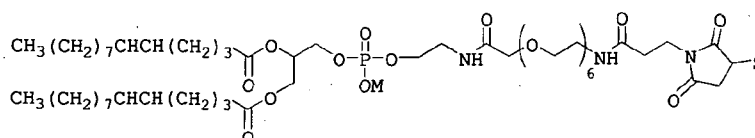
In an exemplifying **seventh** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:



where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-Hil3(M23) (n=6).

In an exemplifying **eighth** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:

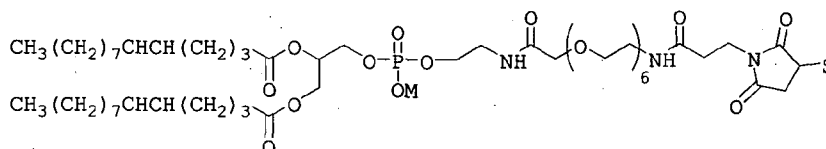
GlnThrAsnAspLysHisLysArgAspThrTyrSerSerGlnThrAsnAspMetHisLysArgAspThrTyrGlySerGlySerGlyCys



where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-PTS-Milt(K,M).

In an exemplifying **ninth** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:

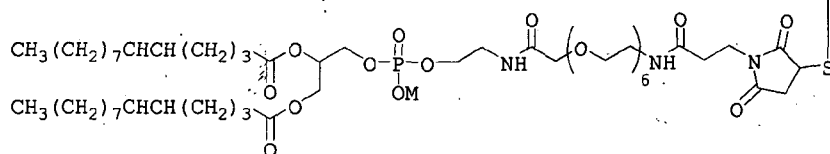
GlnThrAsnAspLysHisLysArgAspThrTyrCys



where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-Milt(K) (M00).

In an exemplifying **tenth** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:

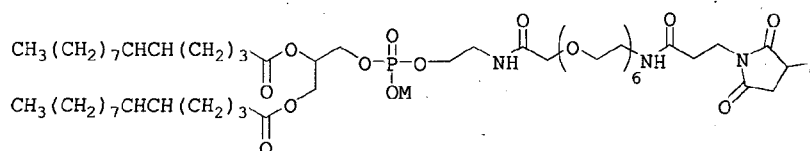
GlnThrAsnAspMetHisLysArgAspThrTyrCys



where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-Milt(M).

- 5 In an exemplifying **eleventh** embodiment of the second aspect the invention provides a peptide-lipid construct of the structure:

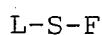
GlnThrAsnAspLysHisLysArgAspThrTyrSerSerGlnThrAsnAspMetHisLysArgAspThrTyrCys



10

where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-Milt(K,M).

- 15 In a **third** aspect the invention provides a peptide-lipid construct of the structure:



where

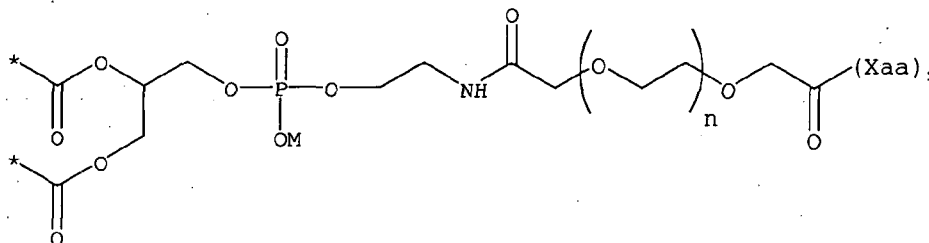
20

F is a peptide;

S is a spacer covalently linking F to L via an oligomer of ethylene glycol; and

- 25 L is a lipid selected from the group consisting of diacyl- and dialkyl-glycerolipids, including glycerophospholipids.

Preferably, the structure of the peptide-lipid construct is:



- 5 where M is a monovalent cation (M^+), n is 6 to 14, z is greater than 5, and * is other than H. More preferably, n is 14.

Optionally, F is a peptide including a terminal sequence
10 selected to promote solubility of the peptide.

In a preferment of this option, the terminal sequence of the peptide is selected from the group consisting of:

SerLysLysLysLysGly

AlaAlaAlaAla

GlySerGlySerGly

15

Preferably, F is a peptide selected from the group consisting of:

(Xaa)_zValMetTyrAlaSerSerGly;

20

where z is the integer 4, 5 or 6.

Preferably, F is a peptide selected from the group consisting of:

SerLysLysLysLysGlyValMetTyrAlaSerSerGly

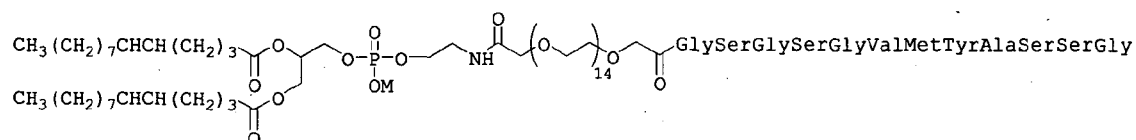
AlaAlaAlaAlaValMetTyrAlaSerSerGly

GlySerGlySerGlyValMetTyrAlaSerSerGly

- 5 Preferably, L is a glycerophospholipid. More preferably, L is a glycerophospholipid selected from the group consisting of: 1,2-O-dioleoyl-*sn*-glycero-3-phosphatidylethanolamine (DOPE) and 1,2-O-distearyl-*sn*-glycero-3-phosphatidylethanolamine (DSPE).

10

In an exemplifying **first** embodiment of the third aspect the invention provides a peptide-lipid construct of the structure:



15

where M is a monovalent cation (M^+) and designated DOPE-PEG₁₄-Syph.

- In a **fourth** aspect the invention provides a method of
 20 preparing a peptide-lipid construct (F-S-L) of the second aspect of the invention including the steps of:

- Preparing a maleimido-derivative of a precursor construct by reacting a maleimido-donating reagent with a precursor
 25 construct of the structure L-S₁-NH₂; and

- Reacting the maleimido-derivative of the precursor construct with a peptide (F) including a Cys residue and solubilised in a solvent.

5 where:

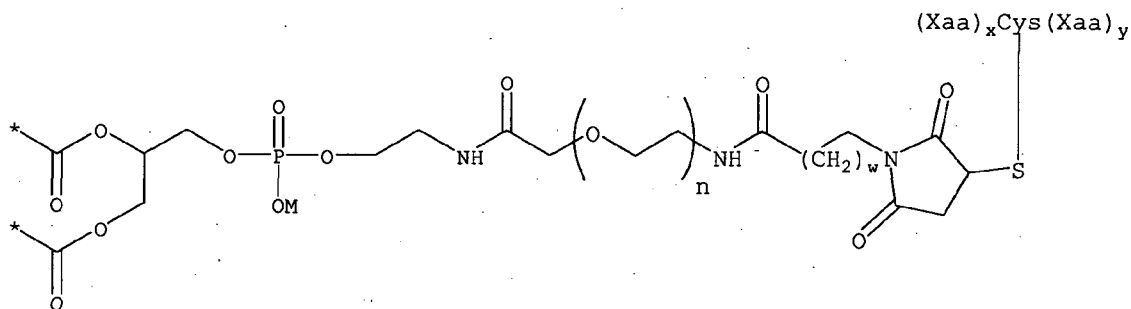
L is a lipid selected from the group consisting of diacyl- and dialkyl-glycerolipids, including glycerophospholipids; and

10

S₁ is selected from the group consisting of oligomers of ethylene glycol.

Preferably, the structure of the peptide-lipid construct is:

15



where n is 6 to 14, w is 1 or 2, the sum of x and y is greater than 5, and * is other than H.

20

Preferably the maleimido-donating reagent is selected from the group consisting of: N-oxysuccinimide ester of maleimidobutyric acid; and N-oxysuccinimide ester of maleimidopropionic acid

25 Preferably, S₁ is an oligomer of ethylene glycol selected from the group consisting of 6 to 14 mer PEG (PEG₆ to PEG₁₄). Most preferably, S₁ is PEG₆.

Preferably, the solvent is selected from the group consisting of: trifluoroethanol; DMSO; or mixtures thereof.

Preferably, the Cys residue is a terminal Cys residue.

5

Optionally, F is a peptide including a proximal terminal sequence (PTS) selected to promote solubility of the peptide in the reaction solvent.

- 10 In a preferment of this option, the PTS of the peptide is selected from the group consisting of:

SerLysLysLysLysGly

AlaAlaAlaAla

GlySerGlySerGly

- 15 Preferably, the terminal sequence of the peptide is selected from the group consisting of:

GlyLysLysLysLysSerCys

AlaAlaAlaAlaCys

GlySerGlySerGlyCys

CysSerLysLysLysLysGly

CysAlaAlaAlaAla

CysGlySerGlySerGly

Preferably, F is a peptide selected from the *List of Peptides*.

- 20 Preferably, F is a peptide selected from the group consisting of:

GlnThrAsnAspLysHisLysArgAspThrTyrAlaAlaAlaAlaAlaCys

GlnThrAsnAspLysHisLysArgAspThrTyrGlySerGlySerGlyCys
 GlnThrAsnAspMetHisLysArgAspThrTyrGlySerGlySerGlyCys
 SerSerGlnThrAsnAspLysHisLysArgAspThrTyrCys
 ThrTyrProAlaHisThrAlaAsnGluValCys
 ProAlaHisThrAlaAsnGluValCys
 SerGlnThrAsnAspLysHisLysArgAspCys

Preferably, L is a glycerophospholipid. More preferably, L is a glycerophospholipid selected from the group consisting of: 1,2-O-dioleoyl-*sn*-glycero-3-phosphatidylethanolamine (DOPE) and 1,2-O-distearyl-*sn*-glycero-3-phosphatidylethanolamine (DSPE).

In a **fifth** aspect the invention provides a method of effecting qualitative and quantitative changes in the levels of peptide expressed at the surface of cells and multi-cellular structures including the step of:

- contacting the cells or multi-cellular structures with a solution of a peptide-lipid construct of the second or third aspects of the invention at a concentration and for a time and temperature sufficient to allow the construct to incorporate into the surface.

Preferably, the peptide-lipid construct is a construct of the second aspect of the invention.

Preferably the cells or multicellular structures are selected from the group consisting of: red blood cells; and embryos. More preferably, the cells or multicellular structures are human cells or multicellular structures.

Preferably, the time and temperature is no greater than 2 hours at 37 °C or 24 hours at 4 °C.

In all aspects of the invention M is typically H, but may be replaced by another monovalent cation such as Na⁺, K⁺ or NH₄⁺.

In the description and claims of the specification the following acronyms, phrases and terms have the meaning provided:

10

"Diagnostic marker" means a molecule, the presence of which in a body fluid of a subject is diagnostic of a phenotype or pathological condition of the subject.

