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(54) **Title**: SMALL EFFICIENT CELL PENETRATING PEPTIDES DERIVED FROM THE SCORPION TOXIN MAUROCALCINE

(57) **Abstract**: The invention relates to small cell penetrating peptides (CPP) derived from the scorpion toxin maurocalcine and to their use as vectors for the intracellular delivery of various drugs and agents.

SMALL EFFICIENT CELL PENETRATING PEPTIDES DERIVED FROM THE SCORPION TOXIN MAUROCALCINE

The invention relates to small cell penetrating peptides (CPP) derived from the scorpion toxin maurocalcine and to their use as vectors for the intracellular delivery of various drugs and agents.

Cell-penetrating peptides (CPP), also called protein transduction domains (PTDs), membrane translocation sequences (MTS) or translocating peptides are capable of crossing the plasma membrane of cells and of carrying cell-impermeable compounds across the plasma membrane, efficiently, rapidly, at low concentration, *in vitro* and *in vivo*, into various cell types. The 60 amino-acid long homeodomain of the *Drosophila* transcription factor Antennapedia (ANTP) was the first CPP discovered and shown to serve as a signal for the internalization of other polypeptides. Its penetration and translocation properties were further restricted to a peptide of 16 residues (penetratine or Pen). Now along with Pen, multiple CPPs including protein transduction domains (PTD) found in proteins such as HIV-1 Tat and HSV-1 VP22, synthetic 7-9 homoarginine peptides and chimera peptides such as transportan, are intensively studied. Little structural resemblances have been found between the different families of CPP. The only characteristic common to all these peptides is that they are unusually enriched in basic amino acids resulting in a high positive net charge. Various molecules or particles of different sizes such as oligonucleotides, peptide nucleic acids (PNAs), siRNAs, cDNA, plasmids, peptides, proteins, antibodies, pharmacologicaly active drugs, imaging agents, liposomes and nanoparticles have been successfully delivered into cells when attached to a CPP. Thus, CPPs represent powerful tools for the delivery of various cargoes to their site of action in a cell, in particular the cytosol and the nucleus. These peptides have opened a new avenue in medicine and research, allowing otherwise impermeable agents of therapeutic, diagnostic and technical value to enter cells and induce biological responses.

Maurocalcine (MCa) is the first demonstrated example of an animal toxin peptide with efficient cell penetration properties. The toxin is a 33-mer peptide (SEQ ID NO: 1) that was initially isolated from the venom of a Tunisian chactid scorpion, *Scorpio maurus palmatus* (Fajloun *et al.*, 2000). Maurocalcine belongs to a

family of peptide that folds according to an Inhibitor Cystine Knot (ICK motif), and thus contains three disulfide bridges with a Cys^1-Cys^4, Cys^2-Cys^5 and Cys^3-Cys^6 connecting pattern (Moshbah *et al.*, 2000). The solution structure, as defined by ^{1}H-NMR, illustrates that MCa contains three β-strands (strand 1 from amino acid residues 9 to 11, strand 2 from 20 to 23, and strand 3 from 30 to 33). One distinctiveness of MCa is the fact that it is greatly enriched in basic amino acid residues. Out of the 33 amino acids that compose MCa, twelve of them are basic, most of them represented by Lys residues. Interestingly, the β-strands of MCa encompass most of the basic domains (Figure 1A). MCa turned to be of interest for research for several reasons.

First, it is an exquisite pharmacological activator of the ryanodine receptor type 1 (RyR1) from skeletal muscle since it promotes high Po gating modes and long-lasting subconductance states of the ion channel (Chen *et al.*, 2003; Lukacs *et al.*, 2008). On myotubes, application of MCa rapidly induces Ca^{2+} release from the sarcoplasmic reticulum (SR) (Estève *et al.*, 2003), a result further confirmed by positive effect of MCa on the release of Ca^{2+} from purified SR vesicles (Chen *et al.*, 2003; Estève *et al.*, 2003). The interaction of MCa with RyR1 has been witnessed by increased [^{3}H]-ryanodine binding onto purified RyR1 (Chen *et al.*, 2003; Estève *et al.*, 2003). The binding site for MCa on RyR1 has also been mapped and shown to correspond to domain(s) that have a predicted localization within the cytoplasm (Altafaj *et al.*, 2005).

Second, MCa has a unique sequence homology with the II-III loop of the L-type calcium channel $Ca_v1.1$ subunit over a domain that is slightly larger than the second β-strand of MCa (Figure 1A) (Estève *et al.*, 2003). This loop is heavily involved in excitation-contraction coupling through direct molecular interactions with RyR1 (Altafaj *et al.*, 2005; Szappanos *et al.*, 2005). This homology turns out to be of tremendous help for understanding how L-type channels are involved in excitation-contraction coupling (Lukacs *et al.*, 2008, Szappanos *et al.*, 2005; Pouvereau *et al.*, 2006).

Third, MCa has been shown to act as a cell penetrating peptide (CPP) (Estève et al., 2005; International PCT Application WO 2006/051224 and corresponding US Patent Application US 2009/0142266). This discovery stemmed

from earlier criticisms that MCa may not be an activator of RyR1 because peptide toxins were not known to cross the plasma membrane, which would be required here to bind to RyR1. Studies that were undertaken to demonstrate the ability of MCa to reach its target showed that i) MCa triggers Ca^{2+} release from the sarcoplasmic reticulum a few seconds after its application in the extracellular medium (Estève *et al.*, 2003), and ii) intracellular accumulation of fluorescent-streptavidine occurs if it incubated first with biotinylated MCa (Estève *et al.*, 2005; International PCT Application WO 2006/0512249 and corresponding US Patent Application US 2009/0142266). Since these pioneering studies, MCa or full-length 33 amino acid analogues thereof proved powerful vectors for the cell entry of proteins, peptides (Ram *et al.*, 2008), nanoparticles, or drugs such as doxorubicine (Aroui *et al.*, Cancer Lett., 2009; Aroui *et al.*, Apoptosis, 2009; Aroui *et al.*, Pharm. Res., 2009). Although the mode of cell penetration of MCa may vary according to cargo nature, cell type or chemical linkage employed, the data gathered so far suggest that the peptide may enter cells according to two priming steps onto the plasma membrane: first an interaction with proteoglycans with an affinity in the micromolar range, followed by a second interaction with negatively charged lipids which occurs with greater affinity (Boisseau *et al.*, 2006; Ram *et al.*, 2008). The mode of cell entry of MCa is not altered by the absence of proteoglycans, but simply reduced quantitatively, suggesting that proteoglycans do not orient the mode of cell penetration. Two modes seem to concur to MCa cell entry, as far as observed, one related to macropinocytosis and another to membrane translocation. The balance between both modes of entry was found correlated to cargo nature and the type of MCa analogue used.

It is of great interest to pursue the study of MCa as CPP in spite of the wealth of new CPP sequences that are discovered yearly. Among the competitive advantage of MCa over other CPP sequences are the facts that it has almost no associated toxicity *in vitro* and *in vivo*, penetrates into cells at very low concentrations, and is extremely stable *in vivo* upon intravenous injection (over 24 hrs). While MCa appears as an elaborate and efficient CPP, its pharmacological properties represent a serious hindrance while envisioning *in vitro* and *in vivo* applications. In addition, because of its length (33 amino acid residues) and the presence of three internal disulfide bridges, MCa is a relatively difficult to synthesize

CPP, comparatively to other CPP. Several attempts were made in the past to try to design MCa analogues which are less complex than MCa, lack the pharmacological effects of wild-type MCa but preserve or enhance its cell penetration efficiencies.

The first strategy, based on single point mutations spanning MCa sequence, preserved the disulfide bridges and the 3D structure of the analogues. The study of the MCa mutants demonstrated that the molecular determinant of MCa implicated in pharmacology and cell penetration overlap partially. In addition, this work confirmed that the main requirement for an efficient cell penetration of MCa is the presence of a basic surface. Many of the amino acids involved in RyR1 binding and pharmacology were located within the cluster of basic amino acids that presented sequence homology with the L-type $Ca_V1.1$ channel. Some of these residues, but not all, were also important for cell penetration properties. Using this approach, full-length MCa analogues with reduced or complete loss of pharmacological effects were defined (Mabrouk *et al.*, 2007). Nevertheless, none of the analogues totally preserved the cell penetration efficiency of MCa. One analogue only had lost entirely its pharmacological action (MCa R24A). However, its cell penetration efficiency was decreased. Some other analogues were better that MCa itself for cell penetration. However, their affinity for RyR1 was unchanged or increased (MCa E12A). Combining a pair of mutations, one aiming at disrupting pharmacology and one at improving penetration, may thus be used in the future to define still better CPP analogues derived of full-length MCa.

The second strategy was based on the chemical synthesis of D-MCa, a full-length analogue entirely based on the use of D-amino acids. This peptide is a mirror image of the natural L-MCa but, like other D-CPP, preserves its cell penetration properties, while losing entirely its ability to interac with RyR1 (Poillot *et al.*, 2010). This CPP analogue has several advantages. It no longer is sensitive to proteases which may be an additional advantage for *in vivo* experiments where the half-life of the circulating peptide matters. In these two strategies while being effective, one may argue that i) the peptides are still among the longest CPP known to date, implying increased costs of production, and ii) the yield of production of these peptides is hampered by the folding process. Also, the use of peptides with internal disulfide bridges, despite having advantageous features in term of stability *in vivo*,

makes chemical coupling of these CPP to cargoes more complicated (difficulty to add extra Cys residues to the peptides for instance without interfering with the correct folding process).

The third strategy that was used to circumvent one of this criticism was the chemical synthesis of a full-length MCa analogue in which all internal Cys residues where replaced by isosteric 2-aminobutyric acid residues (Ram *et al.*, J. Biol. Chem., 2008). The resulting peptide was still 33-mer long but one step in production was saved by avoiding the folding process. In addition, an extra-Cys residue could be added to the N-terminus of the peptide in order to favor simplified cargo grafting on this CPP analogue. This peptide, termed here C-MCaUF1-33 (C for extra-Cys, UF for unfolded, and 1-33 for its length, Figure 1B) has no longer any secondary structures, but efficiently penetrates into cells. Interestingly also, the peptide completely lacks pharmacological activity indicating that folding and secondary structures are essential for binding onto RyR1. While this peptide is an efficient CPP, it remains less potent than MCa in its folded version.

The inventors have developed several truncated Mca peptides that have highly potent cell penetration capabilities, while losing pharmacological activity, preserving lack of cell toxicity, and with facilitated cargo grafting. Here, the inventors demonstrate that several efficient CPP can be derived from maurocalcine by replacing Cys residues by isosteric 2-aminobutyric acid residues and a sequence truncation down to peptides of up to 7 residues in length. A surprising finding is that all the truncated maurocalcine analogues possessed cell penetrating properties indicating that the maurocalcine is a highly specialized CPP. Many of the unfolded truncated MCa peptides are better CPP than unfolded MCa itself.

More surprisingly, the inventors have also found out that poorly charged MCa peptides (net positive charge of 0 to +3) can behave as efficient CPP. This is the case for MCaUF1-9, MCaUF3-9, MCaUF1-9(W3), HadUF1-11 and HadUF3-11 which are ones of the best performing CPPs, especially when low concentration of use is a quality of importance.

Interestingly, the truncated MCa peptides differ somewhat in their mode of cell penetration (direct membrane translocation *versus* endocytosis), some being more prone to enter cells by macropinocytosis than others. Various peptides

were even insensitive to amiloride application suggesting that macropinocytosis did not contribute at all to their entry.

The inventors have also demonstrated that cargo coupling can occur at the N-terminus as well as the C-terminus of the peptide, enhancing the flexibility of cargo coupling to these CPPs.

The CPP potential of these peptides can be optimized by reintroducing one disulphide bond to restore some of the secondary structures that confer a competitive advantage to MCa for cell penetration. Further optimization of these CPPs is obtained by mutagenesis of the region Lys11-Ser18 including the mutation of E12 and D15 as well as further mutagenesis of negatively charged residues including D2 and E29.

The inventors have identified several interesting lead CPP based on unfolded MCa (MCaUF) truncation strategy. This is the case for MCaUF18-33 (macropinocytosis entry-independent), MCaUF1-9 (penetrates better at low concentration), and MCaUF14-25 (yields the greatest cell entry of the dye). These peptides are easy to produce, yield good cell penetration, and their cell penetrating characteristics can be further optimized by mutagenesis or by reintroducing one disulfide bridge to restore some of the secondary structures. This new generation of MCa analogues is predicted to have bright futures for CPP applications *in vitro* and *in vivo*.

In the following description, the standard one letter amino acid code is used. In addition, non-natural amino acids and groups of particular amino acids are referred to using the following one letter code:

- **a** = L-alpha-aminobutyric acid, also named 2-amino butyric acid or Abu,
- **B** = basic amino acid chosen from K and R,
- **J** = hydrophobic amino acid chosen from W, F, L, I, V, M, A and C,
- J^1 = hydrophobic amino acid chosen from W, F, L, I, V, A and C, and
- **O** = S, G, T, A, and V.

One aspect of the present invention relates to the use of a peptide as a vector for the intracellular delivery of a molecular cargo, wherein said peptide is a maurocalcine derived cell penetrating peptide consisting of a sequence selected from the group consisting of:

(I) Z-X_1-X_2-X_3-X_4-X_5-X_6-X_7-Z',

wherein:

- **X_1** represents **J** or another amino acid different from **B**,
- **X_2** represents **J**,
- **X_3** represents **B**, **J**, or another amino different from S, T, D and E,
- **X_4** represents **J** or another amino acid different from **B**, S, T, D and E,
- **X_5** represents **J^1**,
- **X_6** represents **J**, **B**, or another amino acid, and
- **X_7** represents **J**, **B**, or another amino acid, with the proviso that the sequence X_1 to X_7 comprises three or four hydrophobic amino acids and one or two basic amino acids, and no more that two basic amino acids and four hydrophobic amino acids,
- **Z** and **Z'** together represent a sequence of no more than 13 amino acids, or **Z** and/or **Z'** are no amino acid (*i.e.* absent) , and
- said sequence (I) has a net charge of 0 to +2 when Z and Z' are no amino acid or of 0 to +3 when Z and/or Z' are present, and

(II) U-X^aBBJBBBX^b-U',

wherein:

- **X^a** is S, G, T, **J, Q or N,**
- **X^b** is G or **J**, wherein **B** and **J** are as defined above, and
- **U** is a sequence of 1 to 12 amino acids or no amino acid, **U'** is a sequence of 1 to 8 amino acids or no amino acid, with the proviso that only one of U and U' is present.

The peptide according to the present invention is a cell penetrating peptide or CPP. Therefore, it is capable of crossing the plasma membrane of cells and

of carrying small and large non-permeant molecular cargoes across the plasma membrane, efficiently, rapidly, at low concentration, *in vitro* and *in vivo*, into various cell types. Non-permeant molecular cargoes include but are not limited to peptides, proteins including antibodies, small (oligonucleotides, PNAs) and large nucleic acids, small and large chemical compounds, nanoparticles and liposomes. These properties can be readily verified by technique known to those skilled in the art such as those described in the examples of the present application.

The peptide of the invention provides an efficient carrier or vector for the delivery of various drugs and agents of therapeutic, diagnostic and technological value to their site of action in a cell, in particular the cytosol and the nucleus. Therefore, the peptide of the invention can be used for various *in vivo* applications including therapy, diagnosis, medical imaging and research.

Definitions

- "peptide" refers to a chain of natural amino acids (20 gene-encoded amino acids in a L- or D-configuration) linked via a peptide bond and furthermore comprises peptidomimetics of such peptide where the amino acid(s) and/or peptide bond(s) have been replaced by functional analogues. Such functional analogues include all known amino acids other than said 20 gene-encoded amino acids. A non-limitative list of non-coded amino acids is provided in Table 1A of US 2008/0234183 which is incorporated herein by reference. For example L-alpha-aminobutyric acid, also named 2-amino butyric acid (Abu) is an isosteric analogue of cysteine.

- "net charge of a sequence" will refer to the value obtained by adding all the positive and negative charges which are present on the amino acids of a sequence, as shown in Figure 2A; an acidic amino acid (D, E) has one negative charge (-1), a basic amino acid (K, R) has one positive charge (+1) and the other amino acids have no charge (0). H are not taken into consideration.

- " cargo", "molecular cargo", 'impermeant cargo' refers to a substance that can be transported across the plasma membrane of cells and delivered into cells by using a cell penetrating peptide as a delivery vehicle. The cargo may be a molecule such as a small molecule or a macromolecule or a particle such as a nanoparticle or a liposome.

- "cell" refers to a cell in a cell culture (*in vitro*) or in an intact multicellular organism (*in vivo*). The cell can be prokaryotic or eukaryotic. Preferably, the cell is from a mammal (human, animal) or a plant.

The peptide consisting of the sequence (I) is also named peptide (I) or peptide I and the peptide consisting of the sequence (II) is also named peptide (II) or peptide II. "Peptide" refers to both peptides (I) and (II).

The peptide (I) which consists of 7 to 20 amino acids is derived from the maurocalcine peptide 1 to 20 (MCa_{1-20}). The peptide MCa_{1-20} which has the amino acid sequence SEQ ID NO: 2 comprises the sequence X_1 to X_7 in positions 3 to 9. The peptide MCa_{3-9} has the sequence SEQ ID NO: 3, where X_1 is C, X_2 is L, X_3 is P, X_4 is H, X_5 is L, X_6 is K and X_7 is L. Furthermore, X_7 is R in $Opi/IpTx_{3-9}$ (SEQ ID NO: 6); X_2 is I, X_3 is K, X_6 is Q, and X_7 is R in $Hadru_{5-11}$ (SEQ ID NO: 9). Z is derived from the peptide MCa_{1-2} (GD) and Z' is derived from the peptide MCa_{10-20} (SEQ ID NO: 21). Preferably, X_6, X_3 and X_7, X_6 and X_7, X_3 and X_7 or X_6 are basic amino acids, and/or X_1 or X_7, or both, are hydrophobic amino acids. In preferred embodiments, all the hydrophobic amino acids of said peptide (I) are J^1. Preferably, X_2 and X_5 are L or X_2 is I and X_5 is L.

Preferably, the sequence $\mathbf{X_1\text{-}X_2\text{-}X_3\text{-}X_4\text{-}X_5\text{-}X_6\text{-}X_7}$ is chosen from the group consisting of SEQ ID NO: 3 to 20 and the sequences wherein one, two, three, four, five, six or seven amino acids of SEQ ID NO: 3 to 20 have been substituted with a different amino acid. In preferred embodiments, at least the cysteine (C) in position 1 (X_1), the histidine (H) in position 4 (X_4), and/or the lysine (K) in position 6 (X_6) of SEQ ID NO: 3 to 20 have been substituted with a different amino acid. In some embodiments, the cysteine (C) in position 1 is substituted with 2-amino butyric acid. In some preferred embodiments, the sequence $\mathbf{X_1\text{-}X_2\text{-}X_3\text{-}X_4\text{-}X_5\text{-}X_6\text{-}X_7}$ is chosen from the group consisting of SEQ ID NO: 3, 9, 12 and 18.

Preferably, Z consists of a sequence of 1 to 4 amino acids. In some embodiments Z consists of 2, 3 or 4 amino acids. Preferably, Z comprises one or two acidic amino acids (D, E). In some embodiments, Z is chosen from GD, GA, KD and SEKD.

Preferably, Z' is no amino acid or consists of the sequence

(III) $\mathbf{Z'_1\text{-}Z'_2\text{-}Z'_3\text{-}Z'_4\text{-}Z'_5\text{-}Z'_6\text{-}Z'_7\text{-}Z'_8\text{-}Z'_9\text{-}Z'_{10}\text{-}Z'_{11}}$,

wherein:

- Z'_1 is **J**,
- Z'_2 is **B**, J, N, Q or no amino acid,
- Z'_3 is N, Q, **P, G, J**, D, E or no amino acid
- Z'_4 is N, Q, D, E or no amino acid,
- Z'_5 is N, Q, **B** or no amino acid,
- Z'_6 is N, Q,P, G, **J**, D, E or no amino acid,
- Z'_7 is **J** or no amino acid,
- Z'_8 is **J** or no amino acid,
- Z'_9 is S, G, T, **J**, Q, N or no amino acid,
- Z'_{10} is **B** or no amino acid,
- Z'_{11} is **B** or no amino acid, and

wherein Z' does not comprise any internal deletion other than the deletion of Z'_2 to Z_9', Z'_3 to Z_6', or one or more of Z'_3, Z'_6 and Z'_9.

In preferred embodiments, Z' is chosen from the group consisting of:

- SEQ ID NO: 21 to 35,

- the sequences wherein one, two, three, four, five, six, seven, eight, nine, ten or eleven amino acids of SEQ ID NO: 21 to 35 have been substituted. Preferably, the cysteine (C) residues in positions 7 (Z'_7), and eventually also the cysteine(s) in position 1 (Z'_1) and/or 8 (Z'_8) are substituted with Abu, the glutamic acid residue in position 3 (Z'_3) is substituted with N, Q, P, G or J, the aspartic acid residue in position 6 (Z'_6) is substituted with N, Q, P, G or J, and/or the serine or glycine residue in position 9 (Z'_9) is replaced with J, Q or N, and

- the N-terminal fragments of said sequences which consist of the first 1 to 10 amino acids of said sequences, and the fragments wherein the residues in positions 2 to 9 (Z'_2 to Z'_9), the residues in positions 3 to 6 (Z'_3 to Z'_6), or one or more of the residues in position 3 (Z'_3), 6 (Z'_6) and 9 (Z'_9) of SEQ ID NO: 21 to 35 have been deleted.

