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(54) **Title**: A TRANSGLUTAMINE TAG FOR EFFICIENT SITE-SPECIFIC BIOCONJUGATION

(57) **Abstract**: The present invention provides novel peptide sequences for use in microbial transgluatminase-mediated, in particular mTG2-mediated bioconjugations, in particular for the manufacture of antibody-drug-conjugates. Further disclosed are bioconjugation methods employing mTG2 and the novel peptide sequence motifs of the invention. The present invention further provides proteins comprising the novel sequence motifs of the invention as well as polynucleotides encoding the same.

TITLE

A transglutamine tag for efficient site-specific bioconjugation

FIELD OF THE INVENTION

The present invention pertains to the field of bioconjugation, in particular to the field of microbial transglutaminase-mediated bioconjugation and its use for the manufacture of bioconjugates, such as e.g. antibody-drug conjugates.

BACKGROUND

Protein modification with synthetic or naturally occuring molecules is a valuable technique to study protein function or to add additional properties to a protein. Bioconjugations involving natural or synthetic macromolecules, particularly proteins, emerged as a powerful tool to tailor their architecture and engineer functional properties (see e.g. Perez et al. Drug Discovery Today, 2014 Vol 19 (7):869-881). Protein modification or bioconjugation is typically done by either chemical linkage of a further molecule to the protein of interest or enzymatically.

Chemical strategies that are currently utilized for conjugation of biomolecules, make use of the fact that cysteine and lysine residues can be readily be modified. Cysteine residues can be alkylated by reacting them with α-haloketones or Michael acceptors, such as maleimide derivates.The modification of lysine residues is the oldest and and most straightforward method for labeling proteins via the primary lysine amino groups. The ε-amino group of lysine within the protein of interest can be readily reacted with activated esters, sulfonyl chlorides, isocyanates and isothiocyanates to result in the corresponding amides, sulfonamides, ureas and thioureas (see e.g. Takaoka et al., Angew. Chem. Int. Ed. 2013, 52, 4088 – 4106). Although very efficient for bioconjugation these chemical approaches inevitably result in heterogenous mixtures. This effect becomes more pronounced in smaller molecules with fewer lysines, e.g. in antibody fragments lacking an Fc region compared to IgG type molecules. Further examples for bioconjugation include the conjugation of fluorescent proteins, dyes, or the tethering with functional molecules, e.g. PEGs, porphyrins, peptides, peptide nucleic acids, and drugs (Takaoka et al., Angew. Chem. Int. Ed. 2013, 52, 4088 – 4106).

The preparation of protein bioconjugates may involve varying levels of difficulty depending on the desired outcome. For example bioconjugation can range from the simple and non-specific attachment of polyethylene glycol (PEG) to serum albumin (Abuchowski et al. J. of Biological

Chemistry (1977) Vol. 252 (11):3578-3581) to the very demanding preparation of homogenous antibody drug bioconjugates.

This challenge can be addressed, among other approaches, by applying enzyme-mediated conjugations. For example, WO 2014/001325 A1 discloses the use of sortase A for site-specific bioconjugation to Fc regions of an antibody. Sortase A (SrtA) is a bacterial integral membrane protein first described in *Staphylococcus aureus*. SrtA catalyzes a transpeptidation reaction anchoring proteins to the bacterial cell wall. Upon recognition of a sorting signal LPXTG, (X = D, E, A, N, Q, or K) a catalytic cysteine cleaves the peptide bond between residues T and G which results in the formation of a thioacyl intermediate. This thioacyl intermediate subsequently then can reacts with an amino-terminal glycine acting as a nucleophile. SrtA accepts N-terminal (oligo)glycine as a nucleophiles, creating a new peptide bond between two molecules. SrtA functions at physiological conditions and has been used for bioconjugation reactions to label proteins with e.g. biotin, or to functionalize a HER2-specific recombinant Fab with the plant cytotoxin gelonin (see e.g. Popp et al. (2011) Angew Chemie Int. Ed. 50: 5024-5032; Kornberger et al (2014) mAbs 6 (2): 354-366). Typically, target proteins are labeled carboxyterminally with the LPXTG motif followd by a purificaton tag such that the SrtA-mediated transpeptidation removes the purification tag and generates the labeled protein.

One of the major drawbacks in the use of SrtA in bioconjugation reactions is the high concentration of the enzyme that is required to catalyze the transpeptidase reaction. Attempts have been made to improve the reaction kinetics using SrtA molecular evolution which has resulted in an increase of the affinity of the enzme to the LPXTG motif by about 140-fold (see e.g. Proc Natl Acad Sci U S A. 2011 Jul 12; 108(28): 11399-11404). Another disadvantage to the use of SrtA-mediated bioconjugation reactions is the reversibility of catalyzed reactions. Also here attempts have been made to overcome this limitation through the use of chemically modified SrtA substrates LPETGG-isoacyl-serine and LPETGG-isoacyl-homoserine, which can be irreversibly ligated to amino-terminal glycine-containing moieties via the deactivation of SrtA-excised peptide fragments throught the formation of diketopeperazines (see e.g. Liu et al. J. Org. Chem. 2014, 79, 487−492).

Another prominent enzyme-mediated bioconjugation approach involves the use of transglutaminases (TGases), in particular microbial transglutaminases (mTGases). TGases are a large family of enzymes detected in several organisms including mammals, invertebrates, plants and microorganisms. Transglutaminases are protein-glutamine γ-glutamyltransferases (E.C. 2.3.2.13), which typically catalyze pH-dependent transamidation of glutamine residues to lysine residues. Most TGases appear to be promiscuous with respect to the lysine substrate and may even accept 5-amino-pentyl groups as lysine surrogates to serve as the amine donor. However, the selectivity of TGases to recognize a glutamine residue as a substrate appear to be much more stringent in that for a glutamine residue to be accepted by TGases the residue has to be located in a flexible region of the protein (see e.g. Jeger et al. Angew. Chem Int. Ed. 2010, 49, 9995-9997; Fontana et al. Adv Drug Deliv Rev. 2008 Jan 3;60(1):13-28).

Transglutaminases are widely distributed in most tissues and body fluids and are thought to be involved in a variety of physiological functions. One example for a transglutaminase-mediated reaction is the termination of bleeding during blood coagulation by factor XIIIa, which is an activated form of plasma transglutaminase which catalyzes the crosslinking between fibrin molecules (see e.g. Griffin et al. Biochem. J. (2002) 368, 377-396). The biological function of bacterial transglutaminases, however, remains largely unknown. It has been speculated that the mTGase of *Streptomyces mobaraensis* cross-links inhibitory proteins during development of aerial hyphae and spores.

The transglutaminase from *S. mobaraensis* exhibits no significant homology to mammalian TGases and has a unique structure compared to human TG2 being the best characterized member of the human TGase family. In contrast to its mammalian orthologue mTG2 of *S. mobaraensis* is calcium-independent and has only a molecular weight of 37.9 kDa, which is only about half of the molecular weight of factor XIII-like TGases. mTG2 is also characterized by a higher reaction rate than its mammalian orthologue. Another aspect that has contributed to the widespread use of mTG2 is the fact that the enzyme can be easily produced in larger quantities as a recombinant protein which in conjunction with its biochemical properties has led to a wide use of mTG2 also in food industry (see e.g. Sommer at al. (2011) Protein Expression and Purification 77:9-19; Marx et al (2008) Enzyme and Microbial technology 42:568-575). Random mutagenesis of mTG2 has also been employed to increase the thermodynamic stability of the enzyme (see e.g. Journal of Biotechnology 136 (2008) 156-162). Noteably, all mutations that have resulted in an increased stability of mTG2 at elevated temperatures are located within the amino-terminal region of the enzyme.

Microbial Transglutaminase mTG2 has also been used for site-specific and stoichiometric PEGylation of proteins such as α-lactalbumin, human growth hormone and interleukin-2 or for site-specific and stoichiometric modification of antibodies (see e.g. Jeger et al. Angew. Chem Int. Ed. 2010, 49, 9995-9997; Fontana et al. Adv Drug Deliv Rev. 2008 Jan 3;60(1):13-28). Overall, the number of reactive glutamines was found to be low in comparision to the total number of surface-exposed glutamines.

mTG2, when used to catalyze transglutamination on native, fully glycosylated monoclonal antibodies, was found to not recognize any glutamine residues in the respective monoclonal antibody as substrate. Only de- or aglycosylated antibodies were found to be recognized as substrates by mTG2. Interestingly, only one glutamine residue was found to serve as a acyl-glutamine substrate in the de- or aglycosylated antibodies (Q295). This strongly limits the use of mTG2 for site-specific bioconjugation of antibodies for the generation of antibody-drug conjugates, in particular for use in humans. Interestingly, when a Fc mutant (N297Q) antibody was used, this second glutamine residue was also found to be modified by mTG2 with the respective substrate (Fontana et al. Adv Drug Deliv Rev. 2008 Jan 3;60(1):13-28).

One of the best characterized proteins for mTG-mediated PEGylation is human growth hormone (hGH). For hGH, two glutamine residues were identified as major conjugation sites, namely Q40 and Q141. Mutagenesis of mTG resulted in an mTG variant with increased selectivity toward Q141. In another study, it was found that, for salmon calcitonin and human growth hormone, a change in the solvent which presumably results in a change in the secondary structure surrounding the reactive glutamine can be used to limit the conjugation to a single glutamine residue, and therefore increase selectivity.

In the case of human interleukin 2 (hIL-2), a single reactive glutamine (Gln74) was found and conjugated with 12 kDa PEG or galactose-terminated triantennary glycosides.

Artifical peptide sequences have been used in the past to further examine the substrate specificity of mTG2. For example, the sequence effects around the substrate Gln residue were first investigated in context of the heptapeptide substrate (GGGQGGG), where each glycine was individually substituted to several amino acids (Ohtsuka et al. Biosci., Biotechnol., Biochem. 64, 2608−13). It was found that hydrophobic residues at the N-terminus of the Gln accelerated the reaction relative to the GGGQGGG peptide (at the −3, −2, and −1 positions), however the overall reaction kinetics were low.

The preferred substrate sequence of mTG was also assessed using a phage-displayed peptide library utilizing a much larger library of about 10^{11} linear peptides. Most identified clones contained an aromatic amino acid (W, F, or Y) at the −5 to −3 positions, an arginine or hydrophobic residue at the +1 or +2 positions, and hydrophobic residues at the −2 and −1 positions (see e.g. Sugimura et al., Archives of Biochemistry and Biophysics 477 (2008) 379–383).

The use of mTG2 for the generation of antibody-drug-conjugates requires the bioconjugation of a functional payload with a monoclonal antibody counterpart. In antibody-drug conjugates (ADCs) the antibody specifically directs the uptake and release of a highly potent toxin to a cancer cell, a technology which has attracted much attention in recent years as a novel and effective new treatment option for cancer patients.

Examples of ADCs which have received market approval include Kadcyla® (trastuzumab Emtansin) and Adcetris® (brentuximab vedotin) for the treatment of metastatic breast cancer and Hodkin lymphoma. These antibodies as well as other antibody candiates that are currently in clinical development have not been obtained by bioconjugation using e.g. mTG2, but rely on chemical conjugation methods for their production that result in heterogenous mixtures of antibodies with varying numbers of drug molecules attached to them (see e.g. Handbook of Therapeutic Antibodies, 2nd edition, edited by S. Dübel and J.M. Reichert, John Wiley & Sons (2014), pp. 369).

It has been shown that heterogeneity of ADCs can negatively impact drug efficacy, in particular if significant fractions of the material are insufficiently conjugated: Insufficiently conjugated antibodies will compete with ADCs for target binding resulting in a reduced efficacy of the properly conjugated ADCs. Increased drug loading to antibodies can also negatively impact the efficacy of the ADC. Data have demonstrated that ADCs with high drug:antibody ratios are cleared more rapidly from the blood stream resulting in reduced efficacy (see e.g. Sanderson et al. Clin. Cancer Res. 2005; 11:843-52). Studies with anti-CD30 monoclonal antibody – auristatin E (MMAE) conjugates have shown that the ADCs with a antibody:drug stoichiometry of 1:2-1:4 are most effective, with a ratio of 1:4 being most preferable (see e.g. Hamblett et al. Clinical Cancer Research (2004) Vol. 10, 7063–7070).

WO 2013/092983, discloses methods of functionalization of immunoglobulins with drugs employing TGase. This approach, describes the method to obtain new site by directed mutagenesis to generate a Q-donor inside the heavy chain of the antibody. This empiric method needs to test high number of mutants as the rules which govern selection by TGases of glutamine residues for modification are still largely unknown. Consequently, using this method to develop new antibodies bearing Q-donor is time consuming and cost intensive.

WO 2012/059882 further discloses specific engineered polypeptide conjugates and methods of making such conjugates using transglutaminases.

WO 2015/097267 discloses peptide sequences which selectively react as glutamine donors with transglutaminase, such as mTG2 of *S. mobaraensis* which may be utilized for mTG2-mediated conjugation reactions.

Despite the studies on bioconjugation of proteins with mTG2 and exploration of new sequence motifs which may be utilzed as glutamine donors for bioconjugation reactions, neither the sequences nor the structural environment of natural MTG substrate sites are known.

There is thus a need to expand the repertoire of substrates recognized by mTG2 for a more efficient production of bioconjugates, in particular for the manufacture of ADCs with a well defined antibody:drug stoichiometry

SUMMARY OF THE INVENTION

The present inventors have surprisingly found that a acyl glutamine-containing donor sequencederived from the dispase autolysis inducing protein of *Streptomyces mobaraensis* strain 40847 comprising at least the amino acid sequence TYFQAYG can be efficiently used in mTG2-mediated transglutamination reactions.

Accordingly, the present invention provides in a first embodiment a protein comprising at least one acyl glutamine-containing amino donor sequence, which is covalently linked via a γ-glutamyl-amide bond to an amino donor-comprising substrate, wherein the at least one acyl glutamine-containing amino acid donor sequence comprises the amino acid sequence according to SEQ ID NO: 1 (SEQ ID NO: 1 (TYFQAYG)).

According to one embodiment the amino donor-comprising substrate according to the present invention comprises at least an ε-amino group, or at least one tripeptide having the sequence of GGG with a primary aminoterminal amino group.

In one embodiment the amino donor-comprising substrate according to the invention is a lysine residue, a lysine derivative, lysine drug-conjugate, a polypeptide comprising at least one lysine residue.

According to one embodiment the amino donor-comprising substrate according to any one of the above embodiments of the invention is covalently bound to a further molecule.

According to one embodiment the tripeptide GGG of the amino donor-comprising substrate is covalently bound via its carboxy terminus to a further molecule.

In one embodiment the the further moelcule according to the invention is one of a dye, radioisotope, drug, ribozyme, nanobody, enzyme, or linker.

In one embodiment the futher molecule according to the invention is a linker, which is cleavable or non-cleavable.

According to one embodiment the linker according to the invention is coupled or covalently bound to a dye, radioisotope, or cytotoxin.

In a preferred embodiment, the protein of the invention according to any one of the above embodiments comprises an acyl glutamine-containing amino acid donor sequence, which comprises an amino acid sequence according to SEQ ID NO: 2 (X_1X_2 X_3 TYFQAYG $X_4X_5X_6$), wherein

X1 is a hydrophobic amino acid,
X2 is a negatively charged amino acid,
X3 is C or N,
X4 is C or N,
X5 is one of an amino acid with a polar, uncharged side chains, and
X6 is a negatively charged amino acid.

In a preferred embodiment the acyl glutamine-containing amino acid donor sequence of the invention according to any one of the above embodiments comprises an amino acid sequence according to SEQ ID NO: 2, wherein

X1 is any one of A, V, I, L, M or G,
X2 is one of D or E,
X3 is C,
X4 is C or N,
X5, is S, T, or N,
X6 is one of D, or E.

According to a preferred embodiment the acyl glutamine-containing amino acid donor sequence of the invention comprises an amino acid sequence according to SEQ ID NO:2, wherein

X1 is any one of A, V, I, L, M or G,
X2 is one of D or E,
X3 is C,
X4 is C,
X5, is S, T, or N,
X6 is one of D, or E.

According to a more preferred embodiment the acyl glutamine-containing amino acid donor sequence of the invention comprises the amino acid sequence according to SEQ ID NO: 2, wherein

X1 is any one of A, V, I, L, M or G,
X2 is E,
X3 is C,
X4 is C,
X5 is T, and
X6 is E.

According to an even more preferred embodiment the acyl glutamine-containing amino acid donor sequence of the invention comprises an amino acid sequence according to SEQ ID NO: 90.

In one embodiment the protein according to the invention is one of an antibody, antigen-binding antibody fragment, Fc domain, enzyme, a non-immunoglobulin scaffold.

In one embodiment the protein according to the invention is a monoclonal antibody, bivalent antibody, VHH, Fab, $F(ab)_2$, or scFv.

According to a preferred embodiment the protein according to the invention is a human or humanized monoclonal antibody or fragment thereof.

In one aspect the present invention provides for a method of covalently coupling an amino donor comprising substrate of the invention to an acyl glutamine-containing amino acid donor comprising a polypeptide sequence according to SEQ ID NO:2, whereby the method comprises the step of:

- contacting an amino donor-comprising substrate according to the invention and an acyl glutamine-containing amino acid donor according to the invention in the presence of transglutaminase, preferably mTG2, to obtain a protein of the invention according to any one of the above embodiments.

In one embodiment the acyl glutamine-containing amino acid donor of the inventive method is an antibody, antigen-binding antibody fragment, enzyme, or a non-immunoglobulin scaffold.

According to one embodiment, the amino donor-comprising substrate of the inventive method is coupled or covalently bound to a dye, drug, ribozyme, nanobody, enzyme, or linker.

According to one embodiment of the invention the linker is cleavable or non-cleavable and is coupled to a dye, radioisotope, or cytotoxin.

In one embodiment the present invention provides for a protein obtainable by the inventive method as disclosed herein.

In one embodiment the present invention provides for the use of a polypeptide sequence according to any one of SEQ ID NO: 2 in the inventive method according to any one of the embodiments as disclosed herein.
According to one embodiment the present invention provides for a protein comprising the polypeptide comprising the amino acid sequence according to SEQ ID NO:2.

In one embodiment the present invention provides for a polypeptide according to SEQ ID NO:2.

In one embodiment the present invention provides for a polynucleotide encoding a polypeptide sequence according to SEQ ID NO: 2 of the invention.

In one embodiment the present invention provides for a vector comprising the polynucleotide encoding the polypeptide sequence according to SEQ ID NO:2.

In one embodiment the present invention provides a host cell which comprises the polynucleotide of the invention or a vector according to the invention as disclosed herein.

In one embodiment the present invention provides an antibody or antigen-binding fragment thereof, bivalent antibody, or VHH antibody according to the invention which comprises at least one amino acid sequence according to SEQ ID NO:2.

Accordingly, the antibody or antigen-binding fragment thereof, bivalent antibody, or VHH antibody of the invention is humanized or human.

In a preferred embodiment the antibody or antigen-binding fragment thereof according to to the invention as disclosed above is a humanized or human monoclonal antibody.

In a preferred embodiment the antibody of the invention as disclosed above is an IgG1, IgG2, IgG3, IgG4, or IgM type antibody.

In one embodiment the inventive antibody as disclosed above is covalently coupled to at least one linker as disclosed above according to the inventive method as disclosed above.

According to one embodiment the at least one linker of the monoclonal antibody of the invention is further coupled to a dye, radioisotope, or cytotoxin.

In a preferred embodiment the inventive monoclonal antibody as disclosed herein specifically binds to cancer cell surface antigens.

In a more preferred embodiment the monoclonal antibody of the invention as disclosed above is the monoclonal antibody c225 (cetuximab).

In a more preferred embodiment the antibody of the invention as disclosed herein is for use in the treatment of cancer , more preferrably the inventive antibody as disclosed above is for use in the treatment of breast cancer, prostate cancer, ovarian cancer, cervical cancer, skin cancer, pancreatic cancer, preferably colorectal cancer, metastatic (mCRC), non-resctable liver metastases, Squamous Cell Carcinoma of the Head and Neck, Non-Small Cell Lung Cancer (NSCLC), Head and Neck Squamous Cell Carcinoma (HNSCC).

According to one embodiment the present invention provides for a composition comprising the inventive antibody and at least one further pharmaceutically active ingredient.

In one embodiment the present invention provides a pharmaceutical comprising the inventive antibody as disclosed herein or which comprises the composition according to the invention and at least one further ingredient.

In one embodiment the present invention pertains to a method of treating a subject in need thereof inflicted with cancer, wherein the treatment comprises administering to said patient a therapeutically effective amount of the pharmaceutical composition according to to the invention.

BRIEF DESCRIPTON OF DRAWINGS

Figure 1: **a)** Transglutaminase-mediated conjugation of glutamine (Q) with an amine-donor substrate. **b)** Amino acid sequence of a natural transglutaminase recognition sequence taken from the substrate protein DAIP (1) and engineered sequences (2) and (3) used in this study for conjugation. **c)** Schematic depiction of the design of an engineered transglutaminase recognition sequence (MTGtag) mimicking the functional Q298 loop in DAIP.

