YEAST STRAINS PRODUCING MAMMALIAN-LIKE COMPLEX N-GLYCANS

CROSS-REFERENCE TO RELATED

This application claims priority to U.S. Application Serial No. 61/262,828, filed on November 19, 2009. The disclosure of the prior application is incorporated by reference in its entirety.

TECHNICAL FIELD

The invention relates to methods and materials for producing glycoproteins in fungal cells, and more particularly, to genetically engineering fungal cells to produce proteins containing mammalian-like complex N-glycans or proteins containing intermediates within a mammalian glycosylation pathway.

BACKGROUND

High performance expression systems are required to produce most biopharmaceuticals (e.g., recombinant proteins) currently under development. The biological activity of many of these biopharmaceuticals is dependent on their post-translational modification (e.g., phosphorylation or glycosylation). A yeast-based expression system combines the ease of genetic manipulation and fermentation of a microbial organism with the capability to secrete and to modify proteins. However, recombinant glycoproteins produced in yeast cells exhibit mainly heterogeneous high-mannose and hyper-mannose glycan structures, which can be detrimental to protein function, downstream processing, and subsequent therapeutic use, particularly where glycosylation plays a biologically significant role.

SUMMARY

The methods and genetically engineered fungal cells described herein can be used to produce target molecules (e.g., target proteins) that contain mammalian-like N-glycans or contain intermediates within the mammalian (e.g., human) glycosylation pathway. Target molecules isolated from such engineered cells can be used for biopharmaceutical

applications including antibody production, cytokine production, and for treatment of metabolic disorders such as lysosomal storage disorders.

In one aspect, this document features a method of producing a fungal cell (e.g., *Yarrowia lipolytica* or *Arxula adeninivorans*) capable of producing proteins comprising $GlcNAcMan_5GlcNAc_2$ N-glycans. The method includes providing a fungal cell genetically engineered to produce proteins comprising $Man_5GlcNAc_2$ N-glycans; and introducing into the cell a nucleic acid encoding a GlcNAc-transferase I, wherein the nucleic acid includes a nucleotide targeting sequence to target the encoded GlcNAc-transferase I to an intracellular compartment (e.g., Golgi apparatus), wherein expression of the GlcNAc-transferase I in the fungal cell produces proteins including $GlcNAcMan_5GlcNAc_2$ N-glycans. The method further can include introducing into the cell a nucleic acid encoding a target protein, wherein the cell produces the target protein modified to include the $GlcNAcMan_5GlcNAc_2$ N-glycans. The target protein can bind to an Fc receptor. The target protein can be an antibody or fragment thereof. The target protein can be a therapeutic glycoprotein. The target protein can be Interferon-β, GM-CSF, Interferon γ, or erythropoietin.

The fungal cell genetically engineered to produce proteins containing $Man_5GlcNAc_2$ N-glycans can be deficient in OCH1 activity and include a nucleic acid encoding an α-1,2-mannosidase, wherein the nucleic acid encoding the α-1,2-mannosidase includes a nucleotide sequence encoding a targeting sequence to target the encoded α-1,2-mannosidase to the endoplasmic reticulum. The targeting sequence can be an HDEL sequence.

The method further can include introducing into a cell a nucleic acid encoding a mannosidase II, wherein the nucleic acid encoding the mannosidase II includes a nucleotide sequence encoding a targeting sequence to target the encoded mannosidase II to the Golgi apparatus, wherein expression of the mannosidase II in the fungal cell produces proteins containing $GlcNAcMan_3GlcNAc_2$ N-glycans.

The method further can include introducing into a cell a nucleic acid encoding a galactosyltransferase, wherein the nucleic acid encoding the galactosyltransferase includes a nucleotide sequence encoding a targeting sequence to target the encoded galactosyltransferase to the Golgi apparatus, wherein expression of the

galactosyltransferase in the fungal cell produces proteins containing $GalGlcNAcMan_5GlcNAc_2$ or $GalGlcNAcMan_3GlcNAc_2$ N-glycans. The galactosyltransferase can be a fusion of a UDP-Glc-4-epimerase and the catalytic domain of a β-1,4-galactosyltransferase I. Such a method further can include introducing into the cell a nucleic acid encoding a target protein, wherein the cell produces the target protein modified to contain $GalGlcNAcMan_5GlcNAc_2$ or $GalGlcNAcMan_3GlcNAc_2$ N-glycans. The methods can include isolating the target protein modified to contain the $GalGlcNAcMan_5GlcNAc_2$ or $GalGlcNAcMan_3GlcNAc_2$ N-glycans.

In another aspect, this document features a method of producing a target protein containing $GlcNAcMan_3GlcNAc_2$ N-glycans. The method includes providing a fungal cell (e.g., *Yarrowia lipolytica* or *Arxula adeninivorans*) genetically engineered to include a nucleic acid encoding a GlcNAc-transferase I, an α-1,2-mannosidase, and a mannosidase II, wherein the nucleic acid includes a nucleotide sequence encoding a targeting sequence, or nucleotide sequences encoding targeting sequences, to target each encoded protein to an intracellular compartment, wherein the fungal cell is deficient in OCH1 activity; and introducing into the cell a nucleic acid encoding a target protein, wherein the cell produces the target protein containing $GlcNAcMan_3GlcNAc_2$ N-glycans. The nucleic acid encoding the α-1,2-mannosidase can include an endoplasmic reticulum targeting sequence to target the encoded α-1,2-mannosidase to the endoplasmic reticulum. For example, the targeting sequence can be an HDEL sequence. The nucleic acid encoding the GlcNAc-transferase I and the mannosidase II can include a Golgi targeting sequence, or Golgi targeting sequences, to target the encoded GlcNAc-transferase I and mannosidase II to the Golgi apparatus. The target protein can bind to an Fc receptor. The target protein can be an antibody or fragment thereof. The target protein can be a therapeutic glycoprotein. The target protein can be Interferon-β, GM-CSF, Interferon γ, or erythropoietin.

In some embodiments, the method further can include introducing into the cell a nucleic acid encoding a galactosyltransferase, wherein the nucleic acid encoding the galactosyltransferase includes a nucleotide sequence encoding a targeting sequence to target the encoded galactosyltransferase to the Golgi apparatus, wherein expression of the galactosyltransferase in the fungal cell produces the target protein modified to contain

$GalGlcNAcMan_3GlcNAc_2$ N-glycans. The target protein modified to contain $GalGlcNAcMan_3GlcNAc_2$ N-glycans can be isolated from the fungal cell.

This document also features a method of making a fungal cell (e.g., *Yarrowia lipolytica* or *Arxula adeninivorans*) capable of producing proteins containing $GlcNAcMan_3GlcNAc_2$ N-glycans. The method includes providing a fungal cell genetically engineered to produce proteins containing $Man_3GlcNAc_2$ N-glycans; introducing into the cell a nucleic acid encoding a GlcNAc-transferase I, wherein the nucleic acid includes a nucleotide sequence encoding a targeting sequence to target the encoded GlcNAc-transferase I to an intracellular compartment (e.g., Golgi apparatus), wherein expression of the GlcNAc-transferase I in the fungal cell produces proteins containing $GlcNAcMan_3GlcNAc_2$ N-glycans. The method further can include introducing into the cell a nucleic acid encoding a target protein, wherein the cell produces the target protein modified to contain $GlcNAcMan_3GlcNAc_2$ N-glycans. The target protein can bind to an Fc receptor. The target protein can be an antibody or fragment thereof. The target protein can be a therapeutic glycoprotein. The target protein can be Interferon-β, GM-CSF, Interferon γ, or erythropoietin.

The fungal cell genetically engineered to produce proteins containing $Man_3GlcNAc_2$ N-glycans can be deficient in ALG3 activity, and include a nucleic acid encoding an α-1,2-mannosidase, wherein the nucleic acid includes a nucleotide sequence encoding a targeting sequence to target the encoded α-1,2-mannosidase to the endoplasmic reticulum. Such a fungal cell further can be deficient in OCH1 activity and/or further include a nucleic acid encoding α-1,3-glucosyltransferase (e.g., ALG6).

The method further can include introducing into the cell a nucleic acid encoding a GlcNAc-transferase II, wherein the nucleic acid encoding the GlcNAc-transferase II includes a nucleotide sequence encoding a targeting sequence to target the encoded GlcNAc-transferase II to an intracellular compartment, wherein expression of the GlcNAc-transferase II in the fungal cell produces proteins containing $GlcNAc_2Man_3GlcNAc_2$ N-glycans.

The method further can include introducing into the cell a nucleic acid encoding a galactosyltransferase, wherein the nucleic acid encoding the galactosyltransferase includes a nucleotide sequence encoding a targeting sequence to target the encoded

galactosyltransferase to the Golgi apparatus, wherein expression of the galactosyltransferase in the fungal cell produces proteins containing $GalGlcNAcMan_3GlcNAc_2$ or $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans. The galactosyltransferase can be a fusion of a UDP-Glc-4-epimerase and catalytic domain of a β-1,4-galactosyltransferase I. The method further can include introducing into the cell a nucleic acid encoding a target protein, wherein the cell produces the target protein modified to contain $GalGlcNAcMan_3GlcNAc_2$ or $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

The method further can include introducing into the cell a nucleic acid encoding the α and β subunits of a Glucosidase II, wherein expression of the α and β subunits of the Glucosidase II in the fungal cell produces proteins including $GalGlcNAcMan_3GlcNAc_2$ or $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

This document also features a method of producing a target protein containing $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans. The method includes providing a fungal cell genetically engineered to be deficient in ALG3 activity and including a nucleic acid encoding a GlcNAc-transferase I, a GlcNAc-transferase II, and a galactosyltransferase, wherein the nucleic acid encoding the GlcNAc-transferase I, the GlcNAc-transferase II, and the galactosyltransferase include a nucleotide sequence encoding a targeting sequence, or nucleotide sequences encoding targeting sequences, to target each encoded protein to an intracellular compartment (e.g., the Golgi apparatus); and introducing into the cell a nucleic acid encoding a target protein, wherein the cell produces the target protein containing $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans. The fungal cell can be further deficient in OCH1 activity and/or further include a nucleic acid encoding an α-1,3-glucosyltransferase such as ALG6. The fungal cell further can include a nucleic acid encoding the α and β subunits of a Glucosidase II, wherein expression of the α and β subunits of the Glucosidase II in the fungal cell produces the target protein containing $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

In another aspect, this document features an isolated fungal cell genetically engineered to produce proteins containing $GlcNAcMan_3GlcNAc_2$ N-glycans. The fungal cell can be deficient in OCH1 activity and include a nucleic acid encoding an α-1,2-mannosidase, a GlcNAc-transferase I, and a mannosidase II, wherein the nucleic acid encoding the α-1,2-mannosidase, the GlcNAc-transferase I, and the mannosidase II

includes a nucleotide sequence encoding a targeting sequence, or nucleotide sequences encoding targeting sequences, to target each encoded protein to an intracellular compartment, wherein expression of the α-1,2-mannosidase, the GlcNAc-transferase I, and the mannosidase II in the fungal cell produces proteins containing $GlcNAcMan_3GlcNAc_2$ N-glycans. The fungal cell further can include a nucleic acid encoding a target protein, wherein the cell produces the target protein modified to contain $GlcNAcMan_3GlcNAc_2$ N-glycans.

In some embodiments, such a fungal cell further includes a nucleic acid encoding a GlcNAc-transferase II, wherein the nucleic acid encoding the GlcNAc-transferase II includes a nucleotide sequence encoding a targeting sequence to target the encoded GlcNAc-transferase II to an intracellular compartment, wherein expression of the GlcNAc-transferase II in the fungal cell produces proteins containing $GlcNAc_2Man_3GlcNAc_2$ N-glycans.

In some embodiments, such a fungal cell further includes a nucleic acid encoding a galactosyltransferase, wherein the nucleic acid encoding the galactosyltransferase includes a nucleotide sequence encoding a targeting sequence to target the encoded galactosyltransferase to the Golgi apparatus, wherein expression of the galactosyltransferase in the fungal cell produces proteins containing $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

In yet another aspect, this document features an isolated fungal cell genetically engineered to produce proteins containing $GlcNAc_2Man_3GlcNAc_2$ N-glycans. The fungal cell is genetically engineered to be deficient in ALG3 activity and includes a nucleic acid encoding a GlcNAc-transferase I and a GlcNAc-transferase II, wherein the nucleic acid encoding the GlcNAc-transferase I and the GlcNAc-transferase II includes a nucleotide sequence encoding a targeting sequence, or nucleotide sequences encoding targeting sequences, to target each encoded protein to an intracellular compartment, wherein expression of the GlcNAc-transferase I, and the GlcNAc-transferase II in the fungal cell produces proteins containing $GlcNAc_2Man_3GlcNAc_2$ N-glycans. The genetically engineered fungal cell further can be deficient in OCH1 activity and/or further include a nucleic acid encoding an α-1,3-glucosyltransferase. A genetically engineered fungal cell also can include a nucleic acid encoding a target protein, wherein the cell produces the

target protein modified to contain $GlcNAc_2Man_3GlcNAc_2$ N-glycans. A fungal cell further can include a nucleic acid encoding the α and β subunits of a Glucosidase II, wherein expression of the α and β subunits of the Glucosidase II in the fungal cell produces the protein containing $GlcNAc_2Man_3GlcNAc_2$ N-glycans. The fungal cell further can include a nucleic acid encoding a galactosyltransferase, wherein the nucleic acid encoding the galactosyltransferase includes a nucleotide sequence encoding a targeting sequence to target the encoded galactosyltransferase to the Golgi apparatus, wherein expression of the galactosyltransferase in the fungal cell produces proteins containing $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

This document also features a substantially pure culture of *Yarrowia lipolytica* cells, a substantial number of which are genetically engineered to produce glycoproteins containing $Gal_2GlcNac_2Man_3GlcNAc_2$ N-glycans. The cells are genetically engineered to be deficient in ALG3 activity and include a nucleic acid encoding a GlcNAc-transferase I, a GlcNAc-transferase II, and a galactosyltransferase, wherein the nucleic acid encoding the GlcNAc-transferase I, the GlcNAc-transferase II, and the galactosyltransferase include a nucleotide sequence encoding a targeting sequence, or nucleotides sequences encoding targeting sequences, to target each encoded protein to an intracellular compartment, wherein expression of the GlcNAc-transferase I, the GlcNAc-transferase II, and the galactosyltransferase in the cell produces proteins containing $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans. The genetically engineered fungal cell further can be deficient in OCH1 activity and/or further include a nucleic acid encoding an α-1,3-glucosyltransferase (e.g., ALG6). The cells further can include a nucleic acid encoding the α and β subunits of a Glucosidase II, wherein expression of the α and β subunits of the Glucosidase II in the fungal cell produces the target protein containing $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

In another aspect, this document features a substantially pure culture of *Yarrowia lipolytica* cells, a substantial number of which are genetically engineered to produce glycoproteins containing $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans, wherein the cells are genetically engineered to be deficient in OCH1 activity and include a nucleic acid encoding an α-1,2-mannosidase, a GlcNAc-transferase I, a mannosidase II, a GlcNAc-transferase II, and a galactosyltransferase, wherein the nucleic acid encoding the α-1,2-

mannosidase, the GlcNAc-transferase I, the mannosidase II, the GlcNAc-transferase II, and the galactosyltransferase includes a nucleotide sequence encoding a targeting sequence, or nucleotide sequences encoding targeting sequences, to target each encoded protein to an intracellular compartment, wherein expression of the α-1,2-mannosidase, GlcNAc-transferase I, mannosidase II, GlcNAc-transferase II, and galactosyltransferase in the cells produces proteins comprising $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

This document also features a composition that includes a glycoprotein, wherein at least 50% (e.g., at least 70% or at least 85%of the N-glycans on the glycoprotein are $GlcNAc_2Man_3GlcNAc_2$ N-glycans.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the exemplary methods and materials are described below. All publications, patent applications, patents, Genbank® Accession Nos, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present application, including definitions, will control. The materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

DESCRIPTION OF DRAWINGS

FIG. 1A is a representation of $Man_5GLcNAc_2$ and $Man_3GlcNAc_2$ structures.

FIG. 1B is a schematic diagram of plasmid pYlOCH1 PUT TOPO.

FIG. 2 is a series of electroferograms depicting N-glycan analysis of secreted proteins obtained from po1d lnuga *Yarrowia lipolytica* wild-type cells or Δoch1 po1d lnuga *Yarrowia lipolytica* cells. The main N-glycan upon OCH1 inactivation becomes $Man_8GlcNAc_2$. Analysis was performed using DNA sequencer-assisted, fluorophore-assisted carbohydrate electrophoresis (DSA-FACE). "M5," "M6," "M8," and "M9," refer to the number of mannose residues conjugated to the base N-acetylglucosamine structure. The Y-axis represents the relative fluorescence units as an indication of the

amount of each N-glycan structure. The X-axis represents the relative mobility of each N-glycan structure through a capillary. The top electroferogram is an analysis of dextran for use as a mobility standard.

FIG. 3 is a schematic diagram of plasmids pYLHUXdL2preManHDEL and pYLTUXdL2preManHDEL.

FIG. 4 is a series of electroferograms depicting the N-glycan profile after introduction of a ManHDEL (= HDEL-tagged α-1,2-mannosidase) expression cassette (either under TEF1 or Hp4d promoter control) into strain G014. "Rd" stands for "random integration" via the zeta sequences present on the vectors shown in FIG. 3. The major N-glycan upon mannosidase expression is $Man_5GlcNAc_2$. Curing of the URA3 marker from one of these strains (G018, see Table 2) does not change the N-glycan profile.

FIG. 5 is a schematic of the construction strategy for plasmids JME926 pPTLeu2-ADE2ex-Hp4dManHDEL(Yl) and OXYP289 pPTAxp1-LEU2ex-Hp4dManHDEL(Yl). See FIG. 23 for the construction of vector pYLTmAXrGnTII.

FIG. 6 is a series of electroferograms depicting the N-glycan profile after introduction of a ManHDEL (= HDEL-tagged α-1,2-mannosidase) expression cassette (under Hp4d promoter control) into strain G014 by targeted integration (Tg) in either the LEU2 or the AXP1 locus. $Man_5GlcNAc_2$ becomes the main N-glycan.

FIG. 7 is a depiction of the amino acid sequence (SEQ ID NO:3) and *Yarrowia* codon optimized nucleotide sequence (SEQ ID NO:4) of the fusion protein between the 100 N-terminal amino acids of Kre2p and the catalytic domain of human GlcNAc-transferase I. In bold: Kre2p part of fusion protein; in normal font: GnT I part of fusion protein; underlined: start and stop codons.

FIG. 8 is a schematic diagram of the construction strategy for plasmids pYLTmAXhGnTI and pYLHp4mAXhGnTI.

FIG. 9 is a series of electroferograms depicting the N-glycan profile after introduction of the GnT I activity into strain G036 by transformation with a vector expressing GnT I. "Rd" stands for "random integration" via the zeta sequences present on the vectors shown in FIG. 8. The major N-glycan upon expression of the GnT I activity is $GlcNAcMan_5GlcNAc_2$. *In vitro* treatment with α-1,2-mannosidase does not change the profile significantly, indicating that only small amounts of high-mannose N-glycans other

than $Man_5GlcNAc_2$ are present. *In vitro* hexosaminidase treatment results in a shift from $GlcNAcMan_5GlcNAc_2$ towards $Man_5GlcNAc_2$.

FIG. 10 is a depiction of the amino acid sequence (SEQ ID NO:7) and *Yarrowia* codon optimized nucleotide sequence (SEQ ID NO:8) of the fusion protein between the 36 N-terminal amino acids of Mnn2p and the catalytic domain of Drosophila melanogaster mannosidase II. In bold: Mnn2p part of fusion protein; in normal font: Man II part of fusion protein; underlined: start and stop codons.

FIG. 11 is a schematic depiction of the construction strategy for plasmids pYLTmAXDmManII and pYLTmAXDmManII (LEU2ex).

FIG. 12 is a series of electroferograms depicting the N-glycan profile after introduction of the Man II activity into strain G040 by transformation with a Man II-expressing vector. "Rd" stands for "random integration" via the zeta sequences present on the vectors shown in FIG. 11. Upon expression of the Man II activity a new peak appears with higher electrophoretic mobility, as well as a 'shoulder' peak running at almost the same position as $Man_5GlcNAc_2$. *In vitro* hexosaminidase treatment results in a shift forward for these peaks (next to the observed shift from $GlcNAcMan_5GlcNAc_2$ towards $Man_5GlcNAc_2$), indicating the presence of terminal GlcNAc and thus identifying the peaks as $GlcNAcMan_3GlcNAc_2$ and $GlcNAcMan_4GlcNAc_2$. *In vitro* treatment with α-1,2-mannosidase does not change the profile significantly, indicating that only small amounts of high-mannose N-glycans other than $Man_5GlcNAc_2$ are present.