In preferred embodiments, the peptide (I) has a net charge of zero, +1 or +2. Preferably, X_1 to X_7 and Z together have a net charge of zero.

The peptide (II) which consists of 8 to 20 amino acids is derived

from the maurocalcine peptides 6 to 25 and 18 to 33. The peptide MCa_{6-25} has the amino acid sequence of SEQ ID NO: 106. The peptide MCa_{18-33} has the amino acid sequence of SEQ ID NO: 107. The peptide MCa_{18-25} has the sequence SEQ ID NO: 108. U is derived from the peptide MCa_{6-17} (SEQ ID NO: 109) and U' is derived from the peptide MCa_{26-33} (SEQ ID NO: 110).

In some embodiments X^a is chosen from S, G, T and A. In other embodiments, X^a is chosen from J, Q and N.

Preferably, the central sequence $\mathbf{X^aBBJBBBX^b}$ is chosen from: SKKCKRR and GKKCKRR (SEQ ID NO: 108 and 111), and the sequences wherein one, two, three, four, five, six or seven amino acids of SEQ ID NO: 108 and 111 have been substituted with a different amino acid.

Preferably, U is no amino acid or consists of the sequence

(IV) $\mathbf{U_1\text{-}U_2\text{-}U_3\text{-}U_4\text{-}U_5\text{-}U_6\text{-}U_7\text{-}U_8\text{-}U_9\text{-}U_{10}\text{-}U_{11}\text{-}U_{12}}$,

wherein:

- $\mathbf{U_1}$ is J or another amino acid different from K, R, S, T, D and E,
- $\mathbf{U_2}$ is J or no amino acid
- $\mathbf{U_3}$ is J, B, another amino acid, or no amino acid,
- $\mathbf{U_4}$ is J, B, another amino acid, or no amino acid,
- $\mathbf{U_5}$ is J or no amino acid,
- $\mathbf{U_6}$ is B, N, Q, Jor no amino acid,
- $\mathbf{U_7}$ is N, Q, P, G, J, D, E or no amino acid,
- $\mathbf{U_8}$ is N, Q, D, E or no amino acid,
- $\mathbf{U_9}$ is N, Q, B or no amino acid,
- $\mathbf{U_{10}}$ is N, Q, P, G, J, D, E or no amino acid,
- $\mathbf{U_{11}}$ is J or no amino acid,
- $\mathbf{U_{12}}$ is J or no amino acid, and

wherein U does not comprise any internal deletion other than the deletion of U_7 to U_{10} or the deletion of U_7, U_{10}, or both residues.

In preferred embodiments, U is chosen from:

- the sequences SEQ ID NO: 109 and 112 to 115,
- the sequences wherein one, two, three, four, five, six, seven, eight, nine, ten, eleven or twelve amino acids of SEQ ID NO: 109 and 112 to 115 have been

substituted with a different amino acid. In preferred embodiments, the cysteine (C) residues in positions 11 (U_{11}) and 12 (U_{12}), and eventually also the cysteine in position 5 (U_5) are substituted with Abu; the glutamic acid residue (E) in position 7 (U_7) is substituted with N, Q, P, G or J, the aspartic acid residue (D) in position 10 (U_{10}) is substituted with N, Q, P, G or J, the histidine (H) residue in position 1(U_1), and/or the lysine residue in position 3 (U_3) is substituted with a different amino acid, and

- the N-terminal fragments of said sequences which consist of the first 1 to 11 amino acids of said sequences, and the fragments wherein the residues in positions 7 to 10 (U_7 to U_{10}), the glutamic acid residue in position 7 (U_7), the aspartic acid residue in position 10 (U_{10}) or both residues of SEQ ID NO: 109 and 112 to 115 have been deleted. In some embodiments, the N-terminal fragment consists of the first five amino acids of said sequences.

Preferably, U' is no amino acid or consists of the sequence **U'_1-U'_2-U'_3-U'_4-U'_5-U'_6-U'_7-U'_8,**

wherein:

- **U'_1** is **O**,
- **U'_2** is N, Q, or no amino acid,
- **U'_3** is P, J or no amino acid,
- **U'_4** is J, D, E or no amino acid,
- **U'_5** is B or no amino acid,
- **U'_6** is B or no amino acid,
- **U'_7** is J or no amino acid, and
- **U'_8** is B or no amino acid,

wherein U' does not comprise any internal deletion other than the deletion of U'_1 to U'_4.

In preferred embodiments, U' is chosen from:

- the sequences SEQ ID NO: 110 and 116 to 118,

- the sequences wherein one, two, three, four, five, six, seven or eight amino acids of SEQ ID NO: 110 and 116 to 118 have been substituted with a different amino acid. In preferred embodiments, the cysteine (C) residue in position 7 (U'_7) is substituted with Abu and/or the glutamic acid residue in position 4 (U'_4) is substituted with J, P, Q, N or G, and

- the N-terminal fragments of said sequences which consist of the first 1 to 7 amino acids of said sequences and the fragments of said sequences wherein the residues in positions 1 to 4 (U'_1 to U'_4) of SEQ ID NO: 110 and 116 to 118 have been deleted.

In preferred embodiments of the invention, the peptide (I) has a sequence selected from the group consisting of: SEQ ID NO: 2, 3 and 36 to 43 and the sequences which have at least 60% similarity to the full length sequence of any of SEQ ID NO: 2, 3 and 36 to 43. In some embodiments, the sequences have at least 70%, 80% or 90% similarity with said full-length sequences. In some embodiments, said sequences have also at least 40% identity, preferably at least 50%, 60%, 70% or 80% identity with said full-length sequences.

In preferred embodiments of the invention, the peptide (II) has a sequence selected from the group consisting of: SEQ ID NO: 106, 107, 108 and 119 and the sequences which have at least 60% similarity to the full length sequence of any of SEQ ID NO: 106, 107, 108 and 119. In some embodiments, the sequences have at least 70%, 80% or 90% similarity with said full-length sequences. In some embodiments, said sequences have also at least 40% identity, preferably at least 50%, 60%, 70% or 80% identity with said full-length sequences.

Percentage (%) sequence identity is defined as the percentage of amino acid residues in a candidate sequence that are identical with residues in the given listed sequences (referred to by SEQ ID NO: X) after aligning the sequences and introducing gaps if necessary, to achieve the maximum sequence identity and not considering any conservative substitutions as part of the sequence identity. Sequence identity is preferably calculated over the entire length of the respective sequences.

Percentage (%) sequence similarity is defined as the percentage of amino acid residues in a candidate sequence that are identical with residues in the given listed sequences (referred to by SEQ ID NO: X) after aligning the sequences and introducing gaps if necessary, to achieve the maximum sequence identity and considering any conservative substitutions as part of the sequence identity. Sequence similarity is preferably calculated over the entire length of the respective sequences.

Alignment for purposes of determining percent amino acid sequence identity/similarity can be achieved in various ways known to a person of skill in the

art, for instance using publicly available computer software such as BLAST (Altschul *et al.*, J. Mol. Biol., 1990, 215, 403-). When using such software, the default parameters, e.g., for gap penalty and extension penalty, are preferably used. For amino acid sequences, the BLASTP program uses as default a word length (W) of 3 and an expectation (E) of 10.

In some embodiments, the peptides according to the present invention comprise conservative amino acid replacements which, for example, may be between amino acids within the following groups: G, A, S and T; D and E; R, H and K; N and Q; I, L and V; F, Y and W; C and 2-aminobutyric acid.

In some embodiments, the peptide comprises a unique free cysteine (cysteine not linked to another cysteine via a disulfide bond). Preferably, said unique free cysteine is at the N- or C-terminus of the peptide. Preferaby, the other cysteine residues of maurocalcine which are not linked via a disulfide bond are replaced with 2-amino butyric acid. In preferred embodiments of the present invention, said unique free cysteine is used for coupling the cargo covalently to the peptide by a disulphide, thioether or thiol-maleimide linkage.

In other embodiments, the peptide comprises two cysteines which are linked via a disulfide bond (intramolecular disulphide bond). Preferably, the peptide (I) comprises at least the residues Z'_1 to Z'_8 of the sequence Z', with or without the residue(s) Z'_3, Z_6', and/or Z'_9, Z'_2 to Z'_9, or Z'_3 to Z_6', and X_1 and Z'_8 or X_1 and Z'_1 are cysteine residues which are linked via a disulfide bond. Preferably, the peptide (II) comprises at least the residues U_5 to U_{12} of the sequence U and U_5 and the residue J of the central sequence of said peptide II are cysteine residues which are linked via a disulfide bond. The presence or absence of disulphide bonds can be advantageous to improve the cell penetration efficiency and/or the conformational stability of the peptides according to the present invention.

The peptide according to the invention may consist of L-amino acids, D-amino acids or mixtures thereof. Preferably, the peptides comprise D-amino acids. In preferred embodiments of the present invention, the peptide consists of D-amino acids. Peptides comprising D-amino acids have the advantage of being more stable *in vivo* due to their increased resistance to proteolytic cleavage.

Preferred peptides (I) according to the present invention have a

sequence selected from the group consisting of: SEQ ID NO: 2 to 105, 148, 150, 152, 154, 158, 160, 162, 164, 166, 168 and 170. More preferred peptides (I) are selected from the group consisting of SEQ ID NO: 2, 3, 9, 12, 18, 36, 37, 44, 46, 66, 150, 152 and 154.

Preferred peptides (II) according to the present invention have a sequence selected from the group consisting of: SEQ ID NO 106 to 108, 111 and 119 to 133.

In preferred embodiments, the peptide is modified. The modifications include esterification, glycosylation, acylation such as acetylation or linking myristic acid, amidation, phosphorylation, biotinylation, PEGylation, coupling of farnesyl and similar modifications which are well-known in the art. Modifications can be introduced at the the N-terminus, the C-terminus of the peptide or if deemed suitable, also to any amino acid other than the terminal amino acids (e.g. farnesyl coupling to a cysteine side chain). Conversion of the acid function on the C-terminus into an aldehyde and alkylation of the thiol function of a cysteine residue are used for chemoselective ligation or the formation of reduced peptide bonds.

Preferably, the peptide is used as a complex comprising at least the peptide and a molecular cargo.

The use according to the present invention comprises contacting the complex comprising the peptide and the cargo with cells, *in vitro* or *in vivo*, wherein the complex crosses the plasma membrane of the cells and the cargo is delivered into the cells, *in vitro* or *in vivo*. Preferably, the cargo is delivered into the cytoplasm and/or the nucleus of the cells.

The cargo can be a small molecule, a macromolecule or a particle. In a preferred embodiment, the cargo is selected from the group consisting of: oligonucleotides including antisense oligonucleotides, peptide nucleic acids (PNAs), small interfering RNAs, locked nucleic acids (LNAs), phosphorodiamidate morpholino oligonucleotides (PMOs) and decoy DNA molecules; plasmids; cDNAs; aptamers including DNA, RNA or peptide aptamers; peptides; proteins including antibodies; small and large chemical compounds including bioactive substances like drugs for the treatment of human, animal or plant diseases; labels such as fluorescent or radioactive molecules; imaging agents; liposomes, micelles and nanoparticles

including liposomes, micelles and nanoparticles carrying an active agent such as nanocarriers. For example, the active agent can be encapsulated into the particles or grafted onto said particles by means well-known in the art. It is within the present invention that the complex comprises more than one peptide according to the present invention, *i.e.*, a plurality of such peptides, whereby the plurality of the peptides may comprise a plurality of the same or of different peptides. Aso, the complex according to the present invention may also comprise more than one cargo molecule, whereby the plurality of the cargo molecules may comprise a plurality of the same or of different cargo molecules.

In a preferred embodiment, the cargo is covalently or non-covalently bound to the peptide of the invention.

The cargo may be coupled to the peptide, directly or indirectly. Indirect coupling of the cargo to the peptide may be through a linker that is attached to the peptide of the invention. Linkers, also named spacers, that can be used to physically separate the peptide of the invention to the cargo are known in the art and include a peptide bond, an amino acid, a peptide of appropriate length or a different molecule providing the desired feature. The linker may be attached to the the N-terminus, the C-terminus of the peptide or if deemed suitable, also to any amino acid other than the terminal amino acids.

The peptide of the invention can be chemically linked to the cargo by covalent bonds using standard conjugation techniques. The cargo can be linked to the N-terminus, the C-terminus of the peptide, or if applicable, to any amino acid other than the terminal amino acids. Functional groups, modifications also called derivatizations or a linker may also be introduced into the peptide for conjugating the peptide to the cargo. Such covalent bonds are preferably formed between either a suitable reactive group of the peptide and the cargo and more preferably between a terminus of the peptide according to the present invention and the cargo molecule(s). Depending on the chemical nature of the cargo molecules, the moiety, group or radical with which such covalent bond is formed varies and it is within the skills of a person of the art to create such bond. Chemical linkage may be via a disulphide bond, thioether, thiol-maleimide or amide linkage. Other ways of linking the peptide to the cargo include use of a C-terminal aldehyde to form an oxime, use of a click reaction

or formation of a morpholino linkage with a basic amino acid on the peptide. For coupling the peptide to the cargo using click chemistry, an alcyne or azido function may be added to the peptide using the N-alpha-(9-Fluorenylmethyloxycarbonyl)-L-propargylglycine, (S)-2-(Fmoc-amino)-4-pentynoic acid or N-alpha-(9-Fluorenylmethyloxycarbonyl)-4-azido-L-homoalanine or (S)-2-(9-Fluorenylmethyloxycarbonylamino)-4-azidobutanoic acid reagents. This type of construct is produced by well-known peptide chemical synthesis methods, preferably by solid phase synthesis.

In addition, when the cargo is a peptide or a protein including an antibody, the complex may be a fusion protein/peptide in which the cargo is fused to the N-terminus or the C-terminus of the peptide of the invention, directly or via a peptide spacer. This complex is produced by making a fusion in frame of a nucleotide sequence encoding the peptide of the invention to a nucleotide sequence encoding the peptide/protein cargo, and expressing the resulting chimeric gene using standard recombinant DNA techniques. The resulting fusion protein/peptide is of heterologous origin, *i.e.*, it is different from naturally occurring peptides or proteins such as maurocalcine or other toxins of the same family.

The peptide can also be bound to the cargo (molecule or particle carrying the molecule) via non-covalent bounds such as ionic bonds, hydrogen bonds or hydrophobic interactions or a combination of such bonds. Non-limitative examples include streptavidine-biotin interactions between a biotinylated peptide and a cargo (for example nanoparticles like Quantum dots) that is conjugated to streptavidine or a biotinylated cargo and a peptide that is conjugated to streptavidine.

In some embodiments, the complex further comprises a targeting moiety, for example a targeting peptide for targeting the complex to specific cell types.

In a preferred embodiment, the cargo is linked covalently to the peptide of the invention via a cysteine linker that is attached to the N-terminus or the C-terminus of the peptide of the invention. Preferably, the cysteine residues of the peptide are replaced with 2-amino butyric acids, so that the cysteine linker is the unique cysteine of the peptide which is used for coupling the cargo covalently to the peptide by a linkage such a disulphide, thioether or thiol-maleimide linkage.

Examples of such peptides are SEQ ID NO: 134 to 139, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169 and 171. Preferred peptides (I) are selected from the group consisting of: SEQ ID NO: 134-136, 151, 153, 155 and 157.

The invention provides a peptide according to the present invention. Peptides according to the present invention may be provided in isolated or purified form, with or without the cargo.

The invention provides a complex comprising a peptide of the invention and a cargo.

The invention provides a pharmaceutical composition comprising (1) a complex comprising a peptide of the invention and an active agent, and (2) a pharmaceutically acceptable carrier.

The pharmaceutical composition comprises a therapeutically effective amount of the complex, *e.g.*, sufficient to show benefit to the indidual to whom it is administered. The pharmaceutical composition is formulated for administration by a number of routes, including but not limited to oral, parenteral and nasal.

The invention provides a method of treatment of a patient or subject in need for treatment for a disease condition, comprising the step of administering a therapeutically effective amount of a complex comprising a peptide of the invention and an active agent to the patient or subject.

The invention provides also a complex comprising a peptide of the invention and an active agent for treating a disease.

The active agent is a pharmaceutical agent or therapeutic capable of preventing, treating or ameliorating a disease in humans or animals. The active agent may be a protein including an antibody, an oligonucleotide including an antisense oligonucleotide, peptide nucleic acid (PNA), small interfering RNA, locked nucleic acids (LNA), phosphorodiamidate morpholino oligonucleotides (PMO) and decoy DNA molecule, a plasmid, an aptamer including DNA, RNA or peptide aptamer, a small or large chemical drug, or mixtures thereof. In particular, the active agent may be a chemotherapeutic drug used for treating cancer. Coupling anti-tumoral drugs to the cell penetrating peptides represent a valuable strategy to overcome drug resistance. The active agent is also an antigen or a nucleic acid molecule encoding said antigen

(DNA vaccine) for use as a vaccine for the prevention or the treatement of an infectious disease or a cancer. The complex may comprise particles like nanoparticles, micelles or liposomes carrying both the peptide(s) and the active(s) agent(s).

Diseases to be prevented, treated or ameliorated may include any disease where improved penetration of the plasma and/or nuclear membrane by a pharmaceutical or therapeutical molecule may lead to an improved therapeutic effect. Diseases to be treated may include cancer, genetic, neurological, cardiovascular, metabolic, inflammatory, auto-immune and infectious diseases.

The invention provides a detection reagent, for example a diagnostic reagent, comprising a complex comprising a peptide of the invention and a detection agent. Preferably, the detection agent is covalently or non-covalently bound to the peptide. Detection agents are known in the art and include but are not limited to antibodies and oligonucleotide probes that are used for the detection (qualitative or quantitative detection) of an intracellular target, for example a protein or a nucleic acid target. When the intracellular target is associated with a disease (*e.g.*, diagnostic marker), the detection agent is a diagnostic agent. According to a preferred embodiment, the complex further comprises a detectable moiety that produces a detectable signal when the intracellular target reacts with the detection agent. For example, the detectable moiety can be a fluorescent reporter system.

The invention provides a method of detecting an intracellular target, comprising:

- contacting the detection reagent of the invention with cells, *in vitro* or *in vivo,* wherein the detection reagent is capable of reacting with an intracellular target, and
- detecting the intracellular target that has reacted with the reagent, by any appropriate means.

The invention provides a method of diagnosis a disease, comprising:

- contacting the diagnostic reagent of the invention with cells, *in vitro* or *in vivo,* wherein the diagnostic reagent is capable of reacting with an intracellular diagnostic marker, and
- detecting the intracellular diagnostic marker that has reacted

with the reagent, by any appropriate means.

The invention provides an imaging reagent, comprising a complex comprising a peptide of the invention and a label or a contrast agent. Preferably, the label or contrast agent is covalently or non-covalently bound to the peptide.

In optical imaging methods, the imaging reagent comprises a complex comprising a peptide of the invention and a label. The label is any molecule that produces a signal that can be detected *in situ* in living cells or tissues. The label can be a fluorescent molecule. This imaging reagent can be applied in optical imaging methods for research or diagnostic purposes.

In magnetic resonance imaging (MRI) the imaging reagent comprises a complex comprising a peptide of the invention and a contrast agent, usually a paramagnetic contrast agent (usually a gadolinium compound) or a superparamagnetic contrast agent (iron oxide nanoparticles). MRI was primarily used in medical imaging to demonstrate pathological or other physiological alteration of living tissues.

In positron emission tomography (PET), the imaging reagent comprises a complex comprising a peptide of the invention and a short-lived radioactive tracer isotope which has been chemically incorporated into a metabolically active molecule (usually a sugar, fluorodeoxyglucose, FDG) and which decays by emitting a positron. PET is a nuclear medicine imaging technique which produces a three-dimensional image or map of functional processes in the body.

The invention provides a nucleic acid molecule (DNA, RNA) comprising a nucleotide sequence encoding the peptide or the fusion peptide/protein according to the present invention.

The invention provides a nucleic acid recombinant vector comprising said nucleic acid molecule. Preferably, said recombinant vector is an expression vector comprising a regulatory sequence (promoter) operably linked to said nucleotide sequence, wherein the vector is capable of expressing the peptide or fusion peptide/protein of the invention when transfected or transformed into a host cell (mammalian, bacterial or fungal). Recombinant vectors include usual vectors used in genetic engineering and gene therapy including for example plasmids and viral vectors.

The invention provides a cell transformed with said recombinant vector.

The nucleic acid molecule, vector, cell of the invention are useful for the production of the peptide or fusion peptide/protein of the invention using well-known recombinant DNA techniques.

The invention provides a kit comprising one or more of:

- a peptide of the invention,
- a complex of the invention,
- a nucleic acid molecule, recombinant vector, cell transformant of the invention.
- a pharmaceutical composition of the invention, and
- a detection, diagnostic or imaging reagent of the invention.