Figure 2: MTG-mediated conjugation of engineered model peptides and fulllength monoclonal antibodies. a) Engineered model peptides 2 and 3 containing a transglutaminase recognition motif were biotinylated in MTG-catalyzed reaction with monobiotinylcadaverine (4, MBC). b) Biotinylation kinetics comparing conformationally constrained peptide 2 (○) (e.g. with an inventive peptide according to SEQ ID NO:4) with linear peptide 3 (•) (e.g. with inventive peptides according to SEQ ID NO:3 or SEQ ID NO:5). Error bars representing standard deviation were calculated from triplicates. SDS-PAGE gel and western blot analysis of biotinylated cetuximab variants with C-terminal MTG-tags (9: with inventive MTG-tag according to SEQ ID NO:90, 10: with inventive MTG-tag according to SEQ ID NO:246). Biotinylation was visualized using streptavidin-alkaline phosphatase conjugate and NBT/BCIP (right panel). d) Overview of cetuximab variants with C-terminal MTG-tags used for MTG-promoted biotinylation (7 and 8) and the respective conjugated antibodies (9 and 10).

Figure 3: Binding of biotinylated cetuximab studied in cell assays and by flow cytometry. **a)** Cell binding assays of biotinylated cetuximab variants 9 and 10 compared to cetuximab wt using EGFR-positive EBC-1 cells and EGFRnegative CHO-K1 cells (+MTG rx., middle and lower panels). Cells were mounted using ProLong® Diamond Antifade Mountant with DAPI (blue) and biotinylation visualized by

labelling with Streptavidin-AF488 (green). Cells were scanned using a confocal microscope. Merged pictures are shown with differential interference contrast (DIC). **b)** Flow cytometry of EGFR-positive EBC-1 cells incubated with biotinylated cetuximab variants 9. Cells bound to biotinylated cetuximab were fluorescence labelled by the addition of Streptavidin Alexa Fluor® 488 conjugate.

Figure 4: RP-HPLC analysis of transglutaminase-promoted biotinylation of oxidized peptide 2 (gradient 10 to 80%). Peak areas of 2 and 5 were analyzed and background subtracted.

Figure 5: Coomassie stained 15% SDS-PAGE gel analysis of purified cetuximab wildtype (lane 1) and cetuximab variants 7 and 8 (e.g. variant 7 corresponds to cetuximab according to the invention, which has been carboxyterminally fused to SEQ ID NO:90 and locked or constrained by a disulfide bridge, and variant corresponds to cetuximab carboxyterminally fused to SEQ ID NO:246 without disulfide bridge formation and not conformationally constrained. Antibodies were reduced in the presence of 2-mercaptoethanol prior to loading (2µg/lane). Prestained protein ladder (New England Biolabs) is indicating protein sizes in kDa.

Figure 6: Control experiment of transglutaminase-mediated cetuximab conjugation. **a)** Coomassie stained 15% SDS-PAGE gel analysis of transglutaminase-mediated conjugation of cetuximab wildtype with monobiotinyl cadaverine (MBC) in the presence of increasing concentration of the anionic surfactant N-lauroylsarcosin (LS), an agent described to release buried endo-glutamines from proteins making them accessible for tranglutaminase. **b)** Western-blot analysis of transglutaminase-mediated conjugation of cetuximab wildtype with monobiotinyl cadaverine (MBC) in the presence of increasing concentration of the anionic surfactant N-lauroylsarcosin (LS). Biotinylation was detected using streptavidin-alkaline phosphatase conjugate and NBT/BCIP. Prestained protein ladder (New England Biolabs) is indicating protein sizes in kDa.

Figure 7: Schematic representation of a heavy chain of 10 used for tryptic-digestion prior to MALDI-MS-analysis.

Figure 8: MALDI-TOF-MS spectra of trypsin digested heavy chain of 10.

Figure 9: MALDI-TOF-MS spectra of trypsin digested heavy chain of 10 in detail.

Figure 10: **(A)** Peptides derived from trypsin digestion were analyzed by using the bioinformatics tool GPMAW. Peptides modified by either carbamidomethyl

(CAM) at cysteine residues or monobiotinyl-cadaverine (MBC) at glutamine residues are underlined in cyan, peptides identified without modifications are underlined in magenta. **(B)** Statistical analysis of residue coverage indicating that a 56% coverage of the residues was achieved.

Figure 11: SDS-PAGE gel analysis of cetuximab wild-type (wt) and variants 9 and 10 comparing antibodies with C-terminal lysine from the wild-type sequence of cetuximab (+K447) and antibodies lacking this C-terminal lysine (-K447). Intramolecular cross-linking catalyzed by MTG has been observed in preliminary experiments between the MTG-tags and the C-terminal Lys residue from the wild-type sequence of cetuximab (+K447). This cross-linkage could be completely abolished by omitting this lysine (-K447).

Figure 12: Determination of antibody conjugation efficiency using TAMRA-cadaverine and fluorescence analysis.

Figure 13: Determination of free thiols in antibodies 7 and 8 using Ellman's reagent.

Figure 14: **(A)** Western Blot using streptavidin-AP, NBT/BCIP for the detection of biotinylated cetuximab. Arrows indicate the position of cetuximab (biotinylated) and of mTG2. (B) Coomassie stained protein gel with lanes loaded as indicated (C) fluorescence readout for the detection cetuximab comprising MTG-tag 1 (SEQ ID NO:90), or MTG-tag2 (SEQ ID NO:246) conjugated to fluorescent amino-donor substrates GGG-TAMRA or TAMRA-cadavarine.

Figure 15: Cytotoxic payloads with different primary amines used in transglutaminase-mediated conjugation reactions. (1) Monomethyl auristatin E (MMAE) with non-cleavable polyethylene glycol (PEG) linker and primary amino group, (2) Monomethyl auristatin E (MMAE) with cleavable valine-citrulline-p-aminobenzylcarbamate (vc-PABC) linker, PEG-spacer and primary amine, (3) Monomethyl auristatin E (MMAE) with cleavable valine-citrulline-p-aminobenzylcarbamate (vc-PABC) linker and aliphatic amino group, (4) Monomethyl auristatin F (MMAF) with cleavable valine-citrulline-p-aminobenzylcarbamate (vc-PABC) linker and aliphatic amino group.

Figure 16: Hydrophobic interaction chromatography (HIC) of antibody-drug-conjugates (ADCs) synthesized by catalysis of microbial transglutaminase (MTG). ADCs were generated by enzyme-mediated conjugation of cytotoxic payloads 1-4 as shown in Figure 15 to an IgG1 antibody (cetuximab) with a carboxy-terminal MTG-tag at each of its heavy chains. (A) Blank run, (B) Unconjugated antibody

control, (C) ADCs with a different drug-to-antibody ratio (DAR) obtained by conjugation to payload 1, (D) ADCs with a different drug-to-antibody ratio (DAR) obtained by conjugation to payload 2, (E) ADCs with a different drug-to-antibody ratio (DAR) obtained by conjugation to payload 3, (F) ADCs with a different drug-to-antibody ratio (DAR) obtained by conjugation to payload 4.

SEQUENCE LISTING

Sequences according to SEQ ID NO:1-SEQ ID NO:294 are according to the invention and may be used in in accordance with the embodiments of the present invention:

SEQ ID NO: 1	TYFQAYG
SEQ ID NO: 2	$X_1X_2X_3$ TYFQAYG $X_4X_5X_6$
SEQ ID NO: 3	X_1X_2C TYFQAYG NX_5X_6
SEQ ID NO: 4	X_1X_2C TYFQAYG CX_5X_6
SEQ ID NO: 5	X_1X_2N TYFQAYG NX_5X_6
SEQ ID NO: 6	X_1X_2N TYFQAYG CX_5X_6
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SEQ ID NO: 8	VDC TYFQAYG CSD
SEQ ID NO: 9	IDC TYFQAYG CSD
SEQ ID NO: 10	LDC TYFQAYG CSD
SEQ ID NO: 11	MDC TYFQAYG CSD
SEQ ID NO: 12	GDC TYFQAYG CSD
SEQ ID NO: 13	AEC TYFQAYG CSD
SEQ ID NO: 14	VEC TYFQAYG CSD
SEQ ID NO: 15	IEC TYFQAYG CSD
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SEQ ID NO: 17	MEC TYFQAYG CSD
SEQ ID NO: 18	GEC TYFQAYG CSD
SEQ ID NO: 19	ADC TYFQAYG NSD
SEQ ID NO: 20	VDC TYFQAYG NSD
SEQ ID NO: 21	IDC TYFQAYG NSD
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SEQ ID NO: 34	LDC TYFQAYG CSE
SEQ ID NO: 35	MDC TYFQAYG CSE
SEQ ID NO: 36	GDC TYFQAYG CSE
SEQ ID NO: 37	AEC TYFQAYG CSE
SEQ ID NO: 38	VEC TYFQAYG CSE
SEQ ID NO: 39	IEC TYFQAYG CSE
SEQ ID NO: 40	LEC TYFQAYG CSE
SEQ ID NO: 41	MEC TYFQAYG CSE
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SEQ ID NO: 81	IDC TYFQAYG CTE
SEQ ID NO: 82	LDC TYFQAYG CTE
SEQ ID NO: 83	MDC TYFQAYG CTE
SEQ ID NO: 84	GDC TYFQAYG CTE
SEQ ID NO: 85	AEC TYFQAYG CTE
SEQ ID NO: 86	VEC TYFQAYG CTE
SEQ ID NO: 87	IEC TYFQAYG CTE
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SEQ ID NO: 95	MDC TYFQAYG NTE
SEQ ID NO: 96	GDC TYFQAYG NTE
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SEQ ID NO: 127	ADC TYFQAYG CNE

SEQ ID NO: 128	VDC TYFQAYG CNE
SEQ ID NO: 129	IDC TYFQAYG CNE
SEQ ID NO: 130	LDC TYFQAYG CNE
SEQ ID NO: 131	MDC TYFQAYG CNE
SEQ ID NO: 132	GDC TYFQAYG CNE
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SEQ ID NO: 135	IEC TYFQAYG CNE
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SEQ ID NO: 293	MEN TYFQAYG NNE
SEQ ID NO: 294	GEN TYFQAYG NNE
SEQ ID NO: 295	GGGSLLQG
SEQ ID NO: 296	5'-TGGCTGAACGGCAAAGAGTAC
SEQ ID NO: 297	5'-CCTGAAAGTAGGTGCACTCGCCGCCAGGGCTCAGGGACAG
SEQ ID NO: 298	5'-CGGGGGATCCTCATTCGGTGCAGCCGTAGGCCTGAAAGTAGGTGCACTCG
SEQ ID NO: 299	5'-CTGAAAGTAGGTGTTCTCGCCGCCAGGGCTCAGGGACAG
SEQ ID NO: 300	5'-CGGGGGATCCTCATTCGGTATTGCCGTAGGCCTGAAAGTAGGTGTTCTCG
SEQ ID NO: 301	5'-$NNN_1NNN_2NNN_3$ACNTAYTTYCARGCNTAYGGN $NNN_4NNN_5NNN_6$
SEQ ID NO: 302	LPXTG, with X=D, E, A, N, Q, or K
SEQ ID NO:303	GGGYK

DETAILED DESCRIPTION OF THE INVENTION

Although the present invention is described in detail below, it is to be understood that this invention is not limited to the particular methodologies, protocols and reagents described herein as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims. Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art.

In the following, the elements of the present invention will be described. These elements are listed with specific embodiments, however, it should be understood that they may be combined in any manner and in any number to create additional embodiments. The variously described examples and preferred embodiments should not be construed to limit the present invention to only the explicitly described embodiments. This description should be understood to support and encompass embodiments which combine the explicitly described embodiments with any number of the disclosed and/or preferred elements. Furthermore, any permutations and combinations of all described elements in this application should be considered disclosed by the description of the present application unless the context indicates otherwise.

Throughout this specification and the claims which follow, unless the context requires otherwise, the term "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated member, integer or step but not the exclusion of any other non-stated member, integer or step. The term "consist of" is a particular embodiment of the term "comprise", wherein any other non-stated member, integer or step is excluded. In the context of the present invention, the term "comprise" encompasses the term "consist of".

The terms "a" and "an" and "the" and similar reference used in the context of describing the invention (especially in the context of the claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. Recitation of ranges of values herein is merely intended to serve as a shorthand method of referring individually to each separate value falling within the range. Unless otherwise indicated herein, each individual value is incorporated into the specification as if it were individually recited herein. No language in the specification should be construed as indicating any non-claimed element essential to the practice of the invention.

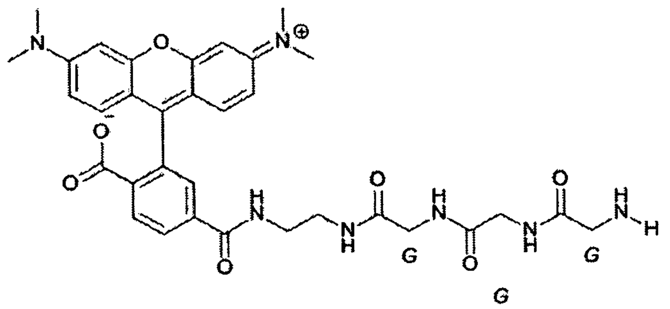
Several documents are cited throughout the text of this specification. Each of the documents cited herein (including all patents, patent applications, scientific publications, manufacturer's specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

The described objectives are solved by the present invention, preferably by the subject matter of the appended claims. More preferably, the present invention is solved according to a first embodiment by a protein which comprises at least one acyl glutamine-containing amino acid donor sequence covalently linked via a γ-glutamyl-amid bond to an amino donor-comprising substrate, wherein the at least one acyl glutamine-containing amino acid donor sequence comprises at least the amino acid sequence according to SEQ ID NO: 1 (SEQ ID NO: 1 (TYFQAYG)). Accordingly, the present invention provides for a protein which comprises at least one, e.g. 1, 2, 3, 4, 5, 6, 7, or 8, preferably 1-6 (e.g. 1, 2, 3, 4, 5, 6), more preferably 1-4 (e.g. 1, 2, 3, 4) acyl glutamine-containing amino acid donor sequences, whereby the at least one acyl glutamine-containing amino acid donor sequence according to the invention is covalently linked via a γ-glutamyl-amid bond to an amino donor-comprising substrate and wherein the at least one acyl glutamine-containing amino acid donor sequence comprises at least the amino acid sequence according to SEQ ID NO: 1 (TYFQAYG). The term "acyl glutamine-containing amino acid donor sequence" according to the invention pertains to an amino acid sequence, which is at least 7 amino acids in length, e.g. at least 7, 8, 9, 10, 11, 12, 13, 14, or 15 amino acids in length and which comprises at least the amino acid sequence according to SEQ ID NO:1. The acyl glutamine-containing amino acid donor sequence according to the invention may e.g. in addition the the amino acid sequence according to SEQ ID NO: 1 comprise natural or non-natural amino acids, or naturally occuring amino acid derivates. For example, the inventive acyl glutamine-containing amino acid donor sequence may comprise 1, 2, 3, 4, 5, 6, 7 or 8 non-natural amino acids, or naturally occuring amino acid derivates.

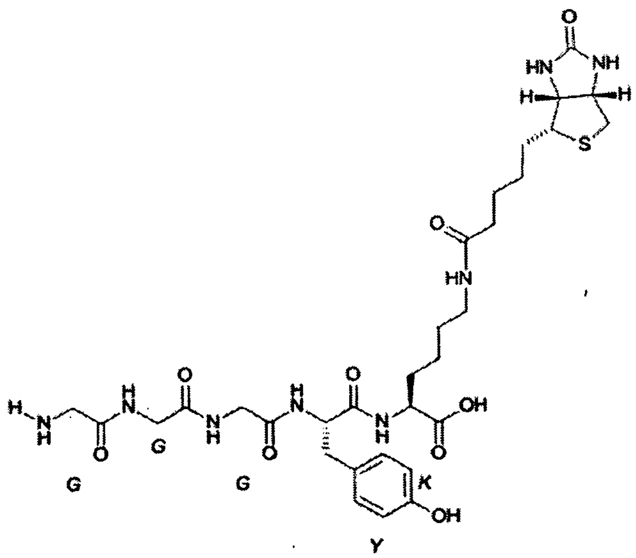
For example, non-natural amino acids which may be comprised in the acyl glutamine-containing amino acid donor sequence of the invention may include azidonorleucine, 3-(1-naphthyl)alanine, 3-(2-naphthyl)alanine, p-ethynyl-phenylalanine, p-propargyl-oxy-phenylalanine, m-ethynyl-phenylalanine, 6-ethynyl-tryptophan, 5-ethynyl-tryptophan, (R)-2-amino~3-(4-ethynyl-1 H-pyrrol-3-yl)propanoic acid, p-bromophenylalanine, p-idiophenylalanine, p-azidophenylalanine, 3-(6-chloroindolyl)alanine, 3-(6-bromoindoyl)alanine, 3-(5-bromoindolyl)alanine, azidohomoalanine, and p-chlorophenylalanine. For example, naturally occuring amino acid derivatives may include 4-hydroxyproline, ε-N,N,N-trimethyllysine, 3-methylhistidine, 5-hydroxylysine, O-phosphoserine, γ-carboxyglutamate, ε-N-acetyllysine, ω-N-methylarginine, N-acetylserine, N,N,N-trimethylalanine.

The term "γ-glutamyl-amid bond" according to the invention refers to an isopeptide bond, e.g. an amide bond, which does not form part of the peptide-bond backbone of the respective polypeptide or protein, which is formed between the gamma-carbon of the glutamyl residue of the inventive acyl glutamine-containing amino acid donor sequence and a primary (1°) amine of the amino donor-comprising substrate accoding to the invention.

According to one embodiment the amino donor-comprising substrate according to the invention comprises at least an ε-amino group or at least one tripeptide having the sequence of GGG with a primary aminoterminal amino group. For example, the amino donor-comprising substrate according to the invention may be lysine, such as L-lysine, or a lysine derivative, or structural mimetics therof, such as e.g. diaminobutyric acid (DAB), 2,3-diaminopropanoic acid, (2S)-2,8-diaminooctanoic acid, ornithinem, thialysine, 1,5-diaminopentane, or N-(biotinyl)cadaverine. The amino donor-comprising substrate according to the invention may e.g. also comprise lysine derivatives which have been coupled to a dye (e.g. TAMRA, or Alexa-Fluor® dyes), or other molecule such as e.g. biotin. The amino donor-comprising substrate according to the invention may e.g. also be a GGG tripeptide, which e.g. may further be coupled to a dye or molecule, such as TAMRA-ethylenediamine or biotin, e.g. :



or e.g. :



In one embodiment the amino donor-comprising substrate according to the invention may e.g. also include polypeptides comprising at least one lysine residue.

According to one embodiment the amino donor-comprising substrate of the invention is covaently bound to a further molecule. For example, the amino donor-comprising substrate according to the invention as disclosed above, such as the tripeptide as disclosed above, may be covalently bound to a further molecule, preferably via its carboxyterminus. For example, the further molecule may be covelently bound via a peptide bond, isopeptide bond, or any other covalent bond, such as e.g. a disulfide bond.

