

Recombinant Glycoproteins with Reduced Antennary Fucosylation

The present invention relates to methods for reducing antennary fucosylation of complex N-glycans in recombinantly expressed glycoproteins, cell lines that can be used in said methods, respective recombinant glycoproteins, and methods for expressing the same in said cell lines.

Most current recombinant therapeutic proteins are glycoproteins. They have sugar residues attached to the amino-group of an asparagine (N-linked glycans) or the hydroxyl-group of a serine or threonine (O-linked glycans). The structure of the glycans is highly variable, depending on the specific protein and the host cell used for recombinant expression.

A very common structure of N-glycans found on glycoproteins expressed with mammalian expression platforms are so-called complex N-glycans, characterized by the core sugar sequence $\text{Man}\alpha 1-6(\text{Man}\alpha 1-3)\text{Man}\beta 1-4\text{GlcNAc}\beta 1-4\text{GlcNAc}\beta 1-\text{Asn}-$. This core structure is extended by “antennae” which are initiated by N-acetylglucosamine (GlcNAc). Typically, complex type N-glycans have two, three, or four antennae, but in rare cases five or six antennae can be found. A typical structure of a di-antennary complex type N-glycan is depicted in Fig. 1A.

Complex N-glycans can be fucosylated. In mammalian cells, fucose is either linked to the proximal GlcNAc by $\alpha 1-6$ linkage (core fucose) or to a distal GlcNAc on one or several of the antennae by $\alpha 1-3$ linkage (antennary fucose; also called Lewis^x antigen (Le^x), CD15, or SSEA-1), displayed in Fig. 1B. If the Lewis^x structure ($\text{Gal}(\beta-4)[\text{Fuc}(\alpha)]\text{GlcNAc-R}$) harbors an additional sialic acid, the resulting structure is called sialyl-Lewis^x, sialyl-Le^x, or SLe^x ($\text{NeuAc}(\alpha 1\rightarrow 4)\text{Gal}(\beta-4)[\text{Fuc}(\alpha 1\rightarrow 3)]\text{GlcNAc-R}$), displayed in Fig. 1C. Sialyl Lewis^x structures emerge by the fucosylation of sialylated complex type N-glycans at the distal GlcNAc catalyzed by various fucosyltransferases. The role of core $\alpha 1-6$ fucosylation has been extensively studied for antibodies. Antibodies of the IgG class typically carry an N-glycan in the CH2 domain of the Fc region. The presence of a core fucose on these N-glycans

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significantly reduces the ADCC (antibody dependent cellular cytotoxicity) response mediated by the antibody *in vivo*. Since ADCC is usually a highly desired effect of a therapeutic antibody, several approaches are being taken to reduce the presence of core-fucose on IgGs. The highly immunogenic core α 1-3 linked fucose structure
5 only exists in plants and in invertebrates and is absent in human cells.

On immunoglobulins, typically no antennary fucose is found, however Lewis^x or sialyl-Lewis^x structures are easily detected on other serum-glycoproteins. Up to date little is known about its physiological role. There is evidence that antennary fucose
10 might increase targeting to sites of inflammation via selectin interactions, but apart from that relatively little is known about the physiological role of antennary fucosylation.

When plasma proteins are recombinantly expressed, the product often shows an
15 elevated level of antennary fucose as compared to the naturally occurring counterpart in the plasma. In order to reduce potential immunogenic effects of recombinant proteins used in replacement therapy, it is desirable that they are as similar to the endogenous protein as possible. A reduction of antennary fucose on recombinant therapeutic proteins is an important step towards this goal.

20 Accordingly, the technical problem underlying the present invention is to provide means for reducing antennary fucosylation (Le^x or SLe^x) of complex N-glycans in recombinantly expressed glycoproteins, as well as respective recombinant glycoproteins and means for producing the same.

25 The solution to the above technical problem is achieved by the embodiments characterized in the claims.

In particular, in a first aspect, the present invention relates to a method for reducing
30 antennary fucosylation of complex N-glycans, either Le^x or sialyl-Le^x in a recombinantly expressed glycoprotein, comprising the step of overexpressing

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together with the glycoprotein β -galactoside α -2,6-sialyltransferase 1 (ST6Gal1) and/or α -2,3-sialyltransferase 4 (ST3Gal4).

As used herein, the term "complex N-glycans" relates to N-glycans that are characterized by the core sugar sequence Man α 1-6(Man α 1-3)Man β 1-4GlcNAc β 1-4GlcNAc β 1-Asn-. This complex N-glycan core sugar sequence can be extended by 2 to 6 antennae which are initiated by N-acetylglucosamine (GlcNAc), wherein two, three or four antennae are typical. Said antennae are sometimes referred to herein as "complex N-glycan antennae". Further, as used herein, the term "antennary fucosylation of complex N-glycans" refers to α 1-3 linkage of fucose to a distal GlcNAc on at least one of the complex N-glycan antennae. In this context, the term "distal GlcNAc" refers to any GlcNAc present in an antenna other than the glycan's initial GlcNAcs.

The term "reducing antennary fucosylation of complex N-glycans" relates to the fact that according to the present invention, by way of overexpressing ST6Gal1 and/or ST3Gal4 together with the glycoprotein, recombinant glycoprotein is generated that has a lower amount of fucosylated complex N-glycan antennae as compared to a conventional recombinant glycoprotein. Preferably, such recombinant glycoprotein is characterized by a significantly reduced antennary fucosylation of complex N-glycans as compared to the same recombinant glycoprotein expressed without overexpression of ST6Gal1 and/or ST3Gal4.