15

"MNS blood group system " means blood group antigens or epitopes of those antigens and mutations which are present on either glycophorin A, glycophorin B or mutations which result in glycophorin A/B hybrids.

20

"Proximal terminal sequence" means that portion of the peptide sequence proximal to the amino- or carboxy- terminus of the peptide (F).

"RBC" means red blood cells.

25

"Reactive antibody" means an immunoglobulin, the presence of which in a body fluid of a subject is diagnostic of a phenotype or pathological condition of the subject.

30

"Via an oligomer of ethylene glycol" means a polymer of ethylene glycol consisting of 2 to 32 mer and specifically excludes via a polymer of ethylene glycol consisting of greater than 32 mer.

"Water soluble" means a stable, single phase system is formed when the construct is contacted with water or saline (such as PBS) at a concentration of at least 100 µg/ml and in the absence of organic solvents or detergents. The phrase is used synonymously with the term "water dispersible".

Exemplifying embodiments of the invention are claimed and will now be described in detail with reference to the Figures of the accompanying drawings pages.

BRIEF DESCRIPTION OF DRAWINGS

Figure 1. ¹H-NMR spectrum of the peptide-lipid construct designated DOPE-PEG₆-βAla-Mal-Milt(K) (**M13**) (5 mg/ml in CD₃OD/CDCl₃/D₂O/0.5M CF₃COOD 60/20/10/1, 600 MHz, 30 °C, δ ppm).

Figure 2. MALDI TOF mass-spectrum of the peptide-lipid construct designated DOPE-PEG₆-βAla-Mal-Milt(K) (**M13**) (2856:Peptide-DOPE (M+H); 2878:Peptide-DOPE (M+Na); 2894:Peptide-DOPE (M+K); 2900:Peptide-DOPE (M+Na, Na salt); 2916:Peptide-DOPE (M+K, Na salt)).

Figure 3. ESI mass-spectrum and analytical HPLC of the peptide SerSerGlnThrAsnAspLysHisLysArgAspThrTyrGlySerGlySerGlyCys of the peptide-lipid construct designated DOPE-PEG₆-βAla-Mal-Milt(K) (**M13**).

Figure 4. ¹H-NMR spectrum of the peptide SerSerGlnThrAsnAspLysHisLysArgAspThrTyrGlySerGlySerGlyCys of the peptide-lipid construct designated DOPE-PEG₆-βAla-Mal-Milt(K) (**M13**) (4.5 mg/ml in D₂O, 600 MHz, 30 °C, δ ppm).

Figure 5. Photomicrographs of zona free embryos modified to incorporate the M2 peptide-lipid construct by contacting the embryos with a dispersion of the construct at a concentration of 1 mg/mL for 2 hours. The upper photomicrograph is the DIC image. The lower photomicrograph is the fluorescent image showing 3.0+ fluorescence.

DETAILED DESCRIPTION

In general terms the invention provides peptide-lipid constructs of the structure $(L-S)_i F(-S-L)_j$ where:

5

F is a peptide;

S is a spacer covalently linking F to L;

L is a lipid selected from the group consisting of diacyl- and dialkyl-glycerolipids, including glycerophospholipids;

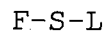
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i and j are independently 0 or 1;

and the use of these peptide-lipid constructs in diagnostic and therapeutic applications.

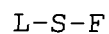
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Where i is 0 and j is 1 the peptide-lipid constructs are of the structure:



20

Where i is 1 and j is 0 the peptide-lipid constructs are of the structure:



25

Where S is linked to F via the amino terminus of the peptide the construct is represented by the structure or substructure L-S-F.

30

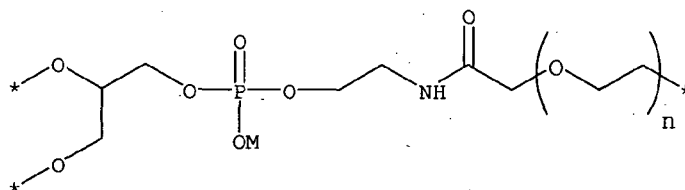
Where S is linked to F via the carboxyl terminus of the peptide the construct is represented by the structure or substructure F-S-L.

Where S is linked to F via a sulphide bond formed via the sulfhydryl group of a Cys residue of the peptide the residue is identified with an underscore (Cys).

- 5 Where S is linked to F via a sulphide bond formed with one or more Cys residues of the peptide, the representation of the peptide-lipid construct by the structure L-S-F-S-L, L-S-F or F-S-L is not intended to imply the sulphide bond is formed exclusively with terminal Cys residues.

10

The use of the peptide-lipid constructs in diagnostic applications is illustrated with reference to the use of constructs including the substructure:



15

where M is a monovalent cation (M^+), n is 6 to 14, * is other than H, and the peptide is selected from the group of peptides consisting of peptides included in the *List of Peptides*
 20 provided on the following pages where z is an integer from 0 to 6.

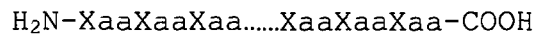
[followed by pages 27 & 28]

List of Peptides	
<u>Cys(Xaa)_zTrpThrProProArgAlaGlnIleThrGlyTyrLeuThrValGlyLeuThrArgArg</u>	ValMetTyrAlaSerSerGly(Xaa) _z Cys
<u>Cys(Xaa)_zTrpThrProProArgAlaGlnIleThrGlyTyrArgLeuThrValGlyLeuThrArgArg</u>	AspTyrHisArgValMetTyrAlaSerSerGly(Xaa) _z Cys
<u>Cys(Xaa)_zValMetTyrAlaSerSerGly</u>	ThrAsnGlyGluThrGlyGlnLeuValHisArgPhe(Xaa) _z Cys
	ThrAsnGlyGluMetGlyGlnLeuValHisArgPhe(Xaa) _z Cys
	AspThrTyrProAlaHisThrAlaAsnGluValSerGlu(Xaa) _z Cys
	ThrTyrProAlaHisThrAlaAsnGluVal(Xaa) _z Cys
	ProAlaHisThrAlaAsnGluVal(Xaa) _z Cys
	TyrProAlaHisThrAlaAsnGlu(Xaa) _z Cys
	ThrTyrProAlaHisThrAlaAsn(Xaa) _z Cys
	ThrTyrProAlaHisThrAlaAsnGlu(Xaa) _z Cys
	TyrProAlaHisThrAlaAsnGluVal(Xaa) _z Cys
	ProAlaHisThrAlaAsnGluValSer(Xaa) _z Cys
	AspThrTyrProAlaHisThrAlaAsnGlu(Xaa) _z Cys
	TyrProAlaHisThrAlaAsnGluValSer(Xaa) _z Cys

List of Peptides	
	SerGlnThrAsnAspLysHisLysArgAsp(Xaa) ₂ Cys
	GlnThrAsnAspLysHisLysArgAspThrTyr(Xaa) ₂ Cys
GlnThrAsnAspLysHisLysArgAspThrTyrSerSerGlnThrAsnAspMetHisLysArgAspThrTyr(Xaa) ₂ Cys	
	GlnThrAsnAspMetHisLysArgAspThrTyr(Xaa) ₂ Cys
	SerSerGlnThrAsnAspLysHisLysArg(Xaa) ₂ Cys
	SerSerGlnThrAsnAspLysHisLysArgAspThrTyr(Xaa) ₂ Cys
	SerSerGlnThrAsnAspMetHisLysArgAspThrTyr(Xaa) ₂ Cys
SerSerGlnThrAsnAspLysHisLysArgAspThrTyrSerSerGlnThrAsnAspMetHisLysArgAspThrTyr(Xaa) ₂ Cys	
	GlnThrAsnAspLysHisLysArgAspThr(Xaa) ₂ Cys
	SerGlnThrAsnAspLysHisLysArgAspThr(Xaa) ₂ Cys
	ThrAsnAspLysHisLysArgAspThrTyrPro(Xaa) ₂ Cys
	GluGluThrGlyGluThrGlyGlnLeuVal(Xaa) ₂ Cys
	GluGluGluThrGlyGluThrGlyGlnLeu(Xaa) ₂ Cys
	GluThrGlyGluThrGlyGlnLeuValHis(Xaa) ₂ Cys
	SerProProArgArgAlaArgValThr(Xaa) ₂ Cys
TyrArgTyrArgTyrThrProLysGluLysThrGlyProMetLysGlu(Xaa) ₂ Cys	
	TrpGlnProProArgAlaArgIle(Xaa) ₂ Cys
	ThrIleThrGlyLeuGluProGlyThrGlu(Xaa) ₂ Cys

The amino acid residues of peptides are identified according to Table 3 of Appendix 2 of Annex C of the *Administrative Instructions under the Patent Cooperation Treaty* dated 7 February 2007 and in accordance with the convention:

5



There is a need for inexpensive and low level sensitivity test systems for a range of diagnostic markers in donated blood, in
10 transfusion recipients, or in antenatal patients (where the unborn child may be at risk of haemolytic disease), e.g. syphilis markers and markers of the MNS blood group system. A particular advantage provided by the invention is the opportunity to employ established blood typing platforms to
15 detect a range of peptide antigen-antibody interactions. The capital costs associated with establishing a new diagnostic assay may therefore be avoided.

Some clinically significant blood group antigens are rare (or
20 rare in some populations). For example mutations of the MNS blood group system resulting in Miltenberger antigens are rare in Europeans, but common in Asians. Being able to create antibody detection and identification panels requires that these antigens be present on the diagnostic screening cells.
25 Obtaining cells suitable for antibody screening/identification having rare antigens is therefore problematic. Being able to add to cells rare antigens prepared exogenously is therefore a major advantage.

30 According to the method of the invention epitope containing peptide sequences for a range of diagnostic markers, such as specific reacting antibodies, can be localized to the surface of red blood cells (RBCs). These modified RBCs may then be

used on existing blood typing platforms to detect blood antibodies or pathologies.

Although the invention is illustrated with reference to the
5 modification of red blood cells and embryos the outer surface
of other cells and multi-cellular structures is contemplated.
However, red blood cells are preferred for use in diagnostic
assays because of the facility with which these modified cells
could be used in blood typing laboratories.

10 The level of peptide-lipid construct incorporated into the
cell membrane of red blood cells is controlled by the
concentration of the construct in the dispersion contacted
with the suspension. The presence of diagnostic markers may
15 then be assessed by agglutination whether direct (induced by
centrifugation of cells) or indirect (induced by adding an
antibody directed against the immunoglobulins of the subject).
Other methods of assessment may be employed including, for
example, rosetting (Indiveri *et al* 1979) and enzyme linked
20 immunosorbant assays (ELISA).