According to one embodiment the further molecule according to the invention as disclosed above is one of a dye, radioisotope, drug, ribozyme, nanobody, enzyme, or linker. For example, a dye which may be covalently bound to the amino donor-comprising substrate according to the invention may be a fluorophore. Accordingly, the amino donor-comprising substrate according to the invention may be covalently bound to a fluorophore. The term "fluorophore" as used in the present invention refers to a chemical compound, which when excited by exposure to a particular wavelength of light, emits light at a different wavelength, e.g. fluorophores that may be covalently bound to the amino donor-comprising substrate according to the invention may include 1,8-ANS, 4-methylumbelliferone, 7-amino-4-methylcoumarin, 7-hydroxy-4-methylcoumarin, Acridine, Alexa Fluor 350™, Alexa Fluor 405™, AMCA, AMCA-X, ATTO Rho6G, ATTO Rho11, ATTO Rho12, ATTO Rho13, ATTO Rho14, ATTO Rho101, Pacific Blue, Alexa Fluor 430™, Alexa Fluor 480™, Alexa Fluor 488™, BODIPY 492/515, Alexa Fluor 532™, Alexa Fluor 546™, Alexa Fluor 555™, Alexa Fluor 594™, BODIPY 505/515, Cy2, cyQUANT GR, FITC, Fluo-3, Fluo-4, GFP (EGFP), mHoneydew, Oregon Green™ 488, Oregon Green™ 514, EYFP, DsRed, DsRed2, dTomato, Cy3.5, Phycoerythrin (PE), Rhodamine Red, mTangerine, mStrawberry, mOrange, mBanana, Tetramethylrhodamine (TRITC), R-Phycoerythrin, ROX, DyLight 594, Calcium Crimson, Alexa Fluor 594™, Alexa Fluor 610™, Texas Red, mCherry, mKate, Alexa Fluor 660™, Alexa Fluor 680™ allophycocyanin, DRAQ-5, carboxynaphthofluorescein, C7, DyLight 750, Cellvue NIR780, DM-NERF, Eosin, Erythrosin, Fluorescein, FAM, Hydroxycoumarin, IRDyes (IRD40, IRD 700, IRD 800), JOE, Lissamine rhodamine B, Marina Blue, Methoxy coumarin, Naphtho fluorescein, PyMPO, 5-carboxy-4',5'-dichloro-2',7'-dimethoxy fluorescein, 5- carboxy-2',4',5',7'-tetrachlorofluorescein, 5-carboxyfluorescein, 5-carboxyrhodamine, 6- carboxyrhodamine, 6-carboxytetramethyl amino, Cascade Blue, Cy2, Cy3, Cy5,6-FAM, dansyl chloride, HEX, 6-JOE, NBD (7-nitrobenz-2-oxa-l,3-diazole), Oregon Green 488, Oregon Green 500, Oregon Green 514, Pacific Blue, phthalic acid, terephthalic acid, isophthalic acid, cresyl fast violet, cresyl blue violet, brilliant cresyl blue, para- aminobenzoic acid, erythrosine, phthalocyanines, azomethines, cyanines, xanthines, succinylfluoresceins, rare earth metal cryptates, europium trisbipyridine diamine, a europium cryptate or chelate, diamine, dicyanins, or La Jolla blue dye. Fluorophores according to the invention may e.g. also include quantum dots. The term quantum dot as used in the present invention refers to a single spherical nanocrystal of semiconductor material where the radius of the nanocrystal is less than or equal to the size of the exciton Bohr radius for that semiconductor material (the value for the exciton Bohr radius can be calculated from data found in handbooks containing information on semiconductor properties, such as the CRC Handbook of Chemistry and Physics, 83rd ed., Lide, David R. (Editor), CRC Press, Boca Raton, Fla. (2002)). Quantum dots are known in the art, as they are described in references, such as Weller, Angew. Chem. Int. Ed. Engl. 32: 41-53 (1993), Alivisatos, J. Phys. Chem. 100: 13226-13239 (1996), and Alivisatos, Science 271: 933-937 (1996). Quantum dots may e.g. be from about 1 nm to about 1000 nm diameter, e.g. 10nm, 20 nm, 30 nm, 40 nm, 50 nm, 60 nm, 70 nm, 80 nm, 90 nm, 100 nm, 150 nm, 200 nm, 250 nm, 300 nm, 350 nm, 400 nm, 450 nm, or 500 nm, preferably at least about 2 nm to about 50 nm, more preferably QDs are at least about 2 nm to about 20 nm in diameter (for example about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nm). QDs are characterized by their substantially uniform nanometer size, frequently exhibiting approximately a 10% to 15% polydispersion or range in size. A QD is capable of emitting electromagnetic radiation upon excitation (i.e., the QD is photoluminescent) and includes a "core" of one or more first semiconductor materials, and may be surrounded by a "shell" of a second semiconductor material. A QD core surrounded by a semiconductor shell is referred to as a "core/shell" QD. The surrounding "shell" material will preferably have a bandgap energy that is larger than the bandgap energy of the core material and may be chosen to have an atomic spacing close to that of the "core" substrate. The core and/or the shell can be a semiconductor material including, but not limited to, those of the groups II-VI (ZnS, ZnSe, ZnTe, US, CdSe, CdTe, HgS, HgSe, HgTe, MgS, MgSe, MgTe, CaS, CaSe, CaTe, SrS, SrSe, SrTe, BaS, BaSe, BaTe, and the like) and III-V (GaN, GaP, GaAs, GaSb, InN, InP, InAs, InSb, and the like) and IV (Ge, Si, and the like) materials, PbS, PbSe, and an alloy or a mixture thereof. Preferred shell materials include ZnS. Quantum dots may be coupled to the inventive linker, enzyme, or protein by any method known in the art such as e.g. the methods disclosed in Nanotechnology. 2011 Dec 9;22(49):494006; Colloids and Surfaces B: Biointerfaces 84 (2011) 360–368.

According to one embodiment the amino donor-comprising substrate of the invention may be covalently bound to a radioisotope such as e.g. ^{47}Ca, ^{14}C, ^{137}Cs, ^{157}Cr, ^{57}Co, ^{60}Co, ^{67}Cu, ^{67}Ga, ^{123}I, ^{125}I, ^{129}I, ^{131}I, ^{32}P, ^{75}Se, ^{85}Sr, ^{35}S, ^{201}Th, ^{3}H, preferably, the radioisotopes are incorporated into a further moelcule, such as e.g. a chelator. Typical chelators that may e.g. be used as a further molecule covalently bound to the amino donor-comprising substrate of the invention are DPTA, EDTA (Ethylenediamine-tetraacetic acid), EGTA (Ethyleneglycol-O, O'-bis(2-aminoethyl)-N, N, N', N'-tetraacetic acid, NTA (Nitrilotriacetic acid), HEDTA (N-(2-Hydroxyethyl)-ethylenediamine-N,N',N'-triacetic acid), DTPA (2-[Bis[2-[bis(carboxymethyl)amino]-ethyl]amino]acetic acid), or DOTA (1,4,7,10-tetraazacyclo-dodecane-1,4,7,10-tetraacetic acid).

For example, in one embodiment the amino donor-comprising substrate according to the invention may be covalently bound to a drug. The term "drug" as used in the present invention refers to any chemical compound or molecule which interferes with the physiological function of a cell, e.g. a cancer or tumor cell. Drugs which may be linked to the amino donor-comprising substrate according to the invention may include cytostatic agents, or cytotoxic agents. For example, cytostatic agents that may be used for covalent coupling to the amino donor-comprising substrate according to the invention include alkylating agents, antimetabolites, antibiotics, mitotic inhibitors, hormones, or hormone antagonists. Alkylating agents may e.g. include Busulfan (Myleran), Carboplatin (Paraplatin), Chlorambucil, Cisplatin, Cyclophosphamide (Cytoxan), Dacarbazine (DTIC-Dome), Estramustine Phosphate, Ifosphamide, Mechlorethamine (Nitrogen Mustard), Melphalan (Phenylalanine Mustard), Procarbazine, Thiotepa, Uracil Mustard, antimetabolites may e.g. include Cladribine, Cytarabine (Cytosine Arabinoside), Floxuridine (FUDR, 5-Fluorodeoxyuridine), Fludarabine, 5-Fluorouracil (5FU), Gemcitabine, Hydroxyurea, 6-Mercaptopurine (6MP), Methotrexate (Amethopterin), 6-Thioguanine, Pentostatin, Pibobroman, Tegafur, Trimetrexate, Glucuronate, antibiotics may e.g. include Aclarubicin, Bleomycin, Dactinomycin (Actinomycin D), Daunorubicin, Doxorubicin (Adriamycin), Epirubicin, Idarubicin, Mitomycin C, Mitoxantrone, Plicamycin (Mithramycin), or mitotic inhibitors may e.g. include Etoposide (VP-16, VePesid), Teniposide (VM-26, Vumon), Vinblastine, Vincristine, Vindesine, hormones, or hormone antagonists which may e.g. be used include Buserelin, Conjugate Equine Estrogen (Premarin), Cortisone, Chlorotriansene (Tace), Dexamethasone (Decadron), Diethylstilbestrol (DES), Ethinyl Estradiol (Estinyl), Fluoxymesterone (Halotestin), Flutamide, Goserelin Acetate (Zoladex), Hydroxyprogesterone Caproate (Delalutin), Leuprolide, Medroxyprogesterone Acetate (Provera), Megestrol Acetate (Megace), Prednisone, Tamoxifen (Nolvadex), Testolactone (Teslac), Testosterone. Cytostatic or antineoplastic compounds such as those disclosed above are known in prior art and may e.g. be found in D. S. Fischer & T. M. Knobf (1989), The cancer chemotherapy handbook (3rd ed.). Chicago: Year Book Medical and Association of Community Cancer Centers (Spring, 1992), Compendia-based drug bulletin, Rockville, MD.

For example, in one embodiment the amino donor-comprising substrate according to the invention may be covalently bound to an enzyme, such as L-Asparaginase.

According to one embodiment the amino donor-comprising substrate of the invention may e.g. be covalently bound to a ribozyme or nanobody. The term "ribozyme" as used in the present invention refers to an enzymatically active RNA molecule having trans-splicing activity and self-splicing activity. For the purpose of the present invention, the ribozyme can serve to inhibit the activity of the cancer-specific gene by a trans-splicing reaction, thereby exhibiting a selective anticancer effect. Any ribozyme may be used in the present invention, as long as it can inactivate a cancer-specific gene and activate the cancer therapeutic gene.

In one embodiment the amino donor-comprising substrate of the invention may e.g. be covalently bound to a nanobody. As used herein, the term "nanobody" refers to an antibody comprising a small single variable domain such as e.g. VHH of antibodies obtained from camelids and dromedaries, e.g. *Camelus baclrianus* and *Calelus dromaderius* including new world members such as llama species (*Lama paccos, Lama glama* and *Lama vicugna*). Antibodies from the species have been characterized with respect to size, structural complexity and antigenicity for human subjects. Certain IgG antibodies from this family of mammals as found in nature lack light chains, and are thus structurally distinct from the typical four chain quarternary structure having two heavy and two light chains, for antibodies from other animals (see e.g. WO94/04678, Hamers-Casterman C, Nature 363: 446–448; Harmsen (2007) Appl Microb Biotechnol 77: 13–22).

According to one embodiment the amino donor-comprising substrate of the invention may e.g. be covalently bound to a linker. The term "linker" or "linker peptide" refers to a synthetic or artifical amino acid sequence that connects or links two molecules, such as e.g. two polypeptide sequences that link two polypeptide domains, or e.g. a protein and a cytostatic drug, or toxin. The term "synthetic" or "artifical" as used in the present invention refers to amino acid sequences that are not naturally occurring.

According to one embodiment the linker which is covalently bound to the amino donor-comprising substrate of the invention is cleavable or non-cleavable. The term "cleavable" as used in the present invention refers to linkers which may be cleaved by proteases, acids, or by reduction of a disulfide body (e.g. glutathion-mediated or glutathion sensitive). For example, cleavable linkers may comprise valine-citrulline linkers, hydrazone linkers, or disulfide linkers.. Non-cleavable linkers which may e.g. be covalently bound to the amino donor-comprising substrate of the invention comprise maleimidocaproyl linker to MMAF (mc-MMAF), N-maleimidomethylcyclohexane-1-carboxylate (MCC), or mercapto-acetamidocaproyl linkers.

According to one embodiment the linker according to the invention is coupled or covalently bound to a dye, radioisotope, or cytotoxin. Accordingly, the linker according to the invention which is covalently bound to the amino donor-comprising substrate of the invention may be e.g. coupled or covalently bound to a dye, radioisotope, or cytotoxin. The term "coupled" as used for the linker according to the invention refers to the fact that the dye, radioisotope or cytoxin is non-covalently attached to the linker molecule according to the invention, e.g. via ionic, or hydrophobic interctions. For example, the linker may comprise streptavidin and the dye, radioisotope or cytotoxin may be covalently bound to biotion. For example, in case of radioisotopes, the radioisotope may be chelated to one of the chelators as disclosed above, which may be covalently bound to biotion. Alternatively, the radioisotope may e.g. be incorporated into the biotin, e.g. [8,9-3H]biotin (see e.g. Robinson et al., J Biol Chem. 1983 May 25;258(10):6660-4.).

Preferably, the linker may e.g. be covalently bound to a cytotoxin, which may e.g. also be referred to as "payloads" (see e.g. Perez et al. Drug Discovery Today Vol 19 (7), July 2014).

Cytotoxins which are suited for covalent attachment to linker molecules include those e.g. disclosed above and may be grouped into two main classes: The first class includes cytotoxins which disrupt microtubule assembly and the second class cytotoxins which target DNA structure. Accordingly, cytotoxins which may e.g. be covalently bound to the linker according to the invention include doxorubicin, calicheamicin, auristatin, maytansine duoarmycin and analogs thereof, α-amaitin, tubulysin and analogs thereof. Methods for covalently attaching cytotoxins to linkers are known in the art and may e.g. be done according to the method disclosed in Mol. Pharmaceutics 2015, 12, 1813–1835. Accordingly, the amino donor-comprising substrate of the invention which is coupled to a cleavable or non-cleavable linker as disclosed above and which are further coupled to a cytotoxin as disclosed above, may e.g. be used in transglutaminase-mediated bioconjugation reations,preferably, the bioconjugation reaction is catalyzed by mTG2. The bioconjugation reaction may e.g. include at least one acyl glutamine-containing amino acid donor sequence substrate according to the invention as disclosed above comprising at least the amino acid sequence according to SEQ ID NO:1 (TYFQAYG) and the amino donor-comprising substrate of the invention as disclosed above in the presence of mTG2 under conditions which allow the mTG2 catalyzed reaction.

According to one embodiment the acyl glutamine-containing amino acid donor sequence of the invention comprises an amino acid sequence according to SEQ ID NO: 2 ($X_1X_2X_3$ TYFQAYG $X_4X_5X_6$), wherein

X_1 is a hydrophobic amino acid,
X_2 is a negatively charged amino acid,
X_3 is C or N,
X_4 is C or N,
X_5 is one of an amino acid with with a polar, uncharged side chains, and X_6 is a negatively charged amino acid.

Accordingly, in the acyl glutamine-containing amino acid donor sequence of the invention X_1 may comprise any one of the amino acids A, I, L, M, F, W, Y, V, X_2 may comrise the amino acids D, E, X_3, X_4 may be one of C or N, X_5 may be one of S, T, N or Q and X_6 may be one of D, or E. Accordingly, the acyl glutamine-containing amino acid donor sequence of the invention may comprise an amino acid sequence according to any one of SEQ ID NO:1 – SEQ ID NO:294, e.g. the acyl glutamine-containing amino acid donor sequence of the invention may comprise any one of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28,

SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO: 139, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 147, SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 151, SEQ ID NO: 152, SEQ ID NO: 153, SEQ ID NO: 154, SEQ ID NO: 155, SEQ ID NO: 156, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 182, SEQ ID NO: 183, SEQ ID NO: 184, SEQ ID NO: 185, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID

NO: 226, SEQ ID NO: 227, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 231, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 234, SEQ ID NO: 235, SEQ ID NO: 236, SEQ ID NO: 237, SEQ ID NO: 238, SEQ ID NO: 239, SEQ ID NO: 240, SEQ ID NO: 241, SEQ ID NO: 242, SEQ ID NO: 243, SEQ ID NO: 244, SEQ ID NO: 245, SEQ ID NO: 246, SEQ ID NO: 247, SEQ ID NO: 248, SEQ ID NO: 249, SEQ ID NO: 250, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 254, SEQ ID NO: 255, SEQ ID NO: 256, SEQ ID NO: 257, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, SEQ ID NO: 261, SEQ ID NO: 262, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 266, SEQ ID NO: 267, SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 273, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 277, SEQ ID NO: 278, SEQ ID NO: 279, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294.

According to one embodiment in the acyl glutamine-containing amino acid donor sequence of the invention X_1 may comprise any one of the amino acids A, V, I, L, M or G, X_2 may comprise the amino acids D, E, X_3 may be C, X_4 may be C or N, X_5 may be one of S, T, or N and X_6 may be one of D, or E. Accordingly, the acyl glutamine-containing amino acid donor sequence of the invention may comprise an amino acid sequence according to any one of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150.

According to a preferred embodiment the acyl glutamine-containing amino acid donor sequence of the invention comprises an amino acid sequence according to SEQ ID NO:4 (X_1X_2 C TYFQAYG CX_5X_6) in which both X_3 and X_4 are C such that a disulfide bond may be formed between the two cysteine residues X3 and X4 which will form a loop-like structure, with amino residues TYFQAG forming the loop-like structure. In the inventive acyl glutamine-containing amino acid donor sequence X_1 may be any one of the amino acids A, V, I, L, M or G, X_2 may be D, or E, X_3 and X_4 are both C, X_5 may be one of S, T or N and X_6 may be one of the amino acids D, or E. Accordingly, the acyl glutamine-containing amino acid donor sequence of the invention may comprise an amino acid sequence according to any one of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138.

The peptides of the invention may be synthesized according to any known method in the art, e.g. according to the methods disclosed in Atherton, E.; Sheppard, R.C. (1989). Solid Phase peptide synthesis: a practical approach. Oxford, England: IRL Press. ISBN 0-19-963067-4, or Stewart, J.M.; Young, J.D. (1984). *Solid phase peptide synthesis* (2nd ed.), ISBN 0-935940-03-0). Peptides may e.g. also be synthesized on an AmphiSpheres 40 RAM resin (Agilent, 0.27 mmol/g) by microwave-assisted Fmoc-SPPS using a Liberty Blue™ Microwave Peptide Synthesizer at a 0.1 mmol scale. Activation of the respective carboxyfunctional amino acid may e.g. be performed by Oxyma/ *N,N'*-Diisopropylcarbodiimide (DIC). Deprotection of the aminoterminal Fmoc-group may e.g. be done using 20% piperidine in DMF in the presence of Oxyma. During the synthesis cycles all amino acids may e.g. be heated to 90°C (cysteines to 50°C). Peptides may then e.g. cleaved from the resin by a standard cleavage cocktail of 94% TFA, 2% triethylsilane, 2% anisole, 2% H_2O. For example, upon synthesis of the acyl glutamine-containing amino acid donor peptide according to SEQ ID NO:4, under non-oxidative synthesis and cleavage conditions, such as e.g. in the presence of dithiotreitol (DTT) in a concentration of e.g. from about 1mM to about 50mM, or from about 10mM to about 40mM. Dislufide bridge formation between residues X_3 and X_4 may be achieved under oxidizing conditions, e.g. 1 mg ml^{-1} in 100 mM $(NH_4)_2CO_3$ aq. pH 8.4, whereby the oxidatoin reation may be monitored by RP-HPLC.

In a more preferred embodiment in the acyl glutamine-containing amino acid donor sequence of the invention X_1 may be any one of amino acids A, V, I, L, M or G, X_2 is E, X_3, X_4 are both C, X_5 is T and X_6 is E. Accordingly, the acyl glutamine-containing amino acid donor sequence of the invention may comprise any one of SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, or SEQ ID NO:90.

According to a more preferred embodiment, in the acyl glutamine-containing amino acid donor sequence of the invention comprises the amino acid sequence according to SEQ ID NO:90 (GECTYFQAYGCTE).

The acyl glutamine-containing amino acid donor sequence according to the invention as disclosed above may e.g. be covalently bound to a protein of interest, such as e.g. enzymes or antibodies. For example, polynucleotides encoding the acyl glutamine-containing amino acid donor sequence of the invention may be added to cDNA constructs encoding light or heavy chains of antibodies by way of polymerase chain reaction (PCR). For example, SOE-PCR may be used according to the principle disclosed in PCR Methods Appl. 1993 May;2(4):301-4, or e.g. in Critical Reviews in Oral Biology and Medicine, 4(3/4):581-590 (1993).

In one embodiment the protein comprising the acyl glutamine-containing amino acid donor sequence according to the invention as disclosed above may be an antibody, antigen-binding antibody fragment, Fc domain, enzyme, a non-immunoglobulin scaffold. Accordingly, the acyl glutamine-containing amino acid donor sequence of the invention may be covalently bound to an antibody, antigen-binding fragment, Fc domain, enzyme, a non-immunoglobulin scaffold.

For example, the protein according to the invention comprising the inventive acyl glutamine-containing amino acid donor sequence may be an antibody, whereby the term “antibody” refers to an immunoglobulin molecule capable of specific binding to a target, such as a carbohydrate, polynucleotide, lipid, polypeptide, etc., through at least one antigen recognition site, located in the variable region of the immunoglobulin molecule. As used in the present invention, the term “antibody” encompasses not only intact polyclonal or monoclonal antibodies, but also, unless otherwise specified, any antigen binding fragment thereof that competes with the intact antibody for specific binding, fusion proteins comprising an antigen binding portion, any other modified configuration of the immunoglobulin molecule that comprises an antigen recognition site, antibody compositions with polyepitopic specificity, multispecific antibodies (e.g., bispecific antibodies).

The term “monoclonal antibody" as used for the protein according to the invention refers to antibodies displaying a single binding specificity and indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma (e.g. murine or human) method first described by Köhler et at., Nature, 256:495 (1975), or may be made by recombinant DNA methods (see, e.g., U.S. Pat.No.4,816,567). A "monoclonal antibody" may also be isolated from phage antibody libraries using the techniques described in Clackson et at., Nature, 352:624-628 (1991) and Marks et at., J. Mol. Biol., 222:581-597 (1991).

The term “human monoclonal antibodies” as used for the protein according to the invention refers to monoclonal antibodies, which have variable and constant regions derived from human germline immunoglobulin sequences. The term “humanized” as used in the context of the present invention preferably refers to a monoclonal antibody in which the amino acid sequence is essentially identical to that of a human variant, despite the non-human origin of some of its complementarity determining region (CDR) segments responsible for the ability of the antibody to bind to its target antigen. The term “chimeric monoclonal antibody” as used in the present invention refers to a monoclonal antibody in which murine Fab fragments are spliced to human Fc.