In particularly preferred embodiments, at least 80%, more preferably at least 90%, and most preferably at least 95%, or more, of the complex N-glycan antennae of the recombinantly expressed glycoprotein are not fucosylated.

The glycoprotein to be subject to the methods of the present invention is not particularly limited, provided that it is a glycoprotein having complex N-glycans and respective complex N-glycan antennae. In preferred embodiments, the glycoprotein is selected from the group consisting of α 1-antitrypsin (AAT), hepatocyte growth factor (HGF), Factor VII (FVII), Factor VIII (FVIII), Factor IX (FIX), von Willebrand-

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Factor (vWF), alkaline phosphatase, and C1 esterase inhibitor (C1-inhibitor; C1 Inh). Further, the glycoprotein is preferably a mammalian, more preferably a human glycoprotein.

- 5 As used herein, the term “recombinantly expressed glycoprotein” relates to glycoproteins that are biotechnologically produced in genetically modified organisms or cells.

Methods for recombinantly expressing glycoproteins, as well as for overexpressing
10 ST6Gal1 and/or ST3Gal4 together with such glycoproteins, are not particularly limited and are known in the art. Further details in this respect are provided hereinafter for the second aspect of the present invention, relating to the cell lines of the present invention.

- 15 In specific embodiments of the present invention, both ST6Gal1 and ST3Gal4 are overexpressed together with the recombinant glycoprotein.

In further specific embodiments of the present invention, (i) β -galactoside α -2,3-sialyltransferase 1 (ST3Gal1) is not overexpressed together with the recombinant
20 glycoprotein, and/or (ii) the expression of α -1,3-mannosyl-glycoprotein 4- β -N-acetylglucosaminyltransferase A (GnTIVa), α -1,3-mannosyl-glycoprotein 4- β -N-acetylglucosaminyltransferase B (GnTIVb), and α -1,6-mannosylglycoprotein 6- β -N-acetylglucosaminyltransferase A (GnTV) is not reduced.

- 25 In this context, the term “ST3Gal1 is not overexpressed together with the recombinant glycoprotein” relates to the fact that ST3Gal1 expression is not increased in any manner as compared to native ST3Gal1 expression. In particular embodiments, ST3Gal1 is not expressed at all. Further, the term “expression of GnTIVa, GnTIVb, and GnTV is not reduced” relates to the fact that expression of
30 said proteins is not decreased in any manner as compared to native expression of said proteins.

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In a second aspect, the present invention relates to a cell line, preferably an insect, avian, or mammalian cell line, more preferably a mammalian, in particular human, cell line, that is genetically modified to overexpress β -galactoside α -2,6-sialyltransferase 1 (ST6Gal1) and/or α -2,3-sialyltransferase 4 (ST3Gal4).

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As used herein, the term "cell line that is genetically modified to overexpress ST6Gal1 and/or ST3Gal4" indicates that upon genetic modification, the individual cells of the cell line display a higher expression of the respective sialyltransferase(s) than they did before the genetic modification.

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Genetic modifications that allow the overexpression of a given protein are not particularly limited and are known in the art. In a particular example, the cell line comprises endogenous gene(s) encoding ST6Gal1 and/or ST3Gal4, such as e.g. human cell lines. In such cases, the cells can be genetically modified by inserting a promoter, enhancing element, and/or stabilizing element into the genome of the cells in a position suitable to cause overexpression of said nucleic acid. This can be done by homologous recombination using TALENS, Zn-finger proteins, CRISPR-CAS9, or other methods known in the art. Thus, in preferred embodiments, the cell line comprises endogenous gene(s) encoding ST6Gal1 and/or ST3Gal4, and further has at least one genetic element, selected from the group consisting of a promoter, an enhancing element, and a stabilizing element inserted into the genome in one or more position(s) suitable to cause overexpression of ST6Gal1 and/or ST3Gal4. Suitable promoters, enhancing elements and stabilizing elements are not particularly limited and are known in the art. For example, promoters include constitutive promoters, e.g. a CMV, EF1 α , SV40, RSV, UbC, CAG, BOS or PGK promoter, and inducible promoters, e.g. tetracycline inducible promoters or other inducible promoters known in the art. Further, enhancing elements (enhancers) include CMV enhancer, β -globin enhancer, immunoglobulin enhancer, and PGK-enhancer. Furthermore, stabilizing elements (chromatin elements) include matrix attachment regions (MARS), locus control regions (LCRs), and ubiquitously acting chromatin opening elements (UCOE).