In contrast with the preparation of constructs where the
function (F) is a carbohydrate, the preparation of constructs
where F is a peptide presents a combination of technical
25 difficulties.

Firstly, it is desirable for the peptide (F) ligated to the L-
S or S-L moiety to be dispersible in the solvents used for the
ligation chemistry. Overcoming this difficulty may require
30 the selection of a proximal terminal sequence (PTS) to promote
solubility without modifying the desired biological properties
of the construct.

Secondly, it is r for the construct (L-S-F-S-L, L-S-F or F-S-L) to be dispersible in water, or at least a biocompatible medium such as buffered saline, according to the requirements of the proposed application (i.e. it is desirable for the
5 construct to be "water soluble" as defined herein).

Overcoming this difficulty requires the selection of a spacer (S) to promote solubility of the construct.

Thirdly, where the proposed application is the modification of
10 cells such as red blood cells (RBCs) for use in diagnostic applications, including use as quality controls in blood group typing or detection of diagnostic antibodies present in patient serum, it is required for the construct to be dispersible without participating in antigen-antibody cross
15 reactivity not specific to the diagnostic marker. Satisfying this requirement requires the identification of suitable structural motifs for the spacer (S) and proximal terminal sequence (PTS) when the latter is present, or the development of sample preparation procedures that neutralize or at least
20 substantially mitigate the undesired cross reactivity and likelihood of false positives.

It should also be noted that where the application is for use in the modification of the surface of cells or multi-cellular
25 structures (e.g. an embryo) with a view to promoting the association of the modified cell or modified multi-cellular structure with a target surface (e.g. the endometrium) exposing the cell or multi-cellular structure to solvents is incompatible with maintaining the cells or multicellular
30 structures in a viable state.

The ability to localise peptides to the surface of cells or multi-cellular structures via a residue proximal to either the

N- or C- terminus of the peptide may also allow the naturally occurring configuration of the peptide sequence relative to the cell surface to be approximated. The presentation of the peptide sequence in the tertiary (or quaternary) structure of the parent polypeptide (or protein) may therefore be mimicked.

Although not demonstrated here it is contemplated that peptides may be localised to the surface of cells via multiple residues. For example, where both a residue proximal to the amino terminus and a residue proximal to the carboxyl terminus are used to localize the peptide, a "looped" configuration of the peptide may be promoted at the surface.

The use of polyethylene glycol (PEG) as a spacer to promote solubility is known. However, polymers of PEG may interfere with the expression and function of the peptide at the surface. In the peptide-lipid constructs of the invention an oligomer of ethylene glycol (6 to 14 mer) is selected as a component (S_1) of the spacer (S) linking the lipid (L) and peptide (F).

Oligomers of ethylene glycol impart less solubility to peptide-lipid constructs of the structure L-S-F than polymers of PEG. The difficulty referred to above therefore arises when it is desired to obtain peptide-lipid constructs that are dispersible in biocompatible solvents and can be used in methods of effecting qualitative and quantitative changes in the levels of peptide expressed at the surface of cells and multi-cellular structures.

The properties of the peptide-lipid constructs must be such that they can be readily dispersed in biologically compatible media in the absence of solvents or detergents, but

incorporate into the lipid bilayer of a membrane when a solution of the construct is contacted with a suspension of cells or multi-cellular structures.

- 5 Peptide-lipid constructs with these potentially conflicting properties are prepared by adopting the combination of structural motifs described here. The preparation of the peptide-lipid constructs where S is linked to F via a sulphide bond formed with a terminal Cys residue of the peptide at the
10 carboxy-terminus of the peptide is preferred as the peptide is less prone to oxidation.

Adopting the combinations of structural motifs in accordance with the description provided here a range of peptides may be
15 prepared as peptide-lipid constructs for use in methods of effecting qualitative and quantitative changes in the levels of peptide expressed at the surface of cells and multi-cellular structures.

- 20 It will be understood that for a non-specific interaction, such as the interaction between diacyl- or dialkyl-glycerolipids or glycerophospholipids and a membrane, structural and stereo-isomers of naturally occurring lipids can be functionally equivalent. For example, it is
25 contemplated that diacylglycerol 2-phosphate could be substituted for phosphatidate (diacylglycerol 3-phosphate). Furthermore it is contemplated that the absolute configuration of phosphatidate can be either R or S.

30 *Preparation of DOPE-PEG₆-NH₂ (7)*

DOPE-PEG₆-NH₂ (L-S₁-NH₂) (7, 800 mg) was prepared by the method of SCHEME 1. To a stirred solution of DOPE (5) (36 mg, 0.0484

mmol) in dry CHCl_3 (3 ml) a solution of Fmoc-PEG-NOS (4) (237 mg, 0.0697 mmol (containing about 80% of active *N*-oxysuccinimide ester)) in dry CHCl_3 (1 ml) and Et_3NH (30 ml) was added.

5

The solution was stirred for 15 h at 20 °C, then Et_3NH (3 ml) was added, and the mixture was maintained for at 8 h at 20°C. The solution was then diluted with toluene (10 ml), evaporated under reduced pressure (10 to 15 torr) and dried under vacuum.

10

The crude residue was dissolved in $\text{H}_2\text{O}/\text{MeOH}/\text{AcOH}$ mixture (10:5:1 (v/v/v), 3 ml) and the solution was slowly applied to a reverse phase C_{16} column (15 ml, water). Salts, *N*-hydroxysuccinimide and H_2N -PEG-DOPE (7) were eluted from the column with $\text{MeOH}/\text{H}_2\text{O}$ 1:2 (v/v) (30 ml), 1:1 (v/v) (15 ml) and 2:1 (v/v) (15 ml). Target H_2N -PEG-DOPE (7) was eluted from the column with MeOH (30 ml) and then with MeOH to $\text{MeOH}/\text{CHCl}_3$ mixtures (4:1 (v/v), 3:1 (v/v), 2:1 (v/v) and 1:1 (v/v); 30 ml each). Fractions containing H_2N -PEG-DOPE (7) were combined, evaporated under reduced pressure (10 to 15 torr) and dried under vacuum.

20

The residue obtained as a thin film on the flask walls was extracted twice with hexane (2 x 5 ml) and dried under vacuum to yield 143 mg of H_2N -PEG-DOPE (7) (78% on DOPE) as a white solid. TLC: R_f = 0.62 (ethanol/water/pyridine/AcOH; 3:1:1:1 (v/v/v/v)).

25

^1H -NMR (500 MHz, CD_3OD , 30 °C): δ = 5.541 (m, 4H; 2 $-\text{CH}=\text{CH}-$), 5.416 (m, 1H; $\text{OCH}_2\text{CHCH}_2\text{O}$), 4.624 (dd, J = 12 Hz, J = 3.2 Hz, 1H; $\text{CO}-\text{OCHCHCH}_2$), 4.373 (dd, J = 12 Hz, J = 6.6 Hz, 1H; $\text{CO}-\text{OCHCHCH}_2$), 4.195 (t, J = 5.6 Hz, 2H; $\text{POCH}_2\text{CH}_2\text{N}$), 4.117 (m, 2H; POCHCHCH_2), 3.968 (m, 4H; $\text{OCH}_2\text{CH}_2\text{O}$, $\text{OCH}_2\text{CH}_2\text{N}$), 3.932 (t, J =

30

6.2 Hz, 2H; $\text{OCH}_2\text{CH}_2\text{CO}$), 3.827 (m, 272 H; $(-\text{OCH}_2\text{CH}_2-)_n$, $n = 68$),
3.683 (m, 2H; $\text{OCH}_2\text{CH}_2\text{O}$), 3.622 (t, $J = 5.6$ Hz, 2H; $\text{OCH}_2\text{CH}_2\text{N}$),
3.397 (t, $J = 5.0$ Hz, 2H; $\text{OCH}_2\text{CH}_2\text{N}$), 2.678 (t, $J = 6.2$ Hz, 2H;
 $\text{OCH}_2\text{CH}_2\text{CO}$), 2.519 (m, 4H; 2 CH_2CO), 2.228 (m, 8H; 2
5 $\text{CH}_2\text{CH}=\text{CHCH}_2$), 1.801 (m, 4H; 2 $\text{CH}_2\text{CH}_2\text{CO}$), 1.508 (m, 40H; $-\text{CH}_2-$),
1.096 (~t, 6H; 2 CH_3) ppm.

Preparation of peptide-lipid constructs

10 Maleimido-derivatives of DOPE-PEG₆-NH₂ were used for the
preparation of peptide-lipid constructs (L-S-F) by the method
of SCHEME 2 via the maleimide-thiol Michael addition reaction.

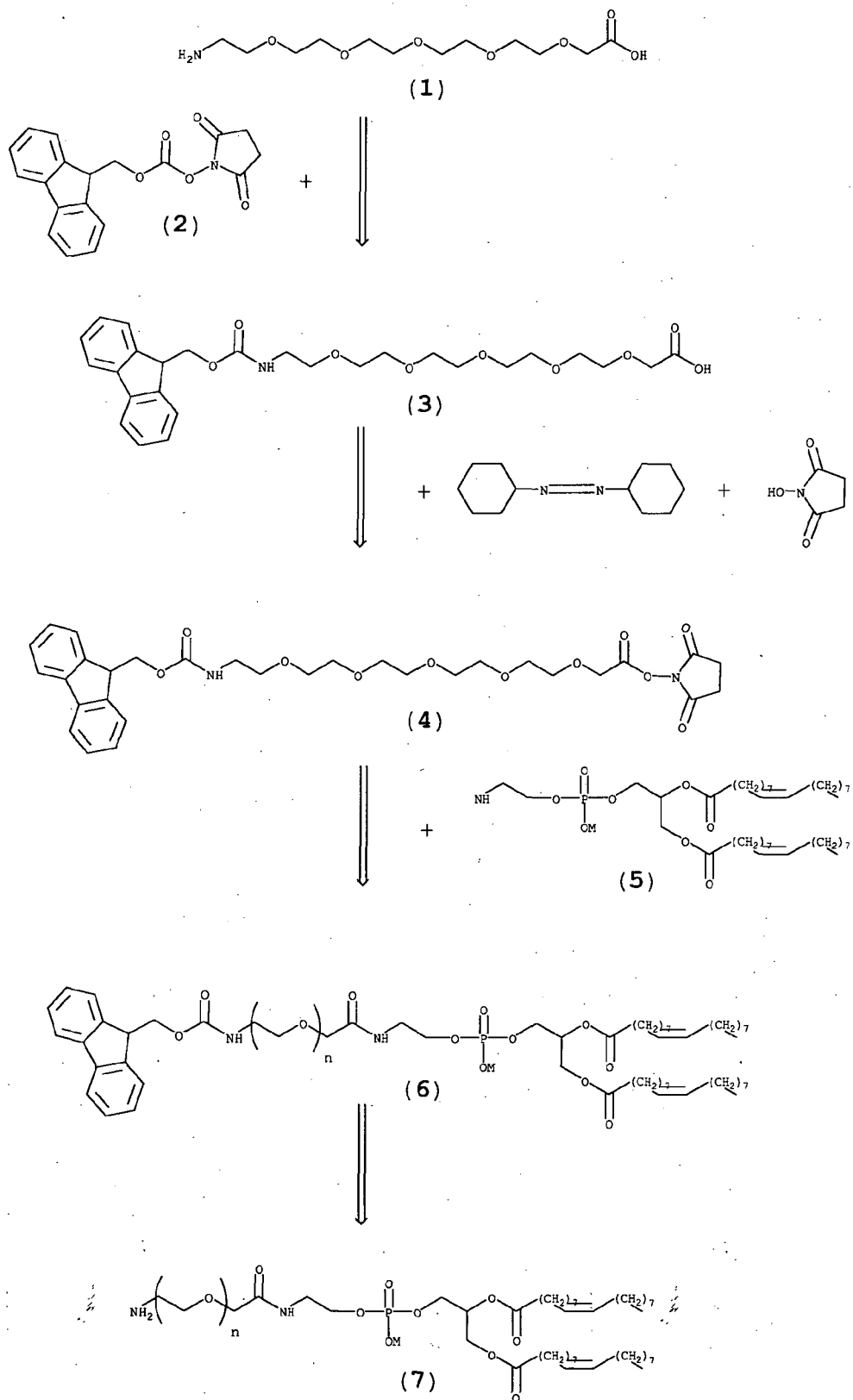
Synthesis via the maleimido-derivatives of DOPE-PEG₆-NH₂ has
15 particular advantages over synthesis via iodoacetate
derivatives as difficulties and low yields as a consequence of
oxidation of the sulfhydryl residues of the peptide and
subsequent dimer formation. Reducing agents (e.g. tertiary
phosphines) may be used during conjugation.