Table I : Peptide sequences

Peptide	Variant	Sequence	SEQ ID NO :
MCa_{1-33}		GDCLPHLKLCKENKDCCSKKC KRRGTNIEKRCR	1
MCa_{1-20}		GDCLPHLKLCKENKDCCSKK	2
MCa_{3-9}		CLPHLKL	3
	H6A	CLPALKL	4
	K8A	CLPHLAL	5
$Opi/IpTx_{3-9}$		CLPHLKR	6
	H6A	CLPALKR	7
	K8A	CLPHLAR	8
$HadruCa_{5-11}$		CIKHLQR	9
	H6A	CIKALQR	10
	K8A	CIKHLAR	11
MCa_{3-9}	C3Abu	aLPHLKL	12
	C3Abu/H6A	aLPALKL	13
	C3Abu/K8A	aLPHLAL	14
$Opi/IpTx_{3-9}$	C3Abu	aLPHLKR	15
	C3Abu/H6A	aLPALKR	16
	C3Abu/K8A	aLPHLAR	17
$HadruCa_{5-11}$	C5Abu	aIKHLQR	18
	C5Abu/H8A	aIKALQR	19
	C5Abu/K10A	aIKHLAR	20
MCa_{10-20}		CKENKDCCSKK	21
	C10,16,17Abu	aKENKDaaSKK	22
	C10,16Abu	aKENKDaCSKK	23
Opi_{10-20}		CKENNDCCSKK	24
	C10,16,17Abu	aKENNDaaSKK	25
	C10,16Abu	aKENNDaCSKK	26
$IpTx_{10-20}$		CKADNDCCGKK	27
	C10,16,17Abu	aKADNDaaGKK	28
	C10,16Abu	aKADNDaCGKK	29
$HemiCa_{10-20}$		CKADKDCCSKK	30
	C10,16,17Abu	aKADKDaaSKK	31
	C10,16Abu	aKADKDaCSKK	32
$HadruCa_{12-22}$		CRENKDCCSKK	33
	C12-18-19Abu	aRENKDaaSKK	34
	C12-18-Abu	aRENKDaCSKK	35
MCa_{1-9}		GDCLPHLKL	36
MCa_{1-15}		GDCLPHLKLCKENKD	37
$MCa_{1-15/\Delta 12-15}$		GDCLPHLKLCK	38
$MCa_{1-15/\Delta 12}$		GDCLPHLKLCKNKD	39
$MCa_{1-15/\Delta 15}$		GDCLPHLKLCKENK	40
$MCa_{1-20/\Delta 12-15}$		GDCLPHLKLCKCCSKK	41
$MCa_{1-20/\Delta 12}$		GDCLPHLKLCKNKDCCSKK	42
$MCa_{1-20/\Delta 15}$		GDCLPHLKLCKENKCCSKK	43
MCa_{1-9}	C3Abu	GDaLPHLKL	44
	D2A/C3Abu	GAaLPHLKL	45
MCa_{1-15}	C3,10Abu	GDaLPHLKLaKENKD	46
	D2A/C3,10Abu	GAaLPHLKLaKENKD	47
	H6A/C3,10Abu	GDaLPALKLaKENKD	48

	K8A/C3,10Abu	GDaLPHLALaKENKD	49
	E12A/C3,10Abu	GDaLPHLALaKANKD	50
	D15A/C3,10Abu	GDaLPHLALaKENKA	51
$MCa_{1-15/\Delta12-15}$	C3,10Abu	GDaLPHLKLaK	52
	D2A/C3,10Abu	GAaLPHLKLaK	53
	H6A/C3,10Abu	GDaLPALKLaK	54
	K8A/C3,10Abu	GDaLPHLALaK	55
$MCa_{1-15/\Delta12}$	C3,10Abu	GDaLPHLKLaKNKD	56
	D2A/C3,10Abu	GAaLPHLKLaKNKD	57
	H6A/C3,10Abu	GDaLPALKLaKNKD	58
	K8A/C3,10Abu	GDaLPHLALaKNKD	59
	D15A/C3,10Abu	GDaLPHLALaKNKA	60
$MCa_{1-15/\Delta15}$	C3,10Abu	GDaLPHLKLaKENK	61
	D2A/C3,10Abu	GAaLPHLKLaKENK	62
	H6A/C3,10Abu	GDaLPALKLaKENK	63
	K8A/C3,10Abu	GDaLPHLALaKENK	64
	E12A/C3,10Abu	GDaLPHLKLaKANK	65
MCa_{1-20}	C3,10,16,17Abu	GDaLPHLKLaKENKDaaSKK	66
	D2A/C3,10,16,17Abu	GAaLPHLKLaKENKDaaSKK	67
	H6A/C3,10,16,17Abu	GDaLPALKLaKENKDaaSKK	68
	K8A/C3,10,16,17Abu	GDaLPHLALaKENKDaaSKK	69
	D15A/C3,10,16,17Abu	GDaLPHLKLaKENKAaaSKK	70
	E12A/C3,10,16,17Abu	GDaLPHLKLaKANKDaaSKK	71
$MCa_{1-20/\Delta12-15}$	C3,10,16,17Abu	GDaLPHLKLaKaaSKK	72
	D2A/C3,10,16,17Abu	GAaLPHLKLaKaaSKK	73
	H6A/C3,10,16,17Abu	GDaLPALKLaKaaSKK	74
	K8A/C3,10,16,17Abu	GDaLPHLALaKaaSKK	75
$MCa_{1-20/\Delta12}$	C3,10,16,17Abu	GDaLPHLKLaKNKDaaSKK	76
	D2A/C3,10,16,17Abu	GAaLPHLKLaKNKDaaSKK	77
	H6A/C3,10,16,17Abu	GDaLPALKLaKNKDaaSKK	78
	K8A/C3,10,16,17Abu	GDaLPHLALaKNKDaaSKK	79
	D15A/C3,10Abu	GDaLPHLKLaKNKAaaSKK	80
$MCa_{1-20/\Delta15}$	C3,10,16,17Abu	GDaLPHLKLaKENKaaSKK	81
	D2A/C3,10,16,17Abu	GAaLPHLKLaKENKaaSKK	82
	H6A/C3,10,16,17Abu	GDaLPALKLaKENKaaSKK	83
	K8A/C3,10,16,17Abu	GDaLPHLALaKENKaaSKK	84
	E12A/C3,10,16,17Abu	GDaLPHLKLaKANKaaSKK	85
MCa_{1-20F}	C10,16Abu	GDCLPHLKLaKENKDaCSKK	86
	D2A/C10,16Abu	GACLPHLKLaKENKDaCSKK	87
	H6A/C10,16Abu	GDCLPALKLaKENKDaCSKK	88
	K8A/C10,16Abu	GDCLPHLALaKENKDaCSKK	89
	D15A/C10,16Abu	GDCLPHLKLaKENKAaCSKK	90
	E12A/C10,16Abu	GDCLPHLKLaKANKDaCSKK	91
$MCa_{1-20/\Delta12-15}$	C10,16,Abu	GDCLPHLKLaKaCSKK	92
	D2A/C10,16Abu	GACLPHLKLaKaCSKK	93
	H6A/C10,16,Abu	GDCLPALKLaKaCSKK	94
	K8A/C10,16Abu	GDCLPHLALaKaCSKK	95
$MCa_{1-20/\Delta12}$	C10,16Abu	GDCLPHLKLaKNKDaCSKK	96
	D2A/C10,16Abu	GACLPHLKLaKNKDaCSKK	97
	H6A/C10,16Abu	GDCLPALKLaKNKDaCSKK	98
	K8A/C10,16Abu	GDCLPHLALaKNKDaCSKK	99
	D15A/C3,10,16Abu	GDCLPHLKLaKNKAaCSKK	100
$MCa_{1-20/\Delta15}$	C10,16,Abu	GDCLPHLKLaKENKaCSKK	101
	D2A/C10,16Abu	GACLPHLKLaKENKaCSKK	102

	H6A/C10,16Abu	GDCLPALKLaKENKaCSKK	103
	K8A/C10,16Abu	GDCLPHLALaKENKaCSKK	104
	E12A/C10,16Abu	GDCLPHLKLaKANKaCSKK	105
MCa_{6-25}		HLKLCKENKDCCSKKCKRRG	106
MCa_{18-33}		SKKCKRRGTNIEKRCR	107
MCa_{18-25}		SKKCKRRG	108
MCa_{6-17}		HLKLCKENKDCC	109
MCa_{26-33}		TNIEKRCR	110
$IpTxa_{18-25}$		GKKCKRR	111
$IpTxa_{6-17}$		HLKRCKADNDCC	112
Opi_{6-17}		HLKRCKENNDCC	113
$Hemi_{6-17}$		HLKLCKADKDCC	114
$Hadru_{8-19}$		HLQRCRENKDCC	115
$IpTxa_{26-33}$		TNAEKRCR	116
Opi1-Hemi-Hadru $_{26-33}$		TNPEKRCR	117
$Opi2_{26-33}$		ANPEKRCR	118
MCa_{14-25}		KDCCSKKCKRRG	119
MCa_{18-33}	C21,32Abu	SKKaKRRGTNIEKRaR	120
$MCa_{18-33\Delta 26-29}$	C21,32Abu	SKKaKRRGKRaR	121
MCa_{6-25}	C10,16,17,21Abu	HLKLaKENKDaaSKKaKRRG	122
MCa_{6-25}	H6A/C10,16,17,21Abu	ALKLaKENKDaaSKKaKRRG	123
MCa_{6-25}	K8A/C10,16,17,21Abu	HLALaKENKDaaSKKaKRRG	124
MCa_{6-25}	E12A/C10,16,17,21Abu	HLKLaKANKDaaSKKaKRRG	125
MCa_{6-25}	D15A/C10,16,17,21Abu	HLKLaKENKAaaSKKaKRRG	126
MCa_{6-25F}	C16,17Abu	HLKLCKENKDaaSKKCKRRG	127
MCa_{6-25F}	H6A/C16,17Abu	ALKLCKENKDaaSKKCKRRG	128
MCa_{6-25F}	K8A/C16,17Abu	HLALCKENKDaaSKKCKRRG	129
MCa_{6-25F}	E12A/C16,17Abu	HLKLCKANKDaaSKKCKRRG	130
MCa_{6-25F}	D15A/C16,17Abu	HLKLCKENKAaaSKKCKRRG	131
MCa_{14-25}	C16,17,21Abu	KDaaSKKaKRRG	132
MCa_{14-25}	D15A/C16,17,21Abu	KAaaSKKaKRRG	133
MCa_{1-20}-C	C3,10,16,17Abu	GDaLPHLKLaKENKDaaSKKC	134
MCa_{1-15}-C	C3,10Abu	GDaLPHLKLaKENKDC	135
MCa_{1-9}-C	C3Abu	GDaLPHLKLC	136
MCa_{18-33}-C	C21,32Abu	SKKaKRRGTNIEKRaRC	137
MCa_{6-25} -C	C10,16,17,21Abu	HLKLaKENKDaaSKKaKRRGC	138
MCa_{14-25}-C	C16,17,21Abu	KDaaSKKaKRRGC	139
MCa_{1-33}-C	C3,10,16,17, 21,32Abu	GDaLPHLKLaKENKDaaSKKaKRRGTNIEKRaRC	140
MCa_{8-33}-C	C10,16,17, 21,32Abu	KLaKENKDaaSKKaKRRGTNIEKRaRC	141
MCa_{11-33}-C	C16,17, 21,32Abu	KENKDaaSKKaKRRGTNIEKRaRC	142
MCa_{14-33}-C	C16,17, 21,32Abu	KDaaSKKaKRRGTNIEKRaRC	143
MCa_{20-33}-C	C21, 32Abu	KaKRRGTNIEKRaRC	144
MCa_{22-33}-C	C32Abu	KRRGTNIEKRaRC	145
MCa_{25-33}-C	C32Abu	GTNIEKRaRC	146
MCa_{1-9}-C	C3A	GDALPHLKLC	147
Imp_{1-9}	C3Abu	GDaLPHLKR	148
Imp_{1-9}-C	C3Abu	GDaLPHLKRC	149
Had_{1-11}	C5Abu	SEKDaIKHLQR	150
Had_{1-11}-C	C5Abu	SEKDaIKHLQRC	151
Had_{3-11}	C5Abu	KDaIKHLQR	152
Had_{3-11}-C	C5Abu	KDaIKHLQRC	153

MCa_{1-9}	C3W	GDWLPHLKL	154
MCa_{1-9}-C	C3W	GDWLPHLKLC	155
MCa_{1-9}-C	D2A, C3Abu	GAaLPHLKLC	156
MCa_{3-9}-C	C3Abu	aLPHLKLC	157
MCa_{1-9}	C3Abu,H6W	GDaLPWLKL	158
MCa_{1-9}-C	C3Abu, H6W	GDaLPWLKLC	159
MCa_{1-9}	C3Abu,L4W	GDaWPHLKL	160
MCa_{1-9}-C	C3Abu,L4W	GDaWPHLKLC	161
MCa_{1-9}	C3Abu,L7F	GDaLPHFKL	162
MCa_{1-9}-C	C3Abu,L7F	GDaLPHFKLC	163
MCa_{1-9}	C3Abu,L9M	GDaLPHLKM	164
MCa_{1-9}-C	C3Abu,L9M	GDaLPHLKMC	165
MCa_{1-9}	C3Q	GDQLPHLKL	166
MCa_{1-9}-C	C3Q	GDQLPHLKLC	167
MCa_{1-9}	C3Abu,L9N	GDaLPHLKN	168
MCa_{1-9}-C	C3Abu,L9N	GDaLPHLKNC	169
MCa_{1-9}	C3Abu,P5R,K8I	GDaLRHLIL	170
MCa_{1-9}-C	C3Abu,P5R,K8I	GDaLRHLILC	171
Tat-C		GRKKRRQRRR-C	172

MCa: Maurocalcine. IpTxa/Imp: Imperatoxine. Opi: Opicalcine. Hemi: Hemicalcine. Hadru/Had: Hadrucalcine

For a better understanding of the invention and to show how the same may be carried into effect, there will now be shown by way of example only, specific embodiments, methods and processes according to the present invention with reference to the accompanying drawings in which:

- Figure 1 shows the efficacy of cargo penetration as a function of grafting position on MCaUF1-33. (A) Amino acid sequence of MCa_F in single letter code. The positions of half-cystine residues and basic amino acids are highlighted in grey. Cys residues are numbered. Secondary structures (β strands) are indicated by arrows. The grey box is the sequence of homology of MCa with the dihydropyridine-sensitive $Ca_v1.1$ channel. (B) Amino acid sequences of unfolded MCa analogues in single letter code. Cys residues are replaced by isosteric 2-aminobutyric acid residues (Abu, in grey) to form MCa_{UF1-33}. An additional N-terminal (C-MCa_{UF1-33}) or C-terminal (MCa_{UF1-33}-C) Cys residue was added in two novel analogues competent for cargo grafting (shown in grey). (C) Comparison of cell penetration efficacy between Cy5-C-MCa_{UF1-33} and MCa_{UF1-33}-C-Cy5 as determined by flow cytometry. CHO cells were incubated 2 hrs with 3 μM peptide, washed, and treated 5 min by 1 mg/ml trypsin before quantification of intracellular fluorescence.

Figure 2 shows the primary structure of truncated MCa_{UF} analogues and comparison of cell penetration efficacies. (A) Primary structures of truncated

MCa_{UF}-C analogues and determination of their net positive charge and percentage of basic amino acid residues within the sequence. A total of 12 truncated MCa_{UF}-C analogues were produced (three with truncations in C-terminus, seven in N-terminus, and two in both N-and C-termini). Positively charged residues are in grey (His residues were not counted), Abu residues that replace Cys residues are indicated. (B) Comparative cell penetration efficacy of all MCa_{UF}-C-Cy5 truncated analogues that possess a net positive charge $\geq +5$. The non-truncated MCa_{UF1-33}-C-Cy5 analogue is shown as reference (black line) for the efficacy of cell penetration of all analogues. Experimental conditions: CHO cell incubation with 1 μM of each analogue for 2 hrs and fluorescence quantification byflow cytometry. (C) Same as (B) but for truncated MCa_{UF}-C-Cy5 analogues with positive net charge $\leq +2$.

- Figure 3 shows the extent of colocalization of the Cy5-labeled peptides with the rhodaminelabeled plasma membrane. NS, non significant; * ≤ 0.1; ** ≤ 0.05; and *** ≤ 0.001.

Figure 4 shows the amiloride sensitivity of truncated MCa_{UF} peptide cell entry. (A) Representative flow cytometry analyses of the effect of 5 mM amiloride on MCa_{UF1-33}-C-Cy5 (upper left panel), MCa_{UF1-15}-C-Cy5 (upper right panel), $MCa_{UF20-33}$-C-Cy5 (lower left panel) and $MCa_{UF18-33}$-C-Cy5 (lower right panel) entries. Numbers in red represent average decrease or increase in peptide entry upon amiloride treatment. Cells were treated 2 hrs with 3 μM peptide concentration with or without 5 mM amiloride. (B) Average effect of amiloride on mean cell entry of the truncated peptides. Positive values reflect increase in cell entries, whereas negative values indicate reduction in cell penetration.

- Figure 5 shows the dose-dependent cell penetration of truncated MCaUF peptides. (A) Representative example of the dose-dependent cell penetration of MCa_{UF8-33}-C-Cy5 in CHO cells as analyzed by flow cytometry. The peptide was incubated 2 hrs with the cells before analyses. There was no saturation of cell entry for a concentration up to 33 μM. (B) Dose-dependent cell penetration of N-terminal truncated MCaUF peptides compared to MCa_{UF1-33}-C-Cy5 (open circle, dotted line). (C) Dose-dependent cell penetration of Cterminal truncated MCaUF peptides. (D)

Dose-dependent cell penetration of N- and C-terminal truncated MCaUF peptides. Note the increase in scale for the penetration of these two peptides.

- Figure 6 shows the lack of pharmacology of the truncated peptides and reduced cell toxicity. (A) Effect of MCaF, MCaUF1-33 and truncated MCaUF peptides on [^{3}H]-ryanodine binding. Data were expressed as x-fold increase in binding induced by the peptides. (B) Effect of 1 and 10 μM MCaUF1-33 and truncated MCaUF peptides on CHO cell viability. Peptides were incubated 24 hrs with the cells *in vitro*.

- Figure 7 shows the dose-dependent cell penetration of the reference peptide $MCa_{UF1\text{-}9(Abu3)}$-C-Cy5 (closed circle) in F98 cells as analyzed by flow cytometry (**A**). **B**. Comparison of the reference peptide (closed circle) with the $MCa_{UF1\text{-}9(A3)}$-C-Cy5 peptide (open circle) in F98 cells.

- Figure 8 shows the dose-dependent cell penetration of the $MCa_{UF1\text{-}9(W3)}$-C-Cy5 (**A**) and $MCa_{UF1\text{-}9(Q3)}$-C-Cy5 (**B**) peptides (both in open circle) in F98 cells compared to the reference peptide $MCa_{UF1\text{-}9(Abu3)}$-C-Cy5 (closed circle) as analyzed by flow cytometry.

- Figure 9 shows the dose-dependent cell penetration of the $MCa_{UF1\text{-}9(A2\text{-}Abu3)}$-C-Cy5 peptide (open circle) in F98 cells compared to the reference peptide $MCa_{UF1\text{-}9(Abu3)}$-C-Cy5 (closed circle) as analyzed by flow cytometry.

- Figure 10 shows the dose-dependent cell penetration of the $MCa_{UF1\text{-}9(Abu3\text{-}W6)}$-C-Cy5 (**A**) and $MCa_{UF1\text{-}9(Abu3\text{-}F7)}$-C-Cy5 (**B**) peptides (open circle) in F98 cells compared to the reference peptide $MCa_{UF1\text{-}9(Abu3)}$-C-Cy5 (closed circle) as analyzed by flow cytometry.

- Figure 11 shows the dose-dependent cell penetration of the $MCa_{UF1\text{-}9(Abu3\text{-}R5\text{-}I8)}$-C-Cy5 peptide (open circle) in F98 cells compared to the reference peptide $MCa_{UF1\text{-}9(Abu3)}$-C-Cy5 (closed circle) as analyzed by flow cytometry.

- Figure 12 shows the dose-dependent cell penetration of the $MCa_{UF3\text{-}9(Abu3)}$-C-Cy5 (**A**) and $Imp_{UF1\text{-}9(Abu3)}$-C-Cy5 (**B**) peptides (open circle) in F98 cells compared to the reference peptide $MCa_{UF1\text{-}9(Abu3)}$-C-Cy5 (closed circle) as analyzed by flow cytometry.

- Figure 13 shows the dose-dependent cell penetration of the $MCa_{UF1\text{-}9(Abu3\text{-}M9)}$-C-Cy5(**A**) and $MCa_{UF1\text{-}9(Abu3\text{-}N9)}$-C-Cy5 (**B**) peptides (open circle) in F98 cells compared to the reference peptide $MCa_{UF1\text{-}9(Abu3)}$-C-Cy5 (closed circle) as analyzed by flow cytometry.

- Figure 14 shows the dose-dependent cell penetration of the $Had_{UF1\text{-}11(Abu5)}$-C-Cy5 (**A**) and $Had_{UF3\text{-}9(Abu5)}$-C-Cy5 (**B**) peptides (open circle) in F98 cells compared to the reference peptide $MCa_{UF1\text{-}9(Abu3)}$-C-Cy5 (closed circle) as analyzed by Flow cytometry.

- Figure 15 shows the comparison of penetration of 3 μM $MCa_{UF1\text{-}9(Abu3)}$-C-Cy5, 1 μM derived peptides ($MCa_{UF3\text{-}9(Abu3)}$-C-Cy5, $MCa_{UF1\text{-}9(W3)}$-C-Cy5, $MCa_{UF1\text{-}9(Abu3\text{-}W4)}$-C-Cy5, $Had_{UF1\text{-}11(Abu5)}$- C-Cy5) and 3 μM TAT-C-Cy5 in F98 cell line as analyzed by confocal microscopy. The membrane is stained by Rhodamine-conjugated concanavalin A. The Cy5 labeled peptide that has penetrated into cells is visualized as intracellular foci.There will now be described by way of example a specific mode contemplated by the Inventors. In the following description numerous specific details are set forth in order to provide a thorough understanding. It will be apparent however, to one skilled in the art, that the present invention may be practiced without limitation to these specific details. In other instances, well known methods and structures have not been described so as not to unnecessarily obscure the description.