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Alternatively, in cases where the cells do not comprise endogenous gene(s) encoding ST6Gal1 and/or ST3Gal4, or additionally, in cases where the cells do comprise endogenous gene(s) encoding ST6Gal1 and/or ST3Gal4, genetic modification of the cells can be achieved by introducing nucleic acid(s), encoding

5 ST6Gal1 and/or ST3Gal4 into the cells. Methods for introducing nucleic acids into cells are not particularly limited and are known in the art. For example, said nucleic acids could be introduced in circular or linearized form into the cells by electroporation, nucleofection, microinjection, via viral vectors, *e.g.* lentiviral vectors, reagent based methods, *e.g.* lipids, calcium phosphate, cationic polymers or other

10 methods known in the art. The nucleic acids can be transiently or stably introduced into the cell by episomal systems or by stable integration of the nucleic acid into the genome. Said nucleic acids can be present in the cells in the form of one or more expression vector(s), *e.g.* pcDNA, pCEP, pLenti, pEntr, pDest, pEF, pEAK, pCMV, pStbl, or other expression vectors known in the art. Expression of ST6Gal1 and/or

15 ST3Gal4 can be under the control of a constitutive promoter, *e.g.* a CMV, EF1alpha, SV40, RSV, UbC, CAG, BOS or PGK promoter, the endogenous promoter, or of an inducible promoter, *e.g.* tetracycline inducible promoter or other inducible promoters known in the art. Further, the nucleic acids encoding ST6Gal1 and/or ST3Gal4 can be present as one continuous nucleic acid, or can be present as separate nucleic

20 acids, *e.g.* as separate expression vectors. Said nucleic acids can contain, in addition to the coding region and a promoter, suitable restriction sites, Kozak sequences, ribosomal binding sites, chromatin modulating elements, selection cassettes, episomal replication systems, *e.g.* Epstein-Barr Nuclear Antigen and ori P, or SV40 ori and SV40 T-large antigen, internal ribosomal entry sites (IRES),

25 splicing signals, and polyadenylation signals known in the art. Thus, in preferred embodiments, the cell line comprises exogenous nucleic acid(s) encoding ST6Gal1 and/or ST3Gal4.

Suitable genes encoding ST6Gal1 and/or ST3Gal4 for transfection of cell lines are

30 not particularly limited and include any genes from any origin that encode proteins having ST6Gal1 or ST3Gal4 activity. Preferably, such genes are mammalian, more preferably human, ST6Gal1 and ST3Gal4 genes.

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The cell lines according to the present invention can be derived from cell lines, *e.g.* mammalian cell lines, known in the art. In preferred embodiments, a cell line of the present invention can be derived from Muscovy Duck cells (AGE.CR®) African green monkey kidney epithelial cells (Vero), Madin Darby canine kidney cells (MDCK),
5 baby hamster kidney cells (BHK), Chinese hamster ovary (CHO) cells, human hepatocarcinoma cell lines (HepG2, Huh7), human embryonic kidney 293 (HEK293) cells, human neuronal precursor cells (AGE1.HN® and NC5T11), human embryonic retinoblasts (Per.C6), myeloma cell lines (HMCLs, MM.1, U266, RPMI8226), CML tumor cell lines (NM, NM-F9.), hybrid HEK293 and lymphoma cell (HKB11), or
10 human amniocytes (CAP; cf. EP 1 230 354 B1), wherein CHO cells, HEK293 cells and CAP cells are preferred, and CAP cells are particularly preferred.

In this context, CAP cells are permanent amniocytic cell lines comprising a nucleic acid encoding the gene products of the adenovirus, in particular adenovirus type 5
15 (Ad5), E1A and E1B regions. CAP cells are derived from primary human amniocytes that are transformed with a nucleic acid encoding Ad5 E1A and E1B.

Accordingly, in a preferred embodiment, the cell lines according to the present invention can be derived from human primary amniocytes comprising at least one
20 nucleic acid encoding the gene products of the adenoviral E1 and pIX region, preferably E1 and pIX region of adenovirus type 5 (Ad5) from nt. 505 to 4079, in which E1A is under the control of the murine phosphoglycerate kinase (pgk) promoter, while E1B and pIX expression is controlled from their natural promoters. The E1B downstream intron, splice acceptor and polyA signal are replaced by
25 corresponding motifs from SV40.

In specific embodiments of the present invention, the cell line of the present invention is genetically modified to overexpress both ST6Gal1 and ST3Gal4.

30 In further specific embodiments of the present invention, the cell line of the present invention is not genetically modified to (i) overexpress β -galactoside α -2,3-sialyltransferase 1 (ST3Gal1), and/or (ii) reduce the expression of α -1,3-mannosyl-

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glycoprotein 4- β -N-acetylglucosaminyltransferase A (GnTIVa), α -1,3-mannosylglycoprotein 4- β -N-acetylglucosaminyltransferase B (GnTIVb), and α -1,6-mannosylglycoprotein 6- β -N-acetylglucosaminyltransferase A (GnTV).

- 5 In this context, the term “the cell line is not genetically modified to overexpress ST3Gal1” relates to the fact that ST3Gal1 expression is not increased in any manner as compared to the cell line’s native ST3Gal1 expression. In particular embodiments, ST3Gal1 is not expressed at all. Further, the term “the cell line is not genetically modified to reduce the expression of GnTIVa, GnTIVb, and GnTV” relates to the fact
10 that expression of said proteins is not decreased in any manner as compared to native expression of said proteins in the cell line.

The cell lines according to this second aspect of the present invention are capable of reducing antennary fucosylation of complex N-glycans in recombinant
15 glycoproteins expressed in said cell lines.

In a third aspect, the present invention relates to a recombinant glycoprotein having complex N-glycans, wherein antennary fucosylation of the complex N-glycans is reduced, so that at least 80%, more preferably at least 90%, and most preferably at
20 least 95%, or more, of the complex N-glycan antennae of the recombinant glycoprotein are not fucosylated.

In this aspect, all relevant definitions and limitations given above for the first and second aspect of the present invention apply in an analogous manner.