20

Maleimido-derivatives were synthesized with 65 to 70% yields
starting from N-oxysuccinimid esters of maleimidobutyric and
maleimidopropionic acids (**8a**, **8b**). An unexpected complication
arose due to the presence of excess Bu₃P which appeared to be
25 highly reactive towards the maleimide function. Phosphine was
therefore used only in sub-equivalent amounts (0.1 to 0.2
equivalents).

30 [followed by page 36]

SCHEME 1



Trifluoroethanol used as a co-solvent in the preparation of **10bC** where the peptide was GlnThrAsnAspMetHisLysArgAspThrTyr-GlySerGlySerGlyCys appeared to be highly efficient for
5 solubilization of both reactants. However, the solvent also caused unwanted acidification of the reaction medium which may inhibit the Michael reaction. The isolated yield of **10bC** in this experiment was ~25%. Preparation of **10aC** where the peptide was GlnThrAsnAspMetHisLysArgAspThrTyrGlySerGlySerGly-
10 Cys (DOPE-PEG₆-βAla-Mal-3MUTM (**M3**)) carried out using DMSO as co-solvent was more successful and provided a 43% yield.

The same solvent strategy in the preparation of **10bC** where the peptide was GlnThrAsnAspLysHisLysArgAspThrTyrSerSerGlnThrAsn-
15 AspMetHisLysArgAspThrTyrAlaAlaAlaAlaCys (DOPE-PEG₆-βAla-Mal-PTS-Milt(K,M)) failed because the peptide supplied appeared to be very acidic and caused solubilization problems. The yield of **10bC** in this experiment was only 23% and about half of the peptide was recovered.

20

Molecular weights for the peptide lipid constructs were determined to be:

DOPE-PEG₆-βAla-Mal-Milt(M) - 3029.48

25

DOPE-PEG₆-βAla-Mal-Milt(K,M) - 4591.12

As expected for peptides bearing the glutamine residue at the N-terminus, all preparations contain variable amounts of
30 related pyroglutamyl derivatives, M-17 in MS, due to loss of NH₃. The formation of related pyroglutamyl derivatives was mitigated in peptides with N-terminal Ser residues.

The use of the peptide-lipid constructs in methods for effecting qualitative and quantitative changes in the levels of peptide expressed at the surface of cells and multi-cellular structures is illustrated with reference to the serodiagnosis.

Modification of red blood cells with peptide-lipid constructs (general method)

Red blood cells are modified by mixing 1 part by volume of washed packed red blood cells with 1 part by volume of peptide-lipid construct dispersed at a concentration of 10 to 1000 µg/ml in cell media (Celpresol™).

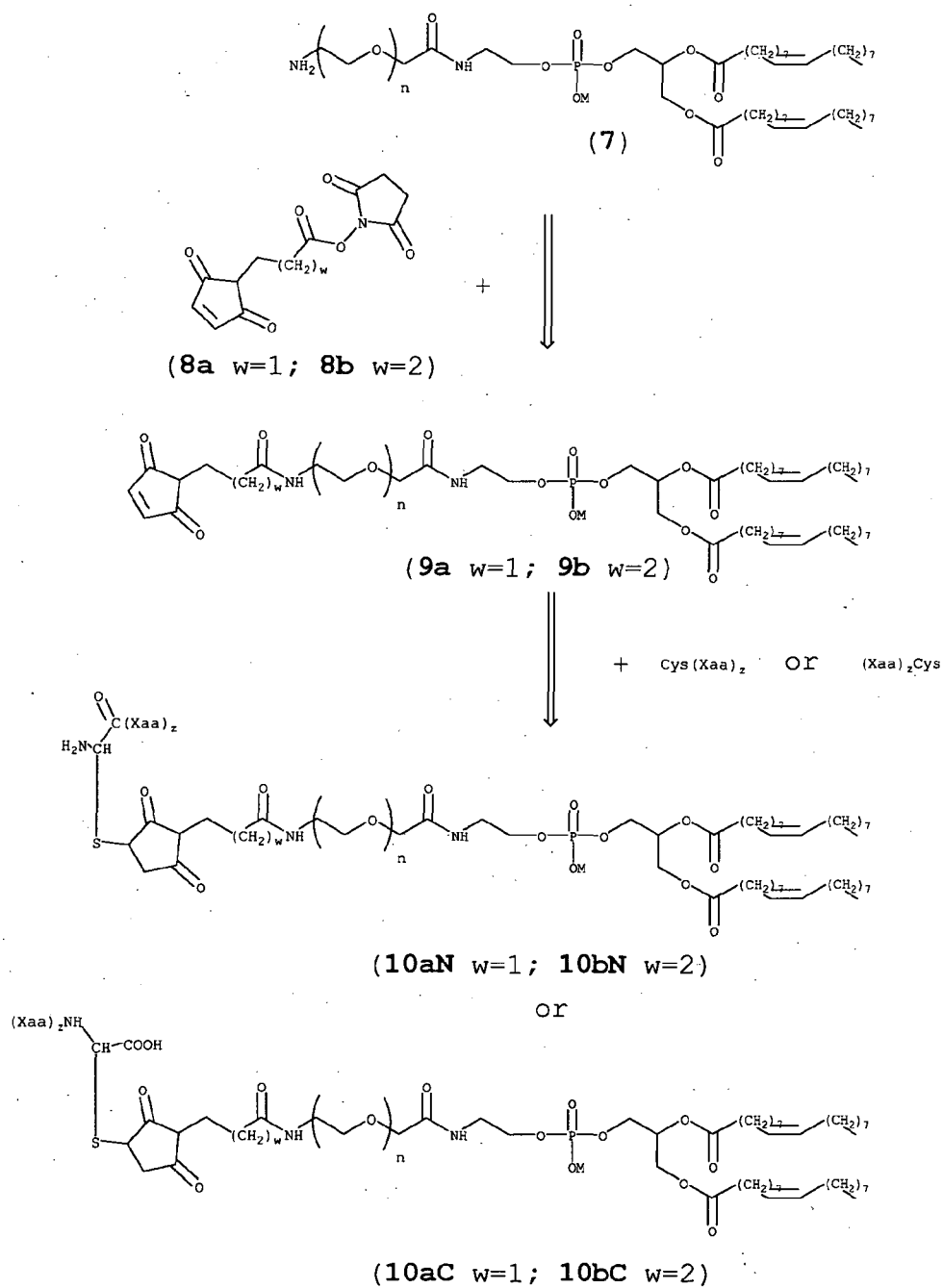
The suspensions are either:

1. incubated for 2 hours at 37 °C before being washed and suspended in a cell medium for serological analysis at a concentration of 0.8 to 3% (Method 1); or
2. incubated for 3 to 4 hours at room temperature (circa 25 °C) followed by 18 hours at 4 °C before being washed and suspended in a cell medium for serological analysis at a concentration of 0.8 to 3% (Method 2).

Modification of red blood cells with DOPE-PEG₆-βAla-Mal-Milt(K) (M00)

4.7 mg of the lipid-peptide construct DOPE-PEG₆-βAla-Mal-Milt(K) (M00) was reconstituted in 0.47 ml of Celpresol™ by sonicating for 10 min and allowing to stand for 1 hour to provide a clear 10 mg/ml stock solution.

SCHEME 2



The stock solution was diluted two-fold to provide a solution of 5 mg/ml and a dilution series then prepared for the peptide-lipid construct at the following concentrations:

- 5 1 mg/ml (1:5 dilution in Celpresol™)
- 0.5 mg/ml (1:10 dilution in Celpresol™)
- 0.25 mg/ml (1:20 dilution in Celpresol™)

10

200 µl of Miltenberger negative red blood cells (*Milt*⁻ RBCs) were washed two times with PBS and one time with Celpresol™. 40 µl of a washed packed volume of *Milt*⁻ RBCs were mixed with 40 µl of a dilution of the peptide-lipid construct and

15 incubated for 2 hours at 37 °C.

The modified RBCs were then washed with Celpresol™ and stored in Celpresol™ until used in tube serology testing (3 days and 24 days).

20

Tube serology testing of modified red blood cells

Serological reactions are graded or scored by either of two established systems (0 or '-' = no agglutination, 1+ or 3 = very weak agglutination, 2+ or 5 = weak agglutination, 3+ or 8 = moderate strong agglutination, 4+ or 10/12 = strong agglutination)

25

Serological platforms used are Tube (addition of reagents and reactants into plastic or glass serology tubes and after appropriate incubations, washing and centrifugation observing reactions macroscopically by eye and a 10X magnification eyepiece and scoring) and BioVue™ (addition of reactants into

30

cassettes containing beads (including some reactants) and after appropriate incubations and centrifugation observing the reaction patterns trapped within the Gel matrix). BioVue is the serological column agglutination platform of Ortho-Clinical
5 Diagnostics.