In one embodiment the protein according to the invention as disclosed above is an antigen-binding fragment. The term “antigen binding fragement” as used for the inventive protein refers to, for example, Fab, Fab’, $F(ab')_2$, Fd, Fv, domain antibodies, also referred to as “nanobodies” (dAbs, or VHH, e.g., shark and camelid antibodies, see e.g. mAbs (2015) 7:1, 15-25; Current Opinion in Structural Biology 2015, 32:1–8), fragments including complementarity determining regions (CDRs), single chain variable fragment antibodies (scFv), maxibodies, minibodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv, and polypeptides that contain at least a portion of an immunoglobulin that is sufficient to confer specific antigen binding to the polypeptide. A "bispecific antibody" as used according to the invention is an antibody that can bind two different target molecules, "bivalent antibody" as according to the invention is an antibody that can bind two different sites of one target molecule. The term "scFv" as used in the present invention refers to a molecule comprising an antibody heavy chain variable domain (or region; VH) and an antibody light chain variable domain (or region; VL) connected by a linker, and lacks constant domains. For example, the inventive protein may be a nanobody which comprise the acyl glutamine-containing amino acid donor sequence according to the invention, e.g. fused to the carboxyterminus of the nanobody. The nanobody according to the invention may then e.g. be used in a mTG2-mediated bioconjugation, whereby the amino donor-comprising substrate may e.g. be further coupled to a linker-cytotoxin as disclosed above, or may e.g. be further coupled to a radioisotope, or dye as disclosed above. The nanobodies of the invention may e.g. be used for cancer treatment, or imaging purposes. For example, nanobodies of the invention coupled to ^{68}Ga which specifically bind EGFR, or HER2, may be used for Pet imaging to detect or image EGFR or HER2 expressing tumors. The term "specific binding" or any grammatical variation thereof refers to the ability of the inventive antibody, antigen-binding fragment (e.g. Fab, Fab', F(ab')$_2$, Fd, Fv), monoclonal antibody, single-chain antibody (scFv) or nanobody to bind to bind to its respective target (e.g. EGFR, or HER2) with an K_D of at least about 1 x 10^{-6} , e.g. 1 x 10^{-6} M, 1 x 10^{-7} M, 1 x 10^{-8} M, 1 x 10^{-9} M, 1 x 10^{-10} M, 1 x 10^{-11}M, 1 x 10^{-12} M, 1 x 10^{-13} M, 1 x 10^{-14} M, 1 x 10^{-15} M, preferably between 1 x 10^{-10} M and 1 x 10^{-15} M, more preferably between about 1x10^{-12}M to about 1x10^{-15}M.

The term "immunoglobulin" (Ig) as used in the present invention may be used interchangeably with the term "antibody". The basic 4-chain antibody unit is a heterotetrameric glycoprotein composed of two identical light (L) chains and two identical heavy (H) chains. An IgM antibody consists of 5 of the basic heterotetramer units along with an additional polypeptide called a J chain, and contains 10 antigen binding sites, while IgA antibodies comprise from 2-5 of the basic 4-chain units which can polymerize to form polyvalent assemblages in combination with the J chain. In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to an H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each H and L chain also has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable domain (V_H) followed by three constant domains (C_H) for each of the α and γ chains and four CH domains for μ and ε isotypes. Each L chain has at the N-terminus, a variable domain (VL) followed by a constant domain at its other end. The VL is aligned with the VH and the CL is aligned with the first constant domain of the heavy chain (C_{H1}). Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains. The pairing of a VH and VL together forms a single antigen-binding site. For the structure and properties of the different classes of antibodies, see e.g., Basic and Clinical Immunology, 8th Edition, Daniel P. Sties, Abba I. Terr and Tristram G. Parsolw (eds), Appleton & Lange, Norwalk, CT, 1994, page 71 and Chapter 6. The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (CH), immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG and IgM, having heavy chains designated α, δ, ε, γ and μ, respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in the CH sequence and function, e.g., humans express the following subclasses: IgG1, IgG2A, IgG2B, IgG3, IgG4, IgA1 and Igκ1. IgG comprises the major class as it normally exists as the second most abundant protein found in plasma. In immunoglobulin fusion proteins, Fc domains of the IgG1 subclass are often used as the immunoglobulin moiety, because IgG1 has the langest serum half-life of any of the serum proteins. The Fc moiety may, e.g., also comprise Fc variants such as those disclosed in WO 02/094852 (e.g. Fc amino acid sequence with variants Fc-488, Fc4, Fc5, Fe6, Fc7, and Fc8 as disclosed therein) to reduce effctor function of the Fc moeity.

For example, the protein according to the invention may be a fusion protein comprising the the acyl glutamine-containing amino acid donor sequence according to the invention and a Fc domain to extend its serum half-life, whereby the the acyl glutamine-containing amino acid donor sequence according to the invention is fused to the carboxyterminus of the Fc moiety. The terminal lysine (K) residue may e.g. be removed in Fc moieties e.g. in IgG-type antibodies, or in Fc-fusion proteins, by PCR-based site-directed mutagenesis to avoid intermolecular crosslinking. PCR-based site-directed mutagenesis may e.g. be done according to the method disclosed in Nucleic Acids Res. 1989 Aug 25;17(16):6545-51, Biotechniques. 1993 Oct;15(4):700-4, Nucl. Acids Res., 32:e115, 2004 For example, primer pairs which may be used for the site-directed mutagenesis may e.g. also be selected according to the the web-based automated tool available at: http://bioinformatics.org/primerx. Alternatively, the corresponding cDNAs which encode the protein according to the invention lacking a terminal lysine residue may be obtained by custom gene synthesis (see e.g. Nature 432, 1050-1054 (23 December 2004); Nucleic Acids Res. 2007 Apr; 35(8): e61.; ACS Synth. Biol. 3, 97–106 (2014); Nat. Methods 6, 343–345 (2009); Nucleic Acids Res. 40, e55 (2012); Proc. Natl. Acad. Sci. USA 105, 20404–20409 (2008)).

In one embodiment the protein according to the invention is a non-immunoglobulin scaffold comprising the inventive acyl glutamine-containing amino acid donor sequence. The term non-immunoglobulin scaffold as used for the protein according to the invention refers to affinity proteins that are not based on Ig molecules. Non-immunoglobulin scaffold proteins include e.g. those disclosed in Nature Biotechnology 23, 1257-1268, 2005, Trends Biotechnol. 2015 Jul;33(7):408-18. For example, the protein according to the invention may be an albumin binding domain, phytocystaton protein (Adhiron), adnectin, Z-domain of S. aureus protein A, γ-B-crystallin (affilin), stefin A, DNA-binding protein Sac7a, alphabodym lipocalins (anticalins), or homologs of β-catenin (e.g. armadillo protein). For example, the protein according to the invention as disclosed herein may comprise the inventive acyl glutamine-containing amino acid donor sequence, whereby the inventive acyl glutamine-containing amino acid donor sequence may be present at the aminoterminus or at the carboxyterminus of the protein according to the invention. A determining factor in positioning the acyl glutamine-containing amino acid donor sequence of the invention to the amino- or carboxyterminus of the inventive protein as diclosed above is whether or not it will interfere with the intended use of the protein. For example, in case the protein according to the invention is an antibody, e.g. a monoclonal antibody, carboxyterminal fusion proteins with the inventive acyl glutamine-containing amino acid donor sequence are preferred, whereby the acyl glutamine-containing amino acid donor sequence according to SEQ ID NO:2 may be fused to the light chain, or heavy chain, or both heavy and light chain, thereby providing an monoclonal antibody comprising 2 (e.g. on both light chains (LCs), or on both heavy chains (HCs)) or 4 acyl glutamine-containing amino acid donor sequences according to the invention.

In one embodiment the present invention provides for a method of covalently coupling an amino donor-comprising substrate according to the invention as disclosed above to a acyl glutamine-containing amino acid donor of the invention which comprises a polypeptide sequence according to SEQ ID NO:2, whereby the method comprises the step of:

Contacting the amino donor-comprising substrate according to the invention and the acyl glutamine-containing amino acid donor according to the invention in the presence of transglutaminase, preferably mTG2, to obtain the inventive protein as disclosed above. Accordingly, in the inventive method the amino donor-comprising substrate according to the invention as disclosed above and the acyl glutamine-containing amino acid donor according to the invention, e.g. any of SEQ ID NO:7-294 as disclosed herein, are contacted in the presence of mTG2 to obtain the inventive protein as disclosed above. The term "contacted" as used in the inventive method refers to any situation in which two or more molecules, such as the amino donor-comprising substrate and the acyl glutamine-containing amino acid donor in accordance with the invention, are brought into intimate physical contact with one another, e.g. form part of the same reaction mixture or aqueous solution. For example, the mTG2-mediated reaction according to the inventive method may comprise reacting the acyl glutamine-containing amino acid donor according to the invention with an 1-60 molar equivalent, or 1-50 molar equivalent of the amino donor-comprising substrate according to the invention, e.g. with an 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 molar equivalent, or e.g. with a molar equivalent of about 2 molar to about 45molar , from about 5 molar to about 40 molar, from about 10 molar to about 35 molar, from about 12.5 molar to about 30 molar, from about 15 molar to about 32.5 molar, from about 7.5 molar to about 27.5 molar, from about 17.5 molar to about 25molar, from about 0.5 molar to about 1 molar. The concentration of the acyl glutamine-containing amino acid donor according to the invention may be from about 0.1 mg/ml to about 100 mg/ml, e.g. from aboput 0.5mg/ml to about 75 mg/ml, from about 1mg/ml to about 50 mg/ml, from about 2.5 mg/ml to about 45 mg/ml, from about 5mg/ml to about 40 mg/ml, from about 10 mg/ml to about 35 mg/ml, from about 12.5 mg/ml to about 30 mg/ml, from about 15 mg/ml to about 25 mg/ml, from about 17.5 to about

20 mg/ml, e.g. 0.15 mg/ml, 0.2 mg/ml, 0.25mg/ml, 0.3mg/ml, 0.35 mg/ml, 0.4mg/ml, 0.45 mg/ml , 0.5 mg/ml, 0.55 mg/ml, 0.6 mg/ml, 0.7 mg/ml, 0.8 mg/ml, 0.9 mg/ml, 2 mg/ml, 3 mg/ml, 4, mg/ml, 6 mg/ml, 7 mg/ml, 8 mg/ml, 9 mg/ml, 11 mg/ml, 12 mg/ml, 13 mg/ml, 14 mg/ml, 16 mg/ml, 19 mg/ml, 23 mg/ml, 27 mg/ml, 31 mg/ml, 33 mg/ml, 37.5 mg/ml, 41 mg/ml, 42 mg/ml, 43 mg/ml, 44 mg/ml, 46 mg/ml, 47 mg/ml, 48 mg/ml, 49 mg/ml.

In the inventive method mTG2 may be e.g. present in an amount from about 0.01 mol equivalents to about 2 mol equivalents to the substrate, e.g. to the protein comprising the the acyl glutamine-containing amino acid donor sequence, from about 0.05 mol equivalents to about 1.5 mol equivalents, from about 0.1 mol equivalents to about 1.125 mol equivalents, from about 0.125 mol equivalents to about 1.75 mol equivalents, from about 0.25 mol equivalents, 0.3 mol equivalents, 0.4 mol equivalents, 0.5 mol equivalents, 0.6 mol equivalents, 0.7 mol equivalents, 0.8 mol equivalents to about 1 mol equivalents, or from about 1 mol equivalents to about 2.5 mol equivalents, preferably mTG2 is used in the inventive method in an amout of about 1 mol equivalents. In the inventive method the reaction may e.g. be allowed to proceed 25°C-37°C for about 1-5 hours, or for about 2-4 hours, or for about 2.5 hours to about 3.5h, or for about 1 hour, 2 hours, 3 hours, 4 hours. The inventive method may e.g. be carried out in any suitable buffer such as HEPES (4-2-hydroxyethyl-1-piperazineethanesulfonic acid), MOPS (3-(N-morpholino)propanesulfonic acid), or PIPES (piperazine-N,N'-bis(2-ethanesulfonic acid) at a pH of about pH7.0.

According to one embodiment the acyl glutamine-containing amino acid donor according to the invention which may be used in the inventive method may be as disclosed above, e.g. the inventive acyl glutamine-containing amino acid donor may be an antibody, antigen-binding antibody fragment, enzyme, or a non-immunoglobulin scaffold as disclosed above.

Microbial transglutaminease, such as e.g. mTG2 which may be used according to the embodiments of the present invention, may be obtained from *Streptoverticillium mobaraense*, or any of its substrains, such as e.g. 40847, according to the method disclosed in Biochem. J. (1994) 299:825-829. For example, *Streptoverticillium mobaraense* may e.g. cultivated as described by Ando et al. (1989) Agric. Biol. Chem. 53, 2613—2617: In 2L Erlenmeyer flasks, 0.1 ml of the spore suspension may be grown in 500 ml of a medium containing: polypeptone, 2.0%; yeast extract, 0.2%; K_2HPO_4, 0.2%; $MgSO_4{\cdot}7H_2O$, 0.1 % ; potato starch, 2.0 % ; glucose, 0.5 % ; pH 7.0. Cultivation may be continued at 30°C, and the culture may be aerated and shaken at 90 rev. /min for 9-11 days until the maximum of enzyme activity was reached. The culture fluid may then be separated from the mycel by centrifugation at 10000 g for 10 min and subsequent filtration over a folded filter paper. The supernatant may directly be utilized in chromatography or stored at - 20 °C for later use. For scaled-up production, 1.0 ml of the cell suspension may be transferred to 3.5 L of a medium containing 2.5 % potato starch instead of

2.0 %, and 1.0 % glucose instead of 0.5 %. The culture may be grown with aeration (2 litres/min) and stirring at 140-180 rev./min for the first day and subsequently at 300- 350 rev./min. Maximum of enzyme activity is typically achieved after 7 days. *Streptoverticillium mobaraense* may e.g. be obtained from ATCC® (ATCC 29032), or e.g. DSM, Braunschweig, Germany.

In one embodiment the inventive amino donor-comprising substrate which is used in the inventive method is coupled or covalently bound to a dye, drug, ribozyme, nanobody, enzyme, or linker as disclosed above. For example, the acyl glutamine-containing amino acid donor may be an antibody or antigen binding fragment as defined above which comprises at its carboxyterminus the inventive acyl glutamine-containing amino acid sequence according to SEQ ID NO:2, or e.g. according to any one of SEQ ID NO:7-294 as disclosed herein. For example, the amino donor-comprising substrate may be as defined above, e.g. may be a peptide comprising at least one lysine residue, or the tripeptide GGG as disclosed above which may e.g. be coupled to a linker, dye, drug, ribozyme, nanobody, or enzyme as disclosed above.

According to one embodiment the linker used in the inventive method may e.g. be further linked to a cytotoxic drug (payload), dye, or radioisotope as defined above. In the inventive method the acyl glutamine-containing amino acid donor and the amino donor-comprising substrate may e.g. be present in a reaction mixture in a ratio of about 1:40 molar equivalents (antibody: amino donor-comprising substrate) or in any molar equivalent disclosed above, with microbial transglutaminase 2 present in an amount as disclosed above, e.g. in a 1:1 molar equivalent to the antibody comprising the inventive acyl glutamine-containing amino acid donor sequence as disclosed above. According to the inventive method the reaction may e.g. be allowed to proceed about 1-5 hours at 25°-37°C, e.g. 1 hour, 2 hours, 2.5 hours, 3 hours, 3.5 hours, 4 hours or 5 hours at 25°C, 26°C, 27°C, 28°C, 29°C, 30°C, 31°C, 32°C, 33°C, 34°C, 35°C, 36°C, or 37°C.

In one embodiment the present invention provides for a protein according to the invention which is obtainable by the inventive method as disclosed above. Accordingly, the protein obtainable according to the present invention may be any protein as disclosed herein, e.g. an antibody, antigen binding fragment, enzyme, or a non-immunoglobulin scaffold as disclosed herein, which comprises the amino acid sequence according to SEQ ID NO:2. For example, the protein obtainable by the inventive method may comprise an antibody drug conjugate comprising the at least one acyl glutamine-containing amino acid donor sequence according to SEQ ID NO:2 as disclosed herein, preferably 2, more preferably 4 acyl glutamine-containing amino acid donor sequences as disclosed above which are covalently bound via an isopeptide bond formed between the acyl glutamine-containing amino acid donor of the invention (e.g.

X_1X_2 X_3 TYF<u>Q</u>AYG $X_4X_5X_6$), whereby the isopeptide bond is formed between the central glutamine residue (underlined) and the amino group of the amino donor-comprising substrate.

In one embodiment the present invention pertains to the use of a polypeptide sequence according to SEQ ID NO:2 in the inventive method as disclosed above. Accordingly, the present invention pertains to the use of one or more, e.g. 1, 2, 3, 4, 5, or more of the inventive polypeptide sequences disclosed herein in the inventive method. For example, the present invention pertains to the use of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO: 139, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 147, SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 151, SEQ ID NO: 152, SEQ ID NO: 153, SEQ ID NO: 154, SEQ ID NO: 155, SEQ ID NO: 156, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ

ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 182, SEQ ID NO: 183, SEQ ID NO: 184, SEQ ID NO: 185, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 231, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 234, SEQ ID NO: 235, SEQ ID NO: 236, SEQ ID NO: 237, SEQ ID NO: 238, SEQ ID NO: 239, SEQ ID NO: 240, SEQ ID NO: 241, SEQ ID NO: 242, SEQ ID NO: 243, SEQ ID NO: 244, SEQ ID NO: 245, SEQ ID NO: 246, SEQ ID NO: 247, SEQ ID NO: 248, SEQ ID NO: 249, SEQ ID NO: 250, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 254, SEQ ID NO: 255, SEQ ID NO: 256, SEQ ID NO: 257, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, SEQ ID NO: 261, SEQ ID NO: 262, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 266, SEQ ID NO: 267, SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 273, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 277, SEQ ID NO: 278, SEQ ID NO: 279, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, or SEQ ID NO: 294 in the inventive method.

For example, the polypeptide according to SEQ ID NO:2 may be carboxyterminally fused the HC or LC of an antibody as disclosed above. For example, sequences in which both X_3, X_4 are C as disclosed above are preferred, accordingly, the use of polypeptide sequences SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:37, SEQ ID

NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, or SEQ ID NO:138, more preferred is the use of any of SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, or SEQ ID NO:90.

In one embodiment the present invention also provides polynucleotides encoding an inventive polypeptide according to SEQ ID NO:2. Accodingly, the present invention provides for polynucleotides encoding the inventive polypeptide according to SQE ID NO:2 of the following structure:

5'-NNN_1 NNN_2 NNN_3 ACN TAY TTY CAR GCN TAY GGN NNN_4 NNN_5 NNN_6-3'
(SEQ ID NO:301),

wherein N denotes any nucleotide (A, C, T, G), Y denotes a pyrimidine base (C or T), R denotes a purine base (A or G). Base nomenclature is according to the Nomenclature Committee of the International Union of Biochemistry (NC-IUB), see e.g. J. Biol. Chem., 1986, 261, 13-17. NNN_1 – NNN_6 indicate codons 1-6, whereby codon NNN_1 encodes amino acid X_1 of SEQ ID NO:2, NNN_2 amino acid X_2 of SEQ ID NO:2, NNN_3 amino acid X_3 of SEQ ID NO:2, NNN_4 amino acid X_4 of SEQ ID NO:2, NNN_5 amino acid X_5 of SEQ ID NO:2 and NNN_6 amino acid X_6 of SEQ ID NO:2. For example, depending on the intended use of the polynucleotides codon usage should be optimized for the specific host, e.g. in case the polynucleotides are used for expressing the inventive peptide or inventive protein as disclosed above in a mammalian, eukarytoic or prokaryotic host the different codon usage by the respective host should be considered. For example, if the inventive polynucleotide is used for expression in a rodent or human cell lines, such as CHO or HEK 293 cells, for the manufacture of a therapeutic, the corresponding codon usage should be used to increase e.g. protein production (Trends in Molecular Medicine, November 2014, Vol. 20, No. 11). Codons NNN_1 – NNN_6 according to the invention may not, however, code for a stop codon, e.g. TAG (*amber*), TAA (*ochre*), or TGA (*opal*).

Accordingly, NNN_1 may be any one of codons GCT, GCC, GCA, GCG, GTT, GTC, GTA,GTG, ATT, ATC, ATA CTT, CTC, CTA, CTG, TTA, TTG, ATG, GGT, GGC, GGA, GGG, NNN_2 may be any one of codons GAT, GAC, GAA, GAG, NNN_3, NNN_4 may be any one of codons TGT, TGC, AAT, AAC, NNN_5 may be one one of codons TCT, TCC, TCA, TCG, AGT, AGC, ACT, ACC, ACA, ACG, AAT, AAC, CAA, CAG, NNN_6 may be any one of codons GAT, GAC, GAA, GAG.

In one embodiment the present invention also provides for a vector which comprises the inventive polynucleotides as disclosed above. The vector according to the invention may e.g. be an expression vector. The term "expression vector" as used for the vector according to the invention to a nucleic acid vector that comprises a gene expression controlling region, such as a promoter or promoter component, operably linked to a nucleotide sequence encoding at least one polypeptid, e.g. at least the inventive polypeptide sequence according to any of of SEQ ID NO:2- SEQ ID NO:294. Expression vectors which may e.g. include pCMV-based expression vectors, or pD912-based vectors and variants thereof, Gateway® expression vectors, pcDNA-based expressoin vectors, or pJΩ vectors (see e.g. Nucleic Acids Research, Vol. 18, No. 4), or vectors which may be used for retroviral or lentiviral production (see e.g. Front Biosci. 1999 Jun 1;4:D481-96.). In the vector according to the invention the polynucleotides may e.g. be comprised 5' or 3' to an multiple cloning site (MCS), which will allow to generate in-frame fusion proteins when a corresponding cDNA encoding e.g. an antibody light or heavy chain, is cloned into the MCS. Depending on the location of the MCS the inventive polynucleotide will be expressed as an aminoterminal or carboxterminal fusion protein.