Example 1: Experimental procedures

1) Reagents

N-α-Fmoc-L-aminoacid, Wang-Tentagel resin and reagents used for peptide syntheses were obtained from Iris Biotech. Solvents were analytical grade products from Acros Organics. Cy5 maleimide mono-reactive dye was purchased from GE Healthcare.

2) Solid-phase peptide syntheses

Chemical syntheses of MCa analogues were performed as previously described (Poillot *et al.*, 2010). Briefly, analogues of MCa were chemically synthesized by the solid-phase method (Merrifield, R.B., 1969) using an automated peptide synthesizer (CEM© Liberty). Peptide chains were assembled stepwise on 0.24

mEq of Fmoc-D-Arg-Pbf-Wang-Tentagel resin using 0.24 mmol of N-α-fluorenylmethyloxycarbonyl (Fmoc) L-amino-acid derivatives. The side-chain protecting groups were: Trityl for Cys and Asn, tert-butyl for Ser, Thr, Glu and Asp, Pbf for Arg and tert-butylcarbonyl for Lys. Reagents were at the following concentrations: Fmoc-amino-acids (0.2 M Fmoc-AA-OH in dimethylformamide (DMF)), activator (0.5 M 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate in DMF), activator base (2M diisopropylethylamine in N-methyl-pyrrolidone (NMP)) and deprotecting agent (5% piperazine / 0.1 M 1-hydroxybenzotriazole in DMF), as advised by PepDriver (CEM©). After peptide chain assembly, resins were treated 4 hrs at room temperature with a mixture of trifluoroacetic acid/water/triisopropylsilan (TIS)/dithiothreitol (DTT) (92.5/2.5/2.5/2.5). The peptide mixtures were then filtered and the filtrates were precipitated by adding cold t-butylmethyl ether. The crude peptides were pelleted by centrifugation (10.000 × g, 15 min) and the supernatants were discarded. MCa analogues were purified by HPLC using a Vydac C18 column (218TP1010, 25×10 cm). Elutions of the peptides were performed with a 10-60% acetonitrile linear Gradient containing 0.1% trifluoroacetic acid. The purified fractions were analyzed by analytical RP-HPLC (Vydac C18 column 218TP104, 25 × 4.6 cm). All analogues were characterized by MALDI-TOF mass spectrometry.

3) Labeling of peptide with Cy5

Each peptide was labeled with Cy5 according to the manufacturer's protocol (GE HEALTHCARE). Peptides were dissolved at 1 mg/ml in 0.1 M Na_2CO_3 buffer, pH 9.3. 300 µl of the solubilized peptides were added to Cy5-maleimide containing tubes. The mixtures were incubated during 2 hrs at room temperature and then purified by HPLC using an analytical Vydac C18 column. Elution of the Cy5-labeled peptides was performed with a 10-60% acetonitrile linear gradient containing 0.1% trifluoroacetic acid. The pure peak fractions were lyophilized and peptides quantified by UV spectrophotometer at 649 nm.

4) Cell culture

Chinese hamster ovary (CHO) and F98 rat glioma cell lines (from ATCC) were maintained at 37°C in 5% CO2 in F-12K nutrient medium (INVITROGEN) supplemented with 10% (v/v) heat-inactivated fetal bovine serum

(INVITROGEN) and 10,000 units/ml streptomycine and penicillin (INVITROGEN) for the CHO cells, and 2 % heat-inactivated fetal bovine serum and 100 units/ml streptomycine and penicillin for the F98 cells

5) MTT assay

Cells were seeded into 96-well micro plates at a density of approximately 8×104 cells/well. After 2 days of culture, the cells were incubated for 24 hrs at 37°C with MCa analogues at a concentration of 10 μM. Control wells containing cell culture medium alone or with cells, both without peptide addition, were included in each experiment. 0.1% saponin was used as toxic agent for comparison. The cells were then incubated with 3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyl-tetrazolium bromide (MTT) for 30 min. Conversion of MTT intopurple colored MTT formazan by the living cells indicates the extent of cell viability. The crystals were dissolved with dimethyl sulfoxide (DMSO) and the optical density was measured at 540 nm using a microplate reader (Biotek ELx-800, MANDEL SCIENTIFIC INC.) for quantification of cell viability. All assays were run in triplicates.

6) Confocal microscopy

For analysis of the subcellular localization of MCa-Cy5 analogues in living cells, cell cultures were incubated with the fluorescent peptides for 2 hrs, and then washed with phosphate-buffered saline (PBS) alone. The plasma membrane was stained with 5μg/ml rhodamine-conjugated concanavalin A (MOLECULAR PROBES) for 5 min. Cells were washed once more. Live cells were then immediately analyzed by confocal laser scanning microscopy using a Leica TCS-SPE operating system. Rhodamine (580 nm) and Cy5 (670 nm) were sequentially excited and emission fluorescence were collected in z-confocal planes of 10–15 nm steps.

7) Flow cytometry

CHO and F98 cells were incubated with various concentrations of Cy5-labeled peptides in F-12K culture medium without serum at 37°C for 2 hrs. The cells were then washed with PBS to remove excess extracellular peptide and treated with 1 mg/ml trypsin (INVITROGEN) for 5 min at 37°C to detach cells from the surface, and centrifuged at 200 g before suspension in PBS. For experiments with the macropinocytosis inhibitor, amiloride, CHO cells were initially washed with F-12K

and preincubated for 30 min at 37°C with 1 mM amiloride (SIGMA). The cells were then incubated for 2 hrs at 37°C with 1 µM of the Cy5-MCa analogues. For all these experimental conditions, flow cytometry analyses were performed with live cells using a Becton Dickinson flow cytometer LSR II or an Accuri® flow cytometer (BD BIOSCIENCES). Data were obtained and analyzed using FCS express software (DE NOVO) or Accuri® proprietary software CFlow sampler. Live cells were gated by forward/side scattering from a total of 10,000 events.

8) Preparation of heavy SR vesicles

Heavy SR vesicles were prepared following the method of Kim *et al.*, J. Biol. Chem., 1983. Protein concentration was measured by the Biuret method.[3H]-Ryanodine binding assay - Heavy SR vesicles (1 mg/ml) were incubated at 37°C for 2 hrs in an assay buffer composed of 10 nM [^{3}H]-ryanodine, 150 mM KCl, 2 mM EGTA, 2 mM $CaCl_2$ (pCa = 5), and 20 mM MOPS, pH 7.4. Truncated MCa analogues were added prior to the addition of heavy SR vesicles. [^{3}H]-ryanodine bound to heavy SR vesicles was measured by filtration through Whatman GF/B glass filters ollowed by three washes with 5 ml of ice-cold washing buffer composed of 150 mM NaCl, 20 mM HEPES, pH 7.4. [^{3}H]-ryanodine retained on the filters was measured by liquid scintillation. Non-specific binding was measured in the presence of 80 µM unlabeled ryanodine. The data are presented as mean ± S.E. Each experiment was performed in triplicate.

9) Statistical analyses

All data are given as mean ± SD for n number of observations, and statistical significance (p) was calculated using Student's t test.

Example 2: Non folded truncated maurocalcine peptides are efficient CPP

Figure 1A illustrates the primary structure of MCa with its secondary structures (β strands) and its pattern of disulfide bridges. This peptide will be termed MCaF, for folded (F) MCa. An earlier report has demonstrated that replacing the six internal cysteine residues of MCa by Abu residues results in a pharmacologically-inert and unfolded (UF) CPP (MCa_{UF1-33}, Figure 1B). This peptide loses its secondary structures (Ram *et al.*, J. Biol. Chem., 2008). Since the present application aims at identifying shorter CPP sequences based on MCa_{UF1-33} sequence by the delivery of Cy5 cargo, the inventors first determined where at the N-terminus

(C-MCa_{UF1-33}) or C-terminus (MCa_{UF1-33}-C) the cargo could be best grafted after addition of an extra cysteine residue (C) (Figure 1B). As shown, both vector/cargo complexes Cy5-C-MCa_{UF1-33} and MCa_{UF1-33}-C-Cy5 penetrated efficiently within CHO cells, as estimated by confocal microscopy or by flow cytometry (Figure 1C). At 3 μM, a slightly better cell penetration was observed with Cy5 localized at the C-terminus of MCa_{UF1-33}, but this difference was not significant. Since chemical syntheses of truncated MCa_{UF1-33} analogues was facilitated by adding the extra cysteine residue at the C-terminus of the sequence rather than at the N-terminus, the inventors kept on working on the basis of MCa_{UF1-33}-C sequence. Nevertheless, these data indicate for the first time that cargo grafting on the CPP MCa_{UF1-33} can be performed likewise at both extremities of the sequence. Next, the inventors designed a series of truncated MCaUF-C peptides comprising either a C-terminal truncation (3 analogues: MCa_{UF1-20}-C, MCa_{UF1-15}-C and MCa_{UF1-9}-C), a N-terminal truncation (7 analogues: $MCaUF_{8-33-C}$, $MCa_{UF11-33}$-C, $MCa_{UF14-33}$-C, $MCa_{UF18-33}$-C, 33-C, $MCa_{UF20-33}$-C, $MCa_{UF22-33}$-C and $MCa_{UF25-33}$-C), and Both N- and C-terminal truncations (2 analogues: MCa_{UF6-25}-C and $MCa_{UF14-25}$-C) (Figure 2A). All of these analogues were then labeled with Cy5 to investigate their cell penetration properties. Every one of these peptides has been designed in such a way that the cargo would be removed from the peptide upon trypsin cleavage. This was useful for the flow cytometry experiments in which the fluorescence associated to the cells is measured after trypsin treatment, thereby potentially removing the cargo from peptides that would eventually be associated to the outer part of the plasma membrane. The net positive charges of the peptides were drastically different, ranging from 0 (MCa_{UF1-15}-C and MCa_{UF1-9}-C) to +8 (MCa_{UF8-33}-C). However, many of the peptides contained a percentage of positively charged residues equal ($MCa_{UF-25-33}$-C) or superior to MCaF or MCa_{UF1-33} (8 out of twelve analogues). Three analogues had a lower percentage of basic residues than MCaF (all three C-terminal truncated analogues, MCa_{UF1-20}-C, MCa_{UF1-15}-C and MCa_{UF1-9}-C). The inventors first evaluated by flow cytometry the fluorescence accumulation within CHO cells that occurred after 2 hrs incubation with 3 μM of positively charged MCa peptides (net charge $\geq$ +5; Figure 2B). This first study revealed several unexpected findings. First, all of the charged peptides (8 tested) demonstrated CPP properties. These peptides had all the

$K_{22}R_{23}R_{24}$ sequence in common, a cluster of basic amino acid residues shown to contribute to the dose-efficacy of cell penetration of MCaF in an earlier study (Mabrouk *et al.*, 2007). Interestingly, removing the last 8 C-terminal amino acids of MCa had little impact on the cell penetration properties (if one compares $MCa_{UF14-25}$-C with $MCa_{UF14-33}$-C). Similarly, the removal of the amino acid region His6-Asn13 did not drastically change cell penetration properties (MCa_{UF6-25}-C versus $MCa_{UF14-25}$-C). Second, all peptides appeared to behave better than the reference peptide MCa_{UF1-33}-C, suggesting that sequence truncation of MCaUF may represent a potent strategy to define more efficient CPP. Less positively charged peptides were also tested for their ability to penetrate into CHO cells (Figure 2C). No less surprisingly, all peptides showed CPP properties, including two peptides with no net positive charge (MCa_{UF1-9}-C and MCa_{UF1-15}-C). MCa_{UF1-9}-C appeared as a better CPP than MCa_{UF1-15}-C suggesting that the Abu-Asp region introduces no competitive advantage and confirming results shown in Figure 2B. This may represent an inhibitory region because of the presence of Glu12 and and Asp15, two negatively charged residues. The finding that mutation of Glu12 to Ala enhances cell penetration of both MCaF (Mabrouk *et al.*, 2007) and MCaUF (Ram *et al.*, J. Biol. Chem., 2008) further supports this conclusion. MCaUF25-33-C turned out to have also CPP properties, even though this sequence did not confer a competitive advantage to other MCa CPP analogues as shown in Figure 2B. The overall message from this first study is that all truncated MCaUF analogues can behave as CPP at the concentration tested. The findings suggest that MCa is a peptide fully specialized to achieve cell penetration including in domains that are not highly charged.

<u>Example 3</u>: The intracellular distribution of all truncated MCaUF analogues bear resemblance with that of the full length MCaUF

While all truncated derivatives of MCaUF1-33 show cell penetration properties according to the flow cytometry analyses, the inventors examined whether there were differences in intracellular distribution among these peptides. This question was investigated by confocal microscopy after 2 hrs of peptide accumulation into CHO cells. Interestingly, all peptides showed very resembling intracellular distributions, although the degree of accumulated cell fluorescence varied somewhat with peptide sequences. In confirmation of the flow cytometry results, the peptide that

appeared to penetrate the least was the full length unfolded MCa, MCa_{UF1-33}-C-Cy5. The vast majority of the fluorescence appears in punctuate dots within the cells. In many cases, these dots appear at higher concentrations within one pole of the cell (MCa_{UF8-33}-C-Cy5, $MCa_{UF11-33}$-C-Cy5, $MCa_{UF25-33}$-C-Cy5, and MCa_{UF1-9}-C-Cy5 for instance). On various occasions also, all of the peptides tend to present a sub-plasma membrane distribution, forming a rim of smaller circumference than the concanavalin A labeling itself. This sub-plasma membrane rim localization was more evident for CHO cells labeled with $MCa_{UF14-25}$-C-Cy5. Finally, more rarely, a direct plasma membrane labeling by the peptide-cargo complex was observable. This type of labeling could be observed with N-terminal truncated vectors exclusively and was most evident or $MCa_{UF22-33}$-C-Cy5. The staining of the plasma membrane was always diffuse in contrast to intracellular staining which was mainly punctuated. Diffuse membrane labeling was also observed for $MCa_{UF25-33}$-C-Cy5 and $MCaUF_{20-33}$-C-Cy5, two peptides that differ from 2 to 3 amino acids with $MCa_{UF22-33}$-C-Cy5. It was difficult to evidence for the other vector/cargo complexes. The inventors propose that this staining coincides with an alteration of the duration of peptide plasma membrane residency for these truncated MCa_{UF} analogues. The lower occurrence of this diffuse staining for the other truncated variants may reflect faster internalization by endocytosis and/or membrane translocation. Globally, these effects reflect cell entry and distribution tendencies that were hard to quantify and they should therefore be interpreted with caution. In an attempt to better apprehend peptide behavior at the plasma membrane, the inventors quantified the extent of Cy5/rhodamine staining colocalization. Rhodamine-positive staining was also Cy5-positive for 63% to 86% of the pixels (best performing peptides were $MCa_{UF14-33}$-C-Cy5, $MCa_{UF18-33}$-C-Cy5, $MCa_{UF20-33}$-C-Cy5 and $MCa_{UF22-33}$-C-Cy5). This finding indicates that the peptides invade large membrane areas and that membrane interaction is not limited to small specialized surface areas. In contrast, Cy5-positive pixels were rhodamine-positive to far more variable extents (Figure 3). For instance, 10.1 ± 2.6% of MCa_{UF1-33}-C-Cy5, the reference compound, was colocalized with the plasma membrane indicator. In spite of the fact that short plasma membrane staining times were used (few minutes), a fraction of the colocalization that is quantified also corresponds to intracellular staining following ongoing endocytosis. Nevertheless, this result indicates that this

peptide does not remain stuck within the plasma membrane during its 2 hrs incubation with CHO cells. It indicates relatively fast cell penetration thus. Many of the other peptides however behaved differently from MCa_{UF1-33}-C-Cy5. Indeed, several peptides show surprisingly higher colocalization with rhodamine (21.3 ± 2.6% for $MCa_{UF11-33}$-C-Cy5 and 30.4 ± 1.4% for MCa_{UF1-20}-C-Cy5 for instance). These higher values of colocalization indicate that some peptides remain for longer periods of time or at higher concentration within the plasma membrane. Alternatively, these peptides may rely more heavily on endocytosis for cell penetration and are present within intracellular organelles to which subsequent endocytotic vesicles that contain rhodamine labeling will fuse. Peptides most concerned by these behaviors were $MCa_{UF11-33}$-C-Cy5 and $MCa_{UF14-33}$-C-Cy5, that contained two or one of the CPP inhibitory negative charges (Glu12 and Asp15), and MCa_{UF1-9}-C-Cy5 and MCa_{UF1-20}-C-Cy5, that were poorly charged peptides.

Example 4: Amiloride-sensitivity of the cell penetration of truncated MCa_{UF} analogues

In earlier studies, the inventors have demonstrated that the cell entry of MCa_{UF1-33} was largely sensitive to amiloride, suggesting a predominant macropinocytosis mechanism for its cell penetration (Ram *et al.*, J. Biol. Chem., 2008, 283, 24274-24284). However, it was likely that such a predominant reliance on macropinocytosis was also conferred by the cargo type transported (streptavidine in that report). The inventors therefore conducted an in depth analysis of the amiloride-sensitivity of the various truncated MCaUF peptides with Cy5 as cargo and quantified by flow cytometry the degree of cell penetration inhibition in CHO cells. Figure 4A illustrates the amiloride-sensitivity of four different truncated peptides. As shown, amiloride inhibits the cell penetration of MCa_{UF1-33}-C-Cy5 by 19.6% and of MCa_{UF1-15}-C-Cy5 by 39%. The finding that amiloride blocks to a far lesser extend the penetration of Cy5 compared to that of streptavidin (Ram *et al.*, J. Biol. Chem., 2008, 283, 24274-24284) when MCa_{UF1-33} is the vector indicates the influence of the cargo nature on the mechanism of cell entry. Surprisingly, blocking macropinocytosis was found to enhance rather than inhibit the cell penetration of $MCa_{UF20-33}$-C-Cy5 and $MCa_{UF18-33}$-C-Cy5 (Figure 4A). Preserving the plasma membrane from undergoing macropinocytosis may free surface areas for enhanced peptide translocation trough the

membrane. The effect of amiloride was always associated with a sharpening of the fluorescence intensity distribution in the x axis (see for instance MCa_{UF1-15}-C-Cy5), reflecting reduced cell heterogeneity for the mechanisms underlying peptide penetration. The amiloride-sensitivity of cell penetration was further investigated for all truncated MCaUF peptides and the results presented in Figure 4B. Four peptides showed higher amiloride-sensitivity than MCa_{UF1-33}-C-Cy5 ($MCa_{UF11-33}$-C-Cy5, $MCa_{UF25-33}$-C-Cy5, MCa_{UF1-15}-C-Cy5 and $MCa_{UF14-25}$-C-Cy5). All other peptides showed reduced amiloride-sensitivities or a tendency for greater cell penetration under the effect of amiloride. The inventors conclude that the Cy5 cargo does not promote macropinocytosis as the main route of peptide entry, and that truncation of MCaUF may lead to analogues that rely to a lesser extent on macropinocytosis for cell entry.

Example 5: Comparative dose-dependent cell penetration of the MCa_{UF} analogues

While the inventors compared the properties of cell penetration of truncated peptides at rather mild concentrations, the inventors also aimed at comparing the dose-dependence of cell penetration of these peptides by flow cytometry (Figure 5). One example of such an analysis is shown for peptide $MCaUF_{8-33}$-C-Cy5 in Figure 5A. 33 μM was the highest concentration that could be tested on CHO cells and obviously cell penetration did not show any sign of saturation for cell incubation times with this peptide for 2 hrs. The dose-dependent cell penetration were compared for all N-terminal truncated peptides (Figure 5B), C-terminal truncated peptides (Figure 5C), and double truncated analogues (Figure 5D) with the same settings. These analyses confirm that MCa_{UF1-33}-C-Cy5 is the least-performing cell penetrating peptide. Most truncated peptides show detectable cell penetration at concentrations equal or above 1 μM. One remarkable exception to this rule was noticeable. MCa_{UF1-9}-C-Cy5 shows an unusual dose-dependent penetration with detectable cell penetration at 10 nM and only small progressive increases in fluorescence intensity with higher peptide concentrations (Figure 5C). This peptide was therefore the best performing peptide for cell penetration at low concentrations. Finally, additional information that could be taken from these analyses is that the peptides differed significantly with regard to the maximal extent of cell penetration. Among the N-terminal truncated MCa_{UF} analogues, $MCa_{UF18-33}$-C-Cy5

performed drastically better than the other truncated peptides (Figure 5B). The difference in cell penetration among $MCa_{UF11-33}$-C-Cy5 and $MCa_{UF18-33}$-C-Cy5 resides in the removal of KENKDAbuAbu sequence which the inventors presume is inhibitory to some extent because of the presence of Glu12 and Asp15. Among the C-terminal truncated peptides, MCa_{UF1-20}-C-Cy5 was performing as well as MCa_{UF8-33}-C-Cy5, and although not tested at higher concentrations, MCa_{UF1-9}-C-Cy5 would be expected to perform still better. Finally, for N- and C-terminal truncated analogues, the best peptide turns out to be $MCa_{UF14-25}$-C-Cy5 that yields the greatest fluorescence accumulation at 33,μM compared to all other truncated MCaUF analogues.