Serum samples were available from 47 blood donors of negative antibody screen status. These samples were designated "negative samples", but not determined not to have anti-
10 Miltenberger antibodies).

Three serum samples known to have Miltenberger related antibodies T217, T6025, T5896. These samples were designated "positive samples", but not determined to have anti-
15 antibodies against the peptide of the peptide of the construct designated DOPE-PEG₆-βAla-Mal-Milt(K) (M00).

A suspension of 3 % modified RBCs was prepared in PBS and 30 μl of the suspension mixed with 30 μl serum sample. The
20 mixtures were then incubated for 45 min at 37 °C. Following incubation the RBCs were centrifuged for 10 s in an Immufuge™ (setting: "high") and observed for agglutination before being washed 3 times with PBS.

25 After washing one drop of Epiclone™ anti-human globulin (AHG) was added and the tubes then centrifuged for 10 s in an Immufuge™ (setting: "high"). Tubes were then read and serology scores recorded.

[followed by page 42] Age of modified RBCs (days)	Serum	Concentration of DOPE-PEG ₆ - β Ala-Mal-Milt(K) (M00) (mg/ml)					
		1.0 (n = 47)		0.5 (n = 21)		0.25 (n = 21)	
3	Negative samples	AHG+	AHG-	AHG+	AHG-	AHG+	AHG-
		1	46	0	21	0	21

Table 1. Summary of reactivity of samples of serum from 47 blood donors not expected to have anti-Miltenberger activity ("negative samples"). AHG+ means sample reacted by the anti-human globulin test. AHG- means sample is unreactive. RBCs were modified with the peptide-lipid construct designated DOPE-PEG₆- β Ala-Mal-Milt(K) at the concentrations indicated. Sera were tested against modified RBCs following 3 days storage.

Age of modified RBCs (days)	Serum	Concentration of DOPE-PEG ₆ - β Ala-Mal-Milt(K) (M00) (mg/ml)		
		1.0	0.5	0.25
3	T217	2+	1+	-
3	T6025	4+	4+	4+
3	T5896	-	-	-
24	T217	-	-	n.t.
24	T6025	2+	2+	n.t.
24	T5896	-	-	n.t.

Table 2. Results by tube serology of 3 serums known to contain antibodies against antigens of the Miltenberger complex. Score results show sample reactivity by the anti-human globulin test, 1+ = weak, 2+ = medium, 3+ = medium/strong, 4+ = strong, - means sample is unreactive. RBCs were modified with the peptide-lipid construct at the concentrations indicated. Sera were tested against modified RBCs following 3 days and 24 days storage. (n.t. - not tested).

Age of modified RBCs (days)		Concentration of DOPE-PEG ₆ - β Ala-Mal-Milt(K) (M00) (mg/ml)		
		1.0	0.5	0.25
	Serum			
3	T217	-	-	1+
3	T6025	1+	2+	1+
3	T5896	-	-	-
24	T217	-	-	-
24	T6025	2+	2+	1+
24	T5896	-	-	-

Table 3. Results by Diamed column serology of 3 serums known to contain antibodies against the Miltenberger complex. Score results show sample reactivity by the anti-human globulin test, 1+ = weak, 2+ = medium, 3+ = medium/strong, 4+ = strong, - means sample is unreactive. RBCs were modified with the peptide-lipid construct at the concentrations indicated. Sera were tested against modified RBCs following 3 days and 24 days storage.

Peptide inhibition

A 5 mg/ml stock solution of the peptide GlnThrAsnAspLysHisLys-ArgAspThrTyrCys dissolved in Celpresol™ was prepared. A 4 μ l (20 μ g peptide) volume of the stock solution was added to a 30 μ l volume of each serum sample (Test). A 4 μ l volume of Celpresol™ was added to 30 μ l of each serum sample (Control). Serum samples (Test and Control) were then incubated at room temperature (RT) for 10 min.

A 30 μ l volume of a 5% suspension of the modified RBCs was added to each sample and incubated at 37 °C for 45 min. The incubated RBCs were then washed 3 times with PBS in an Immufuge™. One drop of Epiclone™ anti-human globulin (AHG)

reagent was then added to each sample and the tubes centrifuged for 10 s in an Immufuge™ (setting: "high"). Tubes were read and serology scores recorded.

Peptide	Serum	Concentration of DOPE-PEG ₆ - β Ala-Mal-Milt (K) (M00) (mg/ml)	
		1.0	0.5
CONTROL	T217	3+	2+
	T6025	4+	4+
	T5896	-	-
TEST	T217	-	-
	T6025	-	-
	T5896	-	-

5

Table 4. Results by tube serology of 3 serums known to contain antibodies against the Miltenberger complex and inhibited with peptide. Recorded scores show sample reactivity by the anti-human globulin test, 1+ = weak, 2+ = medium, 3+ = medium/strong, 4+ = strong, - means sample is unreactive. RBCs were modified with the peptide-lipid construct at the concentrations indicated.

10

[followed by page 45]

15

Reagent	ID	Type	EIA/Miltenberger Specificity
2	T217	Human group AB serum	Reactive with MUT-T peptides by EIA
3	T165	Human group O serum	Reactive with MUR peptides by EIA
4	T7202	Human group B serum	Reactive with MUT-M peptides by EIA
6	T6025	Human group A serum	Reactive with MUT-T peptides by EIA
7	T8445	Human group O serum	Uncertain
8	T5896	Human group O serum	Uncertain
9	MIII	Monoclonal antibody	Reactive with Mi III red cells
10	Mia	Monoclonal antibody	Reactive with Mi III red cells
11	Mur	Monoclonal antibody	Reactive with Mur positive red cells
12	Gam	IgG monoclonal antibody	Reactive with Mi III red cells
13	BoxH	Human serum	Uncertain
14	TAP1	Human group O serum	Presumed MUT-K specificity
15	TAP2	Human serum	Presumed MUR specificity

Table 5. Identification of polyclonal sera and monoclonal antibodies employed as reagents.

Cell ID	Antigen	Polyclonal sera								Monoclonal antibodies				
		2	3	4	6	7	8	14	15	9	10	11	12	
		T217	T165	T7202	T6025	T8445	T5896	TAP1	TAP2	MIII	Mia	Mur	Gam	
9422184	Vw	8	5	3	0	8	0	5	0	0	10	0	12	
11297161	MiIII	12	10	12	12	10	10	10		10	10	12	12	
4131850	MiIV	12			12				10	0	10	12	12	
1523	MiVI	12			12				8	0	10	12	10	
T1569	MiVII	0	0	0	0	10	0	0		0	0	0	0	
C.BR	Mi?X	12	10	12	12	8	12	12	8	0	10	10	10	

Table 6. Identification of naturally occurring Miltenberger antigen positive (Milt⁺) human red cells as determined in BioVue AHG cards. The specificity of C.BR is uncertain.

Designation		Peptide sequence													Terminal sequence	S ₁
M	Antigen	1	2	3	4	5	6	7	8	9	10	11	12	13		
1	MUTK			Gln	Thr	Asn	Asp	Lys	His	Lys	Arg	Asp	Thr	Tyr	AlaAlaAlaAlaAla*	PEG ₆
2	MUTK			Gln	Thr	Asn	Asp	Lys	His	Lys	Arg	Asp	Thr	Tyr	GlySerGlySerGlyCys	PEG ₆
3	MUTM			Gln	Thr	Asn	Asp	Met	His	Lys	Arg	Asp	Thr	Tyr	GlySerGlySerGlyCys	PEG ₆
13	MUTK	Ser	Ser	Gln	Thr	Asn	Asp	Lys	His	Lys	Arg	Asp	Thr	Tyr	Cys	PEG ₆
16	Mur		Thr	Tyr	Pro	Ala	His	Thr	Ala	Asn	Glu	Val			Cys	PEG
18	Mur				Pro	Ala	His	Thr	Ala	Asn	Glu	Val			Cys	PEG
21	MUTK		Ser	Gln	Thr	Asn	Asp	Lys	His	Lys	Arg	Asp			Cys	PEG
23	Hi1		Glu	Glu	Thr	Gly	Glu	Thr	Gly	Gln	Leu	Val			Cys	PEG

Table 7. Identification of peptide-lipid constructs. Cys denotes the cysteine residue via the sulphhydryl residue of which the spacer (S) is covalently linked to the peptide or PTS-peptide (F). * Where Cys is absent the spacer (S) is covalently linked to the peptide (F) via the terminal amino residue. All peptide-lipid constructs (F-S-L or L-S-F) were prepared as the DOPE (L) variant.

Identity of constructs used in modification of RBCs (see Table 7)		Identity of polyclonal sera and monoclonal antibodies (see Table 5)													
M	µg/ml	4	8	2	6	3	14	7	9	10	11	12	13	15	
1	500	T7202	T5896	T217	T6025	T165	TAP1	T8445	MIII	Mia	Mur	Gam	BoxH	TAP2	
2	500	8	8	8	8	5	nt	0	0	5	0	8	nt	nt	
3	1000	8	10	0		5	nt	0	0	0	0	nt	5	nt	
13	250	8	3	8	8	0	nt	0	0	0	0	0	8	nt	
21	200	0	0	0	8	8	nt	0	0	0	0	3	nt	5	

Table 8. Analysis of sorted data for cells modified to incorporate MUT peptide constructs and reactivity against the Miltenberger Antibody Positive Panel. 'nt' denotes not tested.

Identity of constructs used in modification of RBCs (see Table 7)		Identity of polyclonal sera and monoclonal antibodies (see Table 5)												
M	ug/ml	3	6	7	4	8	2	15	9	10	11	12	13	
		T165	T6025	T8445	T7202	T5896	T217	TAP2	MIII	Mia	Mur	Gam	BoxH	
16	100	10	5	12	5	0	0	nt	0	0	0	0	0	
18	100	10	10	8	0	0	0	nt	0	0	0	0	nt	

Table 9. Analysis of sorted data for cells modified to incorporate MUR peptide constructs and reactivity against the Miltenberger Antibody Positive Panel. 'nt' denotes not tested.

The majority of polyclonal sera demonstrated cross reactivity with one or more modified red blood cell populations (Tables 8 and 9).

- 5 Where false positives were observed these could be substantially eliminated by pre-treatment of the sample of serum with the peptide of the peptide-lipid constructs (Table 10 and 11).