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Respective recombinant glycoproteins can be produced as described herein, *e.g.* by overexpression of ST6Gal1 and/or ST3Gal4 together with the recombinant glycoprotein. Preferably, said glycoproteins are produced in a cell line according to the present invention as described herein.

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In a fourth aspect, the present invention relates to a method for the expression of a recombinant glycoprotein according to the present invention, comprising the steps of:

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- (a) providing a cell line according to the present invention,
- (b) expressing the recombinant glycoprotein in said cell line; and
- (c) isolating the recombinant glycoprotein from the cells or the cell culture supernatant.

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In this aspect, all relevant definitions and limitations given above for the first, second and third aspect of the present invention apply in an analogous manner. In particular, the recombinant glycoprotein and the cell line are as defined above.

- 10 Means for the expression of proteins in the cell lines of the present invention are not particularly limited and are known in the art. In this context, the step (b) of expressing the glycoprotein of interest in said cell line encompasses the transfection of a respective coding nucleic acid into said cell line prior to the actual expression of the glycoprotein. Further, means for isolating a glycoprotein of interest from a cell
- 15 culture are not particularly limited and are known in the art.

In a related aspect, the present invention relates to the use of a cell line according to the present invention for the production of recombinant glycoproteins according to the present invention.

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In this aspect, all of the definitions and preferred and/or specific embodiments described for the recombinant glycoproteins of the present invention and the cell lines of the present application apply in an analogous manner where applicable.

- 25 The figures show:

Figure 1:

The Lewis glyco-epitope family, showing a subset of possible variants. The Le^x glyco-epitopes carry fucose in an α 1-3 linkage to the GlcNAc monosaccharide. A) sialylated, non-fucosylated GlcNAc; B) Lewis X (Le^x) also called CD15 or SSEA-1; C) Sialyl Lewis X (sLe^x).

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Figure 2:

IEF (isoelectric focusing) analysis shows increased sialylation of hAAT purified from glyco-optimized CAP cells stably, recombinantly expressing hAAT and ST3Gal4 or ST6Gal1 compared to hAAT purified from non-engineered hAAT expressing CAP cells. 5 µg of affinity purified hAAT per lane were subjected to isoelectric focusing. Different time points during pool generation are shown. Samples: CAP-hAAT-ST3Gal4, hAAT from CAP cell stably expressing human AAT as well as sialyltransferase ST3Gal4, CAP-hAAT-ST6Gal1, hAAT from CAP cell stably expressing human AAT as well as sialyltransferase ST6Gal1. Plasma derived hAAT (Prolastin), hAAT from non-glyco-optimized CAP cells, and desialylated hAAT from CAP cells served as controls.

Figure 3:

Comparative lectin blot analysis of recombinant AAT reveals that a decreased amount of fucosylation correlates with increased amounts of sialylation. Purified human rAAT from either wild-type CAP cells, CAP-ST3Gal4 cells or CAP-ST6Gal1 cells were separated by SDS-PAGE, blotted on nitrocellulose membrane and detected by specific lectins. The corresponding densitometrical analysis (B) was normalized on the AAT protein content in the matching western blot. The *Erythrina crista-galli* lectin (ECL-lectin) analysis detects free galactoses on N-glycans which indicates incomplete sialylation. α 1-3 linked fucose is detected by *Lotus tetragonolobus* agglutinin (LTA).

Figure 4:

FACS analysis of cell surface glycoproteins of glyco-optimized CAP cells stably expressing ST3Gal4 or ST6Gal1 in comparison to non-engineered CAP cells reveals that overexpression of one of these two sialyltransferases not only increases the degree of sialylation on the majority of expressed glycoproteins. It also decreases the amount of antennary fucose on N-glycan structures, resulting in a reduced amount of Lewis^x structures.

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Figure 5:

Increasing amounts of sialic acid (NANA) and reduced amounts of fucose (Fuc) in hAAT purified from CAP cells stably expressing either ST3Gal4 or ST6Gal1 compared to hAAT purified from cell culture supernatant from non-engineered CAP cells. Plasma derived hAAT (Prolastin) shown as control. Monosaccharide analysis was performed by high performance anion exchange chromatography with pulsed amperometric detection (HPAEC PAD).

Figure 6:

Comparative lectin blot analysis of recombinant C1-Inhibitor reveals that an increase in sialylation correlates with a decrease in antennary fucosylation. Purified C1-Inhibitor from either wild-type CAP cells, CAP-ST3Gal4 cells or CAP-ST6Gal1 cells were separated by SDS-PAGE, blotted on nitrocellulose membrane and detected by specific lectins. The corresponding densitometrical analysis (B) was normalized to the C1-Inh protein content in the matching western blot. The *Erythrina crista-galli* lectin (ECL-lectin) analysis (A and B) detects free galactoses on N-glycans which indicates incomplete sialylation. α 1-3 linked fucose is detected by *Lotus tetragonolobus* agglutinin (LTA).

Figure 7:

MS-MS analysis of recombinant C1-Inhibitor: PNGase F released permethylated N-glycans from purified C1-Inhibitor either from wild-type CAP cells, from CAP-ST3Gal4 cells or from CAP-ST6Gal1 cells were analyzed by MALDI TOF/TOF. Only the signal at 3196.8 in MS1 of wildtype derived C1-Inhibitor (A) contained two fucose residues and the characteristic fragmentation pattern for antennary fucose (M/z 638, 505, 260; D) in MS2. In CAP-ST3Gal4 (B) and CAP-ST6Gal1 (C) the signal at 3196.8 could not be detected, also no other signal of MS1 contained a fragmentation pattern of antennary fucose in MS2.