FIG. 13 is the amino acid sequence (SEQ ID NO:9) and *Yarrowia* codon optimized nucleotide sequence (SEQ ID NO:10) of the fusion protein between the 46 N-terminal amino acids of Mnn2p, the Schizosaccharomyces pombe UDP-Glc-4-epimerase-like protein and the catalytic domain of human β-1,4-galactosyl transferase I. The Mnn2p part of the fusion protein is from 1-46, linker sequences are from 47-49 and 405-408, epimerase sequences of the fusion protein are from 50-404, and the Man II part of the fusion protein is from 409-763 of SEQ ID NO:9. The Mnn2p part is from nucleotides 1-138, linker sequences are from nucleotides 139-147 and 1213-1224, epimerase sequences are from nucleotides 148-1212, and Man II part is from 1225-2289 of SEQ ID NO:10. Start and stop codons are underlined.

FIG. 14 is a schematic depiction of the construction strategy for plasmids pYLTmAXSpGal10hGalTI and pYLTmAXSpGal10hGalTI (ADE2ex).

FIG. 15 is a series of electroferograms depicting the N-glycan profile after introduction of the Gal10-GalTI activity into strain G040. The resulting transformant G044 was cultivated in 2 different media. "Rd" stands for "random integration" via the zeta sequences present on the vectors shown in FIG. 14. Upon expression of the Gal10-GalTI activity a new peak appears running at a position between $Man_7GlcNAc_2$ and $Man_8GlcNAc_2$. *In vitro* galactosidase treatment results in a shift forward for this peak and an equal increase of $GlcNAcMan_5GlcNAc_2$ (the latter being confirmed as representing this N-glycan by the double treatment with galactosidase and hexosaminidase). This indicates the presence of terminal galactose and thus identifying the new peak of the G044 profile as $GalGlcNAcMan_5GlcNAc_2$. *In vitro* treatment with α-1,2-mannosidase indicates the presence of a large amount of high-mannose N-glycans (especially $Man_8GlcNAc_2$) that were not yet trimmed to $Man_5GlcNAc_2$.

FIG. 16 is a schematic depiction of plasmid pYLalg3PUT-ALG6.

FIG. 17 is a series of electroferograms depicting the N-glycan profile after introduction of pYLalg3PUT-ALG6 into strain G036. Overexpression of *ALG6* results in a significant amount of glucosylated peaks ($GlcMan_5{\cdot}GlcNAc_2$ and $Glc_2Man_5{\cdot}GlcNAc_2$), indicating that the $Glc_3Man_5{\cdot}GlcNAc_2$ structure that was transferred to the nascent protein is not completely trimmed towards $Man_5{\cdot}GlcNAc_2$ by glucosidase II. Depending on the growth medium, the generated $Man_5{\cdot}GlcNAc_2$ is partially (still some $Man_5{\cdot}GlcNAc_2$ and $Man_4{\cdot}GlcNAc_2$) or almost completely trimmed towards $Man_3GlcNAc_2$ by the action of the ER-localized HDEL-tagged *T. reesei* α-1,2-mannosidase. The $Man_5{\cdot}GlcNAc_2$ and $Man_4{\cdot}GlcNAc_2$ peaks are identified as such, by their sensitivity towards α-1,2-mannosidase. Because of the capping glucoses, $GlcMan_5{\cdot}GlcNAc_2$ and $Glc_2Man_5{\cdot}GlcNAc_2$ are insensitive towards this treatment. Jack Bean mannosidase is partially capable of removing the free α-1,6-linked mannose while it also converts $Man_{3\text{-}5}{\cdot}GlcNAc_2$ into $Man_1GlcNAc_2$.

FIG. 18 is a schematic depiction of the construction strategy for plasmid pYLTmAXhGnTI (Hygr ex).

FIG. 19 is a series of electroferograms depicting the N-glycan profiles after introduction of the GnT I activity into either the non-cured (G039) or cured (G045) version of the Δ*alg3*-Hp4d*ALG6* strain by transformation with a GnT I-expressing vector. The generation of $GlcNAcMan_3GlcNAc_2$ was proven via a hexosaminidase digest. The new peak completely shifts back towards $Man_3GlcNAc_2$. In strain G048 conversion towards $GlcNAcMan_3GlcNAc_2$ was not complete since some $Man_3GlcNAc_2$ could still be observed. This strain also has some remnant $Man_5GlcNAc_2$ as shown by the α-1,2-mannosidase digest.

FIG. 20 is a schematic depiction of the construction strategy for plasmid JME925 pPTAde2-URA3ex-Hp4dhGnTI.

FIG. 21 is a series of electroferograms depicting N-glycan profiles after introduction of the GnT I activity into the cured version of the Δ*alg3*-Hp4d*ALG6* strain (=G045); integration of an Hp4d-driven expression construct into the *ADE2* locus (Tg-*ade2*). In this cultivation the amount of glucosylated N-glycans was high and conversion of $Man_{4,5}GlcNAc_2$ to $Man_3GlcNAc_2$ was not complete. A new peak running next to $Man_4GlcNAc_2$ was observed in transformant G057 and could be designated as $GlcNAcMan_3GlcNAc_2$ based on the result if the hexosaminidase digest: the new peak completely shifts back towards $Man_3GlcNAc_2$.

FIG. 22 is the amino acid sequence (SEQ ID NO:17) and *Yarrowia* codon optimized nucleotide sequence (SEQ ID NO:18) of the fusion protein between the 36 N-terminal amino acids of Mnn2p and the catalytic domain of rat GlcNAc-transferase II. In bold: Mnn2p part of fusion protein; in normal font: GnT II part of fusion protein; underlined: start and stop codons.

FIG. 23 is a schematic depiction of the construction strategy for plasmids pYLTmAXrGnTII and pYLTmAXrGnTII (ADE2 ex).

FIG. 24 is a series of electroferograms depicting N-glycan profiles after introduction of the GnT II activity into a strain synthesizing $GlcNAcMan_3GlcNAc_2$. The resulting strains were either obtained via double transformation of G045 with the GnTI and GnT II expression constructs or via transformation of G047 with the GnTII expression construct. In both cases, the peak representing $GlcNAcMan_3GlcNAc_2$ almost completely disappeared and a new peak, about one glucose unit larger, appeared.

Hexosaminidase treatment indicates the presence of two terminal GlcNAc residues onto the new N-glycan; the peak shifts about two glucose units to the left and thus represents $GlcNAc_2Man_3GlcNAc_2$. α-1,2-mannosidase treatment does not result into major differences, indicating that there are only limited amounts of $Man_{4-5}GlcNAc_2$ present.

FIG. 25 is a schematic diagram of plasmids pYLTUXdL2preAnGlcII and pYLeu2ExTEFpreLip2AnGlucIIβ for expression of the glucosidase II activity.

FIG. 26 is a schematic of the construction strategy for plasmids JME923 pPTura3-LEU2ex-TefL2preAnGlcIIa+b[alt1].

FIG. 27 is a schematic of the construction strategy for plasmids JME923 pPTura3-LEU2ex-Hp4dL2preAnGlcIIa+b[alt1] and Zeta-LEU2ex-Hp4dL2preAnGlcIIa+b[alt].

FIG. 28 is a series of electroferograms depicting N-glycan profiles after introduction of the glucosidase II activity into a strain synthesizing GlcNAcMan3GlcNAc2. The resulting strains were either obtained via random (G060) or targeted (G061) integration of a dual expression construct for the gls2α and gls2β subunit. In both cases, a reduction of glucosylated peaks is observed. α-1,2-mannosidase treatment indicates that not all of the generated $Man_5GlcNAc_2$ was converted towards $Man_3GlcNAc_2$ by the heterologous HDEL-tagged α-1,2-mannosidase. Because of the capping glucoses, $GlcMan_5GlcNAc_2$ and $Glc_2Man_5GlcNAc_2$ are insensitive towards this treatment. Jack Bean mannosidase is partially capable of removing the free α-1,6-linked mannose on both the remaining glucosylated N-glycans and $GlcNAcMan_3GlcNAc_2$. Furthermore, this treatment converts $Man_{3-5}GlcNAc_2$ into $Man_1GlcNAc_2$. "Rd" stands for "random integration" via the zeta sequences present on the vectors shown in FIG. 27. "Tg-ade2" and "Tg-ura3" stands for targeted integration in the ADE2 resp. URA3 locus.

FIG. 29 is a series of electroferograms depicting the N-glycan profile of the secretome of strains G070 and G071, which were generated via the introduction of GlcNAc-transferase II into strain G061. The N-glycans were treated with either α-1,2-mannosidase (removing all terminal α-1,2-linked mannose residues) or hexosaminidase (which removes terminal β-1,2-linked GlcNAc residues) to allow identification of the peaks in the G070 and G071 native profiles. The glucose-containing N-glycans are not sensitive to either of the two enzymes. The α-1,2-mannosidase treatment results in the

trimming of Man5'GlcNAc2 and Man4GlcNAc2 towards Man3GlcNAc2. The hexosaminidase treatment removes the β-1,2-linked terminal GlcNAc residues that have been added by GlcNAc-transferase I and II to generate Man3GlcNAc2.

FIG. 30A is the nucleotide sequence of the synthetic preproLip2-light chain (LC) (SEQ ID NO:32).

FIG. 30B is the amino acid sequence of the synthetic preproLip2-LC (SEQ ID NO:33)

FIG. 31A is the nucleotide sequence of the synthetic preproLip2-heavy chain (HC) (SEQ ID NO:34).

FIG. 31B is the amino acid sequence of the synthetic preproLip2-HC (SEQ ID NO:35).

FIG. 32 is a series of electroferograms depicting the N-glycan profile analysis of SuperT/glycerol shake-flask cultivations of glyco-engineered strains G045, G057, G061 and G071 that were transformed with pYLHp4L2preproHerHC/LC (GUT2ex)-ori2. See Table 2 for a description of strains G045, G057, G061 and G071.

FIG. 33 is a graph of the results from a functional ELISA at different time-points in the G096 fed-batch fermentation.

FIG. 34A and B are series of electroferograms depicting the N-glycan profile analysis of the secretome at different time-points within the G096 fed-batch fermentation.

DETAILED DESCRIPTION

As described herein, *in vivo* synthesis of mammalian-like complex N-glycans on yeast-secreted glycoproteins can be based on either a $Man_5GlcNAc_2$ or $Man_3GlcNAc_2$ base structure (see FIG. 1A, "Man" refers to mannose, and "GlcNAc" refers to N-glucosamine). To produce the $Man_5GlcNAc_2$ base structure, yeast cells can be engineered such that α-1,2-mannosidase activity is increased in an intracellular compartment and Outer CHain elongation (OCH1)activity is decreased. To produce the $Man_3GlcNAc_2$ base structure, activity of Asparagine Linked Glycosylation 3 (ALG3) and, in some embodiments, OCH1 is decreased, activity of α-1,2-mannosidase and, in some embodiments, activity of α-1,3-glucosyltransferase is increased. The N-glycan profile of proteins produced in such yeast cells can be altered by further engineering the

yeast cells to contain one or more of the following activities: GlcNAc transferase I (GnT I) activity, mannosidase II activity, GlcNAc transferase II (GnT II) activity, glucosidase II activity, and galactosyltransferase (Gal T) activity. For example, expressing GnT I in a yeast cell producing $Man_5GlcNAc_2$ or $Man_3GlcNAc_2$ N-glycans results in the transfer of a GlcNAc moiety to the $Man_5GlcNAc_2$ or $Man_3GlcNAc_2$ N-glycans such that $GlcNAcMan_5GlcNAc_2$ or $GlcNAcMan_3GlcNAc_2$ N-glycans, respectively, are produced. In cells producing $GlcNAcMan_5GlcNAc_2$ N-glycans, expressing a mannosidase II results in two mannose residues being removed from $GlcNAcMan_5GlcNAc_2$ N-glycans to produce $GlcNAcMan_3GlcNAc_2$ N-glycans. In cells producing $GlcNAcMan_3GlcNAc_2$ N-glycans, expressing GnT II results in the transfer of another GlcNAc moiety to $GlcNAcMan_3GlcNAc_2$ N-glycans to produce $GlcNAc_2Man_3GlcNAc_2$ N-glycans. Expressing Gal T in cells producing $GlcNAcMan_3GlcNAc_2$ or $GlcNAc_2Man_3GlcNAc_2$ N-glycans results in the transfer of galactose to the $GlcNAcMan_3GlcNAc_2$ or $GlcNAc_2Man_3GlcNAc_2$ N-glycans to produce $GalGlcNAcMan_3GlcNAc_2$ or $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans. In some embodiments, glucosidase II (e.g., by expressing α and β subunits) can be expressed to increase production of the $Man_3GlcNAc_2$ base structure.

Target Molecules

Target molecules, as used herein, refer to any molecules that undergo N-glycosylation in a genetically engineered cell (e.g., a fungal cell such as *Yarrowia lipolytica*, *Arxula adeninivorans*, or other related species dimorphic yeast cell; a plant cell, or an animal cell). In some embodiments, the target molecules are capable of being trafficked through one or more steps of the *Yarrowia lipolytica* or *Arxula adeninivorans* (or other related species dimorphic yeast) secretory pathway, resulting in their N-glycosylation by the host cell machinery. The target molecules can be endogenous or exogenous.

Suitable target proteins include pathogen proteins (e.g., tetanus toxoid; diptheria toxoid; viral surface proteins (e.g., cytomegalovirus (CMV) glycoproteins B, H and gCIII; human immunodeficiency virus 1 (HIV-1) envelope glycoproteins; Rous sarcoma virus (RSV) envelope glycoproteins; herpes simplex virus (HSV) envelope glycoproteins;

Epstein Barr virus (EBV) envelope glycoproteins; varicella-zoster virus (VZV) envelope glycoproteins; human papilloma virus (HPV) envelope glycoproteins; Influenza virus glycoproteins; and Hepatitis family surface antigens), lysosomal proteins (e.g., glucocerebrosidase, cerebrosidase, or galactocerebrosidase), insulin, glucagon, growth factors, cytokines, chemokines, a protein binding to an Fc receptor, antibodies or fragments thereof, or fusions of any of the proteins to antibodies or fragments of antibodies (e.g., protein-Fc). Growth factors include, e.g., vascular endothelial growth factor (VEGF), Insulin-like growth factor (IGF), bone morphogenic protein (BMP), Granulocyte-colony stimulating factor (G-CSF), Granulocyte-macrophage colony stimulating factor (GM-CSF), Nerve growth factor (NGF); a Neurotrophin, Platelet-derived growth factor (PDGF), Erythropoietin (EPO), Thrombopoietin (TPO), Myostatin (GDF-8), Growth Differentiation factor-9 (GDF9), basic fibroblast growth factor (bFGF or FGF2), Epidermal growth factor (EGF), Hepatocyte growth factor (HGF). Cytokines include, e.g., interleukins (e.g., IL-1 to IL-33 such as IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-12, IL-13, or IL-15) and interferons (e.g., interferon β or interferon γ). Chemokines include, e.g., I-309, TCA-3, MCP-1, MIP-1α, MIP-1β, RANTES, C10, MRP-2, MARC, MCP-3, MCP-2, MRP-2, CCF18, MIP-1γ, Eotaxin, MCP-5, MCP-4, NCC-1, Ckβ10, HCC-1, Leukotactin-1, LEC, NCC-4, TARC, PARC, or Eotaxin-2. Also included are tumor glycoproteins (e.g., tumor-associated antigens), for example, carcinoembryonic antigen (CEA), human mucins, HER-2/neu, and prostate-specific antigen (PSA) [Henderson and Finn, *Advances in Immunology*, 62, pp. 217-56 (1996)]. In one embodiment, the target protein is an anti-HER2/neu antibody. In some embodiments, the target protein can be one associated with a lysosomal storage disorder, which target proteins include, e.g., alpha-L-iduronidase, beta-D-galactosidase, beta-glucosidase, beta-hexosaminidase, beta-D-mannosidase, alpha-L-fucosidase, arylsulfatase B, arylsulfatase A, alpha-N-acetylgalactosaminidase, aspartylglucosaminidase, iduronate-2-sulfatase, alpha-glucosaminide-N-acetyltransferase, beta-D-glucoronidase, hyaluronidase, alpha-L-mannosidase, alpha-neuraminidase, phosphotransferase, acid lipase, acid ceramidase, sphingomyelinase, thioesterase, cathepsin K, and lipoprotein lipase.

Target proteins also can be fusion proteins. Fusions proteins include, e.g., a fusion of (i) any protein described herein or fragment thereof with (ii) an antibody or fragment thereof. As used herein, the term "antibody fragment" refers to (a) an antigen-binding fragment or (b) an Fc part of the antibody that can interact with an Fc receptor. An antigen binding fragment can be, for example, a Fab, $F(ab')_2$, Fv, and single chain Fv (scFv) fragment. An scFv fragment is a single polypeptide chain that includes both the heavy and light chain variable regions of the antibody from which the scFv is derived. In addition, diabodies [Poljak (1994) *Structure* 2(12):1121-1123; Hudson *et al.* (1999) J. *Immunol. Methods* 23(1-2):177-189] and intrabodies [Huston *et al.* (2001) *Hum. Antibodies* 10(3-4):127-142; Wheeler *et al.* (2003) *Mol. Ther.* 8(3):355-366; Stocks (2004) *Drug Discov. Today* 9(22): 960-966] can be used in the methods of the invention.

Target proteins can also be joined to one or more of a polymer, a carrier, an adjuvant, an immunotoxin, or a detectable (e.g., fluorescent, luminescent, or radioactive) moiety. For example, a target protein can be joined to polyethyleneglycol, which can be used to increase the molecular weight of small proteins and/or increase circulation residence time.

In some embodiments, the target molecule can be, or contain, dolichol.

Genetically Engineered Cells

Genetically engineered cells described herein can be used to produce target molecules that contain mammalian-like N-glycans or target molecules that contain intermediates within the mammalian glycosylation pathway. For example, as described herein, nucleic acids encoding one or more enzymes can be introduced into a fungal cell such that the cell produces the desired N-glycan (e.g., $GlcNAcMan_5GlcNAc_2$, $GlcNAcMan_3GlcNAc_2$, $GlcNAc_2Man_3GlcNAc_2$, $GalGlcNAcMan_3GlcNAc_2$ or $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans). Thus, in any of the embodiments described herein, a fungal cell may contain a nucleic acid encoding one enzyme, or a nucleic acid may encode multiple enzymes. Each such nucleic acid also can contain a targeting sequence as discussed below. In addition, a nucleic acid encoding a target molecule also can be introduced into the fungal cell such that the target molecule is produced and modified to contain the desired N-glycan (e.g., $GlcNAcMan_5GlcNAc_2$,

$GlcNAcMan_3GlcNAc_2$, $GlcNAc_2Man_3GlcNAc_2$, $GalGlcNAcMan_3GlcNAc_2$ or $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans).

The terms “nucleic acid” and “polynucleotide” are used interchangeably herein, and refer to both RNA and DNA, including cDNA, genomic DNA, synthetic DNA, and DNA (or RNA) containing nucleic acid analogs. Nucleic acids can have any three-dimensional structure. A nucleic acid can be double-stranded or single-stranded (i.e., a sense strand or an antisense strand). Non-limiting examples of nucleic acids include genes, gene fragments, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, siRNA, micro-RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers, as well as nucleic acid analogs. “Polypeptide" and "protein" are used interchangeably herein and mean any peptide-linked chain of amino acids, regardless of length or post-translational modification.

An “isolated nucleic acid” refers to a nucleic acid that is separated from other nucleic acid molecules that are present in a naturally-occurring genome, including nucleic acids that normally flank one or both sides of the nucleic acid in a naturally-occurring genome (e.g., a yeast genome). The term “isolated” as used herein with respect to nucleic acids also includes any non-naturally-occurring nucleic acid sequence, since such non-naturally-occurring sequences are not found in nature and do not have immediately contiguous sequences in a naturally-occurring genome.

An isolated nucleic acid can be, for example, a DNA molecule, provided one of the nucleic acid sequences normally found immediately flanking that DNA molecule in a naturally-occurring genome is removed or absent. Thus, an isolated nucleic acid includes, without limitation, a DNA molecule that exists as a separate molecule (e.g., a chemically synthesized nucleic acid, or a cDNA or genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other sequences as well as DNA that is incorporated into a vector, an autonomously replicating plasmid, a virus (e.g., any paramyxovirus, retrovirus, lentivirus, adenovirus, or herpes virus), or into the genomic DNA of a prokaryote or eukaryote. In addition, an isolated nucleic acid can include an engineered nucleic acid such as a DNA molecule that is part of a hybrid or fusion nucleic acid. A nucleic acid existing among hundreds to millions of other nucleic

acids within, for example, cDNA libraries or genomic libraries, or gel slices containing a genomic DNA restriction digest, is not considered an isolated nucleic acid.