In one embodiment the present invention also provides a host cell which comprises the inventive polynucleotide sequence as disclosed above, e.g. according to SEQ ID NO:2, or e.g. any of SEQ ID NO:7-294, or which comprises a vector according to the invention as disclosed above. For example, a host cell according to the invention comprising the inventive polynucleotide or a vector according to the invention as disclosed above refers to any type of cell that can contain the vector according to the invention. The host cell can be a eukaryotic cell, e.g., plant, animal, fungi, or algae (e.g. *Phaeodactylum tricornutum, Chlamydomonas reinhardtii*) or can be a prokaryotic cell, e.g., bacteria or protozoa. The host cell can be a cultured cell or a primary cell, i.e., isolated directly from an organism, e.g., a human. The host cell can be an adherent cell or a suspended cell, i.e., a cell that grows in suspension. A host cell according to the invention may e.g. include HEK293, HEK293T, HEK293E, HEK 293F, NS0, per.C6, MCF-7, HeLa, Cos-1, Cos-7, PC-12, 3T3, Vero, vero-76, PC3, U87, SAOS-2, LNCAP, DU145, A431, A549, B35, H1299, HUVEC, Jurkat, MDA-MB-231, MDA-MB-468, MDA-MB-435, Caco-2, CHO, CHO-K1, CHO-B11, CHO-DG44, BHK, AGE1.HN, Namalwa, WI-38, MRC-5, HepG2, L-929, RAB-9, SIRC, RK13, 11B11, 1D3, 2.4G2, A-10, B-35, C-6, F4/80, IEC-18, L2, MH1C1, NRK, NRK-49F, NRK-52E, RMC, CV-1, BT, MDBK, CPAE, MDCK.1, MDCK.2, D-17, or e.g. *Saccharomyces cerevisiae, Hansenula polymorpha, Schizosaccharomyces pombe, Schwanniomyces occidentalis, Kluyveromyceslactis, Yarrowia lipolytica* and *Pichia pastoris*, or e.g. Sf9, Sf21, S2, Hi5, or BTI-TN-5B1-4 cells, or e.g. DH5α E.coli.

In one embodiment the present invention also provides for an antibody or antigen-binding fragment thereof, bivalent antibody, or VHH antibody comprising at least one amino acid sequence according to SEQ ID NO:2. Antibodies, antigen-binding fragments thereof, bivalent antibodies, or VHH antibodies according to the invention are as disclosed above. For example, an antibody according to the invention may comprise at least one amino acid sequence according to SEQ ID NO:2 (e.g. the acyl glutamine-containing amino acid donor according to the invention), e.g. as a carboxyterminal fusion to a light or heavy chain. The antibody according to the invention preferably comprises 2, or 4 inventive amino acid sequences according to SEQ ID NO:2, e.g. the antibody of the invention may comprise two light chains, or two heavy chains which comprise at their carboxy terminus the inventive amino acid sequence according to SEQ ID NO:2. Preferably, both heavy and light chains comprise as carboxyterminal fusions the inventive amino acid sequence according to SEQ ID NO:2. The inventive antibodies may e.g. also be modified by PCR-based site directed mutagenesis as disclosed above to remove terminal lysine residues in the Fc domain.

According to one embodiment the antibody according to the invention as disclosed above is a human or humanized monoclonal antibody as disclosed above, preferably, an IgG1, IgG2, IgG3, IgG4, or IgM type antibody. The inventive antibody comprises at least one linker covalently coupled to it according to the inventive method disclosed above. For example, the inventive antibody may comprise one, two, three, or four linker (e.g. cleavable or non-cleavable as disclosed above), which have been covalently coupled to the antibody according to the inventive method disclosed herein. According to one embodiment the inventive linker is further coupled to a dye, radioisotope, or cytotoxin as disclosed above.

In one embodiment the inventive antibody as disclosed above specifically binds to cancer cell surface antigens. Cancer cell surface antigens according to the invention include, but are not limited to EGFR (epidermal grwoth factor receptor), HER2, HER4, AFP, $\alpha_v\beta_3$ integrin, MUC16, CD4, CD20, CD22, CD30, CD33, CD52, CD56, CD66e, CD140b, CD227, EpCam, GD3, PSMA, or VEGF. Cancer cell surface antigens according to the invention also include cancer stem cell such as e.g. CD123, CLL-1, combinations of SLAMs (signaling lymphocyte activation molecule family receptors; see Yilmaz et al., "SLAM family markers are conserved among hematopoietic stem cells from old and reconstituted mice and markedly increase their purity," Hematopoiesis 107: 924-930 (2006)), such as CD150, CD244, and CD48, and those markers disclosed in U.S. Patent No. 6,004,528.

In a preferred embodiment the antibody according to the invention is cetuximab (c225), or e.g. a biosimilar thereof which binds to EGFR. The term "biosimilar" as used for the inventive cetuximab is used in a manner that is consistent with the working definition promulgated by the US FDA which defines a biosimilar product to be one that is "highly similar" to a reference product (despite minor differences in clinically inactive components). In practice there can be no clinically meaningful differences between the reference product and the biosimilar product in terms of safety, purity, and potency (Public Health Service (PHS) Act §262).

For example, cetuximab (or e.g. its biosimilar) according to the invention comprises at least one, preferably at least two, more preferably four acyl glutamine-containing amino acid donor sequences according to the invention. For example, cetuximab according to the invention comprises two, or preferably four linkers as defined above further coupled to a cytotoxin as above.

According to one embodiment cetuximab (or e.g. its biosimilar) according to the invention may be used in the treatment of cancer. The term "cancer" as used in the present invention refers to a cellular disorder characterized by uncontrolled or disregulated cell proliferation, decreased cellular differentiation, inappropriate ability to invade surrounding tissue, and/or ability to establish new growth at ectopic sites. The term "cancer" further encompasses primary and metastatic cancers. The inventive antibody cetuximab may e.g. be used to treat one of breast cancer, prostate cancer, ovarian cancer, cervical cancer, skin cancer, pancreatic cancer, preferably colorectal cancer, metastatic (mCRC), non-resectable liver metastases, Squamous Cell Carcinoma of the Head and Neck, Non-Small Cell Lung Cancer (NSCLC), Head and Neck Squamous Cell Carcinoma (HNSCC). Cetuximab (c225, or its biosimilar) may e.g. be used in patients that particularly benefit from such a treatment, e.g. patients with epidermal growth factor receptor (EGFR)- expressing, RAS wild-type metastatic colorectal cancer. Cetuximab according to the invention (or its biosimilar) may also be used in combination with irinotecan-based chemotherapy, or e.g. in first-line treatment in combination with FOLFOX, or e.g. as a single agent in patients who have failed oxaliplatin- and irinotecan-based therapy and who are intolerant to irinotecan.

In one embodiment the present invention provides for a composition which comprises the inventive antibody as disclosed above, which comprises at least one further pharmaceutically active ingredient. For example, the composition according to the invention may comprise cetuximab (or e.g. its biosimilar) in aqueous or lyophilized form and at least one further chemotherapeutic agent, wherein the agent is selected from the group comprising capecitabine, 5-fluoro-2'-deoxyuiridine, irinotecan, 6-mercaptopurine (6- MP), cladribine, clofarabine, cytarabine, floxuridine, fludarabine, gemcitabine, hydroxyurea, methotrexate, bleomycin, paclitaxel, chlorambucil, mitoxantrone, camptothecin, topotecan, teniposide, colcemid, colchicine, pemetrexed, pentostatin, thioguanine; leucovorin, cisplatin, carboplatin, oxaliplatin, or a combination of 5-FU, leucovorin, a combination of 5-fluorouracil/folinic acid (5-FU/FA), a combination of 5-fluorouracil/folinic acid (5-FU/FA) and oxaliplatin (FLOX), a combination of 5-FU, leucovorin, oxaliplatin (FOLFOX), or a combination of 5-FU, leucovorin, and irinotecan (FOLFIRI), or a combination of leucovorin, 5-FU, oxaliplatin, and irinotecan (FOLFOXIRI), or a combination of Capecitabine and oxaliplatin (CapeOx).

According to one embodiment the present invention provides a pharmaceutical composition which comprises the inventive antibody as disclosed above, or the composition according to the invention and at least one further ingredient. Accordingly, the present invention provides for pharmaceutical compositions which comprise the inventive antibody and which may comprise excipients and/or stabilizers and/or surfactants and/or preservatives. The term "excipients" as used herein means a component of a pharmaceutical product that is not an active ingredient such as, for example, diluents. The excipients that are useful in preparing the inventive pharmaceutical composition are generally safe and non-toxic. Surfactants that may be used with the inventive pharmaceutical composition include e.g. anionic surfactants such as e.g. a mixture of sodium alkyl sulfates, cationic surfactants, such as e.g. quaternary ammonium and pyridinium cationic surfactants, or non-ionic surfactants, such as e.g. Sorbitan esters, polysorbates, e.g. Polysorbat 20 (Polyoxyethylen-(20)-sorbitanmonolaurat), Polysorbat 21 (Polyoxyethylen-(4)-sorbitanmonolaurat), Polysorbat 40 (Polyoxyethylen-(20)-sorbitanmonopalmitat), Polysorbat 60 (Polyoxyethylen-(20)-sorbitan-monostearat), Polysorbat 61 (Polyoxyethylen-(4)-sorbitanmonostearat), Polysorbat 65 (Polyoxyethylen-(20)-sorbitantristearat), Polysorbat 80 (Polyoxyethylen-(20)-sorbitanmonooleat), Polysorbat 81 (Polyoxyethylen-(5)-sorbitanmonooleat) Polysorbat 85 (Polyoxyethylen-(20)-sorbitantrioleat), Polysorbat 120 (Polyoxyethylen-(20)-sorbitanmonoisostearat), or poloxamers e.g. poloxamer 105, poloxamer 108, poloxamer 122, poloxamer 124, poloxamer 105 benzoate. Perservatives which may be comprised in the pharmaveutical composition according to the invention may be benzalkonium chlorid in a concentration of 0.004% to 0.01%.

In one embodiment the present invention provides for a method of treating a subject in need thereof inflicted with cancer, wherein the treatment comprises administering to said subject (e.g. a patient, wherein the patient is preferably a human) a therapeutically effective amount of the pharmaceutical composition as disclosed herein. Accordingly, the present invention provides for a method of treating treating a subject in need thereof inflicted with cancer, e.g. as disclosed above, with a therapeutically effective amount of the inventice c225 (cetuximab) antibody, e.g. cetuximab according to the invention may be administered in a concentration of about 125 mg/m^2 to about 500 mg/m^2 body surface, preferably about 250 mg/m^2 to about 400 mg/m^2 body surface, whereby the dosing of cetuximab may e.g. be computed according to the Dubois method, in which the body surface area of a subject (m^2) is computed using the subject's body weight: $m^2 = (wt\ kg^{0.425} \times height\ cm^{0.725}) \times 0.007184$.

Examples

The following Examples are intended to further illustrate the invention. They are not intended to limit the subject matter or scope of the invention thereto.

Example 1

Solid-phase synthesis of peptides and purification

Peptides were synthesized on an AmphiSpheres 40 RAM resin (Agilent, 0.27 mmol/g) by microwave-assisted Fmoc-SPPS using a Liberty BlueTM Microwave Peptide Synthesizer at a 0.1 mmol scale. Activation of the respective carboxyfunctional amino acid was performed by Oxyma/ N,N'-Diisopropylcarbodiimide (DIC). Deprotection of the aminoterminal Fmoc-group was achieved using 20% piperidine in DMF in the presence of Oxyma. During the synthesis cycles all amino acids were heated to 90°C (cysteines to 50°C). Peptides were cleaved from the resin by a standard cleavage cocktail of 94% TFA, 2% triethylsilane, 2% anisole, 2% H2O. Cysteine containing peptides were cleaved in the presence of dithiotreitol (DTT) to suppress unwanted oxidation of cysteins. After 2 h of cleavage, peptides were precipitated in cold diethylether and washed twice with diethylether. The disulfide-bridged crude peptide was oxidized at 1 mg ml-1 in 100 mM $(NH_4)_2CO_3$ aq. pH 8.4 and oxidation monitored by RP-HPLC. Afterwards, peptides were isolated by preparative RP-HPLC.

RP-HPLC.

Peptides were analyzed by chromatography on an analytical RP-HPLC from Varian (920-LC) using a Phenomenex Hypersil 5u BDS C18 LC column (150 x 4.6 mm, 5 µm, 130 Å). Peptides were isolated by semi-preparative RP-HPLC (Varian) using a Phenomenex Luna 5u C18 LC column (250 x12.2 mm, 5 µm, 100 Å). Eluent A (water) and eluent B (90 % aq. MeCN) each contained 0.1% trifluoroacetic acid (TFA).

ESI-MS analysis.

ESI mass spectra were collected on a Shimadzu LCMS-2020 equipped with a Phenomenex Jupiter 5u C4 LC column (50 x 1 mm, 5 µm, 300 Å) by using an eluent system of 0.1% aq. formic acid (eluent A) and acetonitrile containing 0.1% formic acid (eluent B).

Example 2

Peptide biotinylation assays.

Peptides were dissolved at 50 mg/ml in DMSO and diluted to 1.25 mg/ml in 100 mM HEPES pH 7.0 for enzymatic conjugation. Monobiotinyl cadaverine was added at a 5 fold molar excess over peptide and enzymatic reactions initiated by addition of microbial transglutaminase at an enzyme/substrate ratio of 1/50 (w/w). For peptide biotinylation assays involving peptide 2 (SEQ ID NO: 90) and reference peptide GGGSLLQG (SEQ ID NO:295), the amount of microbial transglutaminase was reduced to an enzyme/substrate ratio of 1/385 and 1/182 (w/w), respectively. Reactions were incubated at 37°C. Aliquots of the reaction mixture were collected after 0, 15, 30, 60, 120, and 180 min and reactions stopped by transglutaminase removal using centrifugation dialysis (Microcon-10, 10.000 NMWL, Merck Millipore). Aliquots were analyzed by RP-HPLC by using a gradient from 10 to 80% eluent B (90% aq. MeCN) over 20 min at 1 ml/min (see Figure 4). Fractions collected from the RP-HPLC analyses were further analyzed by ESI-MS.

Example 3

Enzymatic antibody conjugation using transglutaminase.

Antibody expression and purification. Plasmids coding for cetuximab (Erbitux®) wildtype were kindly provided by Merck Serono (Darmstadt). Cetuximab mutants containing the TG-tags at the C-terminus of the heavy chain were prepared by standard SOE PCR techniques as described below. The C-terminal lysine was omitted in both constructs to avoid cross-reactivity of the ε-amino group with transglutaminase-accessible glutamines. Antibodies were transiently expressed from HEK293F cells using the Expi293 Expression System (Life Technologies). Conditioned supernatants were applied to spin columns with PROSEP-A Media (Montage, Merck Millipore) and washed with 1.5 M Glycine/NaOH, 3 M NaCl, pH 9.0. Proteins were eluted with 0.2 M Glycine/HCl pH 2.5 and neutralized with 1M Tris/HCl pH 9.0. Eluted proteins were dialyzed in 1x DPBS (Life Technologies) and stored at 4°C.

PCR-based generation of tagged Cetuximab (lacking the terminal heavy chain lysine). PCR was used to generate c225 (Cetuximab) constructs lacking the carboxyterminal lysine residue of the heavy chain. Plasmids encoding C225 including a terminal lysine residue and the carboxyterminal amino acid sequence according to SEQ ID NO:246 were amplified using primers having the sequences according to SEQ ID NO:296, SEQ ID NO:299 (both at 1pmole) for 10 cycles (PCR conditions: 3min @ 98°C (initial denaturing), 10s @ 98°C, 30s @ 55°C, 15 s @ 72°C), followed by 20 cycles using primers having the sequences according top SEQ ID

NO:296, SEQ ID NO:300 (10 pmole primers) with the following cycling conditions: 10 s @ 98°C, 30s @ 55°C, 15 s @ 72°C, final extension 5min@ 72°C.

The resulting amplification product was gel purified and subsequently subjected to a restrictoin digest using EcoRV/BamHI (3h @ 37°C). The restriction fragment was then purified using a PCR purification kit. The fragment was then cloned into an EcoRV/BamHI digested pTT5_C225_HC vector (encoding the C225 heavy chain).

Antibody conjugation using transglutaminase. Antibodies were adjusted to 0.5 mg/ml and incubated with 40 mol equiv per conjugation site of monobiotinyl cadaverine (MBC) and 1 mol equiv microbial transglutaminase (mTGase) in 100 mM HEPES buffer pH 7.0 for 3 h at 25°C. For analytical issues, reactions were analyzed by 15% SDS-PAGE and biotinylated heavy chains visualized by semi-dry western blot with streptavidin-alkaline phosphatase conjugate and NBT/BCIP. For preparative production of antibody conjugates, excess substrate and mTGase were removed by size exclusion chromatography with 50 mM sodium phosphate buffer, 150 mM NaCl, pH 7.0 (Superdex S200 10/300 GL, GE Healthcare, 0.5 ml/min).

MALDI-TOF-MS analysis of conjugated antibodies. Prior to MS-analysis, antibodies (6 µg) were reduced in SDS-loading dye containing 2-mercaptoethanol and heavy and light chains separated under denaturing conditions using 15% SDS-PAGE. Proteins were visualized by Coomassie-MeOH staining. Protein bands corresponding to modified heavy chains were excised, cut into small pieces and washed twice with MQ water for 15 min to remove AcOH and MeOH from staining. Afterwards, gel pieces were washed twice with 2:3 MeCN:50 mM ammonium bicarbonate pH 8.0 for 30 min to remove stain. Gel pieces were dehydrated with MeCN and dried at 50°C. 20 mM Dithiothreitol (DTT) in 50 mM ammonium bicarbonate was added and the samples incubated at 60°C for 45 min to reduce disulfide bonds. After the samples were cooled to room temperature, the DTT solution was removed and reduced cysteines were alkylated by the addition of 55 mM iodacetamide (IAA) in 50 mM ammonium bicarbonate for 45 min in the dark. Excess alkylation mix was removed and the gel pieces washed twice with 50 mM ammonium bicarbonate pH 8.0. Gel pieces were then twice dehydrated with MeCN and swelled in 50 mM ammonium bicarbonate, before they were dehydrated and swelled in 50 mM ammonium bicarbonate containing 20 ng/µl trypsin (NEB, Trypsin-ultra, Mass Spectrometry grade) to give a final enzyme/substrate ratio of 1:20. Trypsin digest was performed overnight at 37°C. Peptides were extracted twice by the addition of 50% MeCN, 1% formic acid for 30 min shaking. Combined supernatants containing peptides were lyophilized and analyzed by MALDI-TOF-MS. The in-gel digestion procedure was adopted from the literature (M. Wilm, A. Shevchenko, T. Houthaeve, S. Breit, L. Schweigerer, T. Fotsis, M. Mann, Nature 1996, 379, 466-469.).

Determination of antibody conjugation efficiency by fluorescence measurement. Antibody conjugation efficiency was determined by antibody labeling with N-(Tetramethylrodaminyl) cadaverine (TAMRA-cadaverine) and measurement of fluorescence at an excitation wavelength of 547 nm and an emission wavelength of 573 nm. For this purpose, antibodies were adjusted to 1.0 mg/ml and incubated with 20 mol equiv per conjugation site of TAMRA-cadaverine and 0.5 mol equiv microbial transglutaminase (MTG) in 100 mM HEPES buffer pH 7.0 for 3 h at 25°C. Unbound TAMRA-cadaverine was removed by gelfiltration twice using Protein Desalting Spin Columns (Thermo Scientific) equilibrated with PBS. A non-antibody sample was incubated and treated in the same manner to exclude remaining free TAMRA-cadaverine after gelfiltration. The weak fluorescence measured from this control was afterwards subtracted from the fluorescence of the antibody samples. The concentration of TAMRA-cadaverine conjugated antibodies was determined by using a standard curve of TAMRA-cadaverine ranging from 9.72 to 0.19 µM in PBS (40µl per well) and fluorescence readout using a plate reader (Tecan Infinite M1000). The percentage of labeled/unlabeled antibodies was calculated from the total antibody concentration (determined at 280nm, **9**: MW = 148211.72g/mol ε280 = 223400 M-1m-1, **10**: MW = 148259.55 g/mol ε280 = 223150 M-1m-1) assuming each labeled antibody is conjugated to two TAMRA-moieties attached to the MTG-tag at the heavy chains. For analytical issues, reactions were also analyzed by 15% SDS-PAGE and TAMRA labeled heavy chains visualized by fluorescence readout.

Example 4

Cell binding experiments

Cell lines. EBC-1 and CHO-K1 cells were cultured in DMEM with 4 mM L-glutamine (Sigma-Aldrich) and DMEM-F12 + GlutaMax™ (Gibco®), respectively, both supplemented with 10% fetal bovine (Sigma-Aldrich) at 37 °C and 5% CO2.

Cell binding experiments. Cell binding experiments were performed by using EGFR-overexpressing EBC-1[3] and EGFR-negative CHO-K1 cells in combination with confocal fluorescence microscopy and flow cytometry, respectively. Washing and incubation steps were performed at 4 °C using PBS with 1% BSA. For microscopy based experiments, cells were grown on glass coverslips followed by consecutive labelling with 100 nM of respective antibody-conjugates and 1:200 diluted Streptavidin Alexa Fluor® 488 conjugate (Life Technologies). Then, cells were fixed with 4% paraformaldehyde, mounted with ProLong® Diamond Antifade Mountant with DAPI (Life Technologies) and scanned using a Leica TCS SP5 confocal microscope equipped with a 100× objective (Leica Microsystems). For flow cytometry, 2 × 105 cells were incubated with 100 nM of respective antibody-conjugates and in a consecutive step with 1:200 diluted Streptavidin Alexa Fluor® 488 conjugate (Life Technologies). Cell fluorescence was determined using a BD Influx cell sorter and BD FACS Sortware with detection of 2 × 104 events.