Identity of sera	M1 modified cells			M2 cells vs serum		
	#4	#5	#6	#2	#6	#8
Serum alone	5	5	10	8	8	8
Serum + peptide	0	0	0	0	2	0

10

Table 10. Sera reactive with RBCs modified to incorporate the M1 peptide-lipid construct or M2 peptide-lipid construct constructs by contacting the cells with a 500 µg/ml dispersion of the construct (Method 1) were "neutralised" with the peptide QTNDKHKRDTY and retested against the modified cells. Sera were neutralized by adding 10 µL of 1 mg/ml solution of peptide to a 50 µL volume of sera and incubating for 30 minutes at 37 °C. Testing was performed using BioVue™ cards.

15

Identity of sera	M13 modified cells			
	#3	#42	#37	#34
Serum alone	8	8	8	8
Serum + peptide	0	0	0	0

20

Table 11. Sera reactive with RBCs modified to incorporate the M13 peptide-lipid construct by contacting the cells with a 500 µg/ml dispersion of the construct (Method 1) were "neutralised" with the peptide SSQTNDKHKRDTY and retested against the modified cells. Sera were neutralized by adding 10 µL of 1 mg/ml solution of peptide to a 50 µL volume of sera and incubating for 30 minutes at 37 °C. Testing was performed using BioVue™ cards.

25

Modification of embryos with the peptide-lipid construct designated DOPE-PEG6- β Ala-Mal-PTS-Milt(K) (M2)

The zona pellucida of day 3.5 embryos prepared as microdrops
5 were removed by incubation in 0.5% pronase solution for circa
5 minutes at 37 °C. The zona pellucida removed embryos were
transferred to microdrops containing media alone and contacted
with a dispersion of the peptide-lipid construct designated
DOPE-PEG6- β Ala-Mal-PTS-Milt(K) (M2) at a concentration of 1
10 mg/ml for 2 hours. The dispersion of the peptide-lipid
construct contained azide as an anti-microbial agent.

The incubated embryos were washed four times in handling media
and transferred to microdrops containing the Gam monoclonal
15 antibody (see Table 8) and incubated at 37 °C for 40 min. The
embryos were then washed four times in handling media and
transferred to microdrops containing secondary antibody
(FITC anti-mouse) at a 1:50 dilution.

20 The microdrops were incubated at room temperature in the dark
for 30 minutes before being washed four times in handling
media, placed on microscope slides, and overlaid with mineral
oil. The embryos were visualized using an Olympus™ BX51
fluorescent microscope at 200 x magnification with WIB filter
25 550 nm emission wavelength. The scale used for grading
fluorescence was 0 to 4+, where 0 is no fluorescence and 4+ is
very bright fluorescence. The mean fluorescence of the
modified embryos was 2+ versus zero for unmodified embryos.
The grading of fluorescence is recorded in Table 12.

Mean Fluorescence*	
M2 FSL-peptide	Media alone
2.0+	0

Table 12. Fluorescence of embryos modified by contacting with the peptide-lipid construct designated DOPE-PEG6- β Ala-Mal-PTS-Milt(K) (M2) (10 embryos per group; scale is 0 to 4+).

5

A mean fluorescence of 2+ was observed for the zona pellucida removed embryos modified to incorporate the peptide-lipid construct designated DOPE-PEG6- β Ala-Mal-PTS-Milt(K) (M2). No fluorescence was observed for control embryos. The de-
10 compaction of treated embryos was attributed to the presence of azide in the dispersion of the peptide-lipid construct.

Although the invention has been described by way of exemplifying embodiments it should be appreciated that
15 variations and modifications may be made without departing from the scope of the invention. Furthermore where known equivalents exist to specific features, such equivalents are incorporated as if specifically referred to in this specification.

20

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CLAIMS

1) A **method** of detecting reactive antibody in the serum of a subject including the steps of:

5

- Contacting a sample of the serum with a suspension of cells modified to incorporate a peptide-lipid construct of the structure $(L-S)_iF(-S-L)_j$ to provide a mixture;

10

- Incubating the mixture for a time and at a temperature sufficient to allow agglutination; and
- Determining the degree of agglutination of the cells in the mixture;

15

where:

20

F is a peptide comprising an epitope for the reactive antibody;

S is a spacer covalently linking F to L; and

L is a lipid selected from the group consisting of diacyl- and dialkyl-glycerolipids, including glycerophospholipids; and

25

i and j are independently 0 or 1,

2) The method claim 1 where the method includes the preliminary step of:

30

- Adding an amount of the peptide to the sample of the serum;

where the amount of the peptide is sufficient to neutralize non-specific agglutination or confirm specificity of the reactive antibody.

5 3) The method claim 1 where includes the intermediate step of:

- Adding an anti-subject globulin antibody to the mixture prior to determining the degree of agglutination of the cells of the mixture.

10

4) The method claim 1 where the subject is a human.

5) The method claim 1 where the cells are red blood cells.

15

6) The method claim 1 where the anti-subject globulin antibody is anti-human globulin (AHG) antibody.

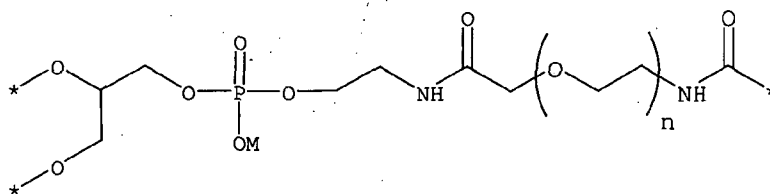
20 7) The method claim 1 where the reactive antibody is reactive to an antigen selected from the group consisting of: Glycophorin A, Glycophorin B, or mutations thereof (including the MNS blood group system).

25

8) The method claim 1 where S is a spacer covalently linking F to L via an oligomer of ethylene glycol.

9) The method claim 1 where the structure of the peptide-lipid construct includes the substructure:

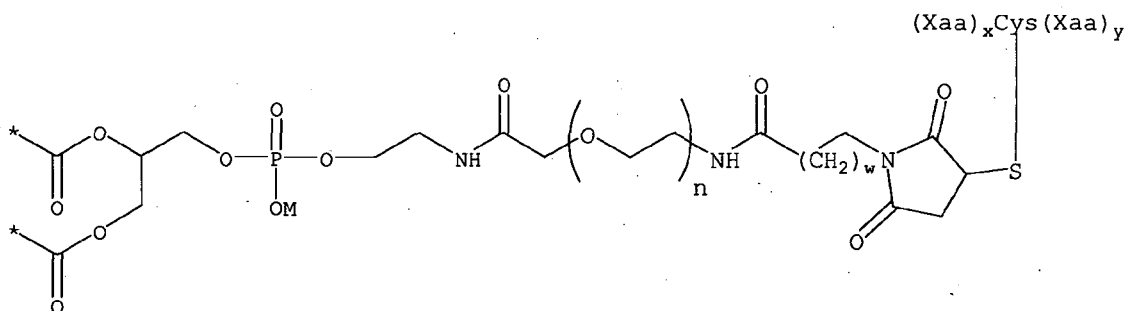
30



where M is a monovalent cation (M^+), n is 6 to 14 and
* is other than H.

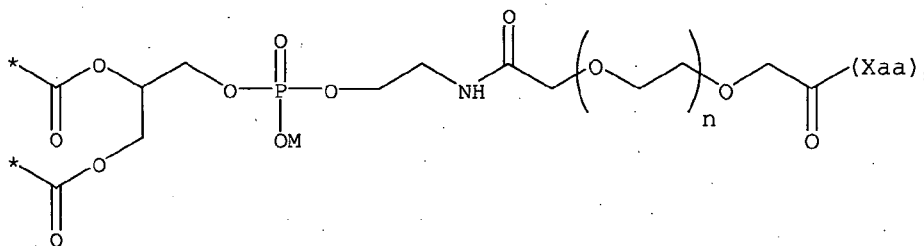
5

- 10) The method claim 1 where the structure of the peptide-lipid construct is either:



10

or



15

where M is a monovalent cation (M^+), n is 6 to 14, w
is 1 or 2, the sum of x and y is greater than 5, z is
greater than 5, and * is other than H.

- 11) The method claim 1 where the sum of i and j is 1.

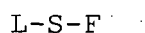
20

- 12) The method claim 1 where F is a peptide including a proximal terminal sequence (PTS) selected to promote solubility of the peptide.
- 5 13) The method claim 12 where the PTS of the peptide is selected from the group consisting of:
- SerLysLysLysLysGly
AlaAlaAlaAla
GlySerGlySerGly
- 10 14) The method claim 1 where F is a peptide comprising an epitope of antigens selected from the group consisting of: Glycophorin A, Glycophorin B, or mutations thereof (including the MNS blood group system).
- 15 15) The method claim 1 where F is a peptide selected from the *List of Peptides*.
- 16) The method claim 1 where F is a peptide selected from the group consisting of:
- GlnThrAsnAspLysHisLysArgAspThrTyrAlaAlaAlaAlaAlaCys
GlnThrAsnAspLysHisLysArgAspThrTyrGlySerGlySerGlyCys
GlnThrAsnAspMetHisLysArgAspThrTyrGlySerGlySerGlyCys
SerSerGlnThrAsnAspLysHisLysArgAspThrTyrCys
ThrTyrProAlaHisThrAlaAsnGluValCys
ProAlaHisThrAlaAsnGluValCys
SerGlnThrAsnAspLysHisLysArgAspCys
AlaAlaAlaAlaValMetTyrAlaSerSerGly
GlySerGlySerGlyValMetTyrAlaSerSerGly

17) The method claim 1 where L is a glycerophospholipid.

18) The method claim 1 where L is a glycerophospholipid
 5 selected from the group consisting of: 1,2-O-dioleoyl-
sn-glycero-3-phosphatidylethanolamine (DOPE) and 1,2-
 O-distearyl-*sn*-glycero-3-phosphatidylethanolamine
 (DSPE).

10 19) A **peptide-lipid construct** of the structure:



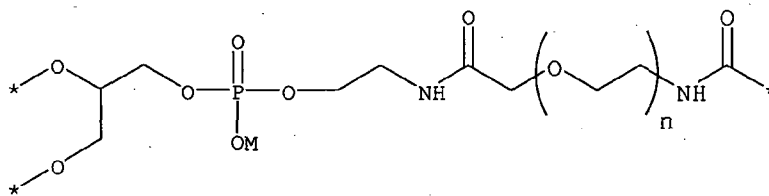
where

15 F is a peptide;

S is a spacer covalently linking F to L via an
 oligomer of ethylene glycol; and

20 L is a lipid selected from the group consisting of
 diacyl- and dialkyl-glycerolipids, including
 glycerophospholipids.

20) The peptide-lipid construct of claim 19 where the
 structure of the peptide-lipid construct includes the
 25 substructure:



30 where M is a monovalent cation (M^+), n is 6 to 14 and
 * is other than H.

21) The peptide-lipid construct of claim 19 where F is a peptide including a proximal terminal sequence (PTS) selected to promote solubility of the peptide.