The term "exogenous" as used herein with reference to nucleic acid and a particular host cell refers to any nucleic acid that does not occur in (and cannot be obtained from) that particular cell as found in nature. Thus, a non-naturally-occurring nucleic acid is considered to be exogenous to a host cell once introduced into the host cell. It is important to note that non-naturally-occurring nucleic acids can contain nucleic acid subsequences or fragments of nucleic acid sequences that are found in nature provided that the nucleic acid as a whole does not exist in nature. For example, a nucleic acid molecule containing a genomic DNA sequence within an expression vector is non-naturally-occurring nucleic acid, and thus is exogenous to a host cell once introduced into the host cell, since that nucleic acid molecule as a whole (genomic DNA plus vector DNA) does not exist in nature. Thus, any vector, autonomously replicating plasmid, or virus (e.g., retrovirus, adenovirus, or herpes virus) that as a whole does not exist in nature is considered to be non-naturally-occurring nucleic acid. It follows that genomic DNA fragments produced by PCR or restriction endonuclease treatment as well as cDNAs are considered to be non-naturally-occurring nucleic acid since they exist as separate molecules not found in nature. It also follows that any nucleic acid containing a promoter sequence and polypeptide-encoding sequence (e.g., cDNA or genomic DNA) in an arrangement not found in nature is non-naturally-occurring nucleic acid. A nucleic acid that is naturally-occurring can be exogenous to a particular cell. For example, an entire chromosome isolated from a cell of yeast x is an exogenous nucleic acid with respect to a cell of yeast y once that chromosome is introduced into a cell of yeast.

Cells suitable for genetic engineering include, e.g., fungal cells (e.g., *Yarrowia lipolytica* or any other related dimorphic yeast cells described herein), plant cells, or animal cells. The cells can be primary cells, immortalized cells, or transformed cells. The cells can be those in an animal, e.g., a non-human mammal. Such cells, prior to the genetic engineering as specified herein, can be obtained from a variety of commercial sources and research resource facilities, such as, for example, the American Type Culture Collection (Rockville, MD).

Genetic engineering of a cell can include genetic modifications such as: (i) deletion of an endogenous gene encoding a protein having N-glycosylation activity; (ii) introduction of a recombinant nucleic acid encoding a mutant form of a protein (e.g., endogenous or exogenous protein) having N-glycosylation activity (i.e., expressing a mutant protein having an N-glycosylation activity); (iii) introduction or expression of an RNA molecule that interferes with the functional expression of a protein having the N-glycosylation activity; (iv) introduction of a recombinant nucleic acid encoding a wild-type (e.g., endogenous or exogenous) protein having N-glycosylation activity (i.e., expressing a protein having an N-glycosylation activity); or (v) altering the promoter or enhancer elements of one or more endogenous genes encoding proteins having N-glycosylation activity to thus alter the expression of their encoded proteins. RNA molecules include, e.g., small-interfering RNA (siRNA), short hairpin RNA (shRNA), anti-sense RNA, or micro RNA (miRNA). It is understood that item (ii) includes, e.g., replacement of an endogenous gene with a gene encoding a protein having greater N-glycosylation activity relative to the endogenous gene so replaced. Genetic engineering also includes altering an endogenous gene encoding a protein having an N-glycosylation activity to produce a protein having additions (e.g., a heterologous sequence), deletions, or substitutions (e.g., mutations such as point mutations; conservative or non-conservative mutations). Mutations can be introduced specifically (e.g., site-directed mutagenesis or homologous recombination) or can be introduced randomly (for example, cells can be chemically mutagenized as described in, e.g., Newman and Ferro-Novick (1987) *J. Cell Biol.* 105(4):1587.

The genetic modifications described herein can result in one or more of (i) an increase in one or more N-glycosylation activities in the genetically modified cell, (ii) a decrease in one or more N-glycosylation activities in the genetically modified cell, (iii) a change in the localization or intracellular distribution of one or more N-glycosylation activities in the genetically modified cell, or (iv) a change in the ratio of one or more N-glycosylation activities in the genetically modified cell. It is understood that an increase in the amount of an N-glycosylation activity can be due to overexpression of one or more proteins having N-glycosylation activity, an increase in copy number of an endogenous gene (e.g., gene duplication), or an alteration in the promoter or enhancer of an

endogenous gene that stimulates an increase in expression of the protein encoded by the gene. A decrease in one or more N-glycosylation activities can be due to overexpression of a mutant form (e.g., a dominant negative form) of one or more proteins having N-glysosylation altering activities, introduction or expression of one or more interfering RNA molecules that reduce the expression of one or more proteins having an N-glycosylation activity, or deletion of one or more endogenous genes that encode a protein having N-glycosylation activity.

Methods of deleting or disrupting one or more endogenous genes are described in the accompanying Examples. For example, to disrupt a gene by homologous recombination, a "gene replacement" vector can be constructed in such a way to include a selectable marker gene. The selectable marker gene can be operably linked, at both 5' and 3' end, to portions of the gene of sufficient length to mediate homologous recombination. The selectable marker can be one of any number of genes which either complement host cell auxotrophy or provide antibiotic resistance, including URA3, LEU2 and HIS3 genes. Other suitable selectable markers include the CAT gene, which confers chloramphenicol resistance to yeast cells, or the lacZ gene, which results in blue colonies due to the expression of β-galactosidase. Linearized DNA fragments of the gene replacement vector are then introduced into the cells using methods well known in the art (see below). Integration of the linear fragments into the genome and the disruption of the gene can be determined based on the selection marker and can be verified by, for example, Southern blot analysis.

As detailed in the accompanying examples, subsequent to its use in selection, a selectable marker can be removed from the genome of the host cell by, e.g., Cre-loxP systems (see below). This process of marker removal is referred to as "curing" throughout the Examples.

Alternatively, a gene replacement vector can be constructed in such a way as to include a portion of the gene to be disrupted, where the portion is devoid of any endogenous gene promoter sequence and encodes none, or an inactive fragment of, the coding sequence of the gene. An "inactive fragment" is a fragment of the gene that encodes a protein having, e.g., less than about 10% (e.g., less than about 9%, less than about 8%, less than about 7%, less than about 6%, less than about 5%, less than about

4%, less than about 3%, less than about 2%, less than about 1%, or 0%) of the activity of the protein produced from the full-length coding sequence of the gene. Such a portion of the gene is inserted in a vector in such a way that no known promoter sequence is operably linked to the gene sequence, but that a stop codon and a transcription termination sequence are operably linked to the portion of the gene sequence. This vector can be subsequently linearized in the portion of the gene sequence and transformed into a cell. By way of single homologous recombination, this linearized vector is then integrated in the endogenous counterpart of the gene.

Expression vectors can be autonomous or integrative.

A recombinant nucleic acid can be in introduced into the cell in the form of an expression vector such as a plasmid, phage, transposon, cosmid or virus particle. The recombinant nucleic acid can be maintained extrachromosomally or it can be integrated into the yeast cell chromosomal DNA. Expression vectors can contain selection marker genes encoding proteins required for cell viability under selected conditions (e.g., URA3, which encodes an enzyme necessary for uracil biosynthesis or TRP1, which encodes an enzyme required for tryptophan biosynthesis) to permit detection and/or selection of those cells transformed with the desired nucleic acids (see, e.g., U.S. Patent No. 4,704,362). Expression vectors can also include an autonomous replication sequence (ARS). For example, U.S. Patent No. 4,837,148 describes autonomous replication sequences which provide a suitable means for maintaining plasmids in *Pichia pastoris*.

Integrative vectors are disclosed, e.g., in U.S. Patent No. 4,882,279. Integrative vectors generally include a serially arranged sequence of at least a first insertable DNA fragment, a selectable marker gene, and a second insertable DNA fragment. The first and second insertable DNA fragments are each about 200 (e.g., about 250, about 300, about 350, about 400, about 450, about 500, or about 1000 or more) nucleotides in length and have nucleotide sequences which are homologous to portions of the genomic DNA of the species to be transformed. A nucleotide sequence containing a gene of interest (e.g., a gene encoding a protein having N-glycosylation activity) for expression is inserted in this vector between the first and second insertable DNA fragments whether before or after the marker gene. Integrative vectors can be linearized prior to yeast transformation to facilitate the integration of the nucleotide sequence of interest into the host cell genome.

An expression vector can feature a recombinant nucleic acid under the control of a yeast (e.g., *Yarrowia lipolytica, Arxula adeninivorans,* or other related dimorphic yeast species) promoter, which enables them to be expressed in yeast. Suitable yeast promoters include the TEF1, HP4D, GAP, POX2, ADC1, TPI1, ADH2, POX, and Gal10 promter. See, e.g., Madzak *et al.*, (2000) *J. Mol. Microbiol. Biotechnol.* 2:207-216; Guarente *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79(23):7410. Additional suitable promoters are described in, e.g., Zhu and Zhang (1999) *Bioinformatics* 15(7-8):608-611 and U.S. Patent No. 6,265,185. Where the expression vector is to be introduced into an animal cell, such as a mammalian cell, the expression vector can feature a recombinant nucleic acid under the control of an animal cell promoter suitable for expression in the host cell of interest. Examples of mammalian promoters include the SV40 and cytomegalovirus (CMV) promoters.

A promoter can be constitutive or inducible (conditional). A constitutive promoter is understood to be a promoter whose expression is constant under the standard culturing conditions. Inducible promoters are promoters that are responsive to one or more induction cues. For example, an inducible promoter can be chemically regulated (e.g., a promoter whose transcriptional activity is regulated by the presence or absence of a chemical inducing agent such as an alcohol, tetracycline, a steroid, a metal, or other small molecule) or physically regulated (e.g., a promoter whose transcriptional activity is regulated by the presence or absence of a physical inducer such as light or high or low temperatures). An inducible promoter can also be indirectly regulated by one or more transcription factors that are themselves directly regulated by chemical or physical cues.

Genetic engineering of a cell also includes activating an endogenous gene (e.g., a gene encoding a protein having N-glycosylation activity) that is present in the host cell, but is normally not expressed in the cells or is not expressed at significant levels in the cells. For example, a regulatory sequence (e.g., a gene promoter or an enhancer) of a endogenous gene can be modified such that the operably-linked coding sequence exhibits increased expression. Homologous recombination or targeting can be used to replace or disable the regulatory region normally associated with the gene with a regulatory sequence which causes the gene to be expressed at levels higher than evident in the corresponding non-genetically engineered cell, or causes the gene to display a pattern of

regulation or induction that is different than evident in the corresponding non-genetically engineered cell. Suitable methods for introducing alterations of a regulatory sequence (e.g., a promoter or enhancer) of a gene are described in, e.g., U.S. Application Publication No. 20030147868.

It is understood that other genetically engineered modifications also can be conditional. For example, a gene can be conditionally deleted using, e.g., a site-specific DNA recombinase such as the Cre-loxP system (see, e.g., Gossen *et al.* (2002) *Ann. Rev. Genetics* 36:153-173 and U.S. Application Publication No. 20060014264).

A recombinant nucleic acid can be introduced into a cell described herein using a variety of methods such as the spheroplast technique or the whole-cell lithium chloride yeast transformation method. Other methods useful for transformation of plasmids or linear nucleic acid vectors into cells are described in, for example, U.S. Patent No. 4,929,555; Hinnen *et al.* (1978) *Proc. Nat. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163; U.S. Patent No. 4,879,231; and Sreekrishna *et al.* (1987) *Gene* 59:115. Electroporation and PEG1000 whole cell transformation procedures may also be used, as described by Cregg and Russel, Methods in Molecular Biology: Pichia Protocols, Chapter 3, Humana Press, Totowa, N.J., pp. 27-39 (1998). Transfection of animal cells can feature, for example, the introduction of a vector to the cells using calcium phosphate, electroporation, heat shock, liposomes, or transfection reagents such as FUGENE® or LIPOFECTAMINE®, or by contacting naked nucleic acid vectors with the cells in solution (see, e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual Second Edition vol. 1, 2 and 3. Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York, USA, Nov. 1989.

Transformed yeast cells can be selected for by using appropriate techniques including, but not limited to, culturing auxotrophic cells after transformation in the absence of the biochemical product required (due to the cell's auxotrophy), selection for and detection of a new phenotype, or culturing in the presence of an antibiotic which is toxic to the yeast in the absence of a resistance gene contained in the transformants. Transformants can also be selected and/or verified by integration of the expression cassette into the genome, which can be assessed by, e.g., Southern blot or PCR analysis.

Prior to introducing the vectors into a target cell of interest, the vectors can be grown (e.g., amplified) in bacterial cells such as *Escherichia coli* (*E. coli*). The vector DNA can be isolated from bacterial cells by any of the methods known in the art which result in the purification of vector DNA from the bacterial milieu. The purified vector DNA can be extracted extensively with phenol, chloroform, and ether, to ensure that no *E. coli* proteins are present in the plasmid DNA preparation, since these proteins can be toxic to mammalian cells.

Genetic engineering, as described herein, can be used to express (e.g., overexpress), introduce modifications into, or delete any number of genes encoding proteins having N-glycosylation activity. Such proteins include, for example, OCH1, ALG3, α-1,3-glucosyltransferase, GnT I, mannosidase II, GnT II, glucosidase II, or Gal T. The genes encoding proteins having N-glycosylation activity can be from any species containing such genes. Exemplary fungal species from which genes encoding proteins having N-glycosylation activity can be obtained include, without limitation, *Pichia anomala, Pichia bovis, Pichia canadensis, Pichia carsonii, Pichia farinose, Pichia fermentans, Pichia fluxuum, Pichia membranaefaciens, Pichia membranaefaciens, Candida valida, Candida albicans, Candida ascalaphidarum, Candida amphixiae, Candida Antarctica, Candida atlantica, Candida atmosphaerica, Candida blattae, Candida carpophila, Candida cerambycidarum, Candida chauliodes, Candida corydalis, Candida dosseyi, Candida dubliniensis, Candida ergatensis, Candida fructus, Candida glabrata, Candida fermentati, Candida guilliermondii, Candida haemulonii, Candida insectamens, Candida insectorum, Candida intermedia, Candida jeffresii, Candida kefyr, Candida krusei, Candida lusitaniae, Candida lyxosophila, Candida maltosa, Candida membranifaciens, Candida milleri, Candida oleophila, Candida oregonensis, Candida parapsilosis, Candida quercitrusa, Candida shehatea, Candida temnochilae, Candida tenuis, Candida tropicalis, Candida tsuchiyae, Candida sinolaborantium, Candida sojae, Candida viswanathii, Candida utilis, Pichia membranaefaciens, Pichia silvestris, Pichia membranaefaciens, Pichia chodati, Pichia membranaefaciens, Pichia menbranaefaciens, Pichia minuscule, Pichia pastoris, Pichia pseudopolymorpha, Pichia quercuum, Pichia robertsii, Pichia saitoi, Pichia silvestrisi, Pichia strasburgensis, Pichia terricola, Pichia vanriji, Pseudozyma Antarctica, Rhodosporidium toruloides, Rhodotorula glutinis,*

Saccharomyces bayanus, Saccharomyces bayanus, Saccharomyces momdshuricus, Saccharomyces uvarum, Saccharomyces bayanus, Saccharomyces cerevisiae, Saccharomyces bisporus, Saccharomyces chevalieri, Saccharomyces delbrueckii, Saccharomyces exiguous, Saccharomyces fermentati, Saccharomyces fragilis, Saccharomyces marxianus, Saccharomyces mellis, Saccharomyces rosei, Saccharomyces rouxii, Saccharomyces uvarum, Saccharomyces willianus, Saccharomycodes ludwigii, Saccharomycopsis capsularis, Saccharomycopsis fibuligera, Saccharomycopsis fibuligera, Endomyces hordei, Endomycopsis fobuligera. Saturnispora saitoi, Schizosaccharomyces octosporus, Schizosaccharomyces pombe, Schwanniomyces occidentalis, Torulaspora delbrueckii, Torulaspora delbrueckii, Saccharomyces dairensis, Torulaspora delbrueckii, Torulaspora fermentati, Saccharomyces fermentati, Torulaspora delbrueckii, Torulaspora rosei, Saccharomyces rosei,Torulaspora delbrueckii, Saccharomyces rosei, Torulaspora delbrueckii, Saccharomyces delbrueckii, Torulaspora delbrueckii, Saccharomyces delbrueckii, Zygosaccharomyces mongolicus, Dorulaspora globosa, Debaryomyces globosus, Torulopsis globosa, Trichosporon cutaneum, Trigonopsis variabilis, Williopsis californica, Williopsis saturnus, Zygosaccharomyces bisporus, Zygosaccharomyces bisporus, Debaryomyces disporua. Saccharomyces bisporas, Zygosaccharomyces bisporus, Saccharomyces bisporus, Zygosaccharomyces mellis, Zygosaccharomyces priorianus, Zygosaccharomyces rouxiim, Zygosaccharomyces rouxii, Zygosaccharomyces barkeri, Saccharomyces rouxii, Zygosaccharomyces rouxii, Zygosaccharomyces major, Saccharomyces rousii, Pichia anomala, Pichia bovis, Pichia Canadensis, Pichia carsonii, Pichia farinose, Pichia fermentans, Pichia fluxuum, Pichia membranaefaciens, Pichia pseudopolymorpha, Pichia quercuum, Pichia robertsii, Pseudozyma Antarctica, Rhodosporidium toruloides, Rhodosporidium toruloides, Rhodotorula glutinis, Saccharomyces bayanus, Saccharomyces bayanus, Saccharomyces bisporus, Saccharomyces cerevisiae, Saccharomyces chevalieri, Saccharomyces delbrueckii, Saccharomyces fermentati, Saccharomyces fragilis, Saccharomycodes ludwigii, Schizosaccharomyces pombe, Schwanniomyces occidentalis, Torulaspora delbrueckii, Torulaspora globosa, Trigonopsis variabilis, Williopsis californica, Williopsis saturnus, Zygosaccharomyces bisporus, Zygosaccharomyces mellis, Zygosaccharomyces rouxii, or any other fungi (e.g.,

yeast) known in the art or described herein. Exemplary lower eukaryotes also include various species of *Aspergillus* including, but not limited to, *Aspergillus caesiellus, Aspergillus candidus, Aspergillus carneus, Aspergillus clavatus, Aspergillus deflectus, Aspergillus flavus, Aspergillus fumigatus, Aspergillus glaucus, Aspergillus nidulans, Aspergillus niger, Aspergillus ochraceus, Aspergillus oryzae, Aspergillus parasiticus, Aspergillus penicilloides, Aspergillus restrictus, Aspergillus sojae, Aspergillus sydowi, Aspergillus tamari, Aspergillus terreus, Aspergillus ustus,* or *Aspergillus versicolor.* Exemplary protozoal genera from which genes encoding proteins having N-glycosylation activity can be obtained include, without limitation, *Blastocrithidia, Crithidia, Endotrypanum, Herpetomonas, Leishmania, Leptomonas, Phytomonas, Trypanosoma* (e.g., *T. bruceii, T. gambiense, T. rhodesiense, and T. cruzi*), and *Wallaceina*. For example, the gene encoding GnT I can be obtained from human (Swiss Protein Accession No. P26572), rat, *Arabidopsis*, mouse, or *Drosophila*; the gene encoding GntII can be obtained from human, rat (Swiss Protein Accession No. Q09326), *Arabidopsis*, or mouse; the gene encoding Man II can be obtained from human, rat, *Arabidopsis*, mouse, *Drosophila* (Swiss Protein Accession No. Q24451); and the gene encoding GalT can be obtained from human (Swiss Protein Accession No. P15291), rat, mouse, or bovine.

In some embodiments, a genetically engineered cell lacks the OCH1 (GenBank Accession No: AJ563920) gene or gene product (mRNA or protein) thereof. In some embodiments, a genetically engineered cell lacks the ALG3 (Genbank® Accession Nos: XM_503488, Genolevures Ref: YALI0E03190g) gene or gene product (mRNA or protein) thereof. In some embodiments, a genetically engineered cell expresses (e.g., overexpresses) an α-1,3-glucosyltransferase (e.g., ALG6, Genbank® Acccession Nos: XM_502922, Genolevures Ref: YALI0D17028g) protein. In some embodiments, a genetically engineered cell expresses an α-1,2-mannosidase (e.g., Genbank Acccession No.:AF212153) protein. In some embodiments, a genetically engineered cell expresses a GlcNAc-transferase I (e.g., Swiss Prot. Accession No. P26572) protein. In some embodiments, a genetically engineered cell expresses a mannosidase II protein or catalytic domain thereof (e.g., Swiss Prot. Accession No. Q24451). In some embodiments, a genetically engineered cell expresses a galactosyltransferase I protein or catalytic domain thereof (e.g., Swiss Prot. Accession No. P15291). In some

embodiments, the genetically engineered cell expresses a GlcNAc-transferase II protein or catalytic domain thereof (e.g., Swiss Prot. Accession No. Q09326). In some embodiments, the genetically engineered cell expresses an alpha or beta subunit (or both the alpha and the beta subunit) of a glucosidase II such as the glucosidase II of *Yarrowia lipolytica*, *Trypanosoma brucei* or *Aspergillus niger*. A genetically engineered cell can have any combination of these modifications.

For example, in some embodiments, a genetically engineered cell can lack the OCH1 gene and express an α-1,2-mannosidase, GlcNAc-transferase I, mannosidase II, and a galactosyltransferase I. In some embodiment, a genetically engineered cell can lack the ALG3 gene, and express an α-1,2-mannosidase, GlcNAc-transferase I, GlcNAc-transferase I, and a galactosyltransferase I. Such a genetically engineered cell further can express an α-1,3-glucosyltransferase and/or express alpha and beta subunits of a glucosidase II and/or lack the OCH1 gene.