Example 5:

Bioconjugation of cetuximab (c225) using mTG2 and GGG amino donor-comprising substrate

Cetuximab heavy chain variants 9 and 10 (9: with inventive MTG-tag according to SEQ ID NO:90, 10: with inventive MTG-tag according to SEQ ID NO:246) with terminal lysine residues (K447) removed were conjugated to biotin-cadavarine, or GGGYK-Biotin.

Assay conditions for carrying out the mTG2-mediated conjugation reactions were as follows:

Assay conditions	Conc [µM]
50 mM Tris-HCl pH 7.5, 150 mM NaCl	1x
mTG (0.4 eq.)	1.364
Cetuximab (according to the invention)	0.5 mg/ml
MBC/GGG-Biotin/GGG-TAMRA/TAMRA-cadaverine (50 molar equivalent)	170.4
Incubation time:	3h@ 22°C

Following the incubation for 3h at 22°C the reaction was stopped by the addition of 2.5µl of SDS loading dye and subsequent denaturation at 98°C for 5min. A 15% SDS polyacrylamide gel was loaded with the samples and run at 300V, 40mA until the desired separation was achieved (see Figure 14B). Western blotting was done (12V, 400 mA, 45 min). Fluorescent detection was done by placing the polyacryamide gel on a UV screen (λ= 260-280nm) (Figure 14C).

Results:

Only cetuximab comprising the inventive MTG-tag1, or MTG-tag2 was fluorescently labled, while wild-type cetuximab without the inventive polypeptide sequences according to SEQ ID

NO:90, SEQ ID NO:246 is not fluorescently labeled indicating that the inventive MTG tags were efficiently recognized my mTG2.

Example 6

MTG-promoted conjugation reactions

Antibody drug conjugates (ADCs) were synthesized in MTG-catalyzed reactions containing 1 mg/ml cetuximab tagged with SEQ ID NO: 246 (e.g. cetuximab comprising at SEQ ID NO: 246 at the carboxyterminus of each of the heavy chains), 20 equivalents of cytotoxic payload 1-4, and 0.1 equivalents of microbial transglutaminase (MTG). Reactions were performed in PBS pH 7.4 at 37°C for 16h and stopped by the addition of 1 volume of HIC buffer A.

ADC analysis by hydrophobic interaction chromatography (HIC)

ADCs were evaluated by hydrophobic interaction chromatography (HIC) on a TSKgel Butyl-NPR column (Tosoh Bioscience, 4.6 mm x 3.5 cm, 2.5 µm) using an Agilent Infinity 1260 HPLC. The HIC method was applied using a mobile phase of 50 mM NaH_2PO_4, 1.5 M $(NH_4)_2SO_2$ pH 7.5 (Buffer A) and 50 mM NaH_2PO_4 pH 7.5 (Buffer B). ADCs (45 µg) in 0.75 M $(NH_4)_2SO_2$ were loaded and eluted with a gradient consisting of 2.5 min 0% Buffer B followed by a linear gradient into 100% Buffer B over 25 min with a flow rate of 0.9 ml/min.

CLAIMS

1. Protein comprising at least one acyl glutamine-containing amino donor sequence covalently linked via a γ-glutamyl-amide bond to an amino donor-comprising substrate, wherein the at least one acyl glutamine-containing amino acid donor sequence comprises at least the amino acid sequence according to SEQ ID NO: 1 (SEQ ID NO: 1 (TYFQAYG))

2. Protein according to claim 1, wherein the amino donor-comprising substrate comprises at least an ε-amino group, or at least one tripeptide having the sequence of GGG with a primary aminoterminal amino group.

3. Protein according to claim 1 or 2, wherein the amino donor-comprising substrate is a lysine residue, a lysine derivative, a polypeptide comprising at least one lysine residue.

4. Protein according to any one of claims 1-3, wherein the amino donor-comprising substrate is covently bound to a further molecule.

5. Protein according to any one of claims 1-4, wherein the tripeptide GGG is covalently bound via its carboxy terminus to a further molecule.

6. Protein according to claim 4 or claim 5, wherein the further molecule is one of a dye, radioisotope, drug, ribozyme, nanobody, enzyme, or linker.

7. Protein according to claims 6, wherein the linker is cleavable or non-cleavable.

8. Protein according to claim 6 or claim 7, wherein the linker is coupled or covalently bound to a dye, radioisotope, or cytotoxin.

9. Protein according to claim 8, wherein the acyl glutamine-containing amino acid donor sequence comprises an amino acid sequence according to SEQ ID NO: 2 ($X_1X_2X_3$ TYFQAYG $X_4X_5X_6$), wherein

   X1 is a hydrophobic amino acid,
   X2 is a negatively charged amino acid,
   X3 is C or N,
   X4 is C or N,
   X5 is one of an amino acid with with a polar, uncharged side chains, and
   X6 is a negatively charged amino acid.

10. Protein according to claim 9, wherein
   X1 is any one of A, V, I, L, M or G,

X2 is one of D, or E,
X3 is C,
X4 is C or N,
X5, is S, T, or N,
X6 is one of D, or E.

11. Protein according to claim 9 or claim 10, wherein
X1 is any one of A, V, I, L, M or G,
X2 is one of D, or E,
X3 is C,
X4 is C,
X5, is S, T, or N,
X6 is one of D, or E.

12. Protein according to any one of claims 9-11, wherein
X1 is any one of A, V, I, L, M or G,
X2 is E,
X3 is C,
X4 is C,
X5 is T, and
X6 is E.

13. Protein according to any one of claims 9-12, wherein
X1 is G,
X2 is E,
X3 is C,
X4 is C,
X5 is T, and
X6 is E. (SEQ ID NO: 90)

14. Protein according to any one of claims 1-13, wherein the protein is one of an antibody, antigen-binding antibody fragment, Fc domain, a non-immunoglobulin scaffold, or enzyme.

15. Protein according to any one of claims 1-14, wherein the protein is a monoclonal antibody, bivalent antibody, VHH, Fab, $F(ab)_2$, , scFv.

16. Protein according to claim 15, wherein the monoclonal antibody is a human or humanized human antibody, or fragment thereof.

17. Method of covalently coupling an amino donor-comprising to an acyl glutamine-containing amino acid donor comprising a polypeptide sequence according to SEQ ID NO:2, comprising the step of:

- contacting said amino donor-comprising substrate and said acyl glutamine-containing amino acid donor in the presence of transglutaminase, preferably mTG2, to obtain a protein according to any one of claims 1-13.

18. Method according to claim 17, wherein the acyl glutamine-containing amino acid donor is an antibody, antigen-binding antibody fragment, a non-immunoglobulin scaffold, or enzyme.

19. Method according to claim 19, wherein the amino donor-comprising substrate is coupled or covalently bound to dye, drug, ribozyme, nanobody, enzyme, or linker.

20. Method according to any one of claims 17-19, wherein the linker is cleavable or non-cleavable and wherein the linker is coupled to a dye, radioisotope, or cytotoxin.

21. Protein obtainable by a method according to the method of any one of claims 17-20.

22. Use of a polypeptide sequence according to SEQ ID NO: 2 in a method according to any one of claims 17-21.

23. Protein comprising the amino acid sequence according to SEQ ID NO:2.

24. Polypeptide according to SEQ ID NO:2.

25. Polynucleotide encoding a polypeptide sequence according to SEQ ID NO: 2.

26. Vector comprising the polynucleotide according to claim 25.

27. Host cell comprising a polynucleotide according to claim 25 or a vector according to claim 26.

28. Antibody or antigen-binding fragment thereof, bivalent antibody, or VHH antibody comprising at least one amino acid sequence according to SEQ ID NO:2.

29. Antibody according to claim 28, wherein the antibody is humanized or human.

30. Antibody according to claim 28 or claim 29, wherein the antibody is a humanized or human monoclonal antibody.

31. Antibody according to any one of claims 28-30, wherein the antibody is an IgG1, IgG2, IgG3, IgG4, or IgM type antibody.

32. Antibody according to any one of claims 28-31, wherein the antibody is covalently coupled to at least one linker according to the method of any one of claims 17-20.

33. Monoclonal antibody according to any one of claims 30-32, wherein the linker is further coupled to a dye, radioisotope, or cytotoxin.

34. Monoclonal antibody according to any one of claims 30-33, wherein the antibody specifically binds to cancer cell surface antigens.

35. Monoclonal antibody according to any one of claims 30-34, wherein the monoclonal antibody is c225 (cetuximab).

36. Antibody according any one of claims 30-35 for use in the treatment of cancer.

37. Antibody according to claim 36, wherein the cancer is breast cancer, prostate cancer, ovarian cancer, cervical cancer, skin cancer, pancreatic cancer, preferably colorectal cancer, metastatic (mCRC), non-resctable liver metastases, Squamous Cell Carcinoma of the Head and Neck, Non-Small Cell Lung Cancer (NSCLC), Head and Neck Squamous Cell Carcinoma (HNSCC).

38. Composition comprising an antibody according to any one of claims 30-35 and at least one further pharmaceutically active ingredient.

39. Pharmaceutical comprising the antibody according to any one of claims 30-35 or the composition according to claim 39 and at least one further ingredient.

40. Method of treating a subject in need thereof inflicted with cancer, wherein the treatment comprises administering to said subject a therapeutically effective amount of the pharmaceutical composition according to claim 39.

DRAWINGS

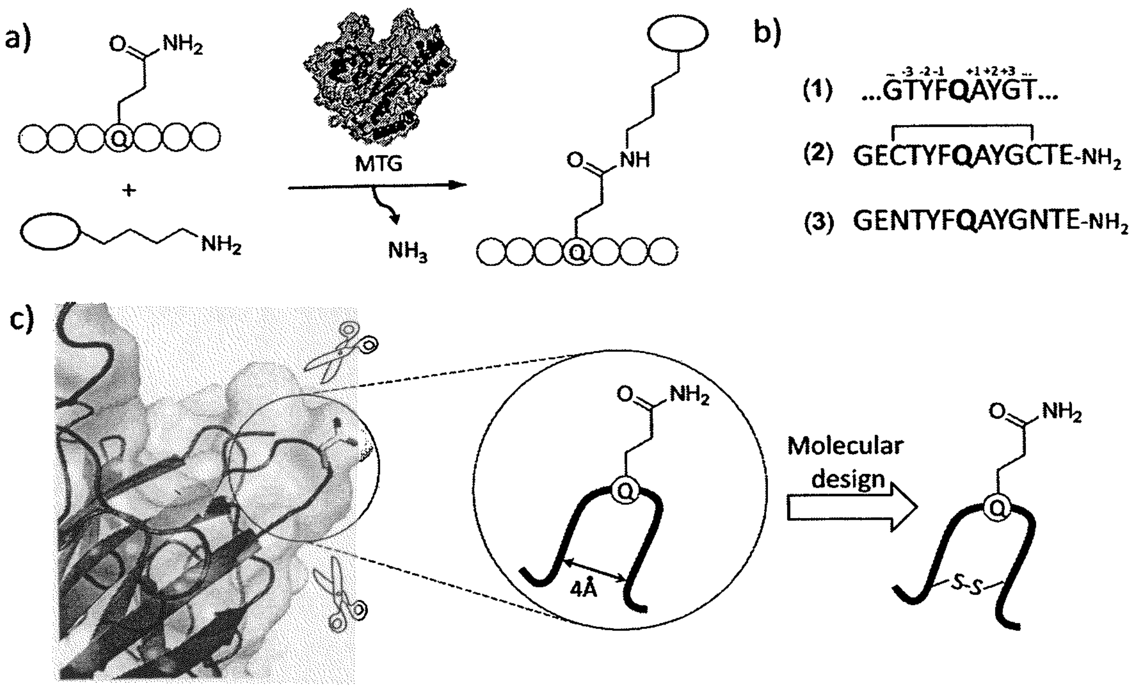


Figure 1

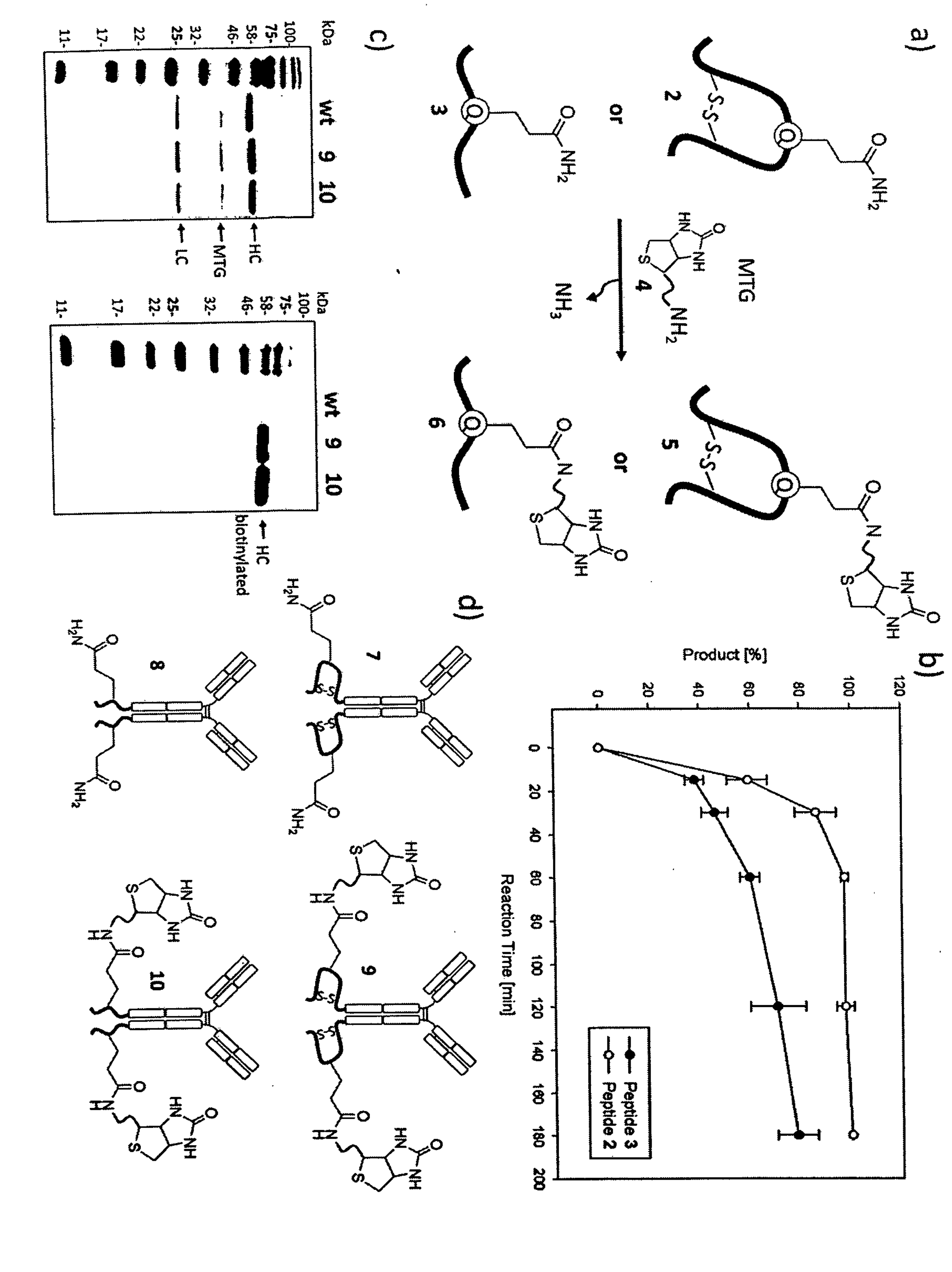

a)
MTG
4
NH_3
or
2
3
5
6
b)
Product [%]
Reaction Time [min]
Peptide 3
Peptide 2
c)
kDa
wt 9 10
HC
MTG
LC
HC biotinylated
d)
7
8
9
10

Figure 2

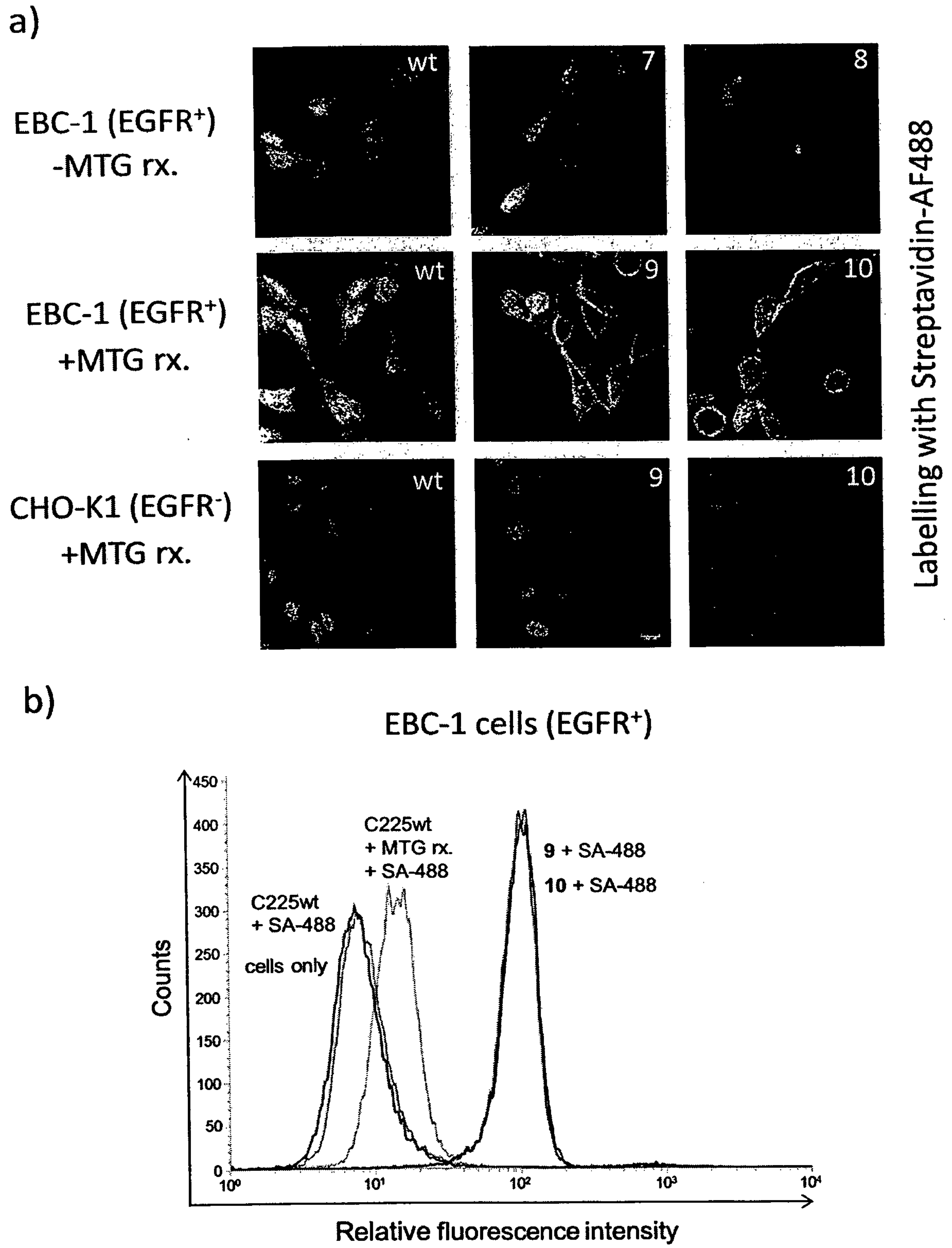

a)
wt
7
8
EBC-1 (EGFR+)
-MTG rx.
wt
9
10
EBC-1 (EGFR+)
+MTG rx.
wt
9
10
CHO-K1 (EGFR-)
+MTG rx.
Labelling with Streptavidin-AF488
b)
EBC-1 cells (EGFR+)
Counts
C225wt
+ MTG rx.
+ SA-488
C225wt
+ SA-488
cells only
9 + SA-488
10 + SA-488
Relative fluorescence intensity