Example 6: Truncated MCaUF peptides lack pharmacological effects and are predominantly non toxic

An earlier report has shown that MCa_{UF1-33} is unable to interact with MCa's target, the ryanodine receptor RyR1 (Ram *et al.*, J. Biol. Chem., 2008). This is due to the loss of secondary structures owing to the lack of internal disulfide bridging. The inventors did therefore expect that truncated analogues of MCa_{UF} should also be pharmacologically inert. This hypothesis was challenged by testing the ability of the Cy5-free peptides to stimulate [^{3}H]-ryanodine binding (Figure 6A). As shown, contrary to MCaF that contains secondary structures and disulfide bridges, none of the peptides the inventors designed had an effect on [^{3}H]-ryanodine binding. Finally, the peptides were challenged for their toxicity by incubating CHO cells with 1 or 10 μM peptide concentrations for an extended duration (24 hrs) that far exceeds the duration challenged for cell penetration (Figure 6B). A 10 μM peptide concentration was generally slightly more toxic than 1 μM except for $MCa_{UF14-25}$-C. At 1 μM, toxicity never exceeded 8% and significances of these effects were negligible. In contrast, toxicity could reach 20% at 10 μM peptide concentration and these effects had higher significance. Most peptides behaved equally well or better than MCa_{UF1-33}-C indicating that truncation did not enhance cell toxicity of the peptides.

Example 7: Synthesis of a peptide containing a disulfide bond and a N-terminal thiol function for coupling to the cargo.

The peptide is synthesized by the solid phase method as described in example 1. The peptide bound to the resin is labeled with N-Succinimidyl-S-acetylthioacetate (SATA) to introduce a protected thiol group at the N-terminus of the peptide.

Labeling of peptide with SATA

SATA(76 mg in 60 µl DMF) and then phosphate buffer saline (PBS), pH 7.4 (540 µl) were added to the peptide bound to the resin (10 mg in 600 µl of PBS, pH 7.4) and the mixture was agitated for 1 hour at room temperature, filtered and washed three times with methanol. The peptide was then deprotected and cleaved from the resin as follows. The preceding mixture was treated 4 hrs at room temperature with a mixture of TFA (Trifluoroacétique acid ; 9.25 ml), triisopropylsilane (250 µl), water (250 µl), and Dithiothreitol (250 mg), filtered, and the filtrate was precipitated by adding cold diethyl ether (40 ml) The crude peptide was pelleted by centrifugation (10,000 g, 15 min). The pellet was washed three times by resuspension in diethyl ether (10 ml) and centrifugation (10,000 g, 15 min). The supernatant was discarded and the peptide was air-dried.

Disulphide bond formation

4,4′-Dipyridyl disulfide (114µL of a 10 mM solution in methanol) was added to the labeled peptide (2 mg in 2 ml of acetonitrile (50 %), water (50 %) and TFA (0.1% TFA) and the mixture was agitated at room temperature for 2 hrs. The solvent was evaporated using a rotavapor. The oxydised peptide (containing an intramolecular disulfide bond) was solubilized in TFA (2 ml of a 0.1 % solution in water), purified by HPLC using a JUPITER™ 4µm PROTEO 90Å column (250 mm x 10 mm; PHENOMENEX) and a 10-60 % acetonitrile gradient (40 minutes, 4 ml/min rate), and lyophilized.

Deprotection of the thiol group

The peptide (2 mg in 1 ml of PBS, pH 7.4) was treated with the deacetylation solution (100 µl of 0.5 M hydroxylamine, 25 mM EDTA in PBS, pH 7.4) for 2 hrs at room temperature, purified by HLPC as described above, and lyophilized.

Example 8: Cell penetration of small peptides derived from MCa_{UF1-9}

Cy5-labeled peptides derived from MCa_{UF1-9} were synthesized and assayed by confocal microscopy or flow cytometry as described in example 1. The results are presented in figures 7-15.

The analysis of the MCa_{UF1-9} truncated variant ($MCa_{UF3-9(Abu3)}$) shows that a peptide of 7 residues derived from MCa_{UF1-9} is an efficient CPP (Figure 12A).

The analysis of the MCa_{UF1-9} variants with point mutations, including Imperatoxin and Hadrucalcine derived peptides, show that the first residues of the MCa_{UF1-9} derived CPP may have various sequences including for example GA ($MCa_{UF1-9(A2-Abu3)}$; figure 9A), SEKD or KD ($Had_{UF1-11(Abu5)}$ and $Had_{UF3-9(Abu5)}$; figure 14A and 14B), and GD ($MCa_{UF1-9(Abu3)}$, figure 7A; all other variants tested).

The residue in position 3 of the MCa_{UF1-9} derived CPP may be, either a hydrophobic amino acid such as a cysteine analog (Abu; $MCa_{UF1-9(Abu3)}$; figure 7A), an alanine ($MCa_{UF1-9(A3)}$; figure 7B) or a tryptophan ($MCa_{UF1-9(W3)}$; figure 8A), or an other amino acid different from K and R, for example a glutamine ($MCa_{UF1-9(Q3)}$; figure 8B). It is preferably a hydrophobic amino acid.

The residue in position 4 of the MCa_{UF1-9} derived CPP is a hydrophobic amino acid, preferably a leucine ($MCa_{UF1-9(Abu3)}$; figure 7A) or an isoleucine ($Had_{UF1-11(Abu5)}$ and $Had_{UF3-9(Abu5)}$; figure 14A and 14B).

The residue in position 5 of the MCa_{UF1-9} derived CPP is a basic amino acid chosen from K ($Had_{UF1-11(Abu5)}$ and $Had_{UF3-9(Abu5)}$; figure 14A and 14B) and R ($MCa_{UF1-9(Abu3-R5-I8)}$; figure 11A), or another amino acid different from S, T, D and E such as P ($MCa_{UF1-9(Abu3)}$; figure 7A). Preferably, it is P, K or R.

The residue in position 6 of the MCa_{UF1-9} derived CPP is either an amino acid different from S, T, D and E, such as H ($MCa_{UF1-9(Abu3)}$, $Had_{UF1-11(Abu5)}$ and $Had_{UF3-9(Abu5)}$; figures 7A, 14A and 14B), or a hydrophobic amino acid, for example a tryptophan ($MCa_{UF1-9(Abu3-W6)}$; figure 10A). Preferably, it is H.

The residue in position 7 of the MCa_{UF1-9} derived CPP is a hydrophobic amino acid, for example a leucine ($MCa_{UF1-9(Abu3)}$, $Had_{UF1-11(Abu5)}$, $Had_{UF3-9(Abu5)}$; figures 7A, 14A and 14B) or a phenylalanine ($MCa_{UF1-9(Abu3-F7)}$; figure 10B). Preferably, it is L.

The residue in position 8 of the MCa_{UF1-9} derived CPP is a basic amino acid, for example a lysine (MCa $_{UF1-9(Abu3)}$, figure 7A), a hydrophobic amino acid, for example an isoleucine (MCa $_{UF1-9(Abu3-R5-I8)}$; figure 11A), or another amino acid different from S, T, D and E, for example a glutamine ($Had_{UF1-11(Abu5)}$, $Had_{UF3-9(Abu5)}$, figure 14A and 14B). Preferably, it is K, Q, R or N.

The residue in position 9 of the MCa_{UF1-9} derived CPP is a hydrophobic amino acid, for example a leucine (MCa $_{UF1-9(Abu3)}$, figure 7A) or a methionine (MCa $_{UF1-9(Abu3-M9)}$, figure 13A), a basic amino acid, for example an arginine ($Imp_{UF1-9(Abu3)}$, $Had_{UF1-11(Abu5)}$, $Had_{UF3-9(Abu5)}$; figures 12B, 14A and 14B), or an other amino acid, for example an asparagine (MCa $_{UF1-9(Abu3-N9)}$, figure 13B). Preferably, it is L, R, I or K.

Interestingly, the hadrucalcine derived peptides $Had_{UF1-11(Abu5)}$ and $Had_{UF3-9(Abu5)}$ perform better as CPP than the maurocalcine derived peptide $MCa_{UF1-9(Abu3)}$ (figure 14A and 14B).

Comparison of MCa and Had derived peptides to a classical CPP (Tat basic peptide : GRKKRRQRRR-C; SEQ ID NO: 172) shows that 3µM MCa $_{UF1-9(Abu3)}$ or 1µM MCa $_{UF3-9(Abu3)}$, MCa $_{UF1-9(W3)}$, MCa $_{UF1-9(Abu3-W4)}$ or Had $_{UF1-11(Abu5)}$ proved better CPP than Tat at 3µM (figure 15).

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5

CLAIMS

1. Use of a peptide as a vector for the intracellular delivery of a molecular cargo, wherein said peptide is a maurocalcine derived cell penetrating peptide consisting of a sequence:

$$Z\text{-}X_1\text{-}X_2\text{-}X_3\text{-}X_4\text{-}X_5\text{-}X_6\text{-}X_7\text{-}Z',$$

wherein:

- X_1 represents a hydrophobic amino acid chosen from 2-amino butyric acid, C, W, F, L, I, V, M and A, or another amino acid different from K and R,
- X_2 represents a hydrophobic amino acid chosen from I, L, W, F, V, M, A and C,
- X_3 represents a basic amino acid chosen from K and R, or another amino acid different from S, T, D and E, such as P,
- X_4 represents an amino acid different from K, R, S, T, D and E, such as H, or a hydrophobic amino acid chosen from W, F, L, I, V, M, A and C,
- X_5 represents a hydrophobic amino acid chosen from L,W, F, I, V, A and C,
- X_6 represents an amino acid other than a basic or hydrophobic amino acid such as Q, a basic amino acid chosen from K and R, or a hydrophobic amino acid chosen from W, F, L, I, V, M, A and C, and
- X_7 represents a basic amino acid chosen from R and K, a hydrophobic amino acid chosen from L, W, F, I, V, M, A and C, or another amino acid, with the proviso that the sequence X_1 to X_7 comprises three or four of said hydrophobic amino acids and one or two of said basic amino acids, and no more than four of said hydrophobic amino acids and two of said basic amino acids,
- **Z** and **Z'** together represent a sequence of no more than 13 amino acids, or Z and/or **Z'**are no amino acid, and

wherein said sequence has a net charge of 0 to +2 when Z and Z' are no amino acid or of 0 to +3 when Z and/or Z' are present, considering that D and E have a negative charge, K and R have a positive charge and the other amino acids have no charge.

2. The use according to claim 1, wherein Z consists of a sequence of 1 to 4 amino acids and Z' is no amino acid or consists of the sequence:

$$Z'_1\text{-}Z'_2\text{-}Z'_3\text{-}Z'_4\text{-}Z'_5\text{-}Z'_6\text{-}Z'_7\text{-}Z'_8\text{-}Z'_9\text{-}Z'_{10}\text{-}Z'_{11},$$

wherein:

- Z'_1 is **J** or 2-amino butyric acid,
- Z'_2 is **B**, **J**, N, Q or no amino acid,
- Z'_3 is **J**, D, E or no amino acid,
- Z'_4 is N, Q, D, E or no amino acid,
- Z'_5 is N, Q, **B** or no amino acid,
- Z'_6 is N, Q, **J**, D, E or no amino acid,
- Z'_7 is **J**, 2-amino butyric acid or no amino acid,
- Z'_8 is **J**, 2-amino butyric acid or no amino acid,
- Z'_9 is S, G, T, **J**, Q, N or no amino acid,
- Z'_{10} is **B** or no amino acid, and
- Z'_{11} is **B** or no amino acid,

wherein **J** is a hydrophobic amino acid chosen from W, F, L, I, V, M, A and C and **B** is a basic amino acid chosen from K and R, and

wherein Z' does not comprise any internal deletion other than the deletion of Z'_2 to Z'_9, Z'_3 to Z'_6, or one or more of Z'_3, Z'_6 and Z'_9.

3. The use according to claim 1 or claim 2, wherein:

- the sequence $\mathbf{X_1\text{-}X_2\text{-}X_3\text{-}X_4\text{-}X_5\text{-}X_6\text{-}X_7}$ is chosen from the group consisting of SEQ ID NO: 3 to 20 and the sequences wherein at least one amino acid of SEQ ID NO: 3 to 20 has been substituted with a different amino acid,
- Z is absent or is chosen from GD, GA, KD and SEKD, and
- Z' is absent or is chosen from the group consisting of the sequences SEQ ID NO: 21 to 35, the sequences wherein at least one amino acid of SEQ ID NO: 21 to 35 has been substituted, the N-terminal fragments of said sequences which consist of the first 1 to 10 amino acids of said sequences, and the fragments of said sequences wherein the residues in positions 2 to 9 or 3 to 6, or one or more residues in position 3, 6 and 9 of SEQ ID NO: 21 to 35 have been deleted.

4. The use according to claim 3, wherein the sequence $\mathbf{X_1\text{-}X_2\text{-}X_3\text{-}X_4\text{-}X_5\text{-}X_6\text{-}X_7}$ is chosen from the group consisting of SEQ ID NO: 3, 9, 12 and 18.

5. The use according to any one of claims 1 to 4, wherein said peptide is selected from the group consisting of: SEQ ID NO: 2 to 105, 148, 150, 152, 154, 158, 160, 162, 164, 166, 168 and 170.

6. The use according to claim 5, wherein said peptide is selected from the group consisting of: SEQ ID NO: 2, 3, 9, 12, 18, 36, 37, 44, 46, 66, 150, 152 and 154.

7. The use according to any one of claims 1 to 6, wherein said peptide consists of L-amino acids, D-amino acids or a mixture thereof.

8. The use according to any one of claims 1 to 7, wherein said peptide comprises two cysteines which are linked via a disulfide bond.

9. The use according to any one of claims 1 to 8, wherein said peptide comprises a unique free cysteine at its N- or C-terminus.

10. A peptide, which is a maurocalcine derived cell penetrating peptide consisting of a sequence as defined in any one of claims 1 to 9.

11. The peptide of claim 10, which further comprises a unique cysteine which is attached to its N- or C-terminus.

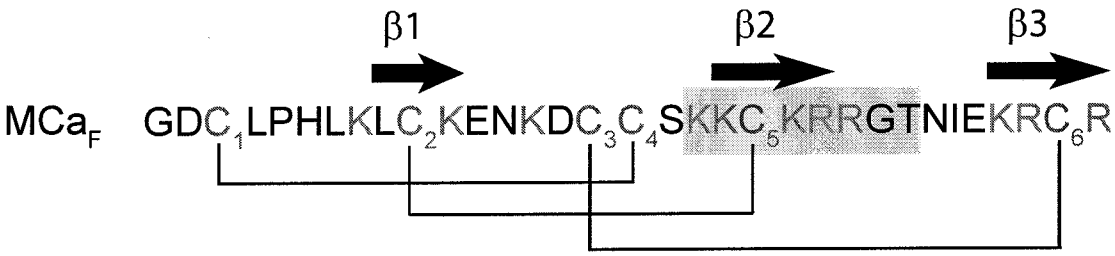
12. The peptide of claim 11, which is selected from the group consisting of SEQ ID NO: 134-136, 151, 153, 155 and 157.

13. A complex comprising a peptide according to any one of claims 10 to 12 bound covalently or not covalently to a molecular cargo.

14. The complex according to claim 13, wherein the cargo molecule is selected from the group consisting of: antisense oligonucleotides, peptide nucleic acids, small interfering RNAs, locked nucleic acids, phosphorodiamidate morpholino oligonucleotides, decoy DNA molecules, plasmids, DNA, RNA or peptide aptamers, peptides, proteins, antibodies, drugs, labels, imaging agents, liposomes, micelles, nanoparticles, and mixtures thereof.

15. A nucleic acid molecule comprising a fusion in frame of a nucleotide sequence encoding the peptide according to any one of claims 10 to 12 to a nucleotide sequence encoding a peptide or protein cargo.

A



B

MCa_{UF1-33} GDAbuLPHLKLAbuKENKDAbuAbuSKKAbuKRRGTNIEKRAbuR

C-MCa_{UF1-33} C-GDAbuLPHLKLAbuKENKDAbuAbuSKKAbuKRRGTNIEKRAbuR

MCa_{UF1-33}-C GDAbuLPHLKLAbuKENKDAbuAbuSKKAbuKRRGTNIEKRAbuR-C

C

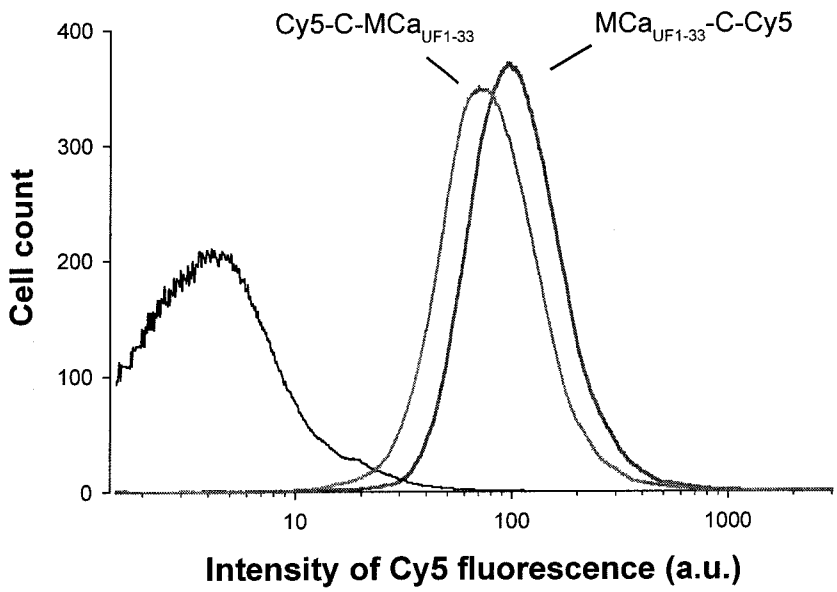
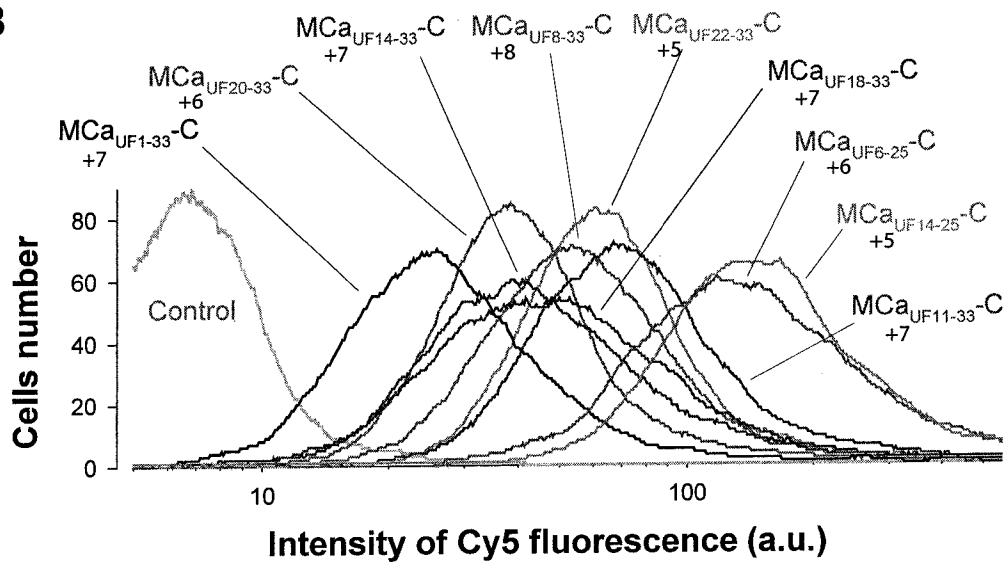


FIGURE 1

A

		Net charge (NC)	%
MCa_{UF1-33}-C	GDAbuLPHLKLAbuKENKDAbuAbuSKKAbuKRRGTNIEKRAbuR-C	+7	33
MCa_{UF1-20}-C	GDAbuLPHLKLAbuKENKDAbuAbuSKK-C	+2	25
MCa_{UF1-15}-C	GDAbuLPHLKLAbuKENKD-C	0	20
MCa_{UF1-9}-C	GDAbuLPHLKL-C	0	11
MCa_{UF8-33}-C	KLAbuKENKDAbuAbuSKKAbuKRRGTNIEKRAbuR-C	+8	42
$MCa_{UF11-33}$-C	KENKDAbuAbuSKKAbuKRRGTNIEKRAbuR-C	+7	43
$MCa_{UF14-33}$-C	KDAbuAbuSKKAbuKRRGTNIEKRAbuR-C	+7	45
$MCa_{UF18-33}$-C	SKKAbuKRRGTNIEKRAbuR-C	+7	50
$MCa_{UF20-33}$-C	KAbuKRRGTNIEKRAbuR-C	+6	50
$MCa_{UF22-33}$-C	KRRGTNIEKRAbuR-C	+5	50
$MCa_{UF25-33}$-C	GTNIEKRAbuR-C	+2	33
MCa_{UF6-25}-C	HLKLAbuKENKDAbuAbuSKKAbuKRRG-C	+6	40
$MCa_{UF14-25}$-C	KDAbuAbuSKKAbuKRRG-C	+5	50