One of more of such proteins can be fusion proteins that contain a heterologous targeting sequence. For example, the α-1,2-mannosidase can have an HDEL endoplasmic reticulum (ER)-retention amino acid sequence (see Examples). It is understood that any protein having N-glycosylation activity can be engineered into a fusion protein comprising an HDEL sequence. Other proteins can have heterologous sequences that target the protein to the Golgi apparatus. For example, the first 100 N-terminal amino acids encoded by the yeast Kre2p gene, the first 36 N-terminal amino acids (Swiss Prot. Accession No. P38069) encoded by the *S. cerevisiae* Mnn2 gene, or the first 46 N-terminal amino acids encoded by the *S. cerevisiae* Mnn2p gene can be used to target proteins to the Golgi. As such, nucleic acids encoding a protein to be expressed in a fungal cell can include a nucleotide sequence encoding a targeting sequence to target the encoded protein to an intracellular compartment. For example, the α-1,2-mannosidase can be targeted to the ER, while the GnT I, GnTII, mannosidase, and Gal T can be targeted to the Golgi.

In embodiments where a protein having N-glycosylation activity is derived from a cell that is of a different type (e.g., of a different species) than the cell into which the protein is to be expressed, a nucleic acid encoding the protein can be codon-optimized for expression in the particular cell of interest. For example, a nucleic acid encoding a

protein having N-glycosylation from *Trypanosoma brucei* can be codon-optimized for expression in a yeast cell such as *Yarrowia lipolytica*. Such codon-optimization can be useful for increasing expression of the protein in the cell of interest. Methods for codon-optimizing a nucleic acid encoding a protein are known in the art and described in, e.g., Gao *et al.* (*Biotechnol. Prog.* (2004) 20(2): 443 -448), Kotula *et al.* (*Nat. Biotechn.* (1991) 9, 1386 – 1389), and Bennetzen *et al.* (*J. Biol. Chem.* (1982) 257(6):2036-3031). Table 1 shows the codon usage for *Yarrowia lipolytica*. Data was derived from 2,945,919 codons present in 5,967 coding sequences. The contents of Table 1 were obtained from a Codon Usage Database, which can be found at world wide web at kazusa.or.jp/codon/cgi-bin/showcodon.cgi?species=284591.

TABLE 1

Yarrowia lipolytica Codon Usage Table

UUU 15.9(46804)	CU 21.8(64161)	AU 6.8(20043)	GU 6.1(17849)
UUC 23.0(67672)	CC 20.6(60695)	AC 23.1(68146)	GC 6.1(17903)
UUA 1.8(5280)	CA 7.8(22845)	AA 0.8(2494)	GA 0.4(1148)
UUG 10.4(30576)	CG 15.4(45255)	AG 0.8(2325)	GG 12.1(35555)
CUU 13.2(38890)	CU 17.4(51329)	AU 9.6(28191)	GU 6.0(17622)
CUC 22.6(66461)	CC 23.3(68633)	AC 14.4(42490)	GC 4.4(12915)
CUA 5.3(15548)	CA 6.9(20234)	AA 9.8(28769)	GA 21.7(63881)
CUG 33.5(98823)	CG 6.8(20042)	AG 32.1(94609)	GG 7.7(22606)
AUU 22.4(66134)	CU 16.2(47842)	AU 8.9(26184)	GU 6.7(19861)
AUC 24.4(71810)	CC 25.6(75551)	AC 31.3(92161)	GC 9.8(28855)
AUA 2.2(6342)	CA 10.5(30844)	AA 12.4(36672)	GA 8.4(24674)
AUG 22.6(66620)	CG 8.5(25021)	AG 46.5(136914)	GG 2.4(7208)
GUU 15.8(46530)	CU 25.5(75193)	AU 21.5(63259)	GU 16.6(48902)
GUC 21.5(63401)	CC 32.7(96219)	AC 38.3(112759)	GC 21.8(64272)
GUA 4.0(11840)	CA 11.2(32999)	AA 18.8(55382)	GA 20.9(61597)
GUG 25.7(75765)	CG 8.9(26190)	AG 46.2(136241)	GG 4.4(12883)

Tablefields are shown as [triplet] [frequency: per thousand] ([number]).

In some embodiments, human proteins can be introduced into the cell and one or more endogenous yeast proteins having N-glycosylation activity can be suppressed (e.g., deleted or mutated). Techniques for "humanizing" a fungal glycosylation pathway are described in, e.g., Choi *et al.* (2003) *Proc. Natl. Acad. Sci. USA* 100(9):5022-5027; Vervecken *et al.* (2004) *Appl. Environ. Microb.* 70(5):2639-2646; and Gerngross (2004) *Nature Biotech.* 22(11):1410-1414.

Where the genetic engineering involves, e.g., changes in the expression of a protein or expression of an exogenous protein (including a mutant form of an endogenous protein), a variety of techniques can be used to determine if the genetically engineered cells express the protein. For example, the presence of mRNA encoding the protein or the protein itself can be detected using, e.g., Northern Blot or RT-PCR analysis or Western Blot analysis, respectively. The intracellular localization of a protein having N-

glycosylation activity can be analyzed by using a variety of techniques, including subcellular fractionation and immunofluorescence.

Methods for detecting glycosylation of a target molecule include DNA sequencer-assisted (DSA), fluorophore-assisted carbohydrate electrophoresis (FACE) or surface-enhanced laser desorption/ionization time-of-flight mass spectrometry (SELDI-TOF MS). For example, an analysis can utilize DSA-FACE in which, for example, glycoproteins are denatured followed by immobilization on, e.g., a membrane. The glycoproteins can then be reduced with a suitable reducing agent such as dithiothreitol (DTT) or β-mercaptoethanol. The sulfhydryl groups of the proteins can be carboxylated using an acid such as iodoacetic acid. Next, the N-glycans can be released from the protein using an enzyme such as N-glycosidase F. N-glycans, optionally, can be reconstituted and derivatized by reductive amination. The derivatized N-glycans can then be concentrated. Instrumentation suitable for N-glycan analysis includes, e.g., the ABI PRISM® 377 DNA sequencer (Applied Biosystems). Data analysis can be performed using, e.g., GENESCAN® 3.1 software (Applied Biosystems). Optionally, isolated mannoproteins can be further treated with one or more enzymes to confirm their N-glycan status. Additional methods of N-glycan analysis include, e.g., mass spectrometry (e.g., MALDI-TOF-MS), high-pressure liquid chromatography (HPLC) on normal phase, reversed phase and ion exchange chromatography (e.g., with pulsed amperometric detection when glycans are not labeled and with UV absorbance or fluorescence if glycans are appropriately labeled). See also Callewaert *et al.* (2001) *Glycobiology* 11(4):275-281 and Freire *et al.* (2006) *Bioconjug. Chem.* 17(2):559-564.

Where any of the genetic modifications of the genetically engineered cell are inducible or conditional on the presence of an inducing cue (e.g., a chemical or physical cue), the genetically engineered cell can, optionally, be cultured in the presence of an inducing agent before, during, or subsequent to the introduction of the nucleic acid. For example, following introduction of the nucleic acid encoding a target protein, the cell can be exposed to a chemical inducing agent that is capable of promoting the expression of one or more proteins having N-glycosylation activity. Where multiple inducing cues induce conditional expression of one or more proteins having N-glycosylation activity, a cell can be contacted with multiple inducing agents.

Target molecules modified to include the desired N-glycan can be isolated from the genetically engineered cell. The modified target molecule can be maintained within the yeast cell and released upon cell lysis or the modified target molecule can be secreted into the culture medium via a mechanism provided by a coding sequence (either native to the exogenous nucleic acid or engineered into the expression vector), which directs secretion of the molecule from the cell. The presence of the modified target molecule in the cell lysate or culture medium can be verified by a variety of standard protocols for detecting the presence of the molecule. For example, where the altered target molecule is a protein, such protocols can include, but are not limited to, immunoblotting or radioimmunoprecipitation with an antibody specific for the altered target protein (or the target protein itself), binding of a ligand specific for the altered target protein (or the target protein itself), or testing for a specific enzyme activity of the modified target protein (or the target protein itself).

In some embodiments, at least about 25% of the target molecules isolated from the genetically engineered cell contain the desired N-glycan. For example, at least about 27%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95%, or at least about 99% of the target molecules isolated from the genetically engineered cell can contain the desired N-glycan.

In some embodiments, in the target molecules produced using the methods described herein, at least 50% (e.g., at least 55, 60, 65, 70, 75, 80, or 85%) of the N-glycans on the glycoprotein can be $GlcNAc_2Man_3GlcNAc_2$ N-glycans. The percentage of $GlcNAc_2Man_3GlcNAc_2$ N-glycans can be estimated from the peak areas in the DSA-FACE electropherograms. See Example 13.

In some embodiments, the isolated modified target molecules can be frozen, lyophilized, or immobilized and stored under appropriate conditions, e.g., which allow the altered target molecules to retain biological activity.

Cultures of Engineered Cells

This document also provides a substantially pure culture of any of the genetically engineered cells described herein. As used herein, a "substantially pure culture" of a genetically engineered cell is a culture of that cell in which less than about 40% (i.e., less than about : 35%; 30%; 25%; 20%; 15%; 10%; 5%; 2%; 1%; 0.5%; 0.25%; 0.1%; 0.01%; 0.001%; 0.0001%; or even less) of the total number of viable cells in the culture are viable cells other than the genetically engineered cell, e.g., bacterial, fungal (including yeast), mycoplasmal, or protozoan cells. The term "about" in this context means that the relevant percentage can be 15% percent of the specified percentage above or below the specified percentage. Thus, for example, about 20% can be 17% to 23%. Such a culture of genetically engineered cells includes the cells and a growth, storage, or transport medium. Media can be liquid, semi-solid (e.g., gelatinous media), or frozen. The culture includes the cells growing in the liquid or in/on the semi-solid medium or being stored or transported in a storage or transport medium, including a frozen storage or transport medium. The cultures are in a culture vessel or storage vessel or substrate (e.g., a culture dish, flask, or tube or a storage vial or tube).

The genetically engineered cells described herein can be stored, for example, as frozen cell suspensions, e.g., in buffer containing a cryoprotectant such as glycerol or sucrose, as lyophilized cells. Alternatively, they can be stored, for example, as dried cell preparations obtained, e.g., by fluidized bed drying or spray drying, or any other suitable drying method.

Disorders Treatable by Altered N-Glycosylation Molecules

The isolated, target molecules modified to contain the desired N-glycan can be used to treat a variety of disorders, including metabolic disorders, cancer, and inflammatory disorders.

(i) Metabolic Disorders

A metabolic disorder is one that affects the production of energy within individual human (or animal) cells. Most metabolic disorders are genetic, though some can be "acquired" as a result of diet, toxins, infections, etc. Genetic metabolic disorders are also known as inborn errors of metabolism. In general, the genetic metabolic disorders are

caused by genetic defects that result in missing or improperly constructed enzymes necessary for some step in the metabolic process of the cell. The largest classes of metabolic disorders are disorders of carbohydrate metabolism, disorders of amino acid metabolism, disorders of organic acid metabolism (organic acidurias), disorders of fatty acid oxidation and mitochondrial metabolism, disorders of porphyrin metabolism, disorders of purine or pyrimidine metabolism, disorders of steroid metabolism disorders of mitochondrial function, disorders of peroxisomal function, and lysosomal storage disorders (LSDs).

Examples of metabolic disorders that can be treated through the administration of one or more glycosylated molecules (or pharmaceutical compositions of the same) described herein can include hereditary hemochromatosis, oculocutaneous albinism, protein C deficiency, type I hereditary angioedema, congenital sucrase-isomaltase deficiency, Crigler-Najjar type II, Laron syndrome, hereditary Myeloperoxidase, primary hypothyroidism, congenital long QT syndrome, tyroxine binding globulin deficiency, familial hypercholesterolemia, familial chylomicronemia, abeta-lipoproteinema, low plasma lipoprotein A levels, hereditary emphysema with liver injury, congenital hypothyroidism, osteogenesis imperfecta, hereditary hypofibrinogenemia, alpha-1antichymotrypsin deficiency, nephrogenic diabetes insipidus, neurohypophyseal diabetes insipidus, adenosine deaminase deficiency, Pelizaeus Merzbacher disease, von Willebrand disease type IIA, combined factors V and VIII deficiency, spondylo-epiphyseal dysplasia tarda, choroideremia, I cell disease, Batten disease, ataxia telangiectasias, ADPKD-autosomal dominant polycystic kidney disease, microvillus inclusion disease, tuberous sclerosis, oculocerebro-renal syndrome of Lowe, amyotrophic lateral sclerosis, myelodysplastic syndrome, Bare lymphocyte syndrome, Tangier disease, familial intrahepatic cholestasis, X-linked adreno-leukodystrophy, Scott syndrome, Hermansky-Pudlak syndrome types 1 and 2, Zellweger syndrome, rhizomelic chondrodysplasia puncta, autosomal recessive primary hyperoxaluria, Mohr Tranebjaerg syndrome, spinal and bullar muscular atrophy, primary ciliary diskenesia (Kartagener's syndrome), giantism and acromegaly, galactorrhea, Addison's disease, adrenal virilism, Cushing's syndrome, ketoacidosis, primary or secondary aldosteronism, Miller Dieker syndrome, lissencephaly, motor neuron disease, Usher's syndrome, Wiskott-Aldrich

syndrome, Optiz syndrome, Huntington's disease, hereditary pancreatitis, anti-phospholipid syndrome, overlap connective tissue disease, Sjögren's syndrome, stiff-man syndrome, Brugada syndrome, congenital nephritic syndrome of the Finnish type, Dubin-Johnson syndrome, X-linked hypophosphophosphatemia, Pendred syndrome, persistent hyperinsulinemic hypoglycemia of infancy, hereditary spherocytosis, aceruloplasminemia, infantile neuronal ceroid lipofuscinosis, pseudoachondroplasia and multiple epiphyseal, Stargardt-like macular dystrophy, X-linked Charcot-Marie-Tooth disease, autosomal dominant retinitis pigmentosa, Wolcott-Rallison syndrome, Cushing's disease, limb-girdle muscular dystrophy, mucoploy-saccharidosis type IV, hereditary familial amyloidosis of Finish, Anderson disease, sarcoma, chronic myelomonocytic leukemia, cardiomyopathy, faciogenital dysplasia, Torsion disease, Huntington and spinocerebellar ataxias, hereditary hyperhomosyteinemia, polyneuropathy, lower motor neuron disease, pigmented retinitis, seronegative polyarthritis, interstitial pulmonary fibrosis, Raynaud's phenomenon, Wegner's granulomatosis, preoteinuria, CDG-Ia, CDG-Ib, CDG-Ic, CDG-Id, CDG-Ie, CDG-If, CDG-IIa, CDG-IIb, CDG-IIc, CDG-IId, Ehlers-Danlos syndrome, multiple exostoses, Griscelli syndrome (type 1 or type 2), or X-linked non-specific mental retardation. In addition, metabolic disorders can also include lysosomal storage disorders such as, but not limited to, Fabry disease, Farber disease, Gaucher disease, GM_1-gangliosidosis, Tay-Sachs disease, Sandhoff disease, GM_2 activator disease, Krabbe disease, metachromatic leukodystrophy, Niemann-Pick disease (types A, B, and C), Hurler disease, Scheie disease, Hunter disease, Sanfilippo disease, Morquio disease, Maroteaux-Lamy disease, hyaluronidase deficiency, aspartylglucosaminuria, fucosidosis, mannosidosis, Schindler disease, sialidosis type 1, Pompe disease, Pycnodysostosis, ceroid lipofuscinosis, cholesterol ester storage disease, Wolman disease, Multiple sulfatase deficiency, galactosialidosis, mucolipidosis (types II ,III, and IV), cystinosis, sialic acid storage disorder, chylomicron retention disease with Marinesco-Sjögren syndrome, Hermansky-Pudlak syndrome, Chediak-Higashi syndrome, Danon disease, or Geleophysic dysplasia.

Symptoms of a metabolic disorder are numerous and diverse and can include one or more of, e.g., anemia, fatigue, bruising easily, low blood platelets, liver enlargement, spleen enlargement, skeletal weakening, lung impairment, infections (e.g., chest

infections or pneumonias), kidney impairment, progressive brain damage, seizures, extra thick meconium, coughing, wheezing, excess saliva or mucous production, shortness of breath, abdominal pain, occluded bowel or gut, fertility problems, polyps in the nose, clubbing of the finger/toe nails and skin, pain in the hands or feet, angiokeratoma, decreased perspiration, corneal and lenticular opacities, cataracts, mitral valve prolapse and/or regurgitation, cardiomegaly, temperature intolerance, difficulty walking, difficulty swallowing, progressive vision loss, progressive hearing loss, hypotonia, macroglossia, areflexia, lower back pain, sleep apnea, orthopnea, somnolence, lordosis, or scoliosis. It is understood that due to the diverse nature of the defective or absent proteins and the resulting disease phenotypes (e.g., symptomatic presentation of a metabolic disorder), a given disorder will generally present only symptoms characteristic to that particular disorder. For example, a patient with Fabry disease can present a particular subset of the above-mentioned symptoms such as, but not limited to, temperature intolerance, corneal whirling, pain, skin rashes, nausea, or dirarrhea. A patient with Gaucher syndrome can present with splenomegaly, cirrhosis, convulsions, hypertonia, apnea, osteoporosis, or skin discoloration.

In addition to the administration of one or more molecules described herein, a metabolic disorder can also be treated by proper nutrition and vitamins (e.g., cofactor therapy), physical therapy, and pain medications.

Depending on the specific nature of a given metabolic disorder, a patient can present these symptoms at any age. In many cases, symptoms can present in childhood or in early adulthood. For example, symptoms of Fabry disease can present at an early age, e.g., at 10 or 11 years of age.

As used herein, a subject "at risk of developing a metabolic disorder" is a subject that has a predisposition to develop a disorder, i.e., a genetic predisposition to develop metabolic disorder as a result of a mutation in a enzyme such as alpha-L-iduronidase, beta-D-galactosidase, beta-glucosidase, beta-hexosaminidase, beta-D-mannosidase, alpha-L-fucosidase, arylsulfatase B, arylsulfatase A, alpha-N-acteylgalactosaminidase, aspartylglucosaminidase, iduronate-2-sulfatase, alpha-glucosaminide-N-acetyltransferase, beta-D-glucoronidase, hyaluronidase, alpha-L-mannosidase, alpha-neurominidase, phosphotransferase, acid lipase, acid ceramidase, sphinogmyelinase, thioesterase,

cathepsin K, or lipoprotein lipase. Clearly, subjects "at risk of developing a metabolic disorder" are not all the subjects within a species of interest.

A subject "suspected of having a disorder" is one having one or more symptoms of a disorder such as any of those described herein.

(ii) Cancer

Cancer is a class of diseases or disorders characterized by uncontrolled division of cells and the ability of these to spread, either by direct growth into adjacent tissue through invasion, or by implantation into distant sites by metastasis (where cancer cells are transported through the bloodstream or lymphatic system). Cancer can affect people at all ages, but risk tends to increase with age. Types of cancers can include, e.g., lung cancer, breast cancer, colon cancer, pancreatic cancer, renal cancer, stomach cancer, liver cancer, bone cancer, hematological cancer, neural tissue cancer, melanoma, thyroid cancer, ovarian cancer, testicular cancer, prostate cancer, cervical cancer, vaginal cancer, or bladder cancer.

As used herein, a subject "at risk of developing a cancer" is a subject that has a predisposition to develop a cancer, i.e., a genetic predisposition to develop cancer such as a mutation in a tumor suppressor gene (e.g., mutation in BRCA1, p53, RB, or APC) or has been exposed to conditions that can result in cancer. Thus, a subject can also be one "at risk of developing a cancer" when the subject has been exposed to mutagenic or carcinogenic levels of certain compounds (e.g., carcinogenic compounds in cigarette smoke such as Acrolein, Arsenic, Benzene, Benz{a}anthracene, Benzo{a}pyrene, Polonium-210 (Radon), Urethane, or Vinyl Chloride). Moreover, the subject can be "at risk of developing a cancer" when the subject has been exposed to, e.g., large doses of ultraviolet light or X-irradiation, or exposed (e.g., infected) to a tumor-causing/associated virus such as papillomavirus, Epstein-Barr virus, hepatitis B virus, or human T-cell leukemia-lymphoma virus. From the above it will be clear that subjects "at risk of developing a cancer" are not all the subjects within a species of interest.