The present invention will be further illustrated in the following examples without being limited thereto.

ExamplesExperimental procedures:5 *Cell culture and fermentation.*

The permanent human amniocyte cell line CAP 1D5 was cultured in suspension, either in chemically defined, animal component free CAP-CDM medium (CEVEC Pharmaceuticals, Germany) supplemented with 6 mM stable glutamine (Biochrom, Germany), or in serum free PEM media (Life Technologies) supplemented with 4 mM stable glutamine (Biochrom, Germany). CAP cells were cultivated at 37 °C in shaker flasks (Corning, #431143, 125 mL (25 mL vv) or #431252, 3000 mL (1000 mL vv)) at 5% CO₂, and 185 rpm. During fermentation, CAP cells were fed at d3, d5, and d7 with 10 % CAP-CDM feed solution (CEVEC Pharmaceuticals, Germany) and 4 mM stable glutamine (Biochrom, Germany).

Cloning.

20 For the generation of CAP cell lines stably expressing ST3Gal4 or ST6Gal1, the cells were nucleofected with the corresponding nucleic acid constructs. Table 1 lists all cell lines created for this project.

For designing the ST3Gal4 cDNA, sequence information of the precursor protein and mature protein was based on the database entry UniProt Q11206 (SEQ ID NO: 1). For cloning, a ClaI restriction site and a Kozak sequence were added 5' of the start codon of the human ST3Gal4 cDNA and an EcoRV restriction site was added 3' of the stop codon to be inserted between the ClaI and EcoRV restriction sites in the pStbl-Neo-CMV-MCS(-) vector resulting in the expression plasmid pStbl-Neo-CMV-ST3Gal4. This vector contains a CMV promoter driving the expression of the gene of interest, followed by an SV40 intron for improved, splicing-mediated mRNA transport and a multiple cloning site for the insertion of the gene of interest. The

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selection marker is driven by the human ubiquitin (UbC) promoter. cDNA synthesis was performed at GeneArt (Germany, Life Technologies).

Table 1: Stable cell lines used in the present invention.

Cell line	rec. protein	overexpression of the sialyltransferase(s)
CAP	/	/
CAP-AAT	AAT	/
CAP-AAT-ST3Gal4	AAT	ST3Gal4
CAP-AAT-ST6Gal1	AAT	ST6Gal1
CAP-C1 Inh	C1 Inh	/
CAP-C1 Inh-ST3Gal1	C1 Inh	ST3Gal4
CAP-C1 Inh-ST3Gal4	C1 Inh	ST6Gal1

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For designing the ST6Gal1 cDNA, sequence information of the precursor protein and mature protein was based on the database entry UniProt P15907 (SEQ ID NO: 2). For cloning, a ClaI restriction site and a Kozak sequence were added 5' of the start codon of the human ST6Gal1 cDNA and an EcoRV restriction site was added 3' of the stop codon to be inserted between the ClaI and EcoRV restriction sites in the pStbl-Neo-CMV-MCS(-) vector resulting in the expression plasmid pStbl-Neo-CMV-ST6Gal1. cDNA synthesis was performed at GeneArt (Germany, Life Technologies).

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Nucleofection and pool generation.

Nucleofection was performed using a Nucleofector II (LONZA) with the appropriate Nucleofector Kit (KitV) according to the manufacturer's protocol. Briefly, during exponential growth phase of the culture 1×10^7 cells were harvested via

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centrifugation (150 g for 5 min) and re-suspended in 100 µl complete Nucleofector solution and mixed with a total of 5 µg plasmid. Nucleofection was performed using the X001 program. After the pulse, cells were recovered in 12 ml complete cell culture media in a 125 ml shaking flask. The cells were cultured as before at 37 °C,
5 5% CO₂, and 185 rpm.

72 to 96 h post-nucleofection cells were selected with 200 µg/ml neomycin in order to generate stable pools.

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Western blot analysis.

Purified protein solutions were separated on a NuPAGE Novex 4-12 % Bis-Tris Gel under reducing conditions, according to the manufacturer's instructions. The
15 separated proteins were transferred via a Blot Module (Invitrogen) (30 V for 60 min at RT) onto an Amersham Hybond ECL membrane (100 V for 60 min at RT). The membrane was blocked for 1 h at RT with PBSTB (phosphate-buffered saline, pH = 7.4, supplemented with 0.1% Tween 20 and 1 % BSA). Afterwards, the membrane was incubated with the specific horseradish peroxidase (HRP)-labeled antibody
20 diluted in PBSTB. After washing the membrane with PBST (phosphate-buffered saline pH = 7.4 supplemented with 0.1% Tween 20), the proteins were detected using the Pierce ECL WB Substrate Kit via a chemiluminescence detector (INTAS).

25 *Lectin immunoblotting.*

Lectins are proteins that bind specific carbohydrate structures. Biotin-coupled lectins can therefore be used to analyze N-linked glycans. *Erythrina crista-galli* (ECL) lectin detects β1-4 linked terminal galactose on N-linked glycans, *Sambucus nigra*
30 agglutinin (SNA) preferentially binds to α2,6-linked sialic acid, whereas *Maackia amurensis* lectin (MAL) preferentially binds to α2,3-linked sialic acids. α1-3 linked

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fucose is detected by *Lotus tetragonolobus* agglutinin (LTA) and *Aleuria aurantia* lectin (AAL) detects α 1-2-, -3, or -6 linked fucose.