B



C

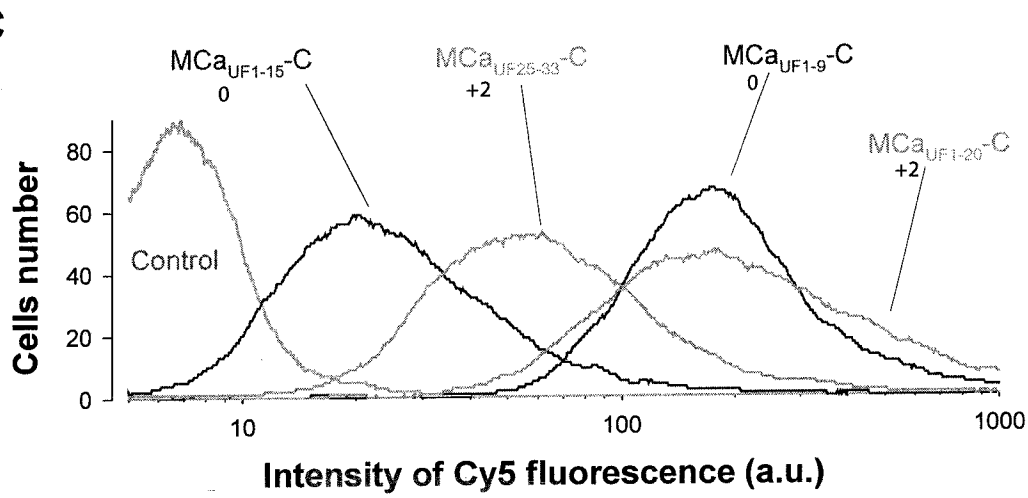
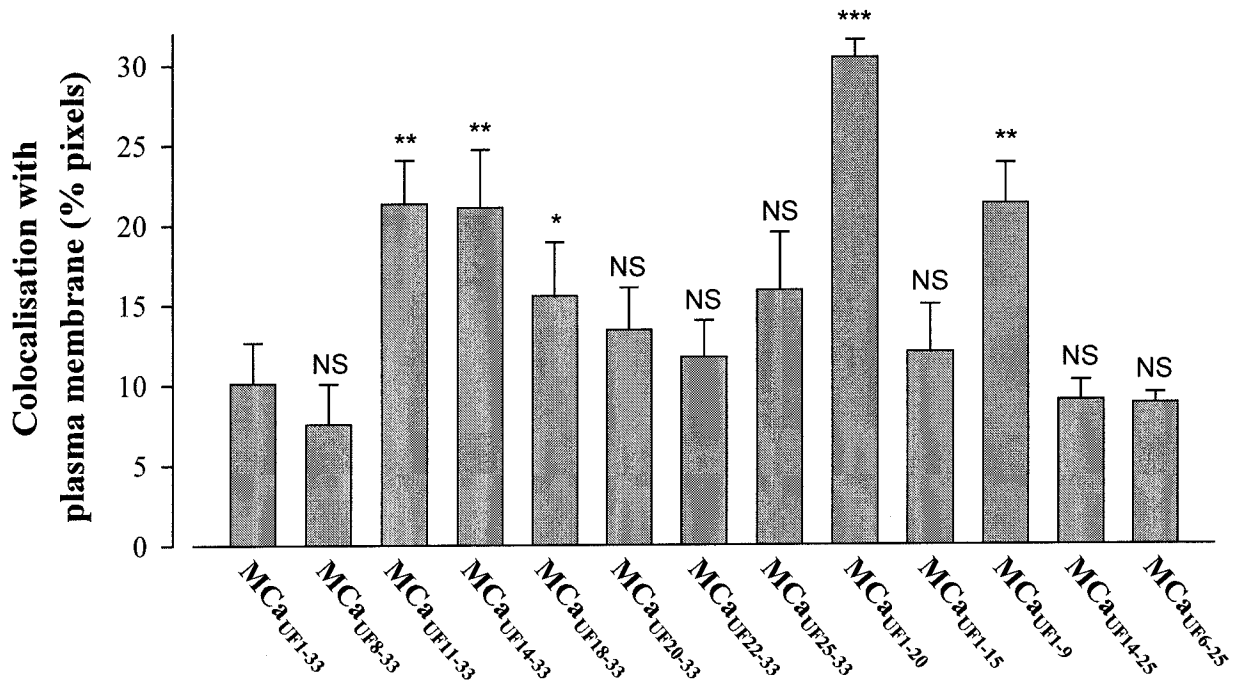


FIGURE 2


Colocalisation with plasma membrane (% pixels)
0
5
10
15
20
25
30
NS
**
**
*
NS
NS
NS
***
NS
**
NS
NS
MCa UF1-33
MCa UF8-33
MCa UF11-33
MCa UF14-33
MCa UF18-33
MCa UF20-33
MCa UF22-33
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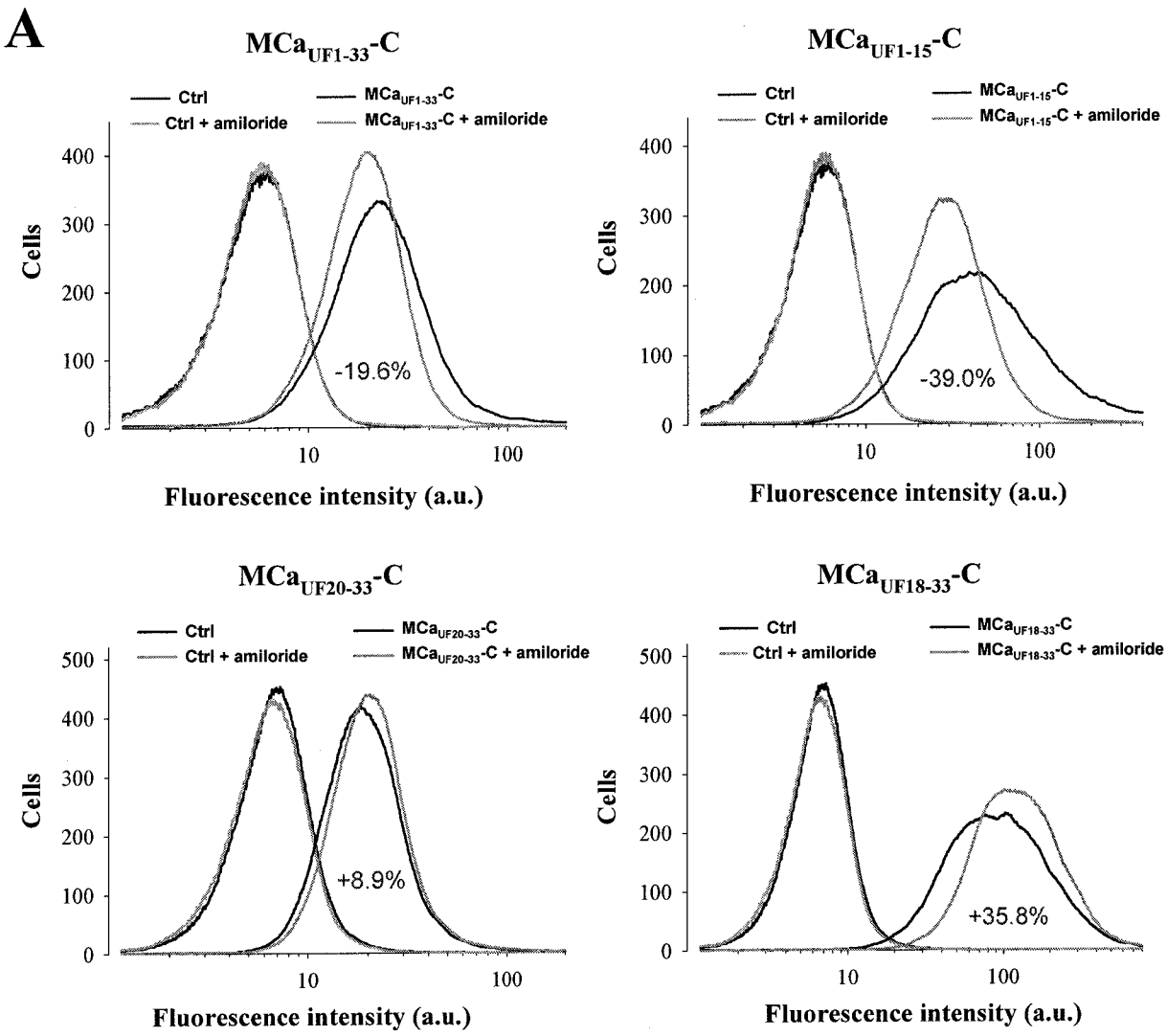
MCa UF1-9
MCa UF14-25
MCa UF6-25

FIGURE 3


A
MCa$_{UF1-33}$-C
Ctrl
Ctrl + amiloride
MCa$_{UF1-33}$-C
MCa$_{UF1-33}$-C + amiloride
Cells
-19.6%
Fluorescence intensity (a.u.)
MCa$_{UF1-15}$-C
Ctrl
Ctrl + amiloride
MCa$_{UF1-15}$-C
MCa$_{UF1-15}$-C + amiloride
Cells
-39.0%
Fluorescence intensity (a.u.)
MCa$_{UF20-33}$-C
Ctrl
Ctrl + amiloride
MCa$_{UF20-33}$-C
MCa$_{UF20-33}$-C + amiloride
Cells
+8.9%
Fluorescence intensity (a.u.)
MCa$_{UF18-33}$-C
Ctrl
Ctrl + amiloride
MCa$_{UF18-33}$-C
MCa$_{UF18-33}$-C + amiloride
Cells
+35.8%
Fluorescence intensity (a.u.)

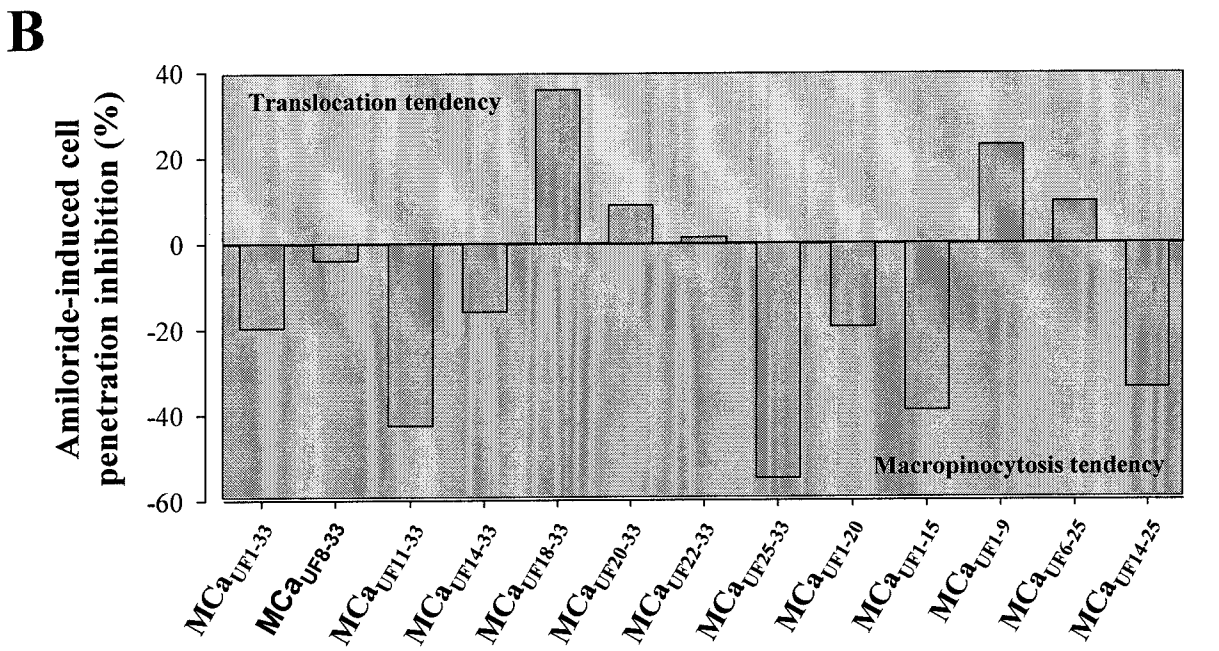

B
Amiloride-induced cell penetration inhibition (%)
Translocation tendency
Macropinocytosis tendency
MCa$_{UF1-33}$
MCa$_{UF8-33}$
MCa$_{UF11-33}$
MCa$_{UF14-33}$
MCa$_{UF18-33}$
MCa$_{UF20-33}$
MCa$_{UF22-33}$
MCa$_{UF25-33}$
MCa$_{UF1-20}$
MCa$_{UF1-15}$
MCa$_{UF1-9}$
MCa$_{UF6-25}$
MCa$_{UF14-25}$

FIGURE 4

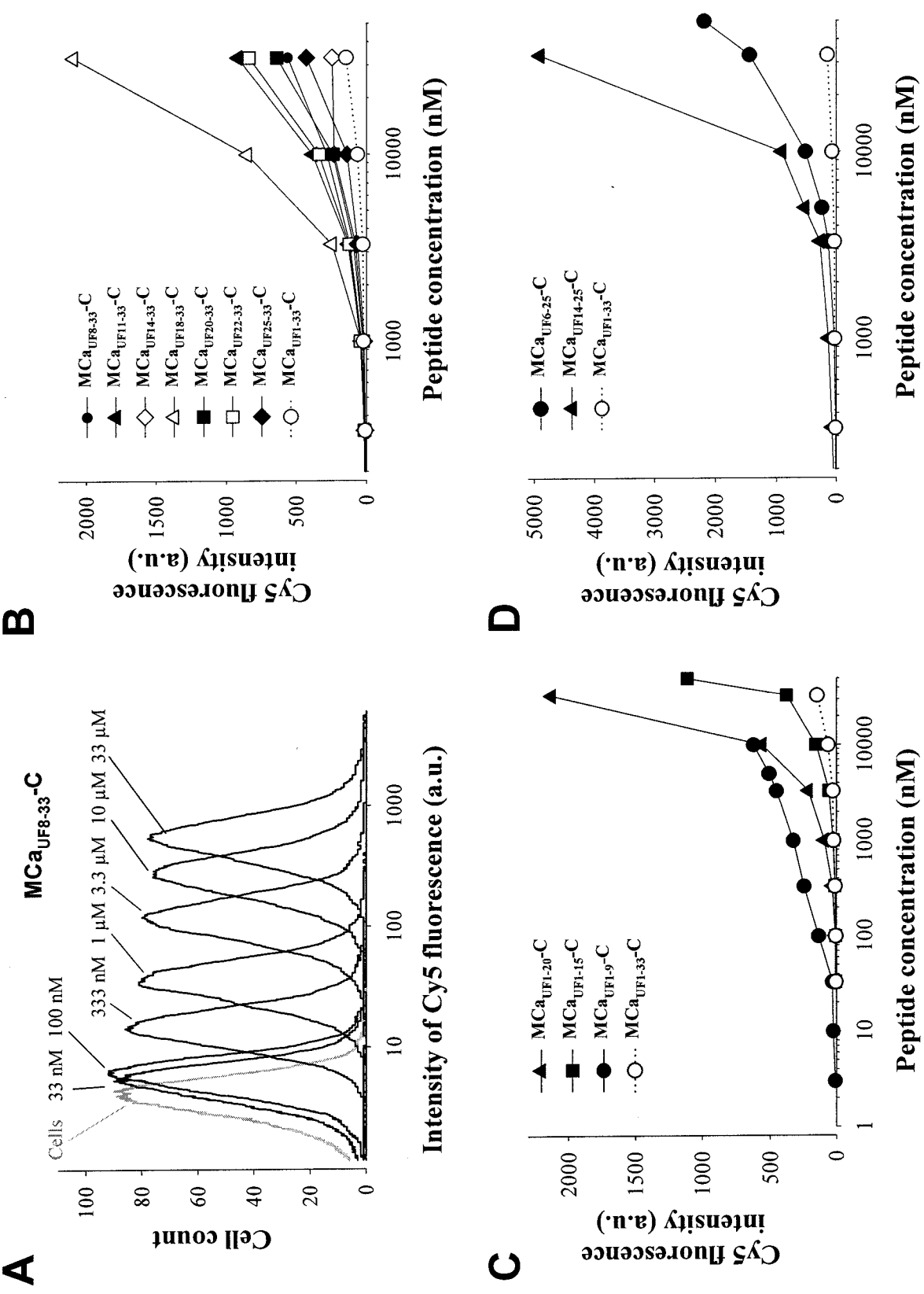

A
MCa$_{UF8-33}$-C
Cells
33 nM
100 nM
333 nM
1 µM
3.3 µM
10 µM
33 µM
Cell count
Intensity of Cy5 fluorescence (a.u.)
B
MCa$_{UF8-33}$-C
MCa$_{UF11-33}$-C
MCa$_{UF14-33}$-C
MCa$_{UF18-33}$-C
MCa$_{UF20-33}$-C
MCa$_{UF22-33}$-C
MCa$_{UF25-33}$-C
MCa$_{UF1-33}$-C
Cy5 fluorescence intensity (a.u.)
Peptide concentration (nM)
C
MCa$_{UF1-20}$-C
MCa$_{UF1-15}$-C
MCa$_{UF1-9}$-C
MCa$_{UF1-33}$-C
Cy5 fluorescence intensity (a.u.)
Peptide concentration (nM)
D
MCa$_{UF6-25}$-C
MCa$_{UF14-25}$-C
MCa$_{UF1-33}$-C
Cy5 fluorescence intensity (a.u.)
Peptide concentration (nM)

FIGURE 5

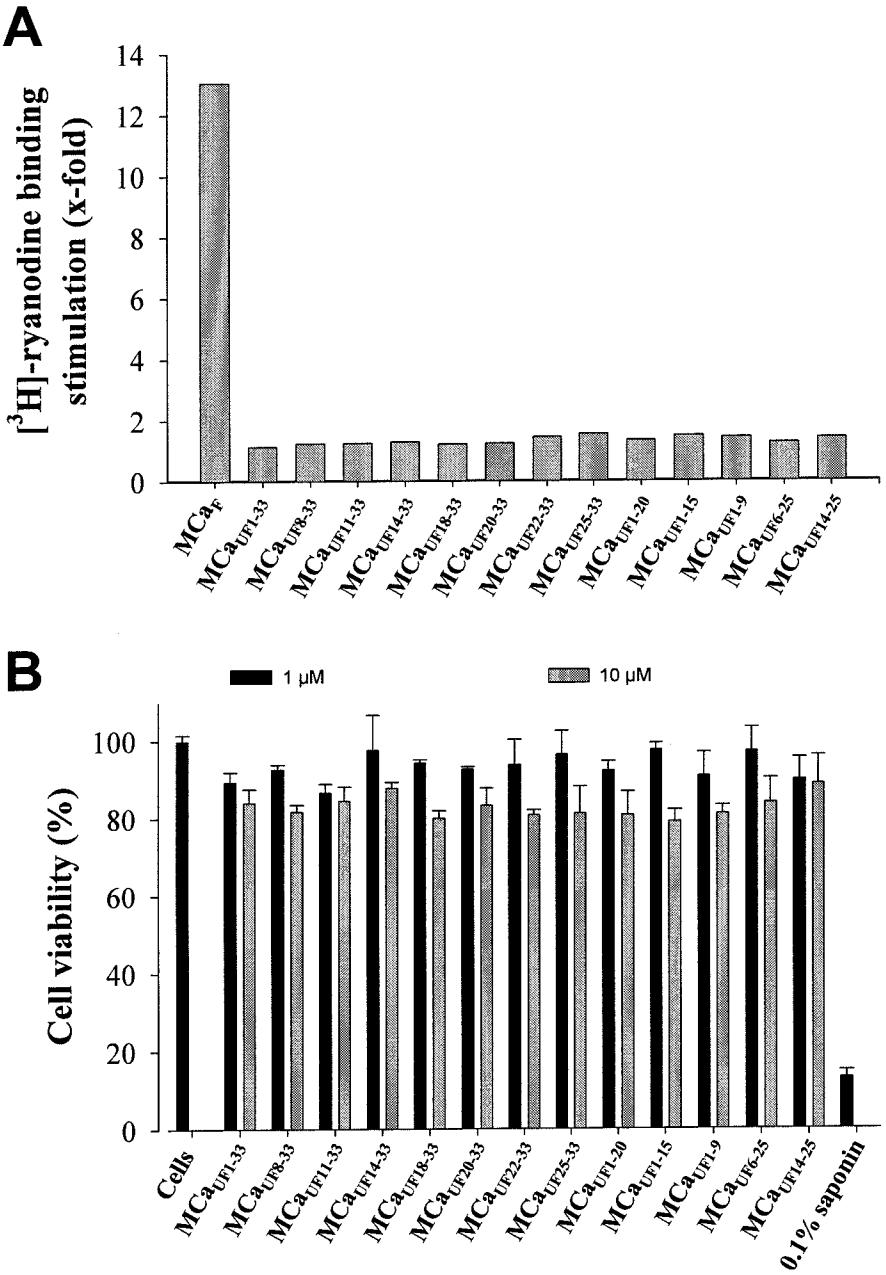
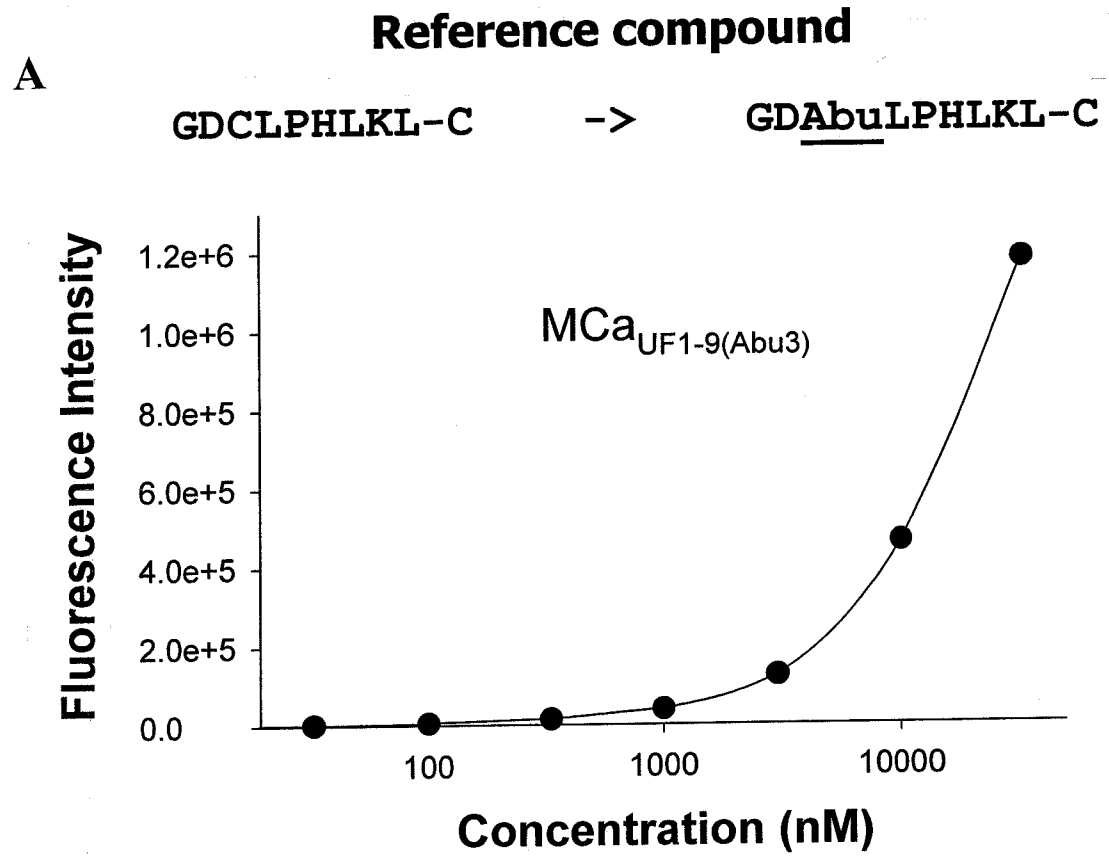