A subject "suspected of having a cancer" is one having one or more symptoms of a cancer. Symptoms of cancer are well-known to those of skill in the art and include, without limitation, breast lumps, nipple changes, breast cysts, breast pain, weight loss,

weakness, excessive fatigue, difficulty eating, loss of appetite, chronic cough, worsening breathlessness, coughing up blood, blood in the urine, blood in stool, nausea, vomiting, liver metastases, lung metastases, bone metastases, abdominal fullness, bloating, fluid in peritoneal cavity, vaginal bleeding, constipation, abdominal distension, perforation of colon, acute peritonitis (infection, fever, pain), pain, vomiting blood, heavy sweating, fever, high blood pressure, anemia, diarrhea, jaundice, dizziness, chills, muscle spasms, colon metastases, lung metastases, bladder metastases, liver metastases, bone metastases, kidney metastases, and pancreas metastases, difficulty swallowing, and the like. From the above it will be clear that subjects "suspected of having a cancer" are not all the subjects within a species of interest.

In addition to the administration of one or more altered N-glycosylation molecules described herein, a cancer can also be treated by chemotherapeutic agents, ionizing radiation, immunotherapy agents, or hyperthermotherapy agents. Chemotherapeutic agents include, e.g., cisplatin, carboplatin, procarbazine, mechlorethamine, cyclophosphamide, camptothecin, adriamycin, ifosfamide, melphalan, chlorambucil, bisulfan, nitrosurea, dactinomycin, daunorubicin, doxorubicin, bleomycin, plicomycin, mitomycin, etoposide, verampil, podophyllotoxin, tamoxifen, taxol, transplatinum, 5-flurouracil, vincristin, vinblastin, and methotrexate.

(iii) Inflammatory Disorders

An "inflammatory disorder," as used herein, refers to a process in which one or more substances (e.g., substances not naturally occurring in the subject), via the action of white blood cells (e.g., B cells, T cells, macrophages, monocytes, or dendritic cells) inappropriately trigger a pathological response, e.g., a pathological immune response. Accordingly, such cells involved in the inflammatory response are referred to as "inflammatory cells." The inappropriately triggered inflammatory response can be one where no foreign substance (e.g., an antigen, a virus, a bacterium, a fungus) is present in or on the subject. The inappropriately triggered response can be one where a self-component (e.g., a self-antigen) is targeted (e.g., an autoimmune disorder such as multiple sclerosis) by the inflammatory cells. The inappropriately triggered response can also be a response that is inappropriate in magnitude or duration, e.g., anaphylaxis. Thus,

the inappropriately targeted response can be due to the presence of a microbial infection (e.g., viral, bacterial, or fungal). Types of inflammatory disorders (e.g., autoimmune disease) can include, but are not limited to, osteoarthritis, rheumatoid arthritis (RA), spondyloarthropathies, POEMS syndrome, Crohn's disease, multicentric Castleman's disease, systemic lupus erythematosus (SLE), multiple sclerosis (MS), muscular dystrophy (MD), insulin-dependent diabetes mellitus (IDDM), dermatomyositis, polymyositis, inflammatory neuropathies such as Guillain Barre syndrome, vasculitis such as Wegener's granulomatosus, polyarteritis nodosa, polymyalgia rheumatica, temporal arteritis, Sjogren's syndrome, Bechet's disease, Churg-Strauss syndrome, or Takayasu's arteritis. Also included in inflammatory disorders are certain types of allergies such as rhinitis, sinusitis, urticaria, hives, angioedema, atopic dermatitis, food allergies (e.g., a nut allergy), drug allergies (e.g., penicillin), insect allergies (e.g., allergy to a bee sting), or mastocytosis. Inflammatory disorders can also include ulcerative colitis and asthma.

A subject "at risk of developing an inflammatory disorder" refers to a subject with a family history of one or more inflammatory disorders (e.g., a genetic predisposition to one or more inflammatory disorders) or one exposed to one or more inflammation-inducing conditions. For example, a subject can have been exposed to a viral or bacterial superantigen such as, but not limited to, staphylococcal enterotoxins (SEs), a streptococcus pyogenes exotoxin (SPE), a staphylococcus aureus toxic shock-syndrome toxin (TSST-1), a streptococcal mitogenic exotoxin (SME) and a streptococcal superantigen (SSA). From the above it will be clear that subjects "at risk of developing an inflammatory disorder" are not all the subjects within a species of interest.

A subject "suspected of having an inflammatory disorder" is one who presents with one or more symptoms of an inflammatory disorder. Symptoms of inflammatory disorders are well known in the art and include, but are not limited to, redness, swelling (e.g., swollen joints), joints that are warm to the touch, joint pain, stiffness, loss of joint function, fever, chills, fatigue, loss of energy, headaches, loss of appetite, muscle stiffness, insomnia, itchiness, stuffy nose, sneezing, coughing, one or more neurologic symptoms such as dizziness, seizures, or pain. From the above it will be clear that

subjects "suspected of having an inflammatory disorder" are not all the subjects within a species of interest.

In addition to the administration of one or more molecules described herein, an inflammatory disorder can also be treated by non-steroidal anti-inflammatory drug (NSAID), a disease-modifying anti-rheumatic drug (DMARD), a biological response modifier, or a corticosteroid. Biological response modifiers include, e.g., an anti-TNF agent. Non-limiting examples of anti-TNF agents include a soluble TNF receptor or an antibody specific for TNF such as adulimumab, infliximab, or etanercept.

Methods suitable for treating (e.g., preventing or ameliorating one or more symptoms of) any of the disorders described herein using any of the altered N-glycosylation molecules (or pharmaceutical compositions thereof) are set forth in the following section.

Pharmaceutical Compositions and Methods of Treatment

A target molecule modified to have the desired N-glycan can be incorporated into a pharmaceutical composition containing a therapeutically effective amount of the molecule and one or more adjuvants, excipients, carriers, and/or diluents. Acceptable diluents, carriers and excipients typically do not adversely affect a recipient's homeostasis (e.g., electrolyte balance). Acceptable carriers include biocompatible, inert or bioabsorbable salts, buffering agents, oligo- or polysaccharides, polymers, viscosity-improving agents, preservatives and the like. One exemplary carrier is physiologic saline (0.15 M NaCl, pH 7.0 to 7.4). Another exemplary carrier is 50 mM sodium phosphate, 100 mM sodium chloride. Further details on techniques for formulation and administration of pharmaceutical compositions can be found in, e.g., Remington's Pharmaceutical Sciences (Maack Publishing Co., Easton, Pa.). Supplementary active compounds can also be incorporated into the compositions.

Administration of a pharmaceutical composition containing molecules with N-glycans can be systemic or local. Pharmaceutical compositions can be formulated such that they are suitable for parenteral and/or non-parenteral administration. Specific administration modalities include subcutaneous, intravenous, intramuscular, intraperitoneal, transdermal, intrathecal, oral, rectal, buccal, topical, nasal, ophthalmic,

intra-articular, intra-arterial, sub-arachnoid, bronchial, lymphatic, vaginal, and intra-uterine administration.

Administration can be by periodic injections of a bolus of the pharmaceutical composition or can be uninterrupted or continuous by intravenous or intraperitoneal administration from a reservoir which is external (e.g., an IV bag) or internal (e.g., a bioerodable implant, a bioartificial organ, or a colony of implanted altered N-glycosylation molecule production cells). See, e.g., U.S. Pat. Nos. 4,407,957, 5,798,113, and 5,800,828. Administration of a pharmaceutical composition can be achieved using suitable delivery means such as: a pump (see, e.g., Annals of Pharmacotherapy, 27:912 (1993); Cancer, 41:1270 (1993); Cancer Research, 44:1698 (1984); microencapsulation (see, e.g., U.S. Pat. Nos. 4,352,883; 4,353,888; and 5,084,350); continuous release polymer implants (see, e.g., Sabel, U.S. Pat. No. 4,883,666); macroencapsulation (see, e.g., U.S. Pat. Nos. 5,284,761, 5,158,881, 4,976,859 and 4,968,733 and published PCT patent applications WO92/19195, WO 95/05452); injection, either subcutaneously, intravenously, intra-arterially, intramuscularly, or to other suitable site; or oral administration, in capsule, liquid, tablet, pill, or prolonged release formulation.

Examples of parenteral delivery systems include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, pump delivery, encapsulated cell delivery, liposomal delivery, needle-delivered injection, needle-less injection, nebulizer, aerosolizer, electroporation, and transdermal patch.

Formulations suitable for parenteral administration conveniently contain a sterile aqueous preparation of the altered N-glycosylation molecule, which preferably is isotonic with the blood of the recipient (*e.g.*, physiological saline solution). Formulations can be presented in unit-dose or multi-dose form.

Formulations suitable for oral administration can be presented as discrete units such as capsules, cachets, tablets, or lozenges, each containing a predetermined amount of the altered N-glycosylation molecule; or a suspension in an aqueous liquor or a non-aqueous liquid, such as a syrup, an elixir, an emulsion, or a draught.

A molecule having N-glycans suitable for topical administration can be administered to a mammal (e.g., a human patient) as, e.g., a cream, a spray, a foam, a gel, an ointment, a salve, or a dry rub. A dry rub can be rehydrated at the site of

administration. Such molecules can also be infused directly into (e.g., soaked into and dried) a bandage, gauze, or patch, which can then be applied topically. Such molecules can also be maintained in a semi-liquid, gelled, or fully-liquid state in a bandage, gauze, or patch for topical administration (see, e.g., U.S. Patent No. 4,307,717).

Therapeutically effective amounts of a pharmaceutical composition can be administered to a subject in need thereof in a dosage regimen ascertainable by one of skill in the art. For example, a composition can be administered to the subject, e.g., systemically at a dosage from 0.01μg/kg to 10,000 μg/kg body weight of the subject, per dose. In another example, the dosage is from 1 μg/kg to 100 μg/kg body weight of the subject, per dose. In another example, the dosage is from 1 μg/kg to 30 μg/kg body weight of the subject, per dose, e.g., from 3 μg/kg to 10 μg/kg body weight of the subject, per dose.

In order to optimize therapeutic efficacy, a molecule containing an N-glycan can be first administered at different dosing regimens. The unit dose and regimen depend on factors that include, *e.g.*, the species of mammal, its immune status, the body weight of the mammal. Typically, levels of such a molecule in a tissue can be monitored using appropriate screening assays as part of a clinical testing procedure, *e.g.*, to determine the efficacy of a given treatment regimen.

The frequency of dosing for a molecule is within the skills and clinical judgement of medical practitioners (e.g., doctors or nurses). Typically, the administration regime is established by clinical trials which may establish optimal administration parameters. However, the practitioner may vary such administration regimes according to the subject's age, health, weight, sex and medical status. The frequency of dosing can be varied depending on whether the treatment is prophylactic or therapeutic.

Toxicity and therapeutic efficacy of such molecules or pharmaceutical compositions thereof can be determined by known pharmaceutical procedures in, for example, cell cultures or experimental animals. These procedures can be used, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD50/ED50. Pharmaceutical compositions that exhibit high therapeutic indices are

preferred. While pharmaceutical compositions that exhibit toxic side effects can be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to normal cells (e.g., non-target cells) and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in appropriate subjects (e.g., human patients). The dosage of such pharmaceutical compositions lies generally within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For a pharmaceutical composition used as described herein (e.g., for treating a metabolic disorder in a subject), the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC50 (i.e., the concentration of the pharmaceutical composition which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma can be measured, for example, by high performance liquid chromatography.

As defined herein, a "therapeutically effective amount" of a molecule containing an N-glycan is an amount of the molecule that is capable of producing a medically desirable result (e.g., amelioration of one or more symptoms of a metabolic disorder) in a treated subject. A therapeutically effective amount (i.e., an effective dosage) can includes milligram or microgram amounts of the compound per kilogram of subject or sample weight (e.g., about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram).

The subject can be any mammal, e.g., a human (e.g., a human patient) or a non-human primate (e.g., chimpanzee, baboon, or monkey), a mouse, a rat, a rabbit, a guinea pig, a gerbil, a hamster, a horse, a type of livestock (e.g., cow, pig, sheep, or goat), a dog, a cat, or a whale.

A molecule or pharmaceutical composition thereof described herein can be administered to a subject as a combination therapy with another treatment, e.g., a

treatment for a metabolic disorder (e.g., a lysosomal storage disorder). For example, the combination therapy can include administering to the subject (e.g., a human patient) one or more additional agents that provide a therapeutic benefit to the subject who has, or is at risk of developing, (or suspected of having) a metabolic disorder (e.g., a lysosomal storage disorder). Thus, the compound or pharmaceutical composition and the one or more additional agents can be administered at the same time. Alternatively, the molecule can be administered first and the one or more additional agents administered second, or vice versa.

It will be appreciated that in instances where a previous therapy is particularly toxic (e.g., a treatment for a metabolic disorder with significant side-effect profiles), administration of a molecule described herein can be used to offset and/or lessen the amount of the previously therapy to a level sufficient to give the same or improved therapeutic benefit, but without the toxicity.

Any of the pharmaceutical compositions described herein can be included in a container, pack, or dispenser together with instructions for administration.

The following are examples of the practice of the invention. They are not to be construed as limiting the scope of the invention in any way.

EXAMPLES

Table 2 contains a list of all of the strains used in the experiments described below. In Table 2, MH = HDEL-tagged α-1,2-mannosidase; ζ = random integration via zeta sequences; docking Δ = integration into a specific locus; and (H) = hygromycin resistant.

TABLE 2

Listing of Strains Used in Examples

Number	Short name	Description	Markers	Expected N-Glycans
G013	Po1d lnuga Δoch1(URA3) cl 26.1	Po1d lnuga transformed with SpeI/Bst1107I- digested pYLOCH1PUT-TOPO	URA3$^+$ leu2$^-$ ade2$^-$ gut2$^-$	Mainly $Man_8GlcNAc_2$
G014	Po1d lnuga Δoch1 (cured) cl 7	Po1d lnuga Δoch1 **(G013)** cured from the URA3 marker using pUB4-Cre	ura3$^-$ leu2$^-$ ade2$^-$ gut2$^-$	Mainly $Man_8GlcNAc_2$
G016	Po1d lnuga Δoch1 TefMH (ζ-Not) cl 1.4	Po1d lnuga Δoch1 (cured) **(G014)** transformed with NotI-digested pYLTUXL2preManHDEL(Yl)	URA3$^+$ leu2$^-$ ade2$^-$ gut2$^-$	$Man_5GlcNAc_2$
G018	Po1d lnuga Δoch1 Hp4dMH (ζ-Not) cl 11.2	Po1d lnuga Δoch1 (cured) **(G014)** transformed with NotI-digested pYLHUXL2preManHDEL(Yl)	URA3$^+$ leu2$^-$ ade2$^-$ gut2$^-$	$Man_5GlcNAc_2$
G036	Po1d lnuga Δoch1 Hp4dMH (ζ-Not)(cured) cl 2.2 (1 copy ManHDEL)	Po1d lnuga Δoch1 Hp4dMH (Not) cl 11.2 **(G018)** cured from the URA3 marker using pRRQ2	ura3$^-$ leu2$^-$ ade2$^-$ gut2$^-$	$Man_5GlcNAc_2$
G039	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 cl 24.1	Po1d lnuga Δoch1 Hp4dMH (ζ-Not-cured) cl 2.2 **(G036)** transformed with NotI/PacI-digested pYlALG3PUT-ALG6	URA3$^+$ leu2$^-$ ade2$^-$ gut2$^-$	$Glc_{1-2}Man_5GlcNAc_2$ and $Man_3GlcNAc_2$
G040	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) TefhGnTI cl 5.4 (1 copy GnT I)	Po1d lnuga Δoch1 Hp4dMH (ζ-Not-cured) cl 2.2 **(G036)**	URA3$^+$ leu2$^-$ ade2$^-$ gut2$^-$	$GlcNAcMan_5GlcNAc_2$

		transformed with NotI-digested pYLTmAx hGnTI		
G043	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) TefhGnTI TefManII cl 15	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) TefhGnTI cl 5.4 **(G040)** transformed with NotI-digested pYLTmAXDmManII (LEU2 ex)	$URA3^{+}$ $LEU2^{+}$ $ade2^{-}$ $gut2^{-}$	$GlcNAcMan_3GlcNAc_2$
G044	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) TefhGnTI TefGalTI cl 12	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) TefhGnTI cl 5.4 **(G040)** transformed with NotI-digested pYLTmAXSpGal10hGalTI (ADE2 ex)	$URA3^{+}$ $leu2^{-}$ $ADE2^{+}$ $gut2^{-}$	$GalGlcNAcMan_5$ $GlcNAc_2$
G045	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 cl 2.16 (cured)	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 cl 24.1 **(G039)** cured from the URA3 marker using pRRQ2	$ura3^{-}$ $leu2^{-}$ $ade2^{-}$ $gut2^{-}$	$Glc_{1-2}Man_5{\cdot}GlcNAc_2$ and $Man_3GlcNAc_2$
G046	Po1d lnuga Δoch1 Hp4dMH (docking Δleu2)	Po1d lnuga Δoch1 (cured) **(G014)** transformed with NotI-digested JME926 pPTleu2-ADE2Ex-Hp4dManHDEL(Yl)	$ura3^{-}$ $leu2^{-}$ $ADE2^{+}$ $gut2^{-}$	$Man_5GlcNAc_2$
G047	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 TefhGnTI(H) cl2 (1 copy GnT I)	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 cl 24.1 **(G039)** transformed with NotI-digested pYLTmAXhGnTI (Hyg^{R} ex)	$URA3^{+}$ $leu2^{-}$ $ade2^{-}$ $gut2^{-}$ Hyg^{R}	$Glc_{1-2}Man_5{\cdot}GlcNAc_2$ and $GlcNAcMan_3GlcNAc_2$
G048	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 (cured) TefhGnTI clone 7.3	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 cl 2.16 (cured) **(G045)** transformed	$URA3^{+}$ $leu2^{-}$ $ade2^{-}$ $gut2^{-}$	$Glc_{1-2}Man_5{\cdot}GlcNAc_2$ and $GlcNAcMan_3GlcNAc_2$

		with NotI-digested pYLTmAXhGnTI		
G050	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 (cured) TefhGnTI TefrGnTII cl. 42.3	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 cl 2.16 (cured) **(G045)** transformed with NotI-digested pYLTmAXhGnTI and pYLTmAXrGnTII (ADE2 Ex)	$URA3^{+}$ $leu2^{-}$ $ADE2^{+}$ $gut2^{-}$	$Glc_{1-2}Man_5$,$GlcNAc_2$ and $GlcNAc_2Man_3GlcNAc_2$
G051	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 TefhGnTI(H) TefrGnTII clone 4.5	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 TefhGnTI cl2 **(G047)** transformed with NotI-digested pYLTmAXrGnTII (ADE2 Ex)	$URA3^{+}$ $leu2^{-}$ $ADE2^{+}$ $gut2^{-}$ Hyg^{R}	$Glc_{1-2}Man_5$,$GlcNAc_2$ and $GlcNAc_2Man_3GlcNAc_2$
G052	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Hp4dhGnTI (ζ) cl one 16	Po1d lnuga Δoch1 Hp4dMH (ζ-Not-cured) cl 2.2 **(G036)** transformed with NotI-digested pYLHp4mAxhGnTI	$URA3^{+}$ $leu2^{-}$ $ade2^{-}$ $gut2^{-}$	$GlcNAcMan_5GlcNAc_2$
G053	Po1d lnuga Δoch1 Hp4dMH (docking Δaxp1)	Po1d lnuga Δoch1 (cured) **(G014)** transformed with NotI-digested OXYP289-pPTAxp1-Leu2Ex-Hp4dManHDEL(Yl)	$ura3^{-}$ $LEU2^{+}$ $ade2^{-}$ $gut2^{-}$	$Man_5GlcNAc_2$
G054	Po1d lnuga Δoch1 Hp4dMH (docking Δaxp1) (cured)	Po1d lnuga Δoch1 Hp4dMH (docking Δaxp1) **(G053)** cured from the LEU2 marker using pUB4-Cre	$ura3^{-}$ $leu2^{-}$ $ade2^{-}$ $gut2^{-}$	$Man_5GlcNAc_2$
G055	Po1d lnuga Δoch1 Hp4dMH (docking Δleu2-cured)	Po1d lnuga Δoch1 Hp4dMH (docking Δleu2) **(G046)** cured from the ADE2 marker using	$ura3^{-}$ $leu2^{-}$ $ade2^{-}$ $gut2^{-}$	$Man_5GlcNAc_2$

		pRRQ2		
G056	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 Hp4dGnTI (ζ) clone E	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 cl 2.16 (cured) **(G045)** transformed with NotI-digested pYLHp4mAxhGnTI	$URA3^{+}$ $leu2^{-}$ $ade2^{-}$ $gut2^{-}$	$Glc_{1-2}Man_5GlcNAc_2$ and $GlcNAcMan_3GlcNAc_2$
G057	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 Hp4dGnTI (docking Δade2) clone G	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 cl 2.16 (cured) **(G045)** transformed with NotI-digested JME925 pPTade2-URA3ex-Hp4dhGnTI	$URA3^{+}$ $leu2^{-}$ $ade2^{-}$ $gut2^{-}$	$Glc_{1-2}Man_5GlcNAc_2$ and $GlcNAcMan_3GlcNAc_2$
G058	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 Hp4dGnTI (ζ-cured)	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 Hp4dGnTI (ζ) **(G056)** cured from the URA3 marker using pRRQ2	$ura3^{-}$ $leu2^{-}$ $ade2^{-}$ $gut2^{-}$	$Glc_{1-2}Man_5GlcNAc_2$ and $GlcNAcMan_3GlcNAc_2$
G059	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 Hp4dGnTI (docking Δade2-cured)	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 Hp4dGnTI (docking Δade2) **(G057)** cured from the URA3 marker using pRRQ2	$ura3^{-}$ $leu2^{-}$ $ade2^{-}$ $gut2^{-}$	$Glc_{1-2}Man_5GlcNAc_2$ and $GlcNAcMan_3GlcNAc_2$
G060	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 Hp4dGnTI (docking Δade2) Hp4dGls2α/β (ζ) clone 6	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 Hp4dGnTI (docking Δade2) (G057) transformed with Not-digested Zeta-LEU2Ex-Hp4dL2preAnGlcII a+b(alt)	URA3+ LEU2+ $ade2^{-}$ $gut2^{-}$	$GlcNAcMan_3GlcNAc_2$