Figure 3

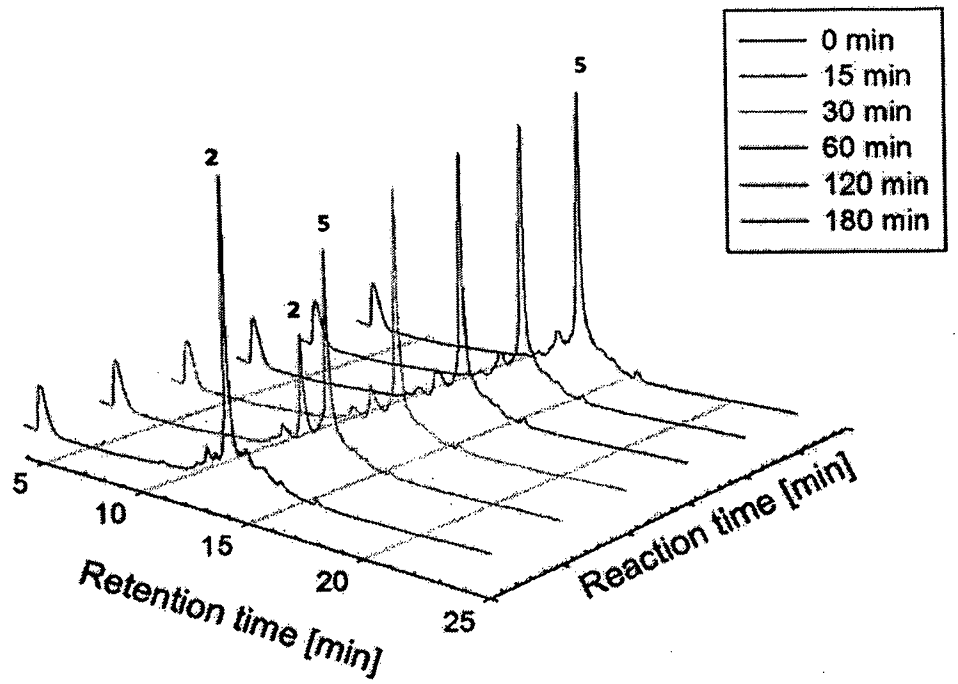


Figure 4

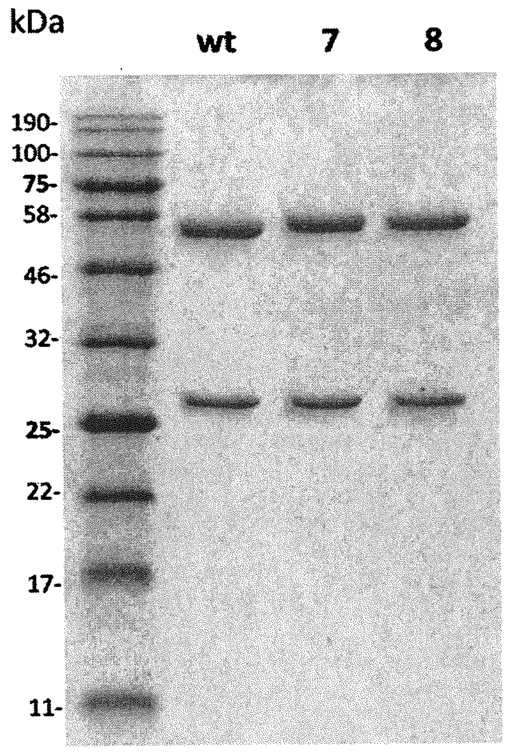


Figure 5

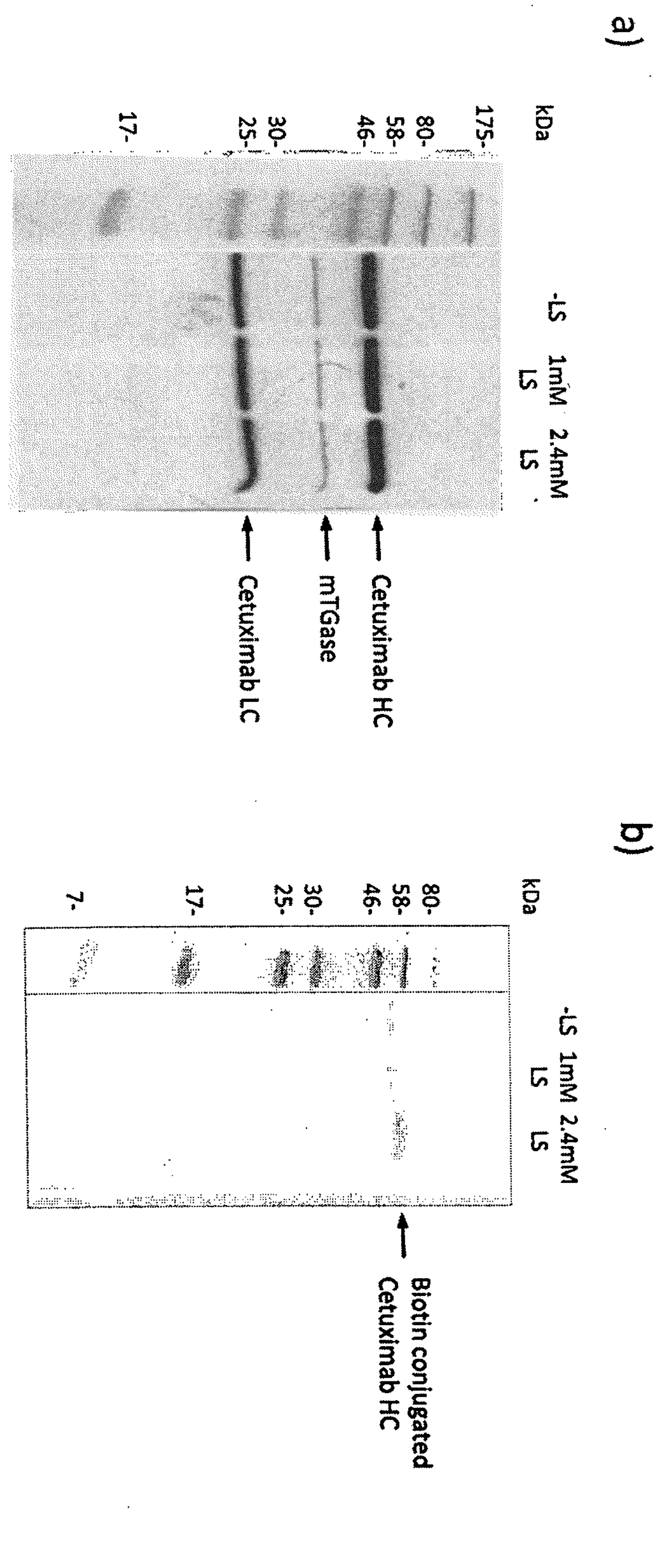

a)
kDa
175-
80-
58-
46-
30-
25-
17-
-LS
1mM LS
2.4mM LS
Cetuximab HC
mTGase
Cetuximab LC
b)
kDa
80-
58-
46-
30-
25-
17-
7-
-LS
1mM LS
2.4mM LS
Biotin conjugated Cetuximab HC

Figure 6

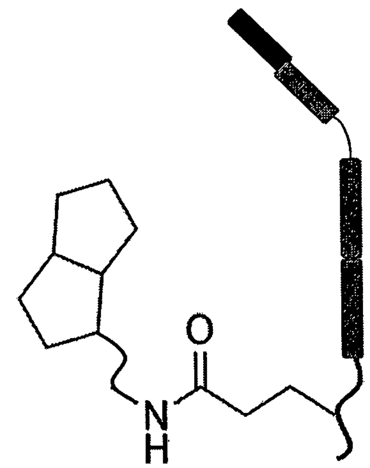


Figure 7

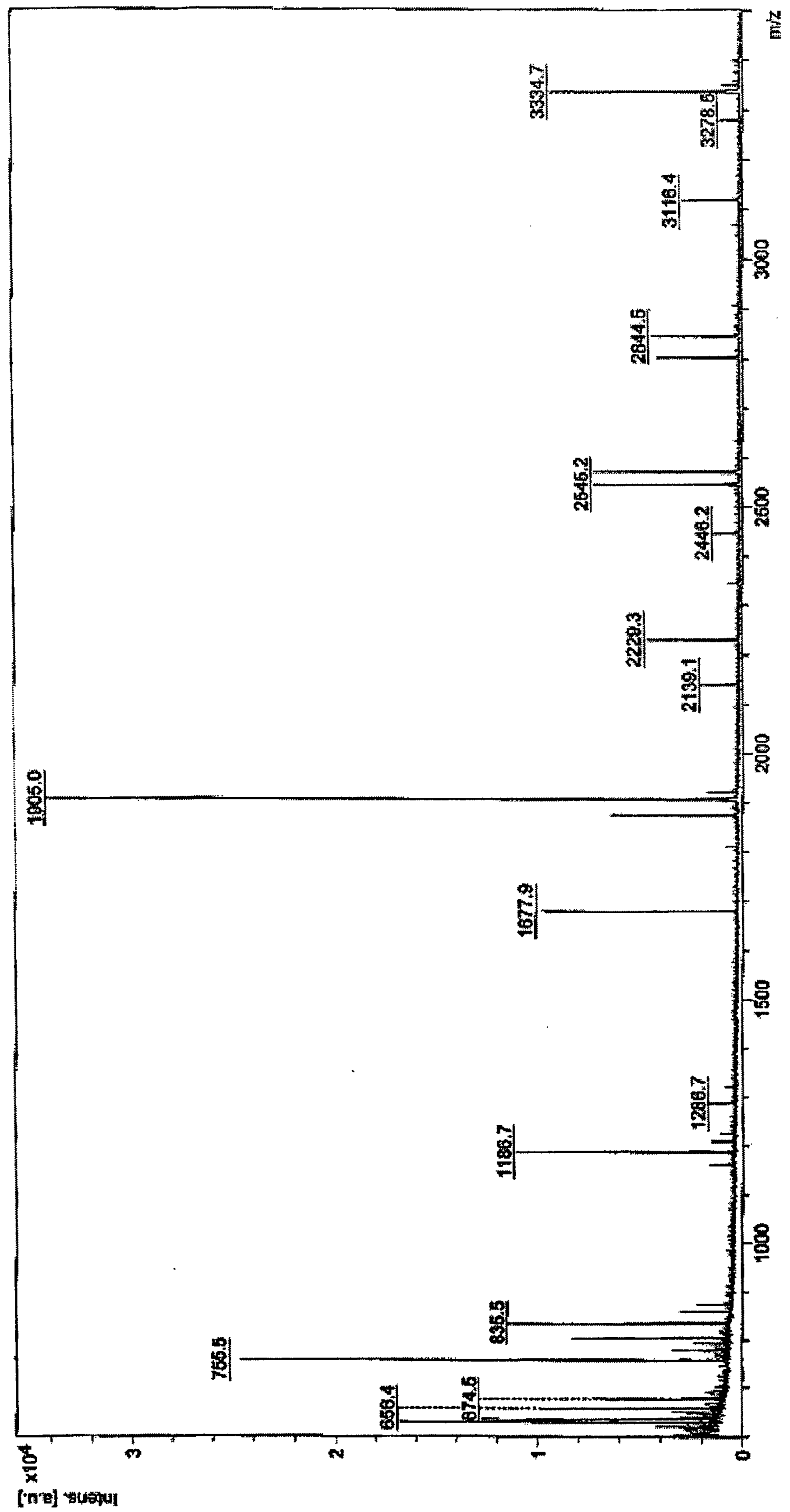

m/z
3334.7
3278.6
3116.4
3000
2844.6
2545.2
2446.2
2500
2229.3
2139.1
2000
1905.0
1677.9
1500
1288.7
1186.7
1000
835.5
755.5
674.5
656.4
Intens. [a.u.]
x10^4
3
2
1
0

Figure 8

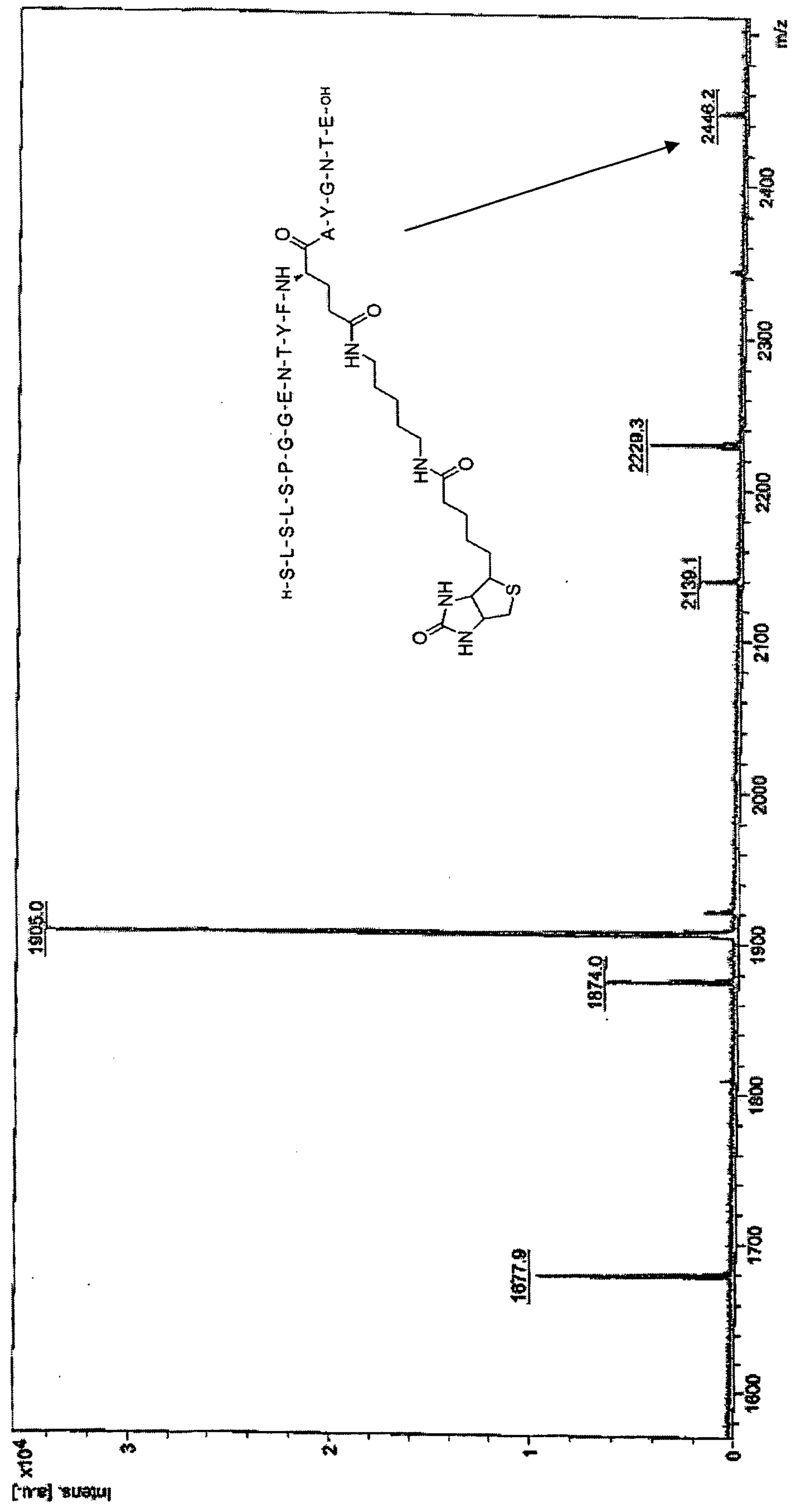

H-S-L-S-L-S-P-G-G-E-N-T-Y-F-NH
A-Y-G-N-T-E-OH
HN
HN
NH
HN
S
O
2446.2
2229.3
2139.1
1905.0
1874.0
1677.9
m/z
Intens. [a.u.]
x10^4

Figure 9

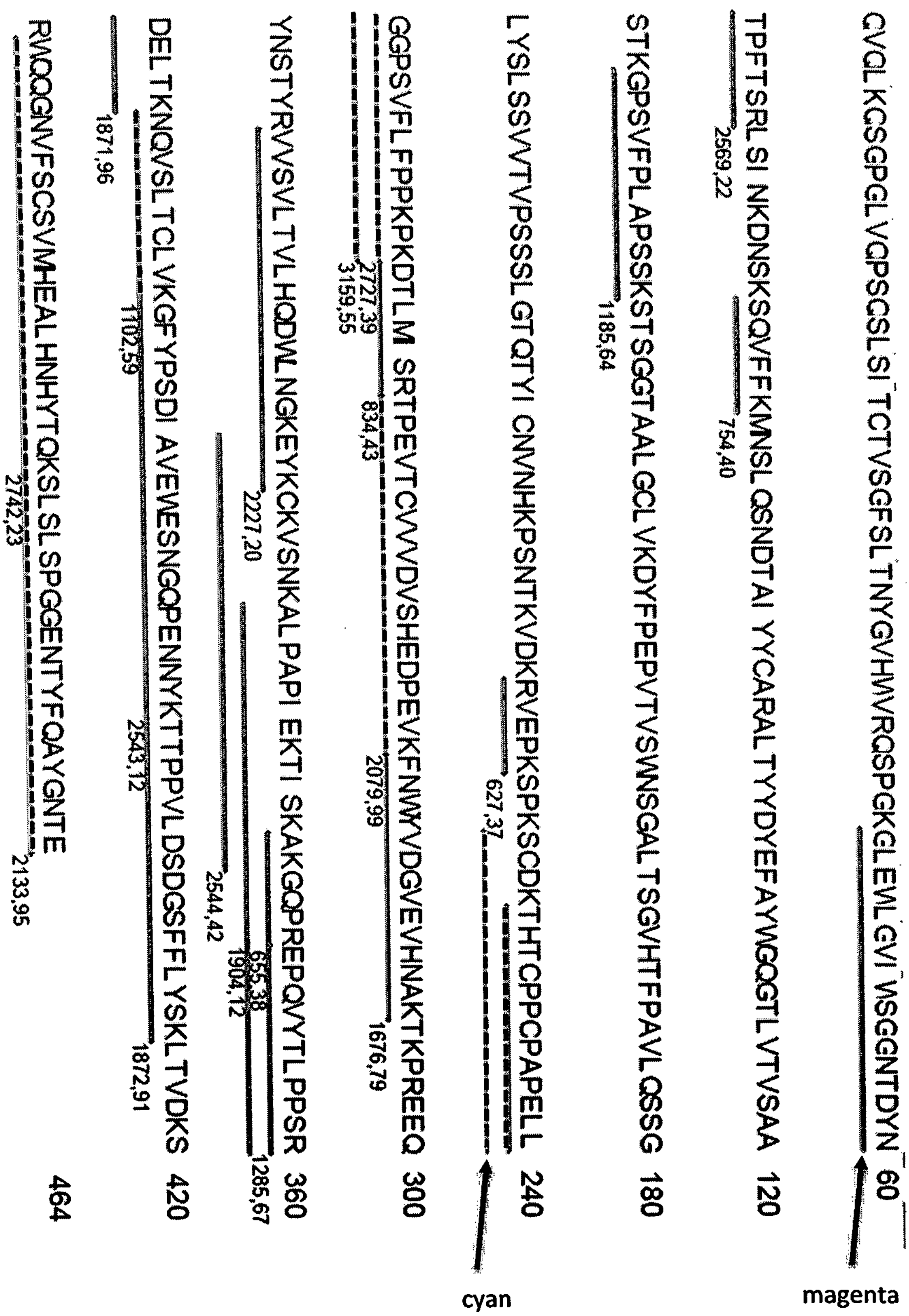

CVQLKQSGPGLVQPSQSLSI TCTVSGFSLTNYGVHWVRQSPGKGLEWLGVI WSGGNTDYN 60
TPFTSRLSI NKDNSKSQVFFKMNSLQSNDTAI YYCARALTYYDYEFAYWGQGTLVTVSAA 120
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
LYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKRVEPKSPKSCDKTHTCPPCPAPELL 240
GGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTI SKAKGQPREPQVYTLPPSR 360
DELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGENTYFQAYGNTE 464
2569,22
754,40
1185,64
627,37
2727,39
3159,55
834,43
2079,99
1676,79
2227,20
655,38
1285,67
1904,12
2544,42
1102,59
2543,12
1872,91
1871,96
2742,23
2133,95
magenta
cyan

Figure 10A

Residue coverage: 56% [261 of 464]
Peptide hits: 14 [12] Modified: 6 [6] Not identified: 8

Peptides identified without modifications:

input	found	dev.	mc	from-to	sequence	
628,400	627,370	-0,022	1	216-220	RVEPK	
656,400	655,377	-0,016	1	344-349	AKGQPR	Missed cleavage
755,500	754,401	-0,091	0	76- 81	SQVFFK	
835,500	834,427	-0,066	0	254-260	DTLMISR	metOx missing
1186,700	1185,639	-0,053	0	124-135	GPSVFPLAPSSK	
1286,700	1285,667	-0,026	0	350-360	EPQVYTLPPSR	
1677,900	1676,795	-0,098	0	280-293	FNWYVDGVEVHNAK	
1874,000	1872,915	-0,078	0	398-414	TTPPVLDSDGSFFLYSK	
1874,000	1871,963	-1,030	1	350-365	EPQVYTLPPSRDELTK	
1905,000	1904,121	0,128	3	332-349	ALPAPIEKTISKAKGQPR	Missed cleavage
2229,300	2227,200	-1,093	1	307-325	VVSVLTVLHQDWLNGKEYK	
2545,200	2544,422	0,230	5	323-345	EYKCKVSNKALPAPIEKTISKAK	Missed cleavage
2545,200	2543,124	-1,069	0	376-397	GFYPSDIAVEWESNGQPENNYK	
2570,290	2569,224	-0,059	0	44- 66	GLEWLGVIWSGGNTDYNTPFTSR	

Peptides identified with modifications:

input	found	dev.	mc	from-to	modification	sequence
1161,700	1102,593	-0,070	0	366-375	CAM	NQVSLTCLVK
2139,100	2079,991	-0,073	0	261-279	CAM	TPEVTCVVVDVSHEDPEVK
2446,200	2133,949	-0,077	-1	445-464	MBC	SLSLSPGGENTYFQAYGNTE
2801,300	2742,231	-0,033	0	422-444	CAM	WQQGNVFSCSVMHEALHNHYTQK
2844,500	2727,392	-0,042	0	228-253	CAM	THTCPPCPAPEL....GPSVFLFPPKPK
3334,700	3159,547	-0,058	1	224-253	CAM	SCDKTHTCPPCP....GPSVFLFPPKPK