Purified protein solutions from parental CAP cells with or without co-expression of
5 ST3Gal4 and/or ST6Gal1 were separated as described above and blotted onto
Amersham Hybond ECL nitrocellulose membrane (GE healthcare). The membrane
was blocked for 1 h at RT with PBSTB (phosphate-buffered saline, pH = 7.4,
supplemented with 0.1% Tween 20 and 1 % BSA). Afterwards, the membrane was
incubated with the lectin diluted in PBSTB. After washing the membrane with PBST
10 (phosphate-buffered saline, pH = 7.4, supplemented with 0.1% Tween 20), the
membrane was stained with streptavidin-coupled horseradish peroxidase (HRP) for
1 h at RT (diluted in PBSTB). The HRP signal was amplified using anti-streptavidin
IgG and anti IgG-HRP. The proteins were detected using the Pierce ECL WB
Substrate Kit via a chemiluminescence detector (INTAS).

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Isoelectric focusing (IEF) analysis.

Isoelectric focusing (IEF) was performed in order to analyze the isoelectric point (pI)
20 of rhAAT purified from CAP cells expressing rhAAT with or without additional
expression of ST3Gal4 or ST6Gal1. The degree of sialylation correlates with a given
proteins acidity and, therefore, with its pI. IEF analysis was done according to the
manufacturers protocol (Invitrogen). Briefly, 5 μ g of purified protein were loaded on
pH 3-7 gels and subjected to electrophoresis (1h 100 V, 1 h 200 V, 30 min 500 V).
25 Proteins were stained with SimplyBlue SafeStain according to the manufacturer`s
protocol (Invitrogen).

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Example 1:

Significantly reduced amount of Lewis^x structures on hAAT protein purified from CAP-ST3Gal4 or ST6Gal1 cells.

- 5 α 1-Antitrypsin (AAT) is a protease inhibitor belonging to the serpin superfamily. AAT is a potent inhibitor of serine proteases, in particular neutrophil elastase. AAT is a 52 kDa glycoprotein carrying 3 N-glycosylation sites.

10 Cells of the human amniocyte cell line CAP already stably expressing human AAT were additionally stably transfected with a plasmid encoding either the sialyltransferase ST3Gal4 to achieve an increase in 2,3-linked sialylation of terminal galactose of N-glycans or the sialyltransferase ST6Gal1 to achieve an increase in 2,6-sialylation of terminal galactose of N-glycans.

- 15 Enhanced 2,3- or 2,6-sialylation upon overexpression of sialyltransferase ST3Gal4 or ST6Gal1 were determined by isoelectric focusing (IEF) analysis of purified hAAT (Figure 2).

20 As the backbones of the different rhAAT (recombinant hAAT) are identical, changes in the IEF indicate changes in the sialic acid content. Recombinant hAAT expressed in CAP cells with additional expression of ST3Gal4 results in a modified rhAAT which shifts significantly towards an acidic pI indicating an increased extent of sialylation; rhAAT expressed in parental CAP cells overexpressing ST6Gal1 also shifts towards a more acidic pI but to a lower degree (Figure 2). This is probably due to the different substrate affinities of ST3Gal4 and ST6Gal1. ST6Gal1 catalyzes sialylation of the primary branches of N-glycans, whereas ST3Gal4 catalyzes the sialylation of the primary branches of N-glycan as well as the additional branches of tri- and tetra-antennary N-glycans. Therefore, ST3Gal4 has more acceptor substrate available than ST6Gal1.

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This result could be confirmed via lectin blot analysis (Figure 3). Increased amounts of α 2,3- or α 2,6-sialylation upon overexpression of sialyltransferase ST3Gal4 or ST6Gal1 were determined via *Erythrina crista-galli* (ECL) lectin blot analysis. ECL

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lectin detects β 1-4 linked terminal galactose on N-linked glycans. Therefore, a diminished signal in the ECL blot correlates to an increased amount of sialylation. Purified AAT from control CAP cells expressing AAT shows a clear signal in the ECL lectin blot, proving an incomplete sialylation. AAT derived from ST6Gal1 or ST3Gal4
5 overexpressing CAP cells, showed a strong reduction or complete absence of the ECL signal, indicating that only minimal amounts of unsialylated β 1-4 linked galactose on the N-linked glycan exist in these preparations (Figure 3).

Remarkably, the degree of antennary fucose (Lewis^x antigen) is reduced on rhAAT
10 upon co-expression of ST6Gal1 or ST3Gal4 as proven by the reduced signal intensity in the *Lotus tetragonolobus* agglutinin (LTA Lectin) blot analysis in Figure 3. *Lotus tetragonolobus* agglutinin (LTA) specifically detects the α 1-3 linked antennary fucose. Therefore, overexpression of the sialyltransferases ST3Gal4 and ST6Gal1 is an unexpected but appropriate way to significantly reduce the amount
15 of the unwanted and potentially immunogenic Lewis^x structures on N-linked glycans.

Example 2:

FACS analysis of glycoproteins on the cell surface of CAP cells expressing ST3Gal4
20 or ST6Gal1.

In order to determine the degree of fucosylation of glycoproteins on the cell surface with increased degree of sialylation by overexpression of sialyltransferases, flow cytometry (FACS) analyses was performed (Figure 4).