G061	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 Hp4dGnTI (docking Δade2) Hp4d Gls2α/β (docking Δura3) clone 18	Po1d lnuga Δoch1 Hp4dMH (ζ-cured) Δalg3ALG6 Hp4dGnTI (docking Δade2) (G057) transformed with Not-digested JME923 pPTUra3-Leu2Ex-Hp4d L2preAnGlcIIa+b(alt)	URA3+ LEU2+ ade2- gut2-	$GlcNAcMan_3GlcNAc_2$
G070	Po1d lnuga Δoch1 Hp4dMH (1 copy-ζ-cured) Δalg3ALG6 (cured) Hp4dGnTI (docking Δade2) Hp4dGls2α/β (docking Δura3) Hp4dGnTII (ζ) cl 6	Po1d lnuga Δoch1 Hp4dMH (1 copy-ζ-cured) Δalg3ALG6 (cured) Hp4dGnTI (docking Δade2) Hp4d Gls2α/β (docking Δura3) **(G061)** transformed with Not-digested pYLHp4mAXrGnTII (ADE2ex)	$URA3^+$ $LEU2^+$ $ADE2^+$ $gut2^-$	$GlcNAc_2Man_3GlcNAc_2$
G071	Po1d lnuga Δoch1 Hp4dMH (1 copy-ζ-cured) Δalg3ALG6 (cured) Hp4dGnTI (docking Δade2) Hp4d Gls2α/β (docking Δura3) Hp4dGnTII (integration in Axp1 locus was aimed at) cl 8	Po1d lnuga Δoch1 Hp4dMH (1 copy-ζ-cured) Δalg3ALG6 (cured) Hp4dGnTI (docking Δade2) Hp4d Gls2α/β (docking Δura3) **(G061)** transformed with Not-digested OXYP289 pPTAxp1-ADE2ex-Hp4dGnTII	$URA3^+$ $LEU2^+$ $ADE2^+$ $gut2^-$	$GlcNAc_2Man_3GlcNAc_2$
G096	Po1d lnuga Δoch1 Hp4dMH (1 copy-ζ-cured) Δalg3ALG6 (cured) Hp4dGnTI (docking Δade2) Hp4d Gls2α/β (docking Δura3) Hp4dGnTII (integration in Axp1 locus was aimed at) Hp4d**PP**-HC/LC clone 13	Po1d lnuga Δoch1 Hp4dMH (1 copy-ζ-cured) Δalg3ALG6 (cured) Hp4dGnTI (docking Δade2) Hp4d Gls2α/β (docking Δura3) Hp4dGnTII (docking Δaxp1) **(G071)** transformed with NotI digested	$URA3^+$ $LEU2^+$ $ADE2^+$ $GUT2^+$	$GlcNAc_2Man_3GlcNAc_2$

		pYLHp4L2preproHerHC&LC (Gut2ex)-ori2		

Example 1: *Yarrowia lipolytica* OCH1 disruption

The generation of a glyco-engineered protein expression strain was done in *Yarrowia lipolytica* strain po1d lnuga (a strain having the auxotrophies *leu2-*, *ura3-*, *gut2-* and *ade2-*). A strategy to knock out the *OCH1* (GenBank Accession No: AJ563920) gene in *Yarrowia lipolytica* was set up as described for the *LIP2* gene (Fickers *et al.*, 2003 *J Microbiol Methods.* 55(3):727-37). The gene construction strategy followed for the *OCH1* gene is described in U.S. Patent Publication No. 20090069232-A1. The resulting vector was called pYlOCH1 PUT TOPO (FIG. 1B).

The OCH1 KO fragment was isolated from the plasmid by a SpeI/Bst1107I restriction digest and transformed to *Yarrowia lipolytica* strain po1d lnuga. Several uracil prototrophic strains were obtained and screened by PCR on genomic DNA (gDNA) using primers *Yloch1 prom fw* (5'-TCGCTATCACGTCTCTAGC-3', SEQ ID NO:1) and *Yloch1 term rev* (5'-ACTCTGTATACTTGTATGTACTGTGAGAC-3', SEQ ID NO:2) to analyze the genomic integration of the plasmid. A fragment of the correct size (i.e., 2328 bp vs. 1894 bp in the wild type) was amplified for several clones tested. The knock-out of the *OCH1* gene also was confirmed by N-glycan analysis of the total glycoprotein pool secreted into the growth medium (= secretome): the $Man_8GlcNAc_2$ structure has become the predominant N-glycan within the sugar profile (FIG. 2). This profile differs from that of the wild-type strain, which contains a higher amount of $Man_9GlcNAc_2$ – the latter most probably containing an additional mannose as a result of Och1p activity – as well as some structures with an even higher number of mannose residues.

To remove the *URA3* gene, a positive Δ*och1* clone (called G013, see Table 2) was transformed with the episomal plasmid pUB4-Cre (Fickers et al., 2003, *supra*) that contains an expression cassette for the Cre recombinase. Removal of the *URA3* gene was screened for by PCR on gDNA using primers *Yloch1 prom fw* and *Yloch1 term rev* (see above). Clones in which the URA3 marker was excised no longer resulted in the amplification of a 2328 bp band; instead a PCR-fragment of 1075 bp (excl. *URA3*) was obtained. Positive clones were checked at the N-glycan level of the secretome and show a profile very similar to that of the non-cured strain (FIG. 2). One of the cured strains (called G014, see Table 2) was selected for further N-glycan engineering.

Example 2: overexpression of an ER-retained α-1,2-mannosidase by either random integration or targeted/docked integration

To enable the generation of $Man_5GlcNAc_2$ attached to glycoproteins expressed by a Δ*och1* strain, an α-1,2-mannosidase was expressed to cleave $Man_8GlcNAc_2$ to $Man_5GlcNAc_2$ (i.e., a Golgi type α-1,2-mannosidase activity). Such a mannosidase should be targeted to the secretion system. *Trichoderma reesei* α-1,2-mannosidase (Genbank accession no. AF212153), fused to the *S. cerevisiae* prepro mating factor and tagged with a HDEL sequence (SEQ ID NO:21) to localize it into the ER, is able to trim $Man_8GlcNAc_2$ to $Man_5GlcNAc_2$ *in vivo* in *Pichia pastoris* as well as in *Trichoderma reesei* and *Aspergillus niger*. Expression constructs were made where a codon-optimized version of the HDEL-tagged *T. reesei* α-1,2-mannosidase was fused to the *Y. lipolytica LIP2* pre signal sequence and placed under the transcriptional control of either the *TEF1*, Hp4d (Madzak *et al.*, 2000, *J. Mol. Microbiol. Biotechnol.* 2:207-216), *GAP* or *POX2* promotor. The construction strategy of these plasmids is described in U.S. Patent Publication No. 20090069232-A1.

Two of these vectors, pYLHUXdL2preManHDEL and pYLTUXdL2preManHDEL (FIG. 3) – with the mannosidase under the transcriptional control of the Hp4d resp. *TEF1* promotor, were used to transform strain G014 (derived from Example 1). The vectors were digested with NotI to allow random integration into the genome via the zeta sequences. *URA3* prototrophic transformants were selected for N-glycan analysis. Several transformants show a clear conversion of $Man_8GlcNAc_2$ towards $Man_5GlcNAc_2$ (FIG. 4). Since clones expressing the mannosidase under *TEF1* promotor control showed a slow and clumpy growth phenotype (one of these clones was called G016), further steps in glyco-engineering were done in a strain background where the gene is under Hp4d transcriptional control.

One positive clone expressing the ManHDEL under control of the hp4d promoter (G018) was chosen, from which the *URA3* marker was cured via transient transformation of plasmid pRRQ2 (Richard *et al.*, 2001 *J. Bacteriol.* 183:3098-3107), expressing the Cre-recombinase. Several *ura3*- clones were selected after the procedure and one clone (G036), showing a clear $Man_5GlcNAc_2$ profile on the secretome, was used for further

engineering work (FIG. 4). Southern analysis of this clone revealed the presence of one randomly integrated mannosidase expression cassette. This Southern analysis was performed on Hind III digested genomic DNA using a DIG-labeled mannosidase-specific PCR fragment that was generated using primers Man for (5'-GCCTTCCAGACCTCTTGGAACGCCTACCACC-3', SEQ ID NO:22) and Man rev (5'-GCCAGGTGGCCGCCTCGTCGAGAAGAAGATCG-3', SEQ ID NO:23).

In an alternative strategy, two constructs were generated that allow targeted integration of the Hp4d-driven mannosidase expression cassette into either the *LEU2* or *AXP1* locus of the *Yarrowia* genome. Construction of these plasmids, JME926_pPTLeu2-ADE2ex-Hp4dManHDEL(Yl) and OXYP289_pPTAxp1-LEU2ex-Hp4dManHDEL(Yl), is described in FIG. 5. Prior to transformation to strain G014, both constructs were digested with NotI and the respective expression cassettes were isolated. Selected *ADE2* prototrophic clones had potentially integrated the mannosidase expression cassette into the *LEU2* locus, whereas *LEU2* prototrophs potentially had integrated the cassette into the *AXP1* locus. The transformants were checked by Southern analysis to assess proper targeting into the genome. This was performed on BamHI digested (integration in *LEU2* locus) or HindIII digested (integration in *AXP1* locus) genomic DNA using a DIG-labeled mannosidase-specific PCR fragment that was generated using primers Man for (5'-GCCTTCCAGACCTCTTGGAACGCCTACCACC-3', SEQ ID NO:22) and Man rev (5'-GCCAGGTGGCCGCCTCGTCGAGAAGAAGATCG-3', SEQ ID NO:23). The selected clones also were checked for the nature of the N-glycans synthesized onto the secreted glycoproteins. In most cases, correctly targeted Hp4d-driven α-1,2-mannosidase expression resulted into the synthesis of predominantly $Man_5GlcNAc_2$ oligosaccharides (FIG. 6). For each targeting locus, one mannosidase expressing clone (G046 in case of *LEU2* docking; G053 in case of *AXP1* docking) was selected for curing via transient expression of the Cre recombinase using plasmid pRRQ2 for strain G046 and pUB4-Cre for strain G053. The resulting cured strains (G055 abd G054, respectively) were re-checked via Southern blotting and their $Man_5GlcNAc_2$ profile confirmed via N-glycan analysis using DSA-FACE.

Example 3: expression of GlcNAc-transferase I

A *Yarrowia* codon-optimized sequence was generated for the expression of a fusion protein consisting of the first 100 N-terminal amino acids of the *S. cerevisiae* Kre2 protein (SwissProt AccNo P27809) followed by the catalytic domain of human GlcNAc-transferase I (SwissProt AccNo P26572)(FIG. 7, SEQ ID NO:3 and SEQ ID NO:4). The yeast Kre2p 100 N-terminal amino acids serve as a Golgi localization signal for the catalytic GnT I domain. In this way, it is ensured that the GnT I fusion protein is localized later in the secretion pathway than the ER-retained HDEL-tagged α-1,2-mannosidase in order to enable the enzyme converting the protein-linked N-glycans from $Man_5GlcNAc_2$ to $GlcNAcMan_5GlcNAc_2$. The codon optimized synthetic gene for the expression of the fusion protein was placed under the transcriptional control of either the *TEF1* or the Hp4d promoter, resulting into the plasmids pYLTmAXhGnTI and pYLHp4mAXhGnTI. The construction strategy is shown in FIG. 8. Functional expression of the Kre2-GnT I fusion protein should result in the addition of a β-1,2-linked GlcNAc residue onto the available $Man_5GlcNAc_2$ glycans resulting in the synthesis of $GlcNAcMan_5GlcNAc_2$.

The plasmids pYLTmAXhGnTI and pYLHp4mAXGnTI were NotI digested before transformation to strain G036 (cf. Example 2), known to produce $Man_5GlcNAc_2$ N-glycans on its secreted proteins. Transformants were selected for uracil prototrophy. Analysis of the N-glycosylation profile on the secretome of several of these clones showed a clear change in the N-glycan pattern: the $Man_5GlcNAc_2$ was significantly reduced and a new peak, representing an N-glycan with higher molecular weight (about one glucose unit extra), appeared. Treatment of the isolated N-glycans with Jack Bean β-N-acetylhexosaminidase, an enzyme capable of removing terminal β-linked GlcNAc residues, indicated that the new N-glycan is $GlcNAcMan_5GlcNAc_2$: the new peak disappeared and was completely converted into $Man_5GlcNAc_2$ (FIG. 9). Depending on the cultivation method used, about 70% of the total N-glycan pool proved to be $GlcNAcMan_5GlcNAc_2$ (with approximately 77% of the available $Man_5GlcNAc_2$ being converted).

One transformant expressing the Kre2-GnT I fusion protein under control of the *TEF1* promotor was named strain G040 and selected for further use. Genomic analysis of

this strain via Southern blot indicated the presence of one expression cassette. Southern analysis was done on BamHI digested genomic DNA using a DIG-labeled GnT I-specific PCR fragment that was generated using primers 5'-GGATGATCACACAATGGCCCTGTTTCTG-3' (SEQ ID NO:5) and 5'-TGCTCTAGACTAGTTCCAAGAGGGGTC-3' (SEQ ID NO:6). Analysis of the glycosylation profile on the secretome of strain G040 versus strains carrying 1 to 3 copies (confirmed by the same southern blot) of the Hp4d-driven Kre2-GnT I expression cassette, did not show significant difference in GlcNAc-transfer capacity.

Example 4: expression of mannosidase II

A *Yarrowia* codon-optimized sequence was generated for the expression of a fusion protein consisting of the first 36 N-terminal amino acids of the *S. cerevisiae* Mnn2 protein (SwissProt AccNo P38069) followed by the catalytic domain of *Drosophila melanogaster* mannosidase II (SwissProt AccNo Q24451)(FIG. 10, SEQ ID NO:7 and SEQ ID NO:8). The yeast Mnn2 36 N-terminal amino acids serve as a Golgi localization signal for the catalytic Man II domain. In this way, it is ensured that the Mnn2-Man II fusion protein is localized at the same or even a later position in the secretion pathway than the Kre2-GnT I fusion protein and is therefore able to convert $GlcNAcMan_5GlcNAc_2$ into $GlcNAcMan_3GlcNAc_2$. The *Yarrowia* codon optimized synthetic gene for the expression of the fusion protein was placed under the transcriptional control of the *TEF1* promoter, resulting into the plasmids pYLTmAXDmManII and pYLTmAXDmManII (LEU2ex). The construction strategy is shown in FIG. 11.

Plasmid pYLTmAXDmManII (LEU2ex) was NotI digested before transformation to strain G040 (see Example 3), which was known to produce $GlcNAcMan_5GlcNAc_2$ N-glycans on its secreted proteins. Transformants were selected for leucine prototrophy. Analysis of the N-glycosylation profile on the secretome of several of these clones showed a change in the N-glycan pattern: a new peak representing an N-glycan with a lower molecular weight of about two glucose units appeared, which could indicate the formation of $GlcNAcMan_3GlcNAc_2$ and thus partial mannosidase II activity. Also another peak appears, running at almost the same position as $Man_5GlcNAc_2$ (i.e. a

shoulder to the peak), potentially representing $GlcNAcMan_4GlcNAc_2$. The latter structure could be the result of a partial trimming event, where the mannosidase II activity has only removed one mannose residue instead of two. Treatment of the isolated N-glycans with Jack Bean β-N-acetylhexosaminidase resulted in a leftward shift of the glycan pattern with about one glucose unit and thus a higher electrophoretic mobility due to the loss of a terminal GlcNAc residue (FIG. 12). This further confirms the generation of $GlcNAcMan_4GlcNAc_2$ and $GlcNAcMan_3GlcNAc_2$ from $GlcNAcMan_5GlcNAc_2$ due to the expression of a functional mannosidase II activity. Depending on the cultivation method used, about 15% of the total N-glycan pool proved to be $GlcNAcMan_3GlcNAc_2$: approximately 35% of the available $GlcNAcMan_5GlcNAc_2$ lost 1 or 2 mannose residues, with 20% being completely trimmed towards $GlcNAcMan_3GlcNAc_2$.

Example 5: expression of galactosyltransferase I

Synthesis of N-glycans with terminal galactose residues not only depends on the presence of a functional and well-localized galactosyltransferase within the secretion pathway, but also on the availability of UDP-Gal, the donor substrate that is used by the enzyme. Although UDP-Glc and UDP-GlcNAc are generally thought to be sufficiently available in the Golgi apparatus of yeast organisms, this is less known for UDP-Gal. To overcome potential UDP-Gal deficiency during glyco-engineering, attempts have been made previously in *Pichia pastoris* to target a fusion protein of the *Schizosaccharomyces pombe* UDP-Glc-4-epimerase (encoded by the *GAL10* like gene SPBC365.14c - SwissProt AccNo Q9Y7X5) and the catalytic domain of the human β-1,4-galactosyltransferase I (GalT I) (SwissProt AccNo P15291) into the yeast Golgi apparatus (Bobrowicz *et al.*, *Glycobiology* 14(9):757-766, 2004). Localization of the Gal10p-GalT I fusion protein within the secretion pathway, preferably at a position where GlcNAc-transfer and mannosidase II activity has already acted on the N-glycans of proteins destined for secretion, was accomplished by using the first 46 N-terminal amino acids of *S. cerevisiae* Mnn2p as N-terminal targeting signal.

Hence, a *Yarrowia* codon-optimized sequence was generated for the expression of a fusion protein consisting of the first 46 N-terminal amino acids of the *S. cerevisiae* Mnn2 protein, followed by the *S. pombe* Gal10-like protein and the catalytic domain of

human GalT I (FIG. 13). The resulting synthetic gene was placed under the transcriptional control of the *TEF1* promoter, resulting into the plasmids pYLTmAXSpGal10hGalTI and pYLTmAXSpGal10hGalTI (ADE2ex). The construction strategy is shown in FIG. 14.

Plasmid pYLTmAXSpGal10hGalTI (ADE2ex) was NotI digested before transformation to strain G040 (see Example 3), known to produce $GlcNAcMan_5GlcNAc_2$ N-glycans on its secreted proteins. Transformants were selected for their adenine prototrophy. Analysis of the N-glycosylation profile on the secretome of several of these clones showed a change in the N-glycan pattern: a new peak appears, running at a position between $Man_7GlcNAc_2$ and $Man_8GlcNAc_2$ (FIG. 15). Treatment of the N-glycans with *Streptococcus pneumonia* β-1,4-galactosidase indicates that the peak represents $GalGlcNAcMan_5GlcNAc_2$ since this *in vitro* digest results in the disappearance of this new peak and an equally high increase in $GlcNAcMan_5GlcNAc_2$.

Using this set-up and depending on the growth conditions, about 75% of $GlcNAcMan_5GlcNAc_2$ was converted into $GalGlcNAcMan_5GlcNAc_2$. The total amount of the galactosylated structure accounted for about 25% of the total N-glycan pool. From an *in vitro* α-1,2-mannosidase digest it is clear, however, that a significant amount of high-mannose N-glycans was not converted to $Man_5GlcNAc_2$ (FIG. 15). Depending on the cultivation medium used, the conversion rate of $Man_5GlcNAc_2$ towards $GlcNAcMan_5GlcNAc_2$ also is lower than that observed in the G040 parent strain. This is most probably related to the slower growth rate observed for transformants of this Mnn2-Gal10-GalT I fusion protein.

Example 6: knock-out of *YlALG3* and simultaneous overexpression of *YlALG6*

To allow the generation of a $Man_3GlcNAc_2$ platform, the *ALG3* gene of strain G036 (po1d lnuga Δ*och1* + Hp4d-driven α-1,2-mannosidase) needs to be inactivated. This results into the loss of the ER-localized Alg3p α-1,6-mannosyltransferase activity and changes the composition of the lipid-linked N-glycan precursor structure. Transfer of this structure to an N-glycosylation site of a nascent polypeptide chain makes it possible to convert the yeast glycosylation profile into mammalian-like N-glycan structures without the need to express the Mannosidase II. However, since this new lipid-linked

structure is not transferred as efficiently to nascent polypeptides, the *Yarrowia ALG6* gene (encoding an ER-localized Alg6p α-1,3-glucosyl transferase) needs to be overexpressed simultaneously to reduce potential protein underglycosylation as much as possible.