A
[3H]-ryanodine binding stimulation (x-fold)
0
2
4
6
8
10
12
14
MCaF
MCaUF1-33
MCaUF8-33
MCaUF11-33
MCaUF14-33
MCaUF18-33
MCaUF20-33
MCaUF22-33
MCaUF25-33
MCaUF1-20
MCaUF1-15
MCaUF1-9
MCaUF6-25
MCaUF14-25
B
1 µM
10 µM
Cell viability (%)
0
20
40
60
80
100
Cells
MCaUF1-33
MCaUF8-33
MCaUF11-33
MCaUF14-33
MCaUF18-33
MCaUF20-33
MCaUF22-33
MCaUF25-33
MCaUF1-20
MCaUF1-15
MCaUF1-9
MCaUF6-25
MCaUF14-25
0.1% saponin

FIGURE 6

A


Reference compound
GDCLPHLKL-C -> GDAbuLPHLKL-C
Fluorescence Intensity
1.2e+6
1.0e+6
8.0e+5
6.0e+5
4.0e+5
2.0e+5
0.0
MCa UF1-9(Abu3)
100
1000
10000
Concentration (nM)

B

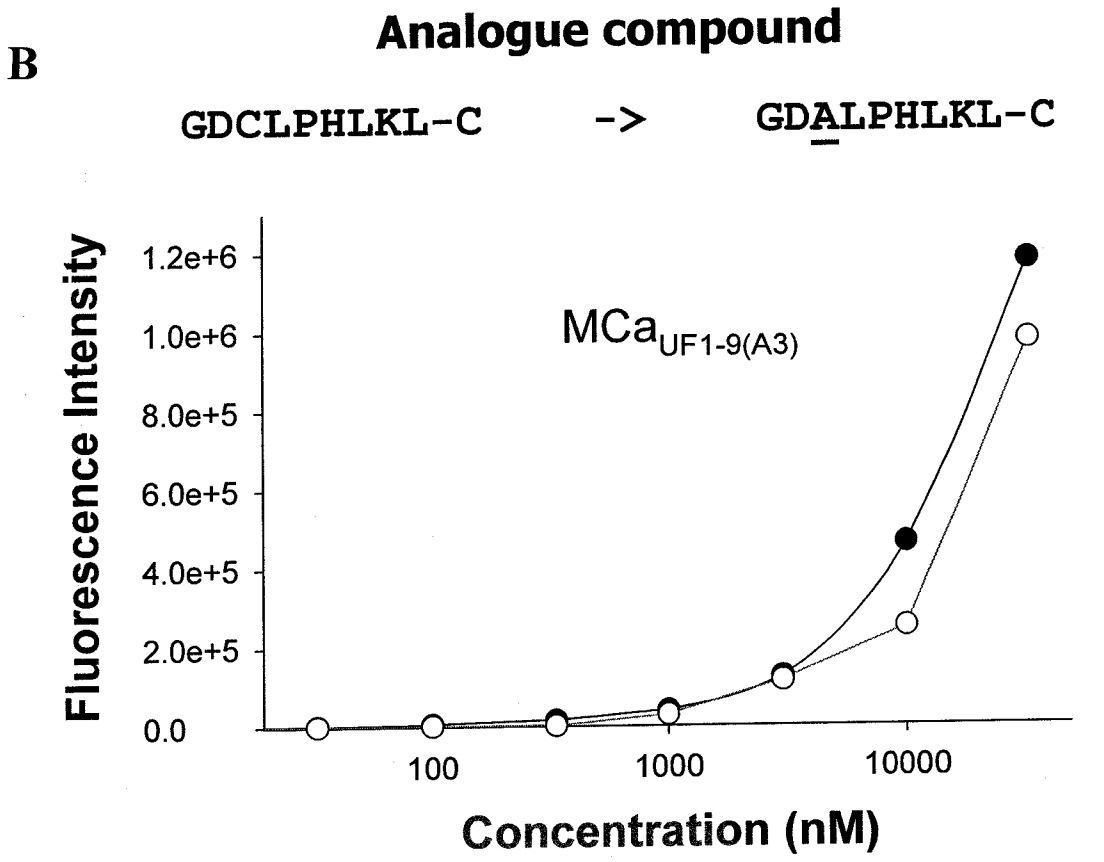
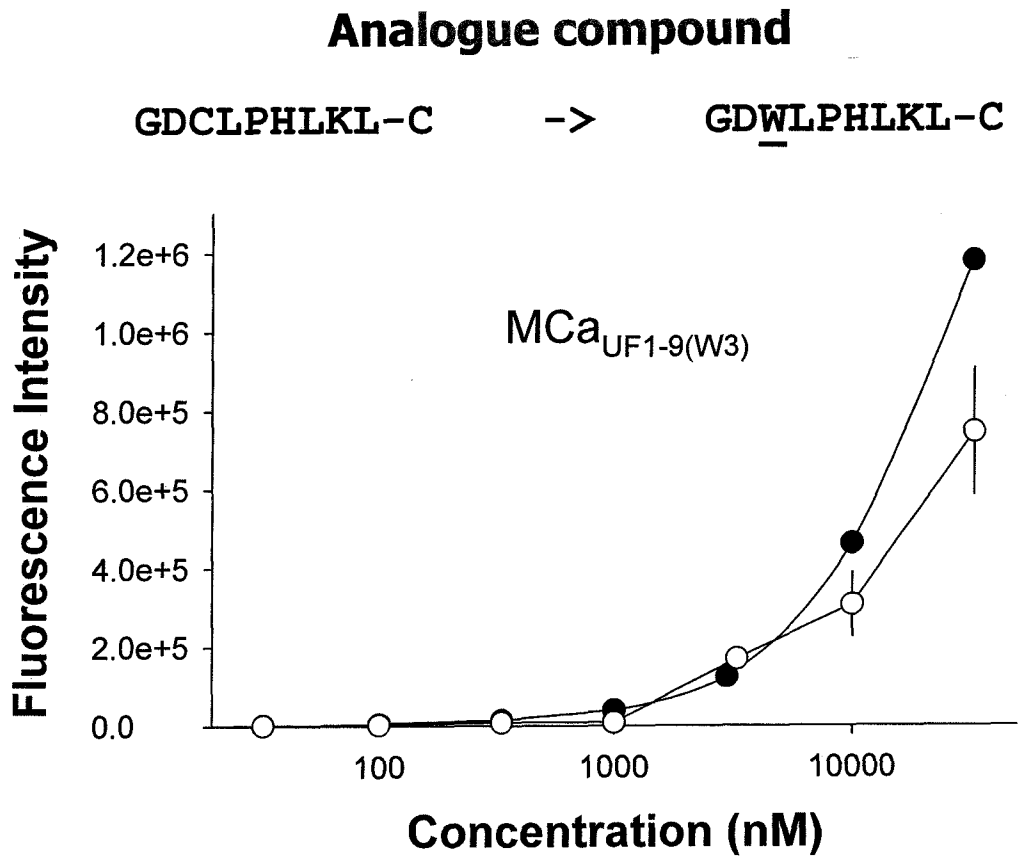

Analogue compound
GDCLPHLKL-C -> GDALPHLKL-C
Fluorescence Intensity
1.2e+6
1.0e+6
8.0e+5
6.0e+5
4.0e+5
2.0e+5
0.0
MCa UF1-9(A3)
100
1000
10000
Concentration (nM)

FIGURE 7

A


Analogue compound
GDCLPHLKL-C -> GDWLPHLKL-C
Fluorescence Intensity
1.2e+6
1.0e+6
8.0e+5
6.0e+5
4.0e+5
2.0e+5
0.0
MCa UF1-9(W3)
100
1000
10000
Concentration (nM)

B

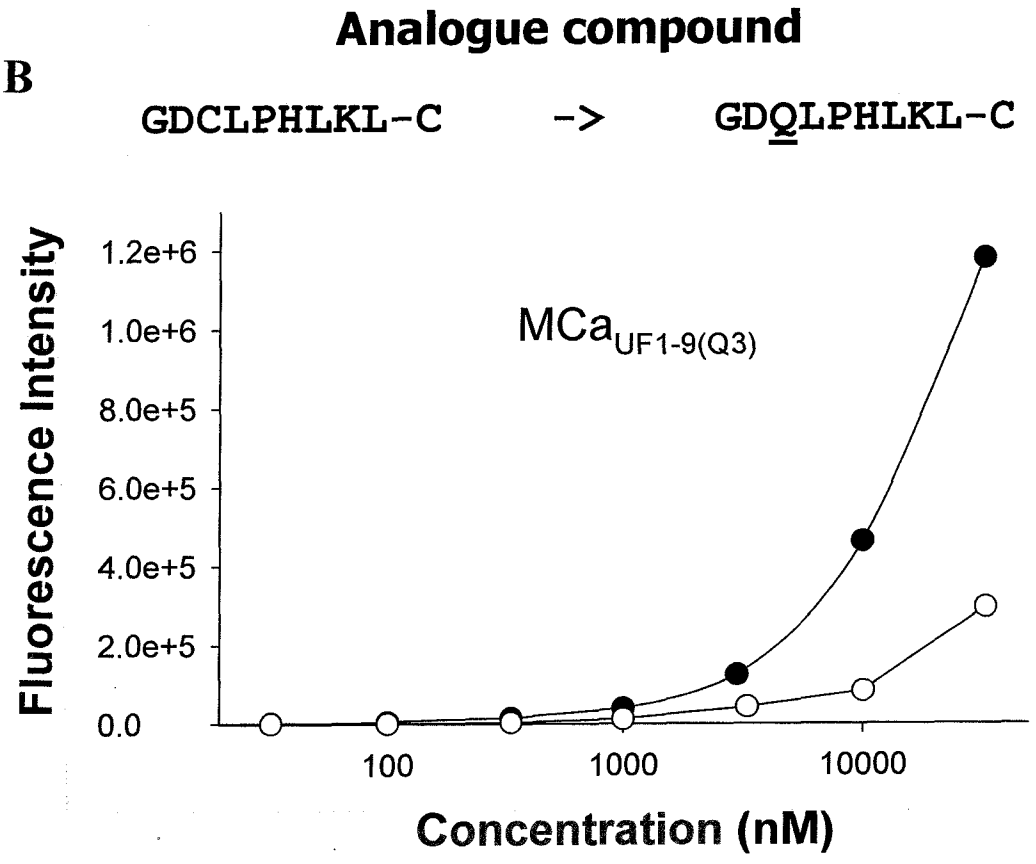

Analogue compound
GDCLPHLKL-C -> GDQLPHLKL-C
Fluorescence Intensity
1.2e+6
1.0e+6
8.0e+5
6.0e+5
4.0e+5
2.0e+5
0.0
MCa UF1-9(Q3)
100
1000
10000
Concentration (nM)

FIGURE 8

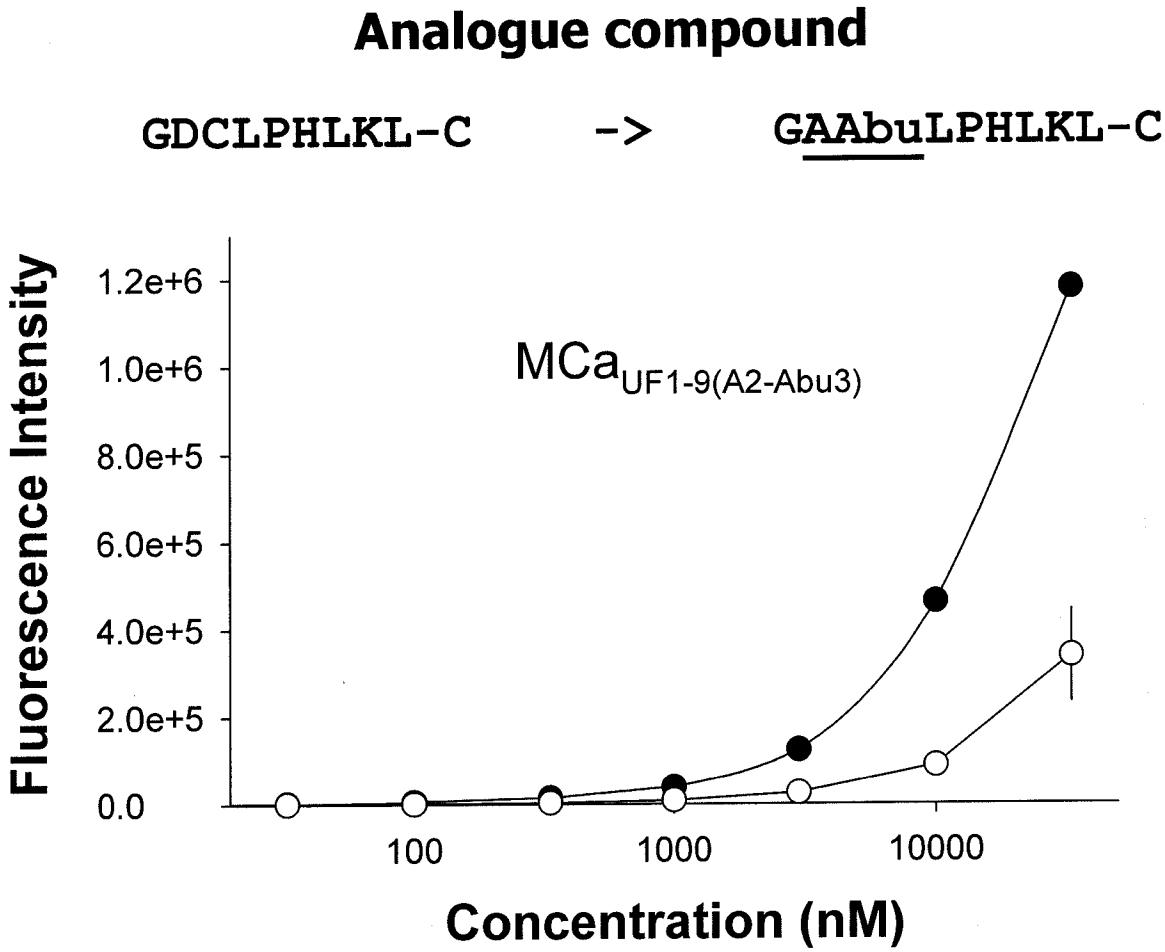
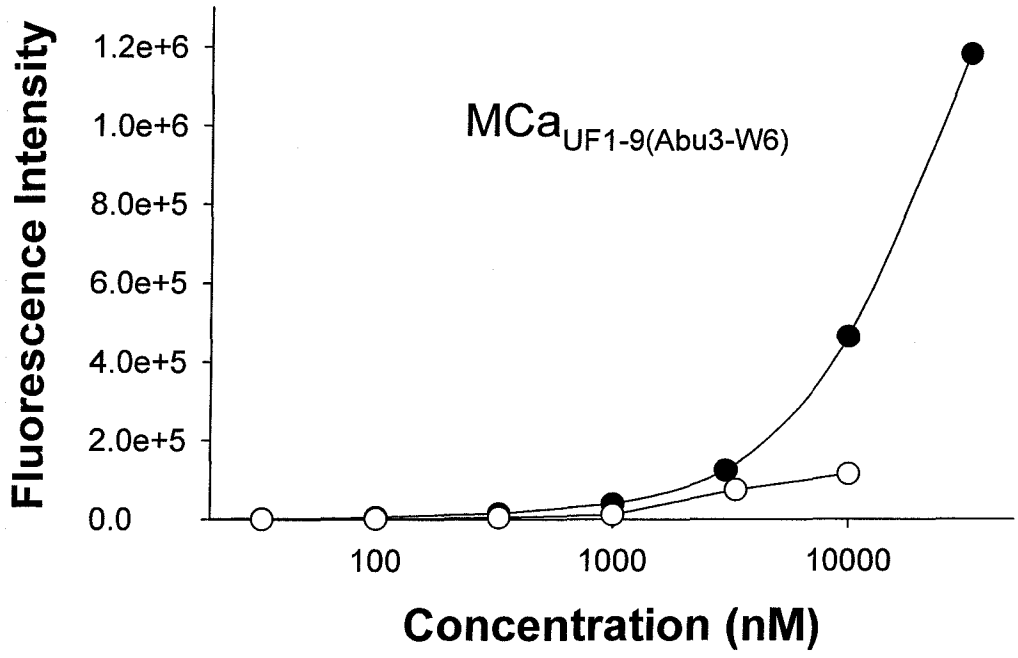

Analogue compound
GDCLPHLKL-C -> GAAbuLPHLKL-C
Fluorescence Intensity
1.2e+6
1.0e+6
8.0e+5
6.0e+5
4.0e+5
2.0e+5
0.0
MCa UF1-9(A2-Abu3)
100
1000
10000
Concentration (nM)