5

22) The peptide-lipid construct of claim 21 where the PTS of the peptide is selected from the group consisting of:

SerLysLysLysLysGly

AlaAlaAlaAla

GlySerGlySerGly

10

23) The peptide-lipid construct of claim 19 where the terminal sequence of the peptide is selected from the group consisting of:

GlyLysLysLysLysSerCys

AlaAlaAlaAlaCys

GlySerGlySerGlyCys

CysSerLysLysLysLysGly

CysAlaAlaAlaAla

CysGlySerGlySerGly

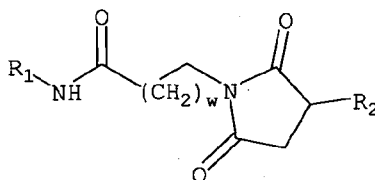
15

24) The peptide-lipid construct of claim 19 where S is covalently linked to F via a sulphide bond formed with the Cys residue of the peptide.

20 25) The peptide-lipid construct of claim 19 where S is covalently linked to F via a sulphide bond formed with a Cys residue of the peptide at or proximal to a terminus of the peptide.

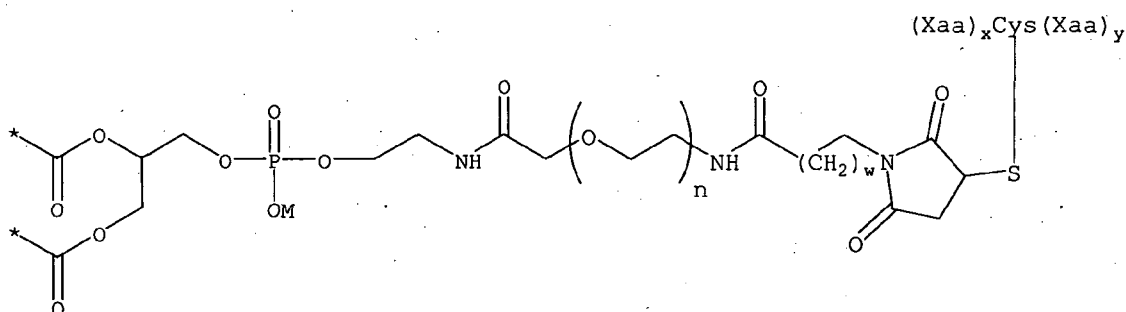
26) The peptide-lipid construct of claim 19 where S is linked to F via a sulphide bond formed with a Cys residue of the peptide at the carboxy-terminus of the peptide.

27) The peptide-lipid construct of claim 19 where S is of the structure $S_1-S_2-S_3$, S_1 is an oligomer of ethylene glycol and S_2-S_3 is selected from the group consisting of:



where R_1 is a terminal carbon of S_1 , R_2 is the sulphur of the Cys residue and w is 1 or 2.

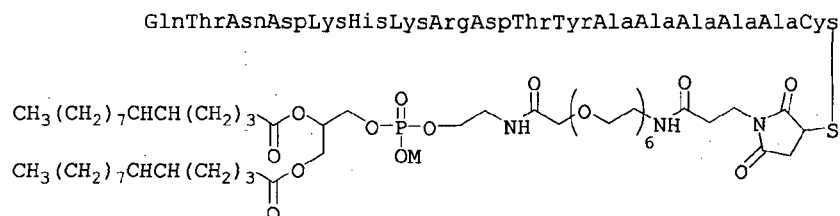
28) The peptide-lipid construct of claim 19 where the structure of the peptide-lipid construct is:



where M is a monovalent cation (M^+), n is 6 to 14, w is 1 or 2, the sum of x and y is greater than 5, and $*$ is other than H.

- 29) The peptide-lipid construct of claim 28 where n is 6.
- 30) The peptide-lipid construct of claim 28 where y is 0.
- 5 31) The peptide-lipid construct of claim 19 where F is a peptide comprising an epitope of antigens selected from the group consisting of: Glycophorin A, Glycophorin B, or mutations thereof (including the MNS blood group system).
- 10 32) The peptide-lipid construct of claim 19 where F is a peptide selected from the *List of Peptides*.
- 15 33) The peptide-lipid construct of claim 19 where F is a peptide selected from the group consisting of:
- GlnThrAsnAspLysHisLysArgAspThrTyrAlaAlaAlaAlaAlaCys
 GlnThrAsnAspLysHisLysArgAspThrTyrGlySerGlySerGlyCys
 GlnThrAsnAspMetHisLysArgAspThrTyrGlySerGlySerGlyCys
 SerSerGlnThrAsnAspLysHisLysArgAspThrTyrCys
 ThrTyrProAlaHisThrAlaAsnGluValCys
 ProAlaHisThrAlaAsnGluValCys
 SerGlnThrAsnAspLysHisLysArgAspCys
- 34) The peptide-lipid construct of claim 19 where L is a glycerophospholipid.
- 20 35) The peptide-lipid construct of claim 19 where L is a glycerophospholipid selected from the group consisting of: 1,2-O-di oleoyl-*sn*-glycero-3-phosphatidylethanolamine (DOPE) and 1,2-O-distearyl-*sn*-glycero-3-phosphatidylethanolamine (DSPE).
- 25

- 36) A **peptide-lipid construct** of the structure:

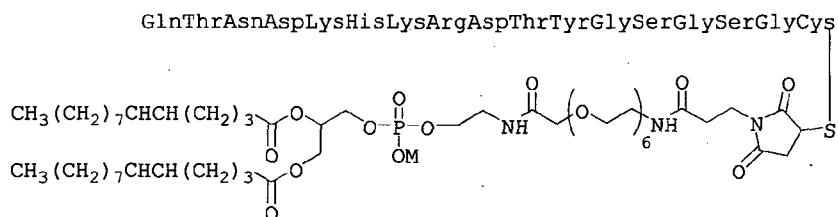


5

where M is a monovalent cation (M^+) and designated DOPE-PEG₆-βAla-Mal-PTS-1MUTK) (**M1**).

- 37) A **peptide-lipid construct** of the structure:

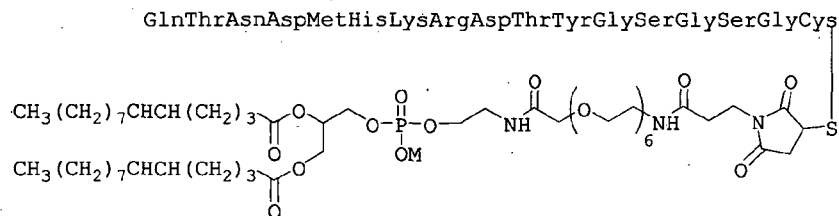
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where M is a monovalent cation (M^+) and designated DOPE-PEG₆-βAla-Mal-PTS-2MUTK) (**M2**).

15

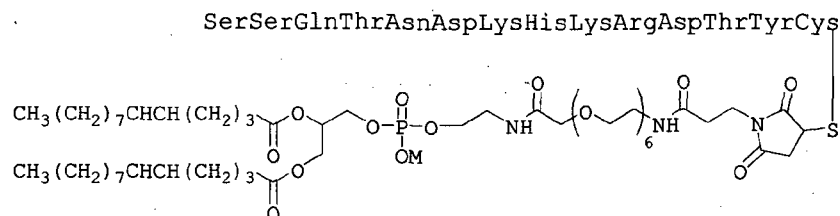
- 38) A **peptide-lipid construct** of the structure:



20

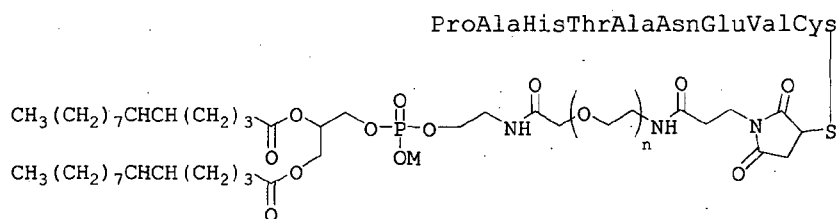
where M is a monovalent cation (M^+) and designated DOPE-PEG₆-βAla-Mal-PTS-3MUTM (**M3**).

- 39) A peptide-lipid construct of the structure:



- 5 where M is a monovalent cation (M^+) and designated DOPE-PEG₆-βAla-Mal-13MUTK (**M13**).

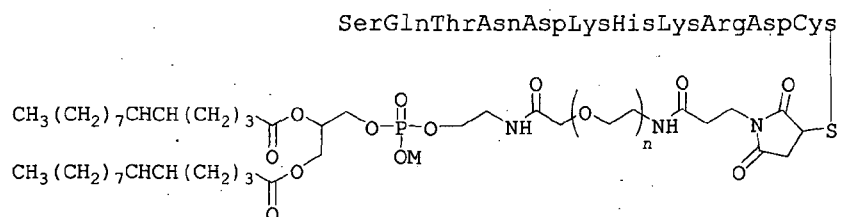
- 40) A peptide-lipid construct of the structure:



10

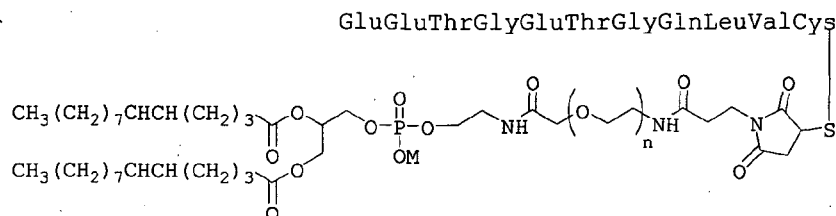
- where M is a monovalent cation (M^+) and designated DOPE-PEG₆-βAla-Mal-18Mur (**M18**) ($n=6$).

- 15 41) A peptide-lipid construct of the structure:



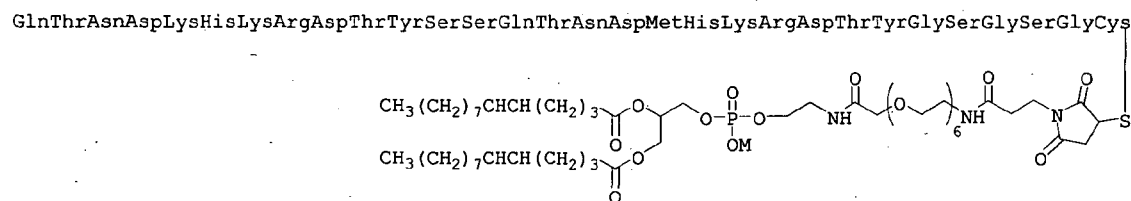
- 20 where M is a monovalent cation (M^+) and designated DOPE-PEG₆-βAla-Mal-21MUTK (**M21**) ($n=6$).