25 CAP-hAAT-ST3Gal4 or CAP-hAAT-ST6Gal1 cells were stained with different antibodies and lectins to analyze sugar epitopes on the surface of the cells. Typically, 1×10^7 cells were centrifuged for 10 min at $140 \times g$ and re-suspended into 100 μ l PBS/BSA. 10 μ l (10^6 cells) were mixed with 10 μ l of antibody or lectin (1mg/ml; FITC conjugated or DIG coupled in combination with a FITC coupled anti-DIG antibody)
30 and 90 μ l PBS/BSA were added. After 10 min at 4 °C, the cells were washed with PBS/BSA. Cell pellets were re-suspended into 500 μ l PBS/BSA and subjected to FACS analysis on a Becton Dickinson FACSCalibur flow cytometer. Dead cells were

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identified and excluded by staining with propidium iodide. Typically, 30000 events were counted and analyzed. FITC or PE stained cells were graphically overlaid with unstained cells.

5 Figure 4 shows parental CAP-hAAT cells or CAP-hAAT cells stably expressing α 2,3 (CAP-hAAT+ST3Gal4) or α 2,6 (CAP-hAAT+ST6Gal1) sialyltransferase, respectively. Cells were either stained with lectins specific for α 2,3 coupled neuraminic acid, MAA (*Maackia amurensis* agglutinin), or α 2,6 coupled neuraminic acid residues, SNA (*Sambucus nigra* agglutinin), or with LTA (*Lotus tetragonolobus*
10 agglutinin) recognizing α 1,3 linked fucose residues (Le^x). Parental CAP-hAAT, HL60 (Le^x pos.), Le^x negative HEK293 cells (Le^x neg.) as well as cells incubated with the FITC coupled anti-DIG antibody only are shown as controls.

As expected, overexpression of α 2,3- or α 2,6- sialyltransferase increases the
15 respective coupled neuraminic acid residues on the N-glycans of cell surface glycoproteins. Interestingly, expression of ST3Gal4 or ST6Gal1 reduces the amount of the non-preferred Le^x structures on glycoproteins on the cell surface, as indicated by significantly reduced staining with lectin LTA.

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Example 3:

Monosaccharide analysis of hAAT expressed in CAP-ST3Gal4 or CAP-ST6Gal1 cells by HPAEC PAD analysis.

25 In order to determine if the total amount of sialic acid and fucose of purified recombinant hAAT from CAP cells changes upon additional expression of the sialyltransferases ST3Gal4 or ST6Gal1, a monosaccharide analysis by high performance anion exchange chromatography with pulsed amperometric detection (HPAEC PAD) was performed.

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Figure 5 shows the relative amounts of sialic acid and fucose as determined by monosaccharide analysis via HPAEC-PAD in CAP-hAAT cells either stably transfected with a plasmid encoding ST3Gal4 or ST6Gal1.

- 5 Figure 5 reveals that by expressing human sialyltransferases, sialic acid content is elevated, whereas the amount of fucose per rhAAT molecule is significantly reduced relative to an un-transfected control, indicating that the amount of the non-preferred Le^x or sialyl-Le^x structure is reduced upon overexpression of sialyltransferases. Of note in this experiment, the total amount of fucose was determined without
10 differentiating between antennary fucose residues (α 1-3 linked fucose) and core fucose (α 1-6 linked fucose) of N-glycans. As additional expression of sialyltransferases only affects the amount of antennary α 1-3 linked fucose but not the relatively abundant core fucose, the determined overall reduction of fucose upon overexpression of sialyltransferases of 25 % (ST6Gal1) and 30 % (ST3Gal4)
15 indicates a pronounced reduction in the absolute amount of antennary α 1-3 linked fucose.

The overall reduction in fucose residues is very surprising as the distal GlcNAc from sialylated complex N-glycans (NeuAc(α 1->4)Gal(β -4)GlcNAc-R), which will be
20 increased upon overexpression of ST3Gal4 and/or ST6Gal1, is a substrate for the fucosyltransferases Fut5, Fut6, and Fut7. Therefore, overexpression of sialyltransferases as ST3Gal4 should rather result in an increase in sialyl-Lewis^x structures than an overall decrease in fucose residues.

25

Example 4:

Reduced amount of Lewis^x structures on hC1 Inhibitor protein purified from CAP-ST3Gal4 or ST6Gal1 cells.

- 30 Cells of the human amniocyte cell line CAP-hC1 Inh were stably transfected with a plasmid encoding either the sialyltransferase ST3Gal4 to achieve increased α 2,3-

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linked sialylation of terminal galactose of N-glycans or sialyltransferase ST6Gal1 to achieve increased α 2,6-sialylation of terminal galactose of N-glycans.

Increased amounts of α 2,3- or α 2,6-sialylation upon overexpression of sialyltransferase ST3Gal4 or ST6Gal1 were determined via *Erythrina crista-galli* (ECL) lectin blot analysis. ECL lectin detects β 1-4 linked terminal galactose on N-linked glycans. As shown in Figure 6, overexpression of ST3Gal4 results in an increased sialylation of the N-linked glycans in comparison to C1 Inh purified from cell culture supernatant from non-glycomodified CAP cells. Overexpression of ST6Gal1 also results in an increased sialylation of terminal galactose on N-linked glycans in comparison to the non-glycomodified C1-Inh, although the effect is not as pronounced as upon overexpression of ST3Gal4. This is most likely due to the different substrate affinities of ST3Gal4 and ST6Gal1 as explained in Example 1.