FIGURE 9

A

Analogue compound

GDCLPHLKL-C -> GDAbuLPWLKL-C



B

Analogue compound

GDCLPHLKL-C -> GDAbuLPHFKL-C

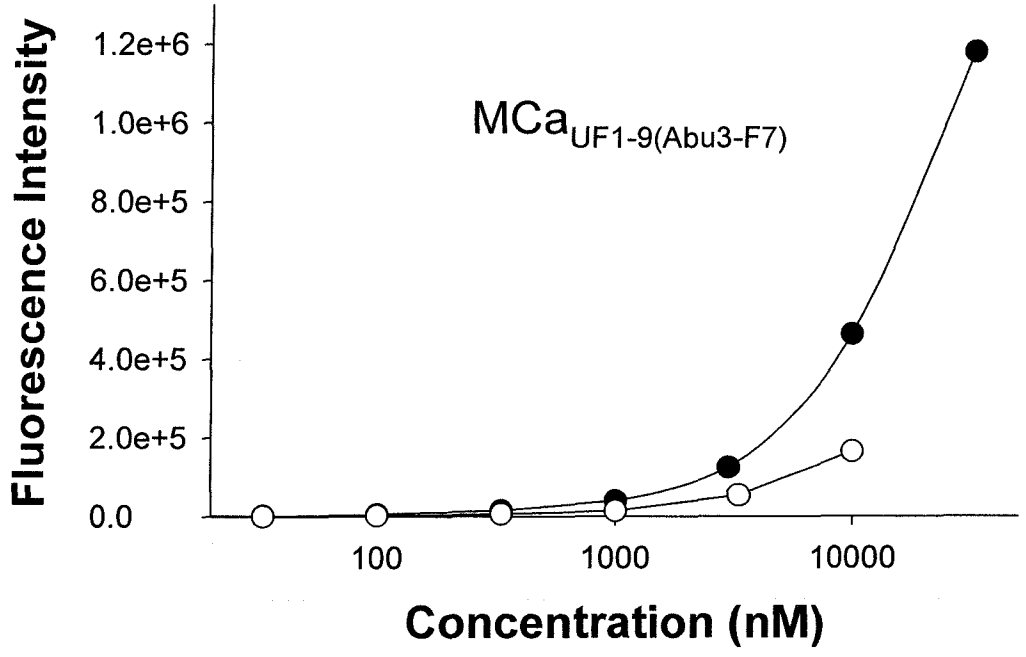


FIGURE 10

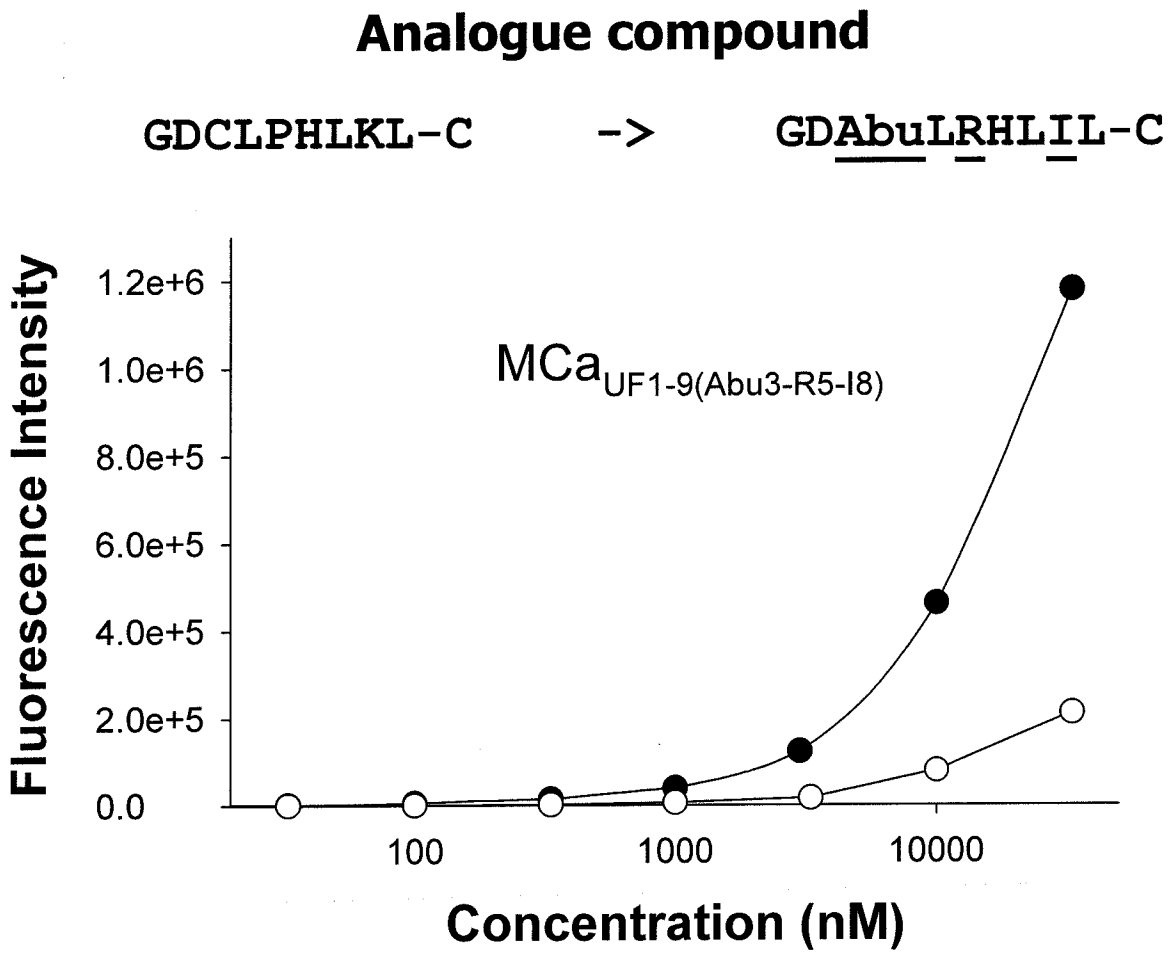
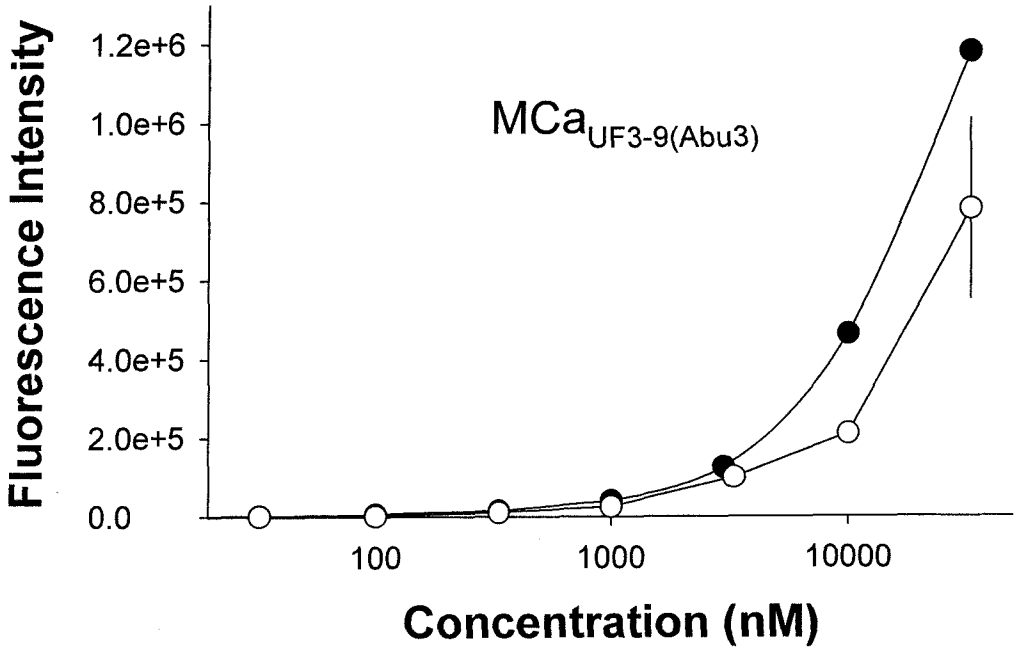

Analogue compound
GDCLPHLKL-C -> GDAbuLRHLIL-C
Fluorescence Intensity
1.2e+6
1.0e+6
8.0e+5
6.0e+5
4.0e+5
2.0e+5
0.0
MCa UF1-9(Abu3-R5-I8)
100
1000
10000
Concentration (nM)

FIGURE 11

A

Analogue compound

GDCLPHLKL-C -> AbuLPHLKL-C



B

Analogue compound

GDCLPHLKL-C -> GDAbuLPHLKR-C

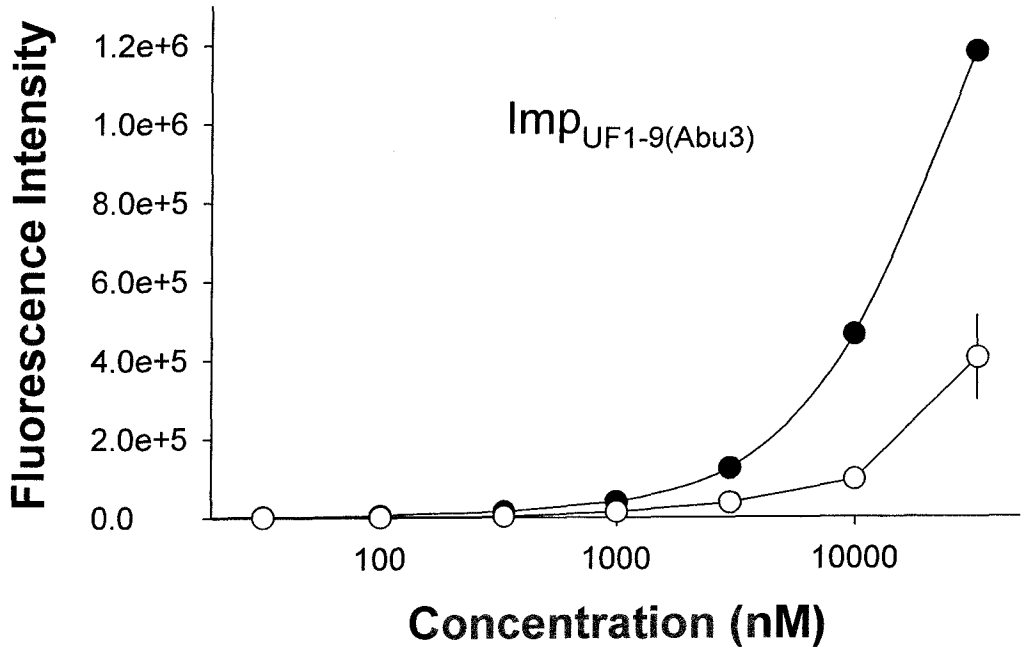
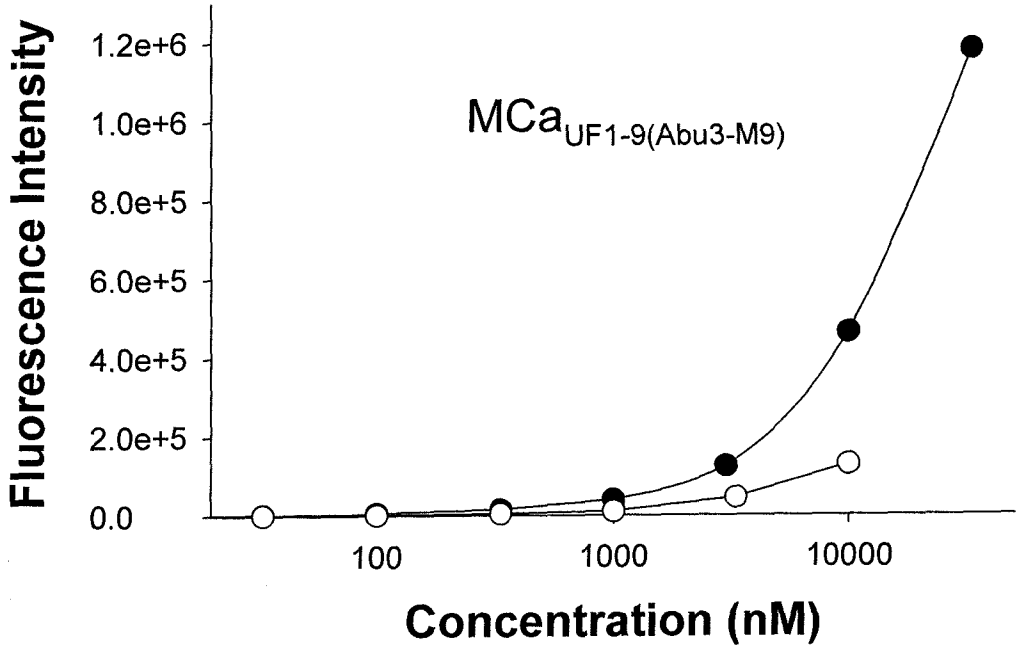


FIGURE 12

A

Analogue compound

GDCLPHLKL-C -> GDAbuLPHLKM-C



B

Analogue compound

GDCLPHLKL-C -> GDAbuLPHLKN-C

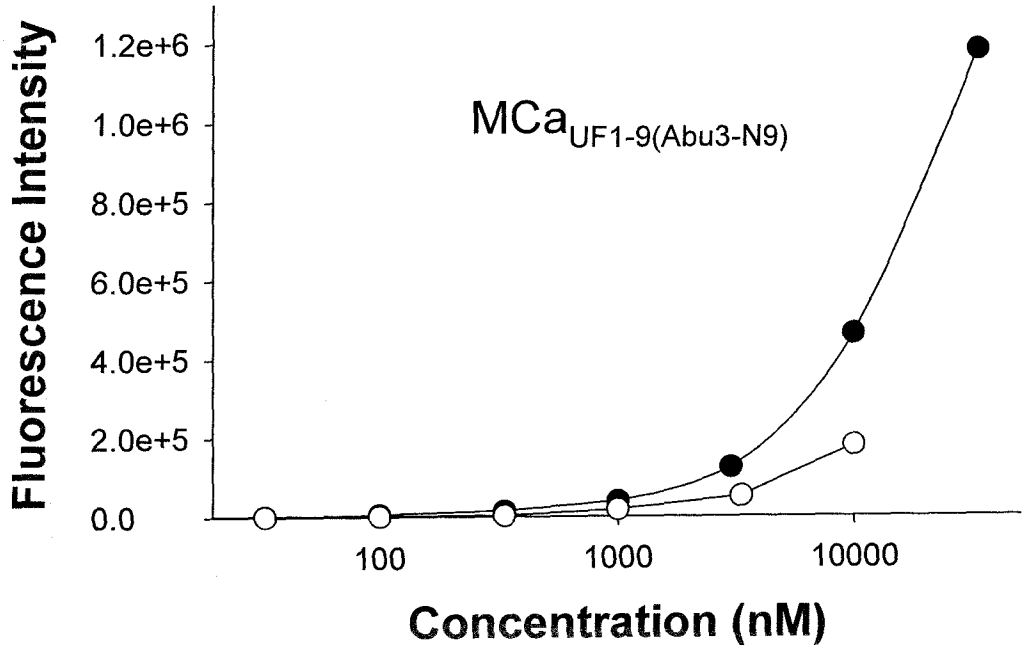
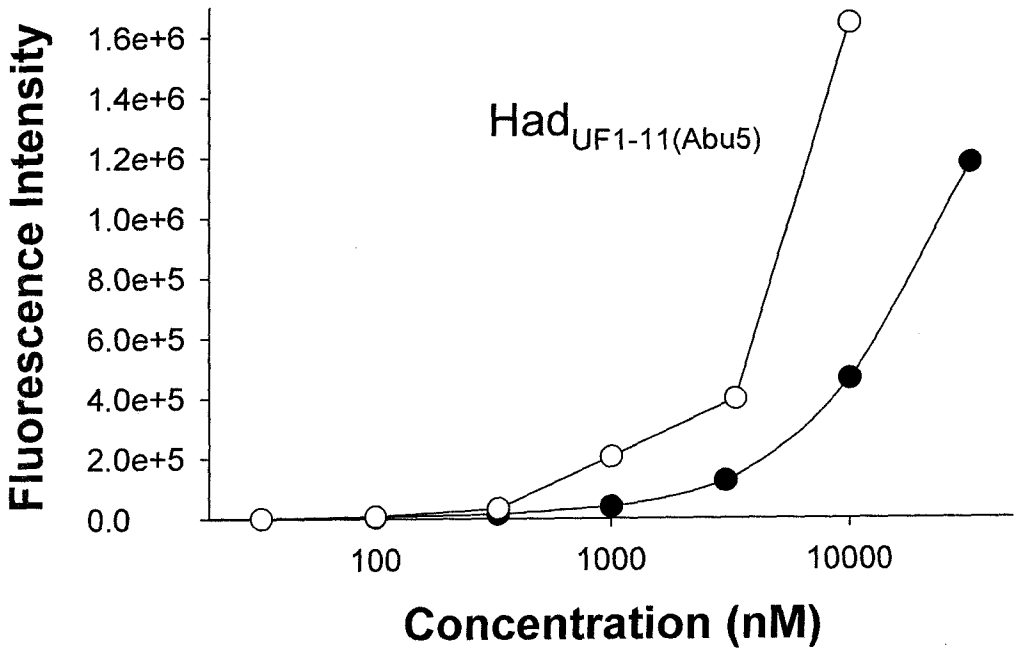


FIGURE 13

A

Analogue compound

GDCLPHLKL-C -> SEKDAbuIKHLQR-C



B

Analogue compound

GDCLPHLKL-C -> KDAbuIKHLQR-C

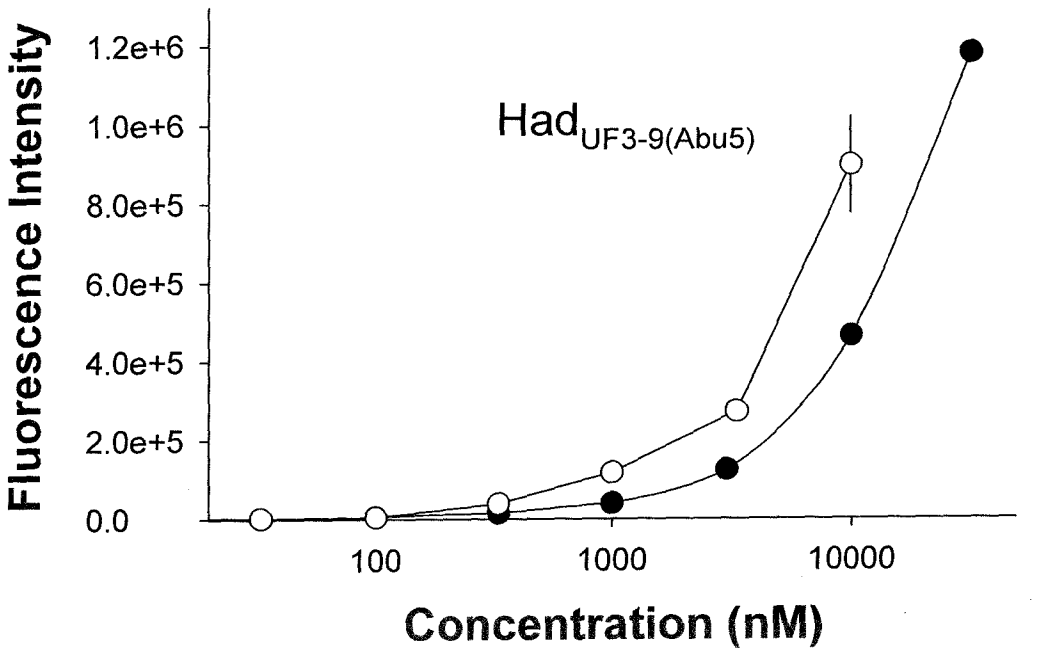


FIGURE 14

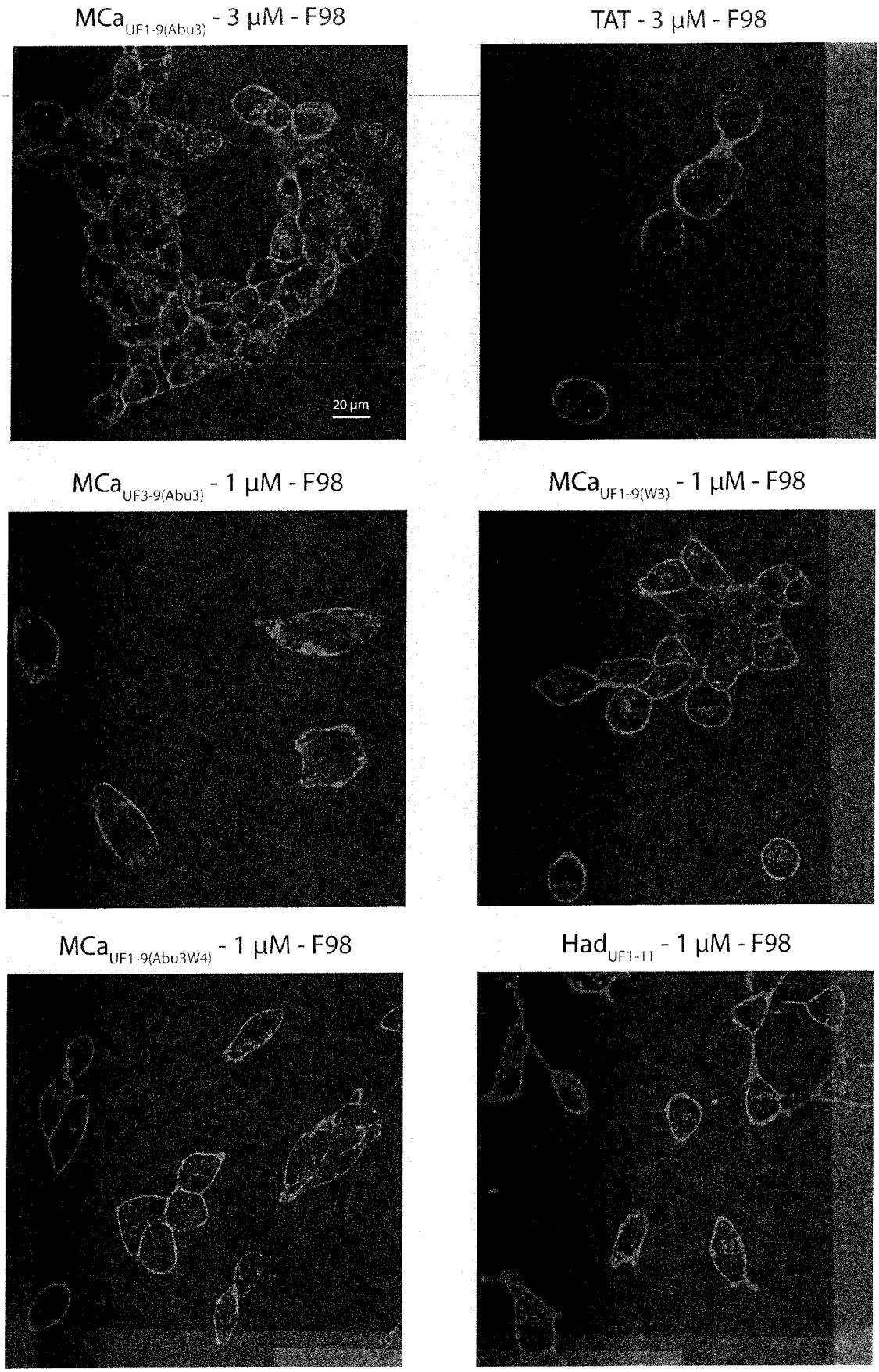

MCa UF1-9(Abu3) - 3 µM - F98
20 µm
TAT - 3 µM - F98
MCa UF3-9(Abu3) - 1 µM - F98
MCa UF1-9(W3) - 1 µM - F98
MCa UF1-9(Abu3W4) - 1 µM - F98
Had UF1-11 - 1 µM - F98

FIGURE 15