- 42) A peptide-lipid construct of the structure:



- 5 where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-Hil3 (**M23**) ($n=6$).

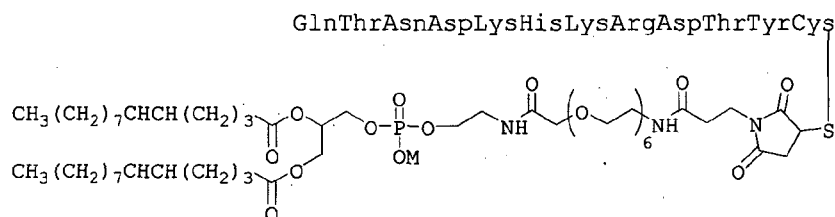
- 43) A peptide-lipid construct of the structure:



10

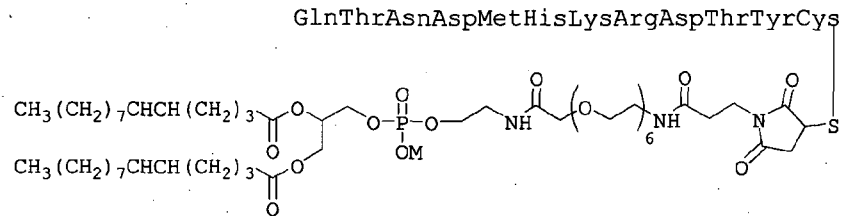
- where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-PTS-Milt (K, M).

- 15 44) A peptide-lipid construct of the structure:



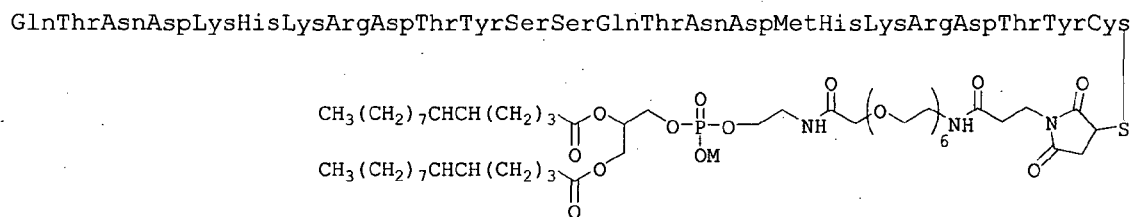
- 20 where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-Milt (K) (**M00**).

- 45) A **peptide-lipid construct** of the structure:



- 5 where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-Milt(M).

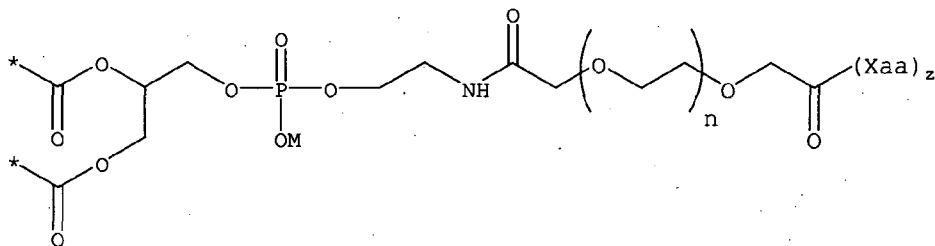
- 46) A **peptide-lipid construct** of the structure:



10

where M is a monovalent cation (M^+) and designated DOPE-PEG₆- β Ala-Mal-Milt(K,M).

- 15 47) The peptide-lipid construct of claim 19 where the structure of the peptide-lipid construct is:



20

where M is a monovalent cation (M^+), n is 6 to 14, z is greater than 5, and * is other than H.

48) The peptide-lipid construct of claim 45 where n is 14.

49) The peptide-lipid construct of claim 45 where F is a peptide including a terminal sequence selected to promote solubility of the peptide.

50) The peptide-lipid construct of claim 47 where the terminal sequence of the peptide is selected from the group consisting of:

SerLysLysLysLysGly

AlaAlaAlaAla

GlySerGlySerGly

51) The peptide-lipid construct of claim 45 where F is a peptide selected from the group consisting of:

$(\text{Xaa})_{z-7}\text{ValMetTyrAlaSerSerGly};$

where z is the integer 4, 5 or 6.

52) The peptide-lipid construct of claim 45 where F is a peptide selected from the group consisting of:

SerLysLysLysLysGlyValMetTyrAlaSerSerGly

AlaAlaAlaAlaValMetTyrAlaSerSerGly

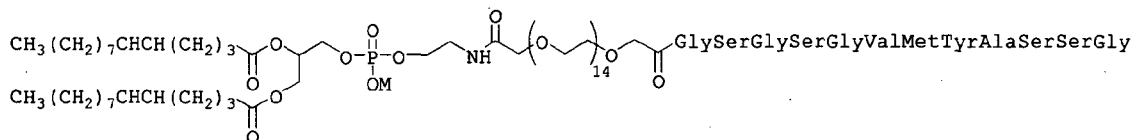
GlySerGlySerGlyValMetTyrAlaSerSerGly

53) The peptide-lipid construct of claim 45 where L is a glycerophospholipid.

54) The peptide-lipid construct of claim 45 where L is a glycerophospholipid selected from the group consisting

of: 1,2-O-dioleoyl-*sn*-glycero-3-phosphatidylethanolamine (DOPE) and 1,2-O-distearyl-*sn*-glycero-3-phosphatidylethanolamine (DSPE).

5 55) A **peptide-lipid construct** of the structure:



where M is a monovalent cation (M^+) and designated
DOPE-PEG₁₄-Syph.

56) A **method** of preparing a peptide-lipid construct (F-S-L) of claim 19 to 47 including the steps of:

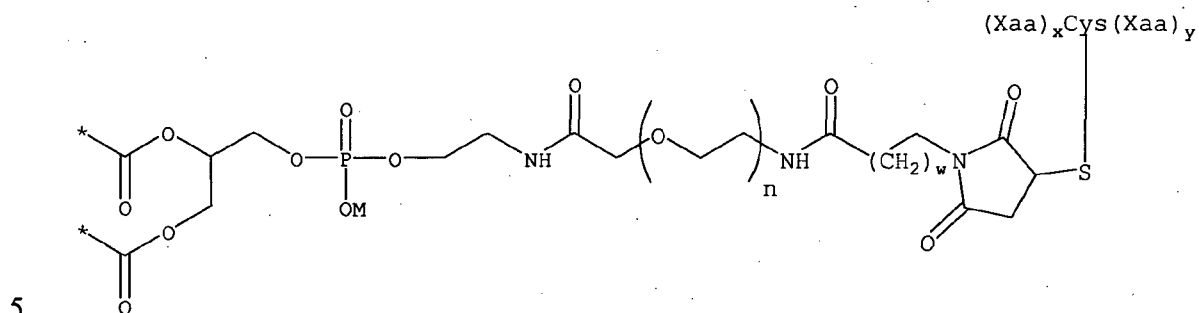
- Preparing a maleimido-derivative of a precursor construct by reacting a maleimido-donating reagent with a precursor construct of the structure L-S₁-NH₂; and
- Reacting the maleimido-derivative of the precursor construct with a peptide (F) including a Cys residue and solubilised in a solvent.

where:

L is a lipid selected from the group consisting of diacyl- and dialkyl-glycerolipids, including glycerophospholipids; and

S₁ is selected from the group consisting of oligomers of ethylene glycol.

- 57) The method of claim 54 where the structure of the peptide-lipid construct is:



where n is 6 to 14, w is 1 or 2, the sum of x and y is greater than 5, and $*$ is other than H.

- 10 58) The method of claim 54 where the maleimido-donating reagent is selected from the group consisting of: N-oxy succinimid ester of maleimidobutyric acid; and N-oxy succinimid ester of maleimidopropionic acid.
- 15 59) The method of claim 54 where S_1 is an oligomer of ethylene glycol selected from the group consisting of 6 to 14 mer PEG (PEG₆ to PEG₁₄).
- 60) The method of claim 54 where S_1 is PEG₆.
- 20 61) The method of claim 54 where the solvent is selected from the group consisting of: trifluoroethanol; DMSO; or mixtures thereof.
- 25 62) The method of claim 54 where the Cys residue is a terminal Cys residue.

63) The method of claim 54 where F is a peptide including a proximal terminal sequence (PTS) selected to promote solubility of the peptide in the reaction solvent.

5 64) The method of claim 61 where the PTS of the peptide is selected from the group consisting of:

SerLysLysLysLysGly

AlaAlaAlaAla

GlySerGlySerGly

10 65) The method of claim 54 where the terminal sequence of the peptide is selected from the group consisting of:

GlyLysLysLysLysSerCys

AlaAlaAlaAlaCys

GlySerGlySerGlyCys

CysSerLysLysLysLysGly

CysAlaAlaAlaAla

CysGlySerGlySerGly

66) The method of claim 54 where F is a peptide selected from the *List of Peptides*.

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67) The method of claim 54 where F is a peptide selected from the group consisting of:

GlnThrAsnAspLysHisLysArgAspThrTyrAlaAlaAlaAlaCys

GlnThrAsnAspLysHisLysArgAspThrTyrGlySerGlySerGlyCys

GlnThrAsnAspMetHisLysArgAspThrTyrGlySerGlySerGlyCys

SerSerGlnThrAsnAspLysHisLysArgAspThrTyrCys

ThrTyrProAlaHisThrAlaAsnGluValCys

ProAlaHisThrAlaAsnGluValCys

SerGlnThrAsnAspLysHisLysArgAspCys

68) The method of claim 54 where L is a glycerophospholipid.

5 69) The method of claim 54 where L is a glycerophospholipid selected from the group consisting of: 1,2-O-dioleoyl-*sn*-glycero-3-phosphatidylethanolamine (DOPE) and 1,2-O-distearyl-*sn*-glycero-3-phosphatidylethanolamine (DSPE).

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70) A **method** of effecting qualitative and quantitative changes in the levels of peptide expressed at the surface of cells and multi-cellular structures including the step of:

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- contacting the cells or multi-cellular structures with a solution of a peptide-lipid construct of any one of claims 19 to 55 at a concentration and for a time and temperature sufficient to allow the construct to incorporate into the surface.

20

71) The method of claim 54 where the peptide-lipid construct is a construct of any one of claims 19 to 47.

25

72) The method of claim 54 where the cells or multicellular structures are selected from the group consisting of: red blood cells; and embryos.

- 73) The method of claim 54 where the cells or multicellular structures are human cells or multicellular structures.
- 5 74) The method of claim 54 where the time and temperature is no greater than 2 hours at 37 °C or 24 hours at 4 °C.