A vector called pYLalg3PUT-ALG6 (FIG. 16) was constructed previously to allow simultaneous knock-out of *YlALG3* and Hp4d-driven overexpression of *YlALG6*. See U.S. Patent Publication No. 20090069232-A1. A NotI/PacI fragment of this vector, containing this knock-out/knock-in cassette, was transformed into *Yarrowia lipolytica* G036 and transformants were selected based on their uracil prototrophy. Clones that had correctly integrated the construct were directly screened via N-glycan analysis on the secretome. Out of 80 screened clones, 2 clones showed an N-glycosylation profile that could fit with the inactivation of *YlALG3* in a strain expressing an ER-located α-1,2-mannosidase. Apart from a fraction $Man_3GlcNAc_2$ glycans, there was still some $Man_4GlcNAc_2$ and $Man_5GlcNAc_2$ as well as a significant amount of glucosylated N-glycans ($GlcMan_5GlcNAc_2$ and $Glc_2Man_5GlcNAc_2$). The latter are the result of an inefficient trimming by glucosidase II (Grinna and Robbins, *J. Biol. Chem.* 255, 2255-2258, 1980). The nature of the structures of $Man_4GlcNAc_2$ and $Man_5GlcNAc_2$ was confirmed by *in vitro* treatment of the N-glycans with α-1,2-mannosidase (FIG. 17). Depending on the growth conditions used, the level of $Man_3GlcNAc_2$ could increase to up to 60% of the total N-glycan pool, with the glucosylated peaks being insensitive towards α-1,2-mannosidase and only slightly sensitive towards Jack Bean α-mannosidase treatment (aspecific α-mannosidase that can act on α-1,2-, α-1,3- and α-1,6-linked mannose residues). In contrast, the latter enzyme converts the generated $Man_3GlcNAc_2$ into $Man_1GlcNAc_2$ (FIG. 17).

One of the two positive transformants was called G039 and used for further glyco-engineering work. The strain was transformed transiently with pRRQ2 expressing the Cre-recombinase to allow the curing of the *URA3* marker that was introduced upon transformation of G036 with vector pYLalg3PUT-ALG6. Analysis shows that the glycosylation profile remains the same after curing. One cured strain was selected for further use and designated G045.

Example 7: expression of GlcNAc-transferase I in a $Man_3GlcNAc_2$ producing strain

Similar to what was done in example 3, the introduction of a GnT I activity was accomplished via the expression of the Kre2-GnT I fusion protein. Random integration of such an expression construct for GnT I was accomplished in three ways: ***1)*** the non cured strain G039 (see Example 6) was transformed with the NotI digested vector pYLTmAXhGnTI (Hygr ex) and GnT I expressing clones were initially selected based on their ability to survive 300 μg/ml of hygromycin added to the selection plates, ***2)*** the cured strain G045 (see Example 6) was transformed with the NotI digested vector pYLTmAXhGnTI (see also Example 3) and GnT I expressing clones were initially selected based on their uracil prototrophy or ***3)*** the cured strain G045 (see Example 6) was transformed with the NotI digested vector pYLHp4mAXhGnTI and GnT I expressing clones were initially selected based on their uracil prototrophy. The construction strategy for pYLTmAXhGnTI (Hygr ex) is shown in FIG. 18. When using plasmids pYLTmAXhGnTI (Hygr ex) and pYLTmAXhGnTI, the expression of GnT I was under the transcriptional control of the *TEF1* promoter; when using plasmid pYLHp4mAXhGnTI, the GnT I expression was under the control of the Hp4d promoter.

Transformation of G039 with pYLTmAXhGnTI (Hygr ex) resulted in three clones that only emerged on the culture plates after a longer incubation period than what was expected. However, analysis of the N-glycosylation profile of the secretome of these clones showed a clear change in the N-glycan pattern: the $Man_3GlcNAc_2$ present in the non-transformed G039 strain was significantly reduced or almost completely absent while a new peak, representing an N-glycan with higher molecular weight (about one glucose unit extra), appeared. Treatment of the isolated N-glycans with Jack Bean β-N-acetylhexosaminidase, an enzyme capable of removing terminal β-linked GlcNAc residues, indicated that the new N-glycan indeed is $GlcNAcMan_3GlcNAc_2$. The new peak disappeared and was completely converted into $Man_3GlcNAc_2$ (FIG. 19). One of the evaluated transformants was used for further glyco-engineering work and named G047. Similar results were also obtained when the cured strain G045 was transformed with pYLTmAXhGnTI (G048) or with pYLHp4mAXhGnTI (G056). Strain G056 was

selected for curing via transient expression of the Cre recombinase using plasmid pRRQ2. The resulting strain was called G058.

Depending on the cultivation method used, about 70% of the total N-glycan pool of strain G047 proved to be $GlcNAcMan_3GlcNAc_2$ with some remaining $Glc_{1-2}Man_5GlcNAc_2$ and almost no $Man_3GlcNAc_2$ was present (conversion rate >> 90%) (FIG. 19). Regardless of the high conversion rate, only one copy of the GnT I expression cassette could be identified in this strain via Southern blot. Southern analysis was done on BamHI digested genomic DNA using a DIG-labeled GnT I-specific PCR fragment that was generated using primers 5'-GGATGATCACACAATGGCCCTGTTTCTG-3'(SEQ ID NO:11) and 5'-TGCTCTAGACTAGTTCCAAGAGGGGTC-3' (SEQ ID NO:12).

In an alternative strategy, a construct JME925 pPTAde2-URA3ex-Hp4dhGnTI was generated to allow targeted integration of the Hp4d-driven GnT I expression cassette into the *ADE2* locus of the *Yarrowia* genome. The construction strategy is depicted in FIG. 20. Prior to transformation to strain G045, the plasmid was NotI digested and the targeting/expression cassette was isolated. Transformants were selected based on their adenine prototrophy. Correct integration of the expression cassette into the *ADE2* locus was checked via PCR using forward primer Ver1Ade2 (5'-CGACGATAGAGCAGGTCTCACTGTTGGGAATGCTG-3', SEQ ID NO:13) reverse primer Ver2Ade2 (5'-CTACACTGACGAAGTGGACATCCCGGCTTGGACTG-3', SEQ ID NO:14) and further confirmed via Southern blotting. This was done on BamHI/SpeI digested genomic DNA using a DIG-labeled GnT I-specific PCR fragment that was generated using primers 5'-GGATGATCACACAATGGCCCTGTTTCTG-3' (SEQ ID NO:15) and 5'-TGCTCTAGACTAGTTCCAAGAGGGGTC-3' (SEQ ID NO:16). Synthesis of $GlcNAcMan_3GlcNAc_2$ onto the secretome was confirmed via N-glycan analysis and *in vitro* Jack Bean β-N-acetylhexosaminidase treatment (FIG. 21). One GnT I expressing transformant (called G057) was selected for curing via transient expression of the Cre recombinase using plasmid pRRQ2. The resulting strain was called G059.

Example 8: expression of GlcNAc-transferase II

A *Yarrowia* codon-optimized sequence was generated for the expression of a fusion protein consisting of the first 36 N-terminal amino acids of the *S. cerevisiae* Mnn2 protein (SwissProt AccNo P38069) followed by the catalytic domain of rat GlcNAc-transferase II (GnT II) (SwissProt AccNo Q09326) (FIG. 22, SEQ ID NO:17 and SEQ ID NO:18). The yeast Mnn2 36 N-terminal amino acids serve as a Golgi localization signal for the catalytic GnT II domain. In this way, it was ensured that the Mnn2-GnT II fusion protein was localized at the same or even a later position in the secretion pathway than the Kre2-GnT I (and Mnn2-Man II) fusion protein and was therefore able to convert $GlcNAcMan_3GlcNAc_2$ into $GlcNAc_2Man_3GlcNAc_2$. The synthetic gene for the expression of the fusion protein was placed under the transcriptional control of the *TEF1* promoter, resulting into the plasmids pYLTmAXrGnTII and pYLTmAXrGnTII (ADE2ex). The construction strategy is shown in FIG. 23.

A strain expressing the GnT II activity was generated in two different ways: ***1)*** strain G045 (see Example 6) was transformed simultaneously with NotI digested pYLTmAXhGnTI and NotI digested pYLTmAXrGnTII (ADE2 ex) and transformants were selected based on their uracil and adenine prototrophy or ***2)*** strain G047 (Example 7) was transformed with NotI digested pYLTmAXrGnTII (ADE2 ex) and transformants were selected based on their adenine prototrophy. Integration of the expression cassettes was checked using forward primer TefPromFW 5'-GTCCCCGAATTACCTTTCC-3' (SEQ ID NO:19) and reverse primer Lip2TermRV 5'-AGGTAGAAGTTGTAAAGAGTG-3' (SEQ ID NO:20). N-glycan analysis on the secretome in combination with *in vitro* treatment of the isolated sugars with Jack Bean β-N-acetylhexosaminidase indicated that several transformants were capable of producing $GlcNAc_2Man_3GlcNAc_2$ and thus of expressing a functional GnT II activity (FIG. 24). In one selected condition, about 40% of the total N-glycan pool consisted of $GlcNAc_2Man_3GlcNAc_2$. The conversion rate of the substrate $GlcNAcMan_3GlcNAc_2$ to $GlcNAc_2Man_3GlcNAc_2$ was 90%. The final selected strains were called G050 (double transformation of G045) and G051 (GnT II expression in G047).

Example 9: expression of glucosidase II alpha and beta subunits (Gls2α and Gls2β)

Based on the experiments described in Examples 6 to 8, the strategy involving the knock-out of *YlALG3* and simultaneous overexpression of *YlALG6* results into the generation of N-glycans carrying one or two terminal glucose residues ($Glc_{1-2}Man_5GlcNAc_2$). The presence of these glucose residues hampers the conversion towards $Man_3GlcNAc_2$ by the ER-localized HDEL-tagged α-1,2-mannosidase. In order for the glucose residues to be removed, the glucosidase II activity within the ER needs to be increased. In a background without α-1,2-mannosidase expression, overexpression of the *Aspergillus niger* glucosidase II alpha and beta subunit resulted in the highest conversion of $Glc_{1-2}Man_5GlcNAc_2$ into $Man_5GlcNAc_2$ (U.S. Patent Publication No. 20090069232-A1). Constructs for the overexpression of the *A. niger* gls2 subunits were produced as follows: ***1)*** a *Yarrowia* codon-optomized cDNA was generated for the expression of the mature (lacking the signal peptide) *A. niger* gls2α and gls2β subunit; ***2)*** the cDNA's were cloned in-frame to the *Y. lipolytica LIP2*pre-sequence; ***3)*** the resulting *LIP2*pre-gls2α and *LIP2*pre-gls2β sequences were cloned under the transcriptional control of the constitutive *TEF1* promoter. The resulting plasmids were called pYLTUXdL2preAnGlcIIα and pYLeu2ExTEFpreLip2AnGlucIIβ (FIG. 25).

Based on these plasmids, new constructs were generated for the simultaneous overexpression of the *A. niger* gls2α and gls2β subunits under either *TEF1* promoter control (vector JME923 pPTura3-LEU2ex-TefL2preAnGlcIIa+b[alt1] for targeted integration – FIG 26) or Hp4d promoter control (vector JME923 pPTura3-LEU2ex-Hp4dL2preAnGlcIIa+b[alt1] for targeted integration and vector Zeta-LEU2ex-Hp4dL2preAnGlcIIa+b[alt] for random integration – FIG. 27).

Strain G057 (see example 7) was transformed with NotI digested plasmids JME923 pPTura3-LEU2ex-Hp4dL2preAnGlcIIa+b[alt1] and Zeta-LEU2ex-Hp4dL2preAnGlcIIa+b[alt] and transformants were selected based on their leucine prototrophy. Several clones were analyzed genomically via PCR and Southern analysis to evaluate the integration of the gls2α and gls2β expression cassette. PCR-analysis and DIG probe generation for the gls2α subunit was done using primers AnGls2α-FW (5'-

GCTGGACTCTTCTTCTATCC-3') (SEQ ID NO:24) and AnGls2α-RV (5'-GGTCTCCTTCAGAGACAGG-3') (SEQ ID NO:25); for the gls2β subunit we made use of primers AnGls2β-FW (5'-CCAAGTTCTACAAGGACACC-3') (SEQ ID NO:26)and AnGlc2β-RV (5'- CCCTTGACGACCTTAGAGG-3') (SEQ ID NO:27). Southern analysis to check for targeted integration of the dual Hp4dGls2α/β expression cassette was done on Eco47III-digested gDNA when using the gls2α probe, and on SpeI/SfiI-digested gDNA when using the gls2β probe. The majority of the selected clones showed correct integration of the dual expression cassette into the *URA3* locus. Southern analysis for random integration of the dual Hp4dGls2α/β expression cassettes was checked on PvuI-digested gDNA with both probes. In all cases, only one copy of the dual expression cassette was integrated.

Next, N-glycan analysis was performed on several clones confirmed to have the dual Hp4dGls2α/β expression cassette (correctly) integrated. N-glycosylation was examined on total secreted protein after three days of falcon cultivation. Several clones showed a significant reduction of the glucosylated sugars and an increase of $Man_3GlcNAc_2$ and $GlcNAcMan_3GlcNAc_2$. The profiles of a clone that has integrated the dual expression cassette randomly (= strain G060) on the one hand and in a targeted way (= strain G061) on the other, are shown in FIG 28. The two smaller peaks represent $Man_4GlcNAc_2$ and $Man_5GlcNAc_2$, since they shift to $Man_3GlcNAc_2$ resp. $Man_1GlcNAc_2$ upon treatment with α-1,2-mannosidase and Jack Bean mannosidase. The latter treatment also results in a partial conversion of the remaining $Glc_{1-2}Man_5GlcNAc_2$ into $Glc_{1-2}Man_4GlcNAc_2$ and of $GlcNAcMan_3GlcNAc_2$ into $GlcNAcMan_2GlcNAc_2$. Presence of $Man_4GlcNAc_2$ and $Man_5GlcNAc_2$ however indicates incomplete conversion towards $Man_3GlcNAc_2$ by the heterologously co-expressed HDEL-tagged α-1,2-mannosidase. Similarly, the presence of $Man_3GlcNAc_2$ indicates incomplete transfer of a GlcNAc-residue by recombinant human GnT I to obtain $GlcNAcMan_3GlcNAc_2$. However, based on results described above (e.g. G047 cultivation in Example 7, FIG. 19), it is clear that differences in cultivation conditions can increase the conversion rates significantly and thus improve the end result.

Example 10: expression of GlcNAc-transferase II in the $GlcNAcMan_3GlcNAc_2$ producing strain G061

As described in Example 8, a *Yarrowia* codon-optimized sequence was generated for the expression of a fusion protein consisting of the first 36 N-terminal amino acids of the *S. cerevisiae* Mnn2 protein (SwissProt AccNo P38069) followed by the catalytic domain of rat GlcNAc-transferase II (GnT II) (SwissProt AccNo Q09326) (FIG. 22, SEQ ID NO:17 and SEQ ID NO:18, respectively). The yeast Mnn2 36 N-terminal amino acids serve as a Golgi localization signal for the catalytic GnT II domain. In this way, it was ensured that the Mnn2-GnT II fusion protein was localized at the same or even a later position in the secretion pathway than the Kre2-GnT I fusion protein and was therefore able to convert $GlcNAcMan_3GlcNAc_2$ into $GlcNAc_2Man_3GlcNAc_2$. The synthetic gene for the expression of the fusion protein was placed under the transcriptional control of the Hp4d promoter resulting in plasmid pYLHp4mAXrGnTII, which was used for random integration of the Hp4d-driven GnT II expression cassette into the *Yarrowia* genome. In an alternative strategy, construct OXYP289 pPTAxp1-ADE2ex-Hp4dhGnTII was generated to allow targeted integration of the Hp4d-driven GnT II expression cassette into the *AXP1* locus of the *Yarrowia* genome.

Prior to transformation of strain G061 (see Example 9), the plasmids were NotI digested and the targeting/expression cassette was isolated. Transformants were selected based on their adenine prototrophy. Correct integration of the expression cassette into the *ADE2* locus was confirmed by Southern blot analysis after digesting the genomic DNA with XmnI. A DIG-labeled probe with specificity for the GnT II coding sequence was generated using forward primer rGnTII-FW (5'-GACCAGATGCTGCGAAACG-3') (SEQ ID NO: 28) and reverse primer rGnTII-RV (5'-CTTGACGTCCACCTTGTCG-3') (SEQ ID NO: 29). This strategy produces a band of 3172 bp when the gene is successfully integrated into the Axp1 locus.

In an alternative strategy, correct integration into the Axp1 locus can be examined via a PCR reaction on genomic DNA using the forward primer AXPVer1b (5'-GCCTGAACGGCACGATGCGATCGTGGCAATCC-3') (SEQ ID NO: 30) and the reversed primer AXPVer2b (5'-CAAGAAGCCTCAGGCTCGGCGAATCTCCA TC-3')

(SEQ ID NO: 31). In case of correct targeting into the Axp1 locus, a PCR fragment of 6489 bp is expected.

N-glycan analysis on the secretome, in combination with *in vitro* treatment of the isolated sugars with Jack Bean β-N-acetylhexosaminidase or *T. reesei* α-1,2-mannosidase, indicated that several transformants were capable of producing $GlcNAc_2Man_3GlcNAc_2$ and thus of expressing a functional GnT II activity (FIG. 29). The analyses indicated that about 25 to 30% of the total N-glycan pool consisted of $GlcNAc_2Man_3GlcNAc_2$, with a $GlcNAcMan_3GlcNAc_2$ to $GlcNAc_2Man_3GlcNAc_2$ conversion rate of about 90%. The final selected strains were called G070 (integration of pYLHp4mAXrGnTII into G061) and G071 (integration of OXYP289 pPTAxp1-ADE2ex-Hp4dhGnTII into G061).

Example 11: construction of a tandem plasmid for simultaneous Hp4d-driven expression of the anti-HER2 heavy chain (HC) and light chain (LC) into *Yarrowia lipolytica*

The amino acid sequences for the anti-HER2 antibody heavy and light chains were obtained from Carter *et al.*, *Proc Natl Acad Sci USA.*, 89(10): 4285–4289 (1992); and Ward *et al.*, *Appl Environ Microbiol.*, 70(5): 2567–2576 (2004). The relevant amino acid sequences were reverse translated, codon-optimized for *Yarrowia lipolitica*, and synthesized by GenArt, Regensburg Germany. Regions of very high (>80%) or very low (<30%) GC content were avoided where possible. During the optimization processes, the following cis-acting sequence motifs were avoided: internal TATA-boxes, chi-sites and ribosomal entry sites, AT-rich or GC-rich sequence stretches, repeat sequences and RNA secondary structures as well as (cryptic) splice donor and acceptor sites. In order to allow secretion of the ectopic proteins, the coding sequence of the Lip2 protein 'prepro' signal (followed by that of a peptide linker 'GGG') was added to the 5' region of the coding sequences. 'GGG' was added to enhance the changes for correct Kex2 processing. FIG. 30A contains the nucleotide sequence of the synthetic preproLip2-LC (= 750 bp) (SEQ ID NO: 32). FIG. 30B contains the amino acid sequence of the preproLip2-LC (= 250 Aa; MW= 27.011 Da; pI= 8.46) (SEQ ID NO: 33). FIG. 31A contains the nucleotide sequence of the synthetic preproLip2-HC (= 1458 bp) (SEQ ID NO: 34). FIG. 31B

contains the amino acid sequence of the preproLip2-HC (= 486 Aa; MW= 52.853 Da; pI= 8.65) (SEQ ID NO: 35). The coding sequences for preproLip2-HC and -LC were introduced into the same vector, called pYLHp4L2preproHerHC/LC (GUT2ex)-ori2.

Example 12: expression of the anti-HER2 antibody HC and LC into *Yarrowia lipolytica* strains with a varying degree of glyco-engineering

Plasmid pYLHp4L2preproHerHC&LC (GUT2ex)-ori2 was digested with NotI and the HC-/LC-tandem expression cassette was isolated before transforming *Yarrowia lipolytica* strains G045, G057, G061 and G071 (see Table 2). Transformants containing the randomly integrated HC-/LC-expression cassette were selected based on their ability to grow on glycerol as the sole carbon source. Expression analysis of the HC and LC was done via western blotting after a 4 day shake flask cultivation of the selected transformants in rich medium containing glycerol as the only carbon source (SuperT/glycerol medium: 0.5% yeast extract; 2% malt extract; 1% trypton; 1.5% glycerol; 200 mM phosphate buffer pH 6.8). LC-detection was performed using a mouse monoclonal to Kappa Free Light Chains (4C11) (Abcam) while HC-detection was done using mouse monoclonal anti-human IgG (γ-chain specific) (Sigma).