Mass values not identified:
674,50 777,40 804,30 860,50 876,50
1208,70 3116,40 3278,50

Mass list checked for modifications [3*]:
CAM (58,029 Da) [C]
MBC (311,167 Da) [Q]

Figure 10 B

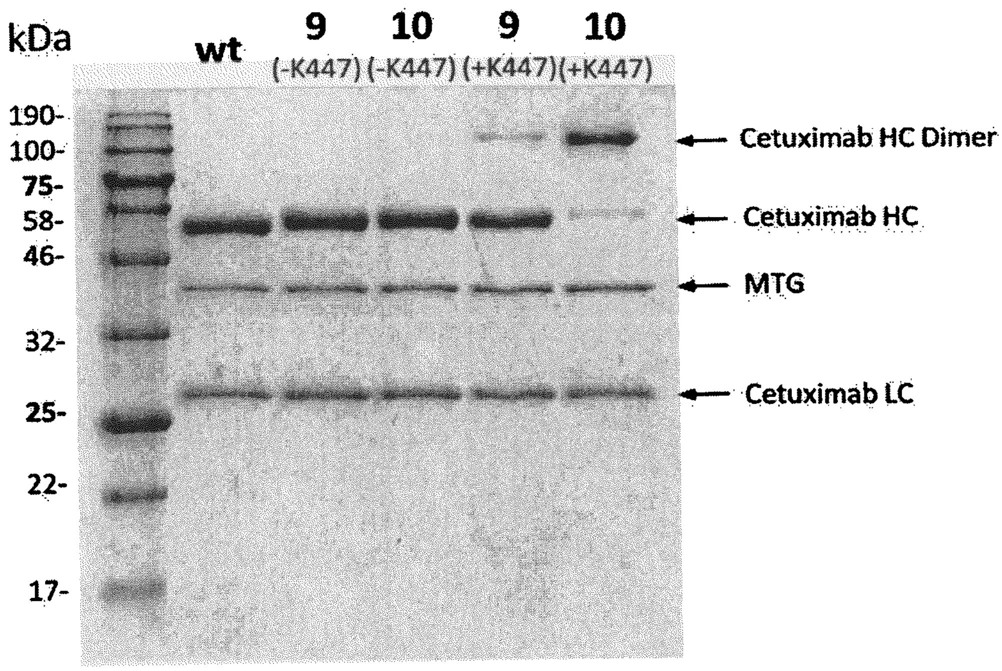
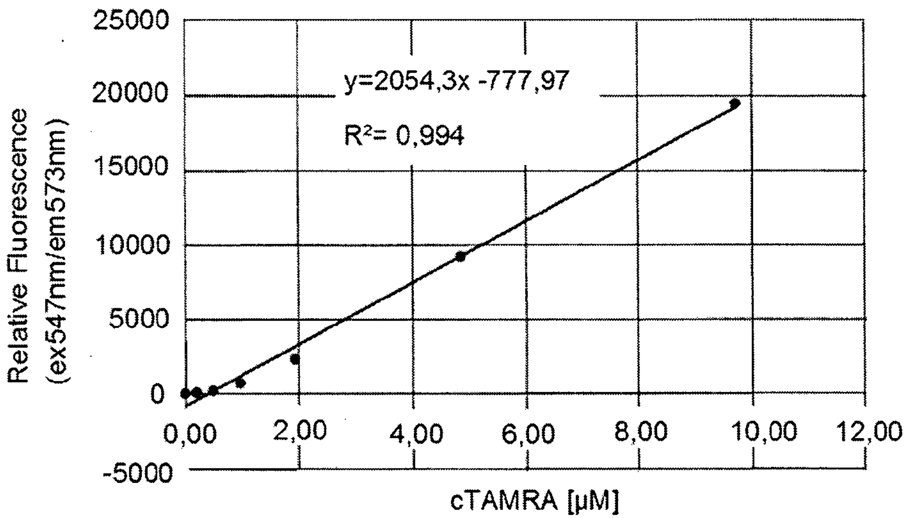


Figure 11

Sample	-Ab control (1:5)	7+TAMRA (1:5)	8+TAMRA (1:5)	-Ab control (1:10)	7+TAMRA (1:10)	8+TAMRA (1:10)
1	18	912	693	9	343	324
2	17	801	671	10	302	255
Mean	18	857	682	10	323	290
Std. dev.	0,5	55,5	11	0.5	20,5	34,5
TAMRA [µM]		0,787*	0,702*		0,531*	0,515*

*: determined using TAMRA-standard curve

Ab	c[µM]	n[pmol]	TAMRA c[µM]	TAMRA n[pmol]	% of labeled Ab
7+TAMRA	2,731	109,24	4,62	184,92	85
8+TAMRA	2,509	100,36	4,33	173,22	86



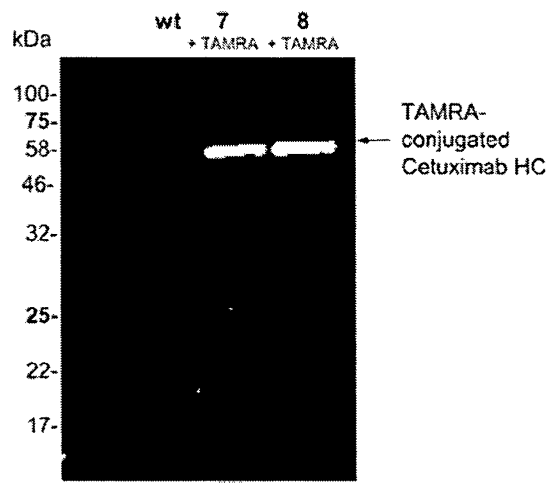


Figure 12

Sample	1	2	3	Mean	Std. dev.	cThiole [mM]	cProtein [mM]	cThiole/cProtein	Thiols/Protein theoretical
Lysozyme (red.)	0,428	0,493	0,463	0,461	0,033	0,497	0,067	7,459	8
Lysozyme	0,110	0,095	0,105	0,104	0,008	0,044	0,062	0,714	8
Cetuximab wt	0,102	0,088	0,122	0,104	0,017	0,045	0,013	3,334	32
7	0,085	0,089	0,093	0,089	0,004	0,026	0,016	1,641	36
8	0,107	0,091	0,106	0,102	0,009	0,042	0,020	2,131	32

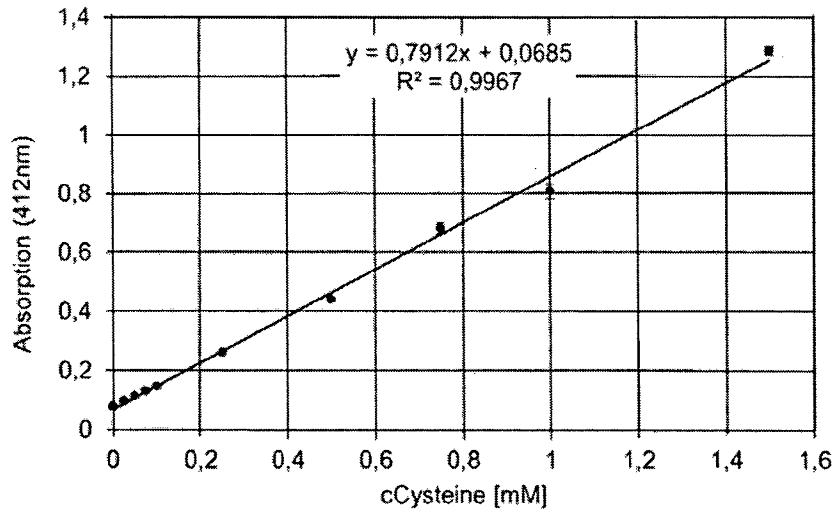
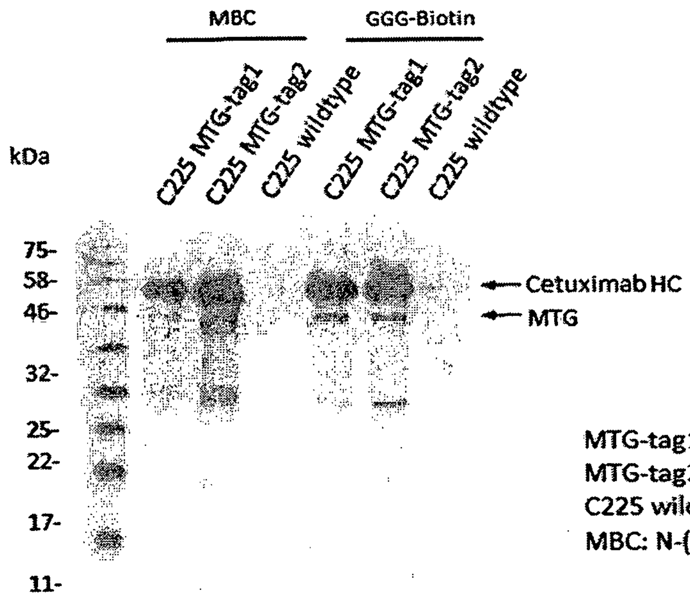


Figure 13

Conjugation of cetuximab with GGG-substrates by microbial transglutaminase (MTG)

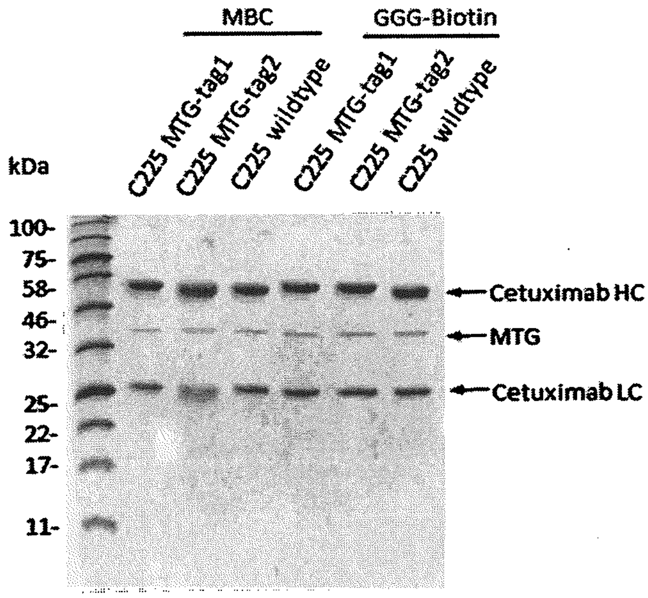
A



MTG-tag1: GECTYFQAYGCTE
MTG-tag2: GENTYFQAYGNTE
C225 wildtype: no MTG-tag
MBC: N-(Biotinyl)cadaverine

Western blot (Streptavidin-AP, NBT/BCIP)

B



15% SDS-PAGE (coomassie stained)

Figure 14 A, B

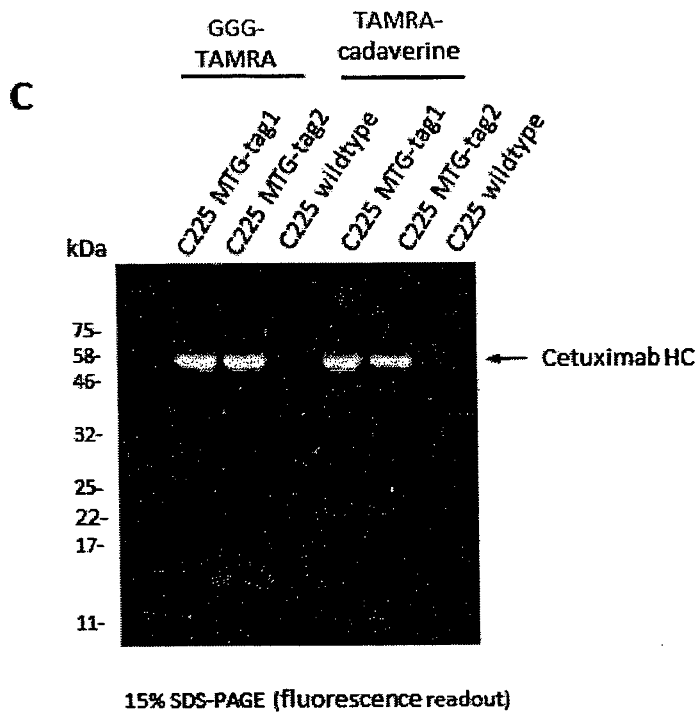
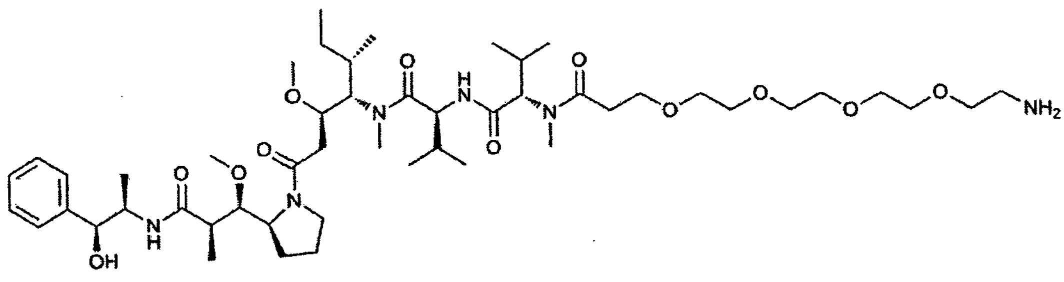
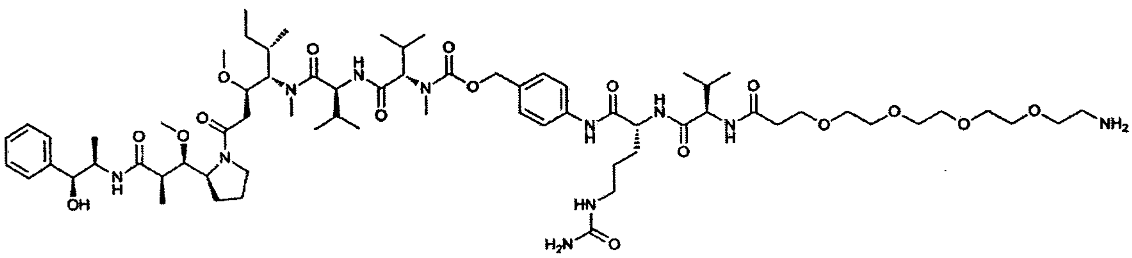

C
GGG-
TAMRA
TAMRA-
cadaverine
C225 MTG-tag1
C225 MTG-tag2
C225 wildtype
C225 MTG-tag1
C225 MTG-tag2
C225 wildtype
kDa
75-
58-
46-
32-
25-
22-
17-
11-
Cetuximab HC
15% SDS-PAGE (fluorescence readout)

Figure 14 C

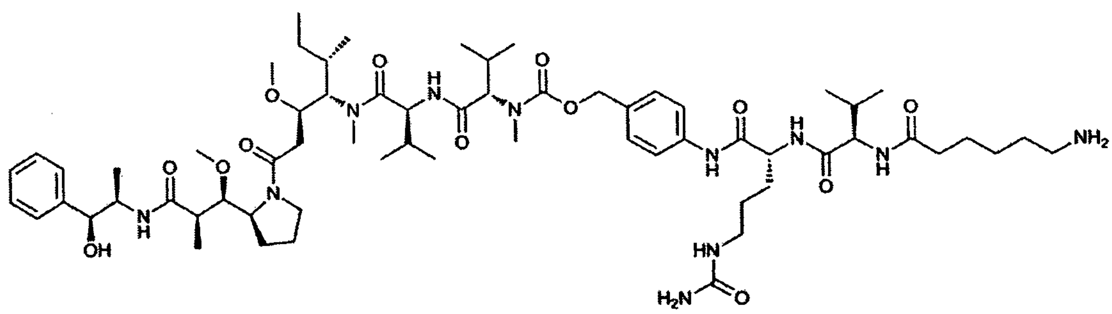
1



2



3



4

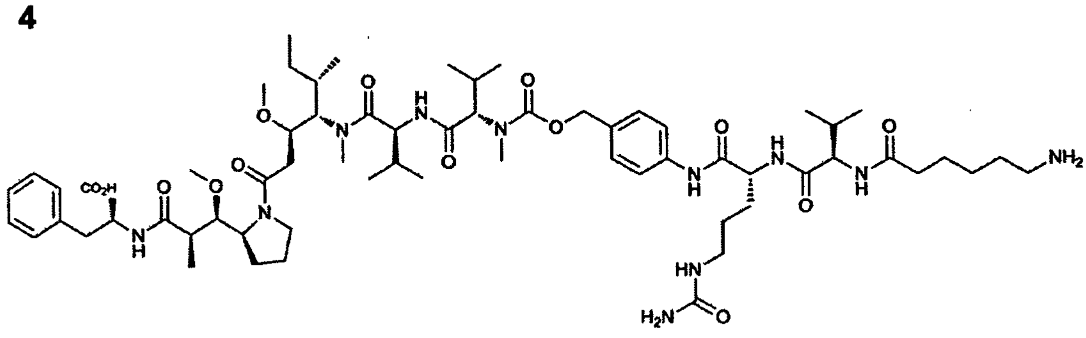


Figure 15

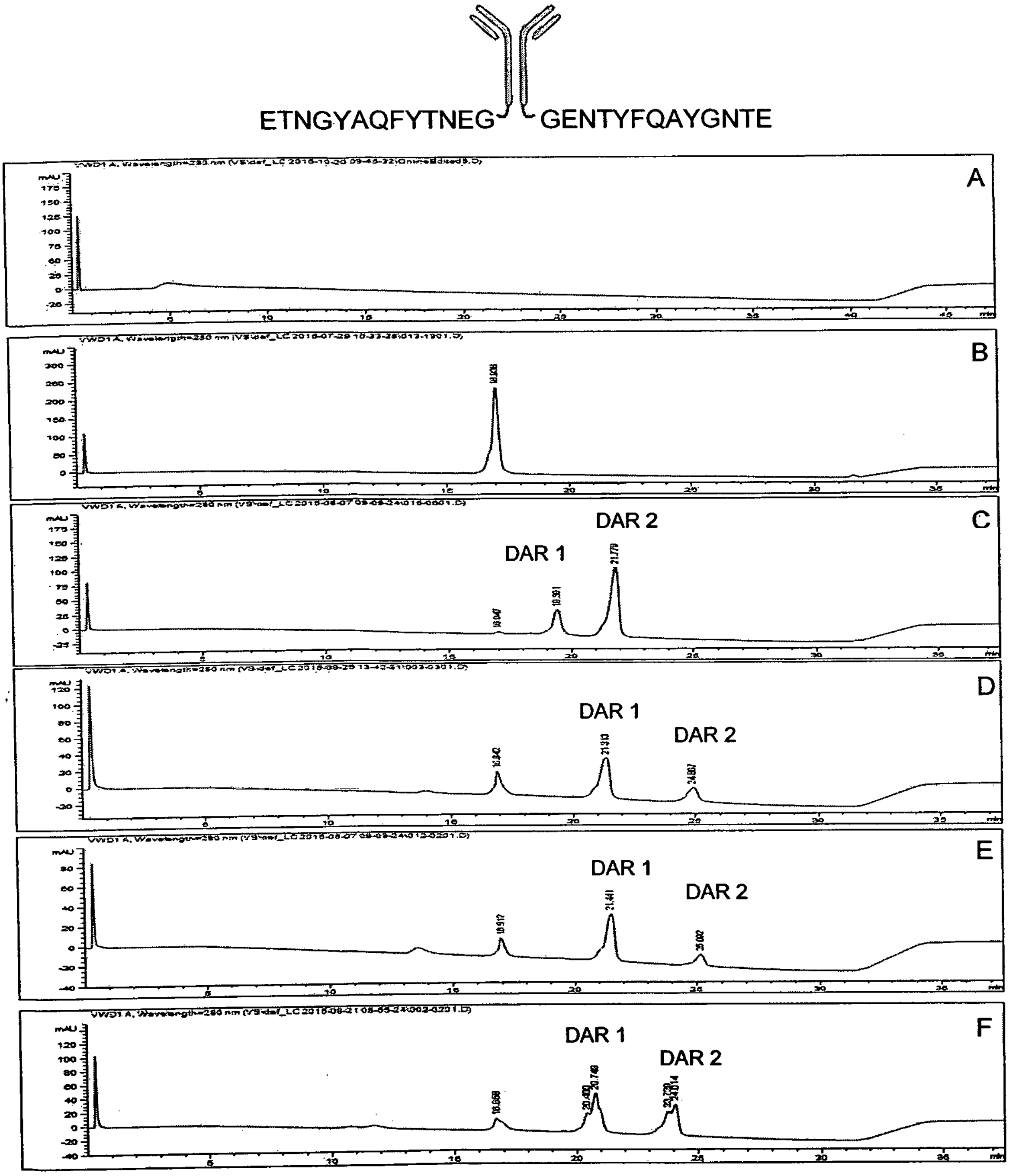

ETNGYAQFYTNEG
GENTYFQAYGNTE
A
B
DAR 2
DAR 1
C
DAR 1
DAR 2
D
DAR 1
DAR 2
E
DAR 1
DAR 2
F

Figure 16