The amount of antennary α 1-3 linked fucose in the different C1 Inh protein preparations (CAP control, CAP-ST3Gal4, CAP-ST6Gal1) was determined by the *Lotus tetragonolobus* agglutinin (LTA) blot analysis. Figure 6 reveals that the increased sialylation upon overexpression of ST6Gal1 or ST3Gal4 correlates with a reduced amount of antennary fucosylation proven by the decreased signal intensity in the LTA lectin blot analysis.

These results were confirmed by MS-MS analysis of N-glycans from C1 Inh derived in CAP control cells, CAP-ST3Gal4, or CAP-ST6Gal1 cells (Figure 7). PNGaseF released permethylated N-glycans from purified C1-Inhibitor either from control CAP cells, from CAP-ST3Gal4 cells or from CAP-ST6Gal1 cells were analyzed by MALDI TOF/TOF. Only the signal at 3196.8 in MS1 in wildtype derived C1-Inhibitor (Figure 7 A) contained two fucose residues and the characteristic fragmentation pattern for antennary fucose (M/z 638, 505, 260; D) in MS2. In CAP-ST3Gal4 and CAP-ST6Gal1 (Figure 7 B and C) the signal at 3196.8 could not be detected. Moreover, no other signal of MS1 contained a fragmentation pattern of antennary fucose in MS2.

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The present invention relates to the following amino acid sequences.

SEQ ID NO: 1

Human ST3Gal4

5

MVSKSRWKL LAM LALVLVVMVWYSISREDRYIELFYFPIPEKKEPCLQGEAESKASKLFGN
YSRDQPIFLRLLEDYFWVKTPSAYELPYGTKGSEDLLLRVLAITSSSIPKNIQSLRCRRCVV
VGNGHRLRNSSLGD AINKYDVVIRLNNAPVAGYEGDVGSKTTMRLFY PESAHFDPKVENNP
DTLLVLVAFKAMDFHWIETILSDKKRVRKGFWKQPPLIWDVNPQIRILNPFMEIAADKL
10 LSLPMQQPRKIKQKPTTGLLAITLALHLCDLVHIAGFGYPDAYNKKQTIHYEQITLKSMA
GSGHNVSQEALAIKRMLEMGAIKNLTSE

SEQ ID NO: 2

Human ST6Gal1

15

MIHTNLKKKFSCCVLVFLLFAVICVWKEKKKGSYYDSFKLQTKEFQVLKSLGKLAMGSDSQ
SVSSSSTQDPHRGRQTLGSLRGLAKAKPEASFQVWNKDSSSKNLIPRLQKIWKNYLSMNKY
KVS YKGP GPGIKFSAEALRCHLRDHVNVSMVEVTDFPFNTSEWEGYLPKESIRTKAGPWGR
CAVVSSAGSLKSSQLGREIDDHDAVLRFN GAPTANFQQDVGTKTTIRLMNSQLVTTEKRFL
20 KDSLYNEGILIVWDPSVYHSDIPKWYQNP DYNFFNNYKTYRKLHPNQPFYILKPQMPWELW
DILQEISPEEIQPNPPSSGMLGIIIMMTLCDQVDIYEFLPSKRKTDVCYYYQKFFDSACTM
GAYHPLLYEKNLVKHLNQGTDEDIYLLGKATLPGFRTIHC

SEQ ID NO: 3

25 Human AAT

MPSSVSWGILLLAGLCCCLVPVSLAEDPQGDAAQKTDTSHHQDHP TFNKITPNLAEFASFSL
YRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQE
LLRTL NQPD SQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAF TVNFGDTEEAKQIND
30 YVEKGTQGKIVDLVKELDRDTV FALVNYIFFKGKWERPF EVKDTEEDFHVDQVTTVKVPM
MKRLGMFNIQHCKKLSSWVLLMKYLG NATAIFFLPDEGKLQHLENELTHDIITKFL ENEDR
RSASLHLPKLSITGT YDLKSVLGQLGITK VFSNGADLSGVTEEAPLKLKSAVHKAVLTIDE
KGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK

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SEQ ID NO: 4Human C1 Inh

MASRLTLLTLLLLLLLAGDRASSNP NATSSSSQDPESLQDRGEGKVATTVISKMLFVEPILE
5 VSSLPTTNSTTNSATKITANTTDEPTTQPTTEPTTQPTIQPTQPTTQLPTDSPTQPTTGSF
CPGPVTLCSDL ESHSTEAVLGDALVDFSLKLYHAFSAMKKVETNMAFSPFSIASLLTQVLL
GAGENTKTNLESILSYPKDFTCVHQALKGFTTKGVTSVSQIFHSPDLAIRDTFVNASRTLY
SSSPRVLSNNSDANLELINTWVAKNTNNKISRLLDSLPSDTRLVLLNAIYLSAKWKTTTFDP
KKTRMEPFHFKN SVIKVPMMN SKKYPVAHFIDQTLKAKVGQLQLSHNLSLVILVPQNLKHR
10 LEDMEQALSPSVFKAIMEKLEMSKFQPTLLTLPRIKVTTSQDMLSIMEKLEFFDFS YDLNL
CGLTEDPDLQVSAMQHQT VLELTETGVEAAAAS AISVARTLLVFEVQQPFLFVLWDQQHKF
PVFMGRVYDPRA