The N-glycans of the secretome of the anti-HER2 antibody producing strains showed a similar profile as the corresponding glyco-engineered strains that were not expressing any HC and LC (FIG. 32). The percentages of N-glycans in strains with the G045, G057, G061, and G071 background were determined after a 6-day shake flask cultivation in SuperT/glycerol medium. In a G045 background, 54.6% of the N-glycans were $Man_3GlcNAc_2$. In the G057 background, 47.5% of the N-glycans were $GlcNAc_1Man_3GlcNAc_2$. In a G061 background, 58.9% of the N-glycans were $GlcNAc_1Man_3GlcNAc_2$. In a G071 background, 37.6% of the N-glycans were $GlcNAc_2Man_3GlcNAc_2$.

Example 13: fermentation of *Yarrowia* strain G096, a $GlcNAc_2Man_3GlcNAc_2$ synthesizing strain expressing the anti-HER2 antibody HC and LC

Several pYLHp4L2preproHerHC&LC (GUT2ex)-ori2 transformants of *Yarrowia lipolytica* G071, a strain capable of synthesizing $GlcNAc_2Man_3GlcNAc_2$, were analyzed

for HC and LC expression levels. One of these clones, G096, was chosen for further analysis.

Fermentation was done in a 14-litre stirred tank bioreactor (MAVAG AG) equipped with a process control and management system (Lucillus PIMS). The relative partial oxygen pressure in the medium, the CO_2 and O_2 concentrations in the exhaust gas, pH value, temperature, reactor overpressure, reactor weight, feed weight and base weight were all monitored on-line. Foam generation was counteracted by adding the antifoaming agent polypropylene glycol (PPG). Adjustments in pH were done by either the addition of a 25% ammonia solution or a 8.5% phosphoric acid solution.

A seed culture of G096 was grown at 28°C in a shake flask containing rich medium. The seed culture was inoculated into the fermentor containing mineral medium to start a batch phase at 28°C with unrestricted growth, using glycerol as only carbon source. This phase was used to rapidly reach a high biomass concentration. From that point onward, the process was shifted to an exponential glycerol fed batch (with glycerol as sole carbon and energy source; pH 6), with a constant growth rate of 0.02. As an example, the results for a fed batch fermentation at 28 °C are described below.

The fed-batch phase lasted for 148 hours. At different time-points of the fermentation, samples were taken to follow up the following parameters: 1) expression of the LC and HC protein backbones via western blot; 2) expression of functional anti-HER2 antibody via an ELISA; and 3) evolution of the N-glycosylation profile of the secretome.. The full-length HC expression level reached a maximum around timepoint 7 (39 hrs) and remains approximately equal from then onwards. The LC expression reached a maximum between time-points 7 (39 hrs) and 10 (73 hrs), but decreased somewhat in the later time-points. Some LC-dimers were produced between time-points 5 (25 hrs) and 9 (62 hrs), but disappeared again from that point onwards.

A functional ELISA was developed to measure the production of anti-HER2 antibody that has at least one functional antigen binding domain. Plates were coated with a recombinant variant of the natural HER2 antigen, the recombinant human ErbB2/Fc chimera (R&D systems). Then a dilution of the medium, harvested at different time-points, was added to the coated plates. Assessment of the amount of antigen binding protein was done using a HRP-conjugated anti-human kappa LC antibody (Sigma). The

evolution of the amount of ErbB2/Fc chimera binding protein (a measure of the amount of secreted functional anti-HER2 antibody) within the fed-batch fermentation is shown in FIG. 33. The data show a gradual increase in the levels of anti-HER2 antibody, with a maximum of 10 to 12 mg/L at the end of the production phase.

N-glycan analysis was done on samples taken at several time-points during the fed-batch fermentation. The results are shown in FIG. 34A and 34B. At the beginning of the fed-batch phase, there was a significant amount of glucose-containing N-glycans present. From time-point 6 onward (34 hrs after start of exponential feeding), the level of glucosylated N-glycans decreased significantly with hardly any left at the time of harvest (time-point 18, 148 hrs). This indicated that proteins originally carrying glucose-containing N-glycans, were diluted out by the end of the fermentation. At that point about 86% of the N-glycans isolated from the secretome had the structure $GlcNAc_2Man_3GlcNAc_2$.

OTHER EMBODIMENTS

While the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

WHAT IS CLAIMED IS:

1. A method of producing a fungal cell capable of producing proteins comprising $GlcNAcMan_5GlcNAc_2$ N-glycans, said method comprising:

a) providing a fungal cell genetically engineered to produce proteins comprising $Man_5GlcNAc_2$ N-glycans;

b) introducing into said cell a nucleic acid encoding a GlcNAc-transferase I, wherein said nucleic acid comprises a nucleotide sequence encoding a targeting sequence to target the encoded GlcNAc-transferase I to an intracellular compartment, wherein expression of said GlcNAc-transferase I in said fungal cell produces proteins comprising $GlcNAcMan_5GlcNAc_2$ N-glycans.

2. The method of claim 1, said method further comprising introducing into said cell a nucleic acid encoding a target protein, wherein said cell produces said target protein modified to comprise said $GlcNAcMan_5GlcNAc_2$ N-glycans.

3. The method of claim 2, wherein said target protein binds to an Fc receptor.

4. The method of claim 3, wherein said target protein is an antibody or fragment thereof.

5. The method of claim 2, wherein said target protein is a therapeutic glycoprotein.

6. The method of claim 2, wherein said target protein is Interferon-β, GM-CSF, Interferon γ, or erythropoietin.

7. The method of claim 1, wherein said intracellular compartment is the Golgi apparatus.

8. The method of claim 1, wherein said fungal cell genetically engineered to produce proteins comprising $Man_5GlcNAc_2$ N-glycans is deficient in OCH1 activity and comprises a nucleic acid encoding an α-1,2-mannosidase, wherein said nucleic acid encoding said α-1,2-mannosidase comprises a nucleotide sequence encoding a targeting sequence to target the encoded α-1,2-mannosidase to the endoplasmic reticulum.

9. The method of claim 8, wherein said targeting sequence is an HDEL sequence.

10. The method of claim 1, wherein said fungal cell is *Yarrowia lipolytica* or *Arxula adeninivorans*.

11. The method of claim 1, said method further comprising introducing into said cell a nucleic acid encoding a mannosidase II, wherein said nucleic acid encoding said mannosidase II comprises a nucleotide sequence encoding a targeting sequence to target the encoded mannosidase II to the Golgi apparatus, wherein expression of said mannosidase II in said fungal cell produces proteins comprising $GlcNAcMan_3GlcNAc_2$ N-glycans.

12. The method of claim 1 or claim 11, said method further comprising introducing into said cell a nucleic acid encoding a galactosyltransferase, wherein said nucleic acid encoding said galactosyltransferase comprises a nucleotide sequence encoding a targeting sequence to target the encoded galactosyltransferase to the Golgi apparatus, wherein expression of said galactosyltransferase in said fungal cell produces proteins comprising $GalGlcNAcMan_5GlcNAc_2$ or $GalGlcNAcMan_3GlcNAc_2$ N-glycans.

13. The method of claim 12, said method further comprising introducing into said cell a nucleic acid encoding a target protein, wherein said cell produces said target protein modified to comprise said $GalGlcNAcMan_5GlcNAc_2$ or $GalGlcNAcMan_3GlcNAc_2$ N-glycans.

14. The method of claim 12, wherein said galactosyltransferase is a fusion of a UDP-Glc-4-epimerase and the catalytic domain of a β-1,4-galactosyltransferase I.

15. The method of claim 13, further comprising isolating said target protein modified to comprise said $GalGlcNAcMan_5GlcNAc_2$ or $GalGlcNAcMan_3GlcNAc_2$ N-glycans.

16. A method of producing a target protein comprising $GlcNAcMan_3GlcNAc_2$ N-glycans, said method comprising:

a) providing a fungal cell genetically engineered to comprise a nucleic acid encoding a GlcNAc-transferase I, an α-1,2-mannosidase, and a mannosidase II, wherein said nucleic acid comprises nucleotide sequences encoding targeting sequences to target each encoded protein to an intracellular compartment, wherein said fungal cell is deficient in OCH1 activity; and

b) introducing into said cell a nucleic acid encoding a target protein, wherein said cell produces said target protein comprising said $GlcNAcMan_3GlcNAc_2$ N-glycans.

17. The method of claim 16, wherein said fungal cell is *Yarrowia lipolytica* or *Arxula adeninivorans*.

18. The method of claim 16, wherein said nucleic acid encoding said α-1,2-mannosidase comprises an endoplasmic reticulum targeting sequence to target the encoded α-1,2-mannosidase to the endoplasmic reticulum.

19. The method of claim 18, wherein said targeting sequence is an HDEL sequence.

20. The method of claim 16, wherein said nucleic acid encoding said GlcNAc-transferase I and said mannosidase II comprises nucleotide sequences encoding Golgi targeting sequences to target the encoded GlcNAc-transferase I and mannosidase II to the Golgi apparatus.

21. The method of claim 16, wherein said target protein binds to an Fc receptor.

22. The method of claim 16, wherein said target protein is an antibody or fragment thereof.

23. The method of claim 16, wherein said target protein is a therapeutic glycoprotein.

24. The method of claim 16, wherein said target protein is Interferon-β, GM-CSF, Interferon γ, or erythropoietin.

25. The method of claim 16, further comprising introducing into said cell a nucleic acid encoding a galactosyltransferase, wherein said nucleic acid encoding said galactosyltransferase comprises a nucleotide sequence encoding a targeting sequence to target the encoded galactosyltransferase to the Golgi apparatus, wherein expression of said galactosyltransferase in said fungal cell produces said target protein modified to comprise $GalGlcNAcMan_3GlcNAc_2$ N-glycans.

26. The method of claim 25, further comprising isolating said target protein modified to comprise said $GalGlcNAcMan_3GlcNAc_2$ N-glycans.

27. A method of making a fungal cell capable of producing proteins comprising $GlcNAcMan_3GlcNAc_2$ N-glycans, said method comprising:

a) providing a fungal cell genetically engineered to produce proteins comprising $Man_3GlcNAc_2$ N-glycans;

b) introducing into said cell a nucleic acid encoding a GlcNAc-transferase I, wherein said nucleic acid comprises a nucleotide sequence encoding a targeting sequence to target said encoded GlcNAc-transferase I to an intracellular compartment, wherein expression of said GlcNAc-transferase I in said fungal cell produces proteins comprising $GlcNAcMan_3GlcNAc_2$ N-glycans.

28. The method of claim 27, said method further comprising introducing into said cell a nucleic acid encoding a target protein, wherein said cell produces said target protein modified to comprise said $GlcNAcMan_3GlcNAc_2$ N-glycans.

29. The method of claim 27, wherein said target protein binds to an Fc receptor.

30. The method of claim 27, wherein said target protein is an antibody or fragment thereof.

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125 31. The method of claim 27, wherein said target protein is a therapeutic glycoprotein.

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127 32. The method of claim 27, wherein said target protein is Interferon-β, GM-CSF,
128 Interferon γ, or erythropoietin.

129

130 33. The method of claim 27, wherein said intracellular compartment is the Golgi
131 apparatus.

132

133 34. The method of claim 27, wherein said fungal cell genetically engineered to produce
134 proteins comprising $Man_3GlcNAc_2$ N-glycans is deficient in ALG3 activity, and
135 comprises a nucleic acid encoding an α-1,2-mannosidase, said nucleic acid comprising a
136 nucleotide sequence encoding a targeting sequence to target the encoded α-1,2-
137 mannosidase to the endoplasmic reticulum.

138

139 35. The method of claim 34, wherein said fungal cell genetically engineered to produce
140 proteins comprising $Man_3GlcNAc_2$ N-glycans further is deficient in OCH1 activity.

141

142 36. The method of claim 34 or 35, wherein said fungal cell genetically engineered to
143 produce proteins comprising $Man_3GlcNAc_2$ N-glycans further comprises a nucleic acid
144 encoding an α-1,3-glucosyltransferase.

145

146 37. The method of claim 36, wherein said α-1,3-glucosyltransferase is ALG6.

147

148 38. The method of claim 27, wherein said fungal cell is *Yarrowia lipolytica* or *Arxula*
149 *adeninivorans*.

150

151 39. The method of claim 27, said method further comprising introducing into said cell a
152 nucleic acid encoding a GlcNAc-transferase II, wherein said nucleic acid encoding said
153 GlcNAc-transferase II comprises a nucleotide sequence encoding a targeting sequence to
154 target the encoded GlcNAc-transferase II to an intracellular compartment, wherein

expression of said GlcNAc-transferase II in said fungal cell produces proteins comprising $GlcNAc_2Man_3GlcNAc_2$ N-glycans.

40. The method of claim 27 or claim 39, said method further comprising introducing into said cell a nucleic acid encoding a galactosyltransferase, wherein said nucleic acid encoding said galactosyltransferase comprises a nucleotide sequence encoding a targeting sequence to target the encoded galactosyltransferase to the Golgi apparatus, wherein expression of said galactosyltransferase in said fungal cell produces proteins comprising $GalGlcNAcMan_3GlcNAc_2$ or $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

41. The method of claim 40, said method further comprising introducing into said cell a nucleic acid encoding a target protein, wherein said cell produces said target protein modified to comprise said $GalGlcNAcMan_3GlcNAc_2$ or $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

42. The method of claim 40, wherein said galactosyltransferase is a fusion of a UDP-Glc-4-epimerase and catalytic domain of a β-1,4-galactosyltransferase I.

43. The method of claim 40 said method further comprising introducing into said cell a nucleic acid encoding the α and β subunits of a Glucosidase II, wherein expression of said α and β subunits of said Glucosidase II in said fungal cell produces proteins comprising $GalGlcNAcMan_3GlcNAc_2$ or $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

44. A method of producing a target protein comprising $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans, said method comprising:

a) providing a fungal cell genetically engineered to be deficient in ALG3 activity and comprising a nucleic acid encoding a GlcNAc-transferase I, a GlcNAc-transferase II, and a galactosyltransferase, wherein said nucleic acid encoding said GlcNAc-transferase I, said GlcNAc-transferase II, and said galactosyltransferase comprises nucleotide sequences encoding targeting sequences to target each encoded protein to an intracellular compartment;

b) introducing into said cell a nucleic acid encoding a target protein, wherein said cell produces said target protein comprising said $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

45. The method of claim 44, wherein said fungal cell further is deficient in OCH1 activity.

46. The method of claim 44 or 45, wherein said fungal cell further comprises a nucleic acid encoding an α-1,3-glucosyltransferase.

47. The method of claim 46, wherein said nucleic acid encoding said α-1,3-glucosyltransferase is ALG6.

48. The method of claim 44, claim 45, or claim 46, wherein said fungal cell further comprises a nucleic acid encoding the α and β subunits of a Glucosidase II, wherein expression of said α and β subunits of said Glucosidase II in said fungal cell produces said target protein comprising said $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

49. An isolated fungal cell genetically engineered to produce proteins comprising $GlcNAcMan_3GlcNAc_2$ N-glycans, wherein said fungal cell is deficient in OCH1 activity and comprises a nucleic acid encoding an α-1,2-mannosidase, a GlcNAc-transferase I, and a mannosidase II, wherein said nucleic acid encoding said α-1,2-mannosidase, said GlcNAc-transferase I, and said mannosidase II comprises nucleotide sequences encoding targeting sequences to target each encoded protein to an intracellular compartment, wherein expression of said α-1,2-mannosidase, said GlcNAc-transferase I, and said mannosidase II in said fungal cell produces proteins comprising $GlcNAcMan_3GlcNAc_2$ N-glycans.

50. The fungal cell of claim 49, wherein said genetically engineered fungal cell further comprises a nucleic acid encoding a target protein, wherein said cell produces said target protein modified to comprise said $GlcNAcMan_3GlcNAc_2$ N-glycans.

51. The fungal cell of claim 49 or claim 50, wherein said genetically engineered fungal cell further comprises a nucleic acid encoding a GlcNAc-transferase II, wherein said nucleic acid encoding said GlcNAc-transferase II comprises a nucleotide sequence encoding a targeting sequence to target the encoded GlcNAc-transferase II to an intracellular compartment, wherein expression of said GlcNAc-transferase II in said fungal cell produces proteins comprising $GlcNAc_2Man_3GlcNAc_2$ N-glycans.

52. The fungal cell of claim 51, said fungal cell further comprising a nucleic acid encoding a galactosyltransferase, wherein said nucleic acid encoding said galactosyltransferase comprises a nucleotide sequence encoding a targeting sequence to target the encoded galactosyltransferase to the Golgi apparatus, wherein expression of said galactosyltransferase in said fungal cell produces proteins comprising $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

53. An isolated fungal cell genetically engineered to produce proteins comprising $GlcNAc_2Man_3GlcNAc_2$ N-glycans, wherein said fungal cell is genetically engineered to be deficient in ALG3 activity and comprises a nucleic acid encoding a GlcNAc-transferase I and a GlcNAc-transferase II, wherein said nucleic acid encoding said GlcNAc-transferase I and said GlcNAc-transferase II comprises nucleotide sequences encoding targeting sequences to target each encoded protein to an intracellular compartment, wherein expression of said GlcNAc-transferase I, and said GlcNAc-transferase II in said fungal cell produces proteins comprising $GlcNAc_2Man_3GlcNAc_2$ N-glycans.

54. The fungal cell of claim 53, wherein said genetically engineered fungal cell further is deficient in OCH1 activity.

55. The fungal cell of claim 53 or claim 54, wherein said genetically engineered fungal cell further comprises a nucleic acid encoding an α-1,3-glucosyltransferase.

56. The fungal cell of claim 53, claim 54, or claim 55, wherein said genetically engineered fungal cell further comprises a nucleic acid encoding a target protein, wherein said cell produces said target protein modified to comprise said $GlcNAc_2Man_3GlcNAc_2$ N-glycans.

57. The fungal cell of any one of claims 53-56, said fungal cell further comprising a nucleic acid encoding the α and β subunits of a Glucosidase II, wherein expression of said α and β subunits of said Glucosidase II in said fungal cell produces said protein comprising said $GlcNAc_2Man_3GlcNAc_2$ N-glycans.

58. The fungal cell of claim 57, said fungal cell further comprising a nucleic acid encoding a galactosyltransferase, wherein said nucleic acid encoding said galactosyltransferase comprises a nucleotide sequence encoding a targeting sequence to target the encoded galactosyltransferase to the Golgi apparatus, wherein expression of said galactosyltransferase in said fungal cell produces proteins comprising $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

59. A substantially pure culture of *Yarrowia lipolytica* cells, a substantial number of which are genetically engineered to produce glycoproteins comprising $Gal_2GlcNac_2Man_3GlcNAc_2$ N-glycans, wherein said cells are genetically engineered to be deficient in ALG3 activity and comprise a nucleic acid encoding a GlcNAc-transferase I, a GlcNAc-transferase II, and a galactosyltransferase, wherein said nucleic acid encoding said GlcNAc-transferase I, said GlcNAc-transferase II, and said galactosyltransferase comprises nucleotide sequences encoding targeting sequences to target each encoded protein to an intracellular compartment, wherein expression of said GlcNAc-transferase I, said GlcNAc-transferase II, and said galactosyltransferase in said cell produces proteins comprising $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

60. The substantially pure culture of claim 49, wherein said cells further are deficient in OCH1 activity.

61. The substantially pure culture of claim 59 or claim 60, wherein said cells further comprise a nucleic acid encoding an α-1,3-glucosyltransferase.

62. The substantially pure culture of claim 59, claim 60, or claim 61, wherein said cells further comprise a nucleic acid encoding the α and β subunits of a Glucosidase II, wherein expression of said α and β subunits of said Glucosidase II in said fungal cell produces said target protein comprising said $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

63. A substantially pure culture of *Yarrowia lipolytica* cells, a substantial number of which are genetically engineered to produce glycoproteins comprising $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans, wherein said cells are genetically engineered to be deficient in OCH1 activity and comprise a nucleic acid encoding an α-1,2-mannosidase, a GlcNAc-transferase I, a mannosidase II, a GlcNAc-transferase II, and a galactosyltransferase, wherein said nucleic acid encoding said α-1,2-mannosidase, said GlcNAc-transferase I, said mannosidase II, said GlcNAc-transferase II, and said galactosyltransferase comprises nucleotide sequences encoding targeting sequences to target each encoded protein to an intracellular compartment, wherein expression of said α-1,2-mannosidase, said GlcNAc-transferase I, said mannosidase II, said GlcNAc-transferase II, and a galactosyltransferase in said cells produces proteins comprising $Gal_2GlcNAc_2Man_3GlcNAc_2$ N-glycans.

64. A composition comprising a glycoprotein, wherein at least 50% of the N-glycans on said glycoprotein are $GlcNAc_2Man_3GlcNAc_2$ N-glycans.

65. The composition of claim 64, wherein at least 70% of the N-glycans on said glycoprotein are $GlcNAc_2Man_3GlcNAc_2$ N-glycans.

66. The composition of claim 64, wherein at least 85% of the N-glycans on said glycoprotein are $GlcNAc_2Man_3GlcNAc_2$ N-glycans.