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(54) Title: SIALYLATED GLYCOPROTEINS

(57) Abstract: Glycoproteins having particular sialylation patterns, and methods of making and using such glycoproteins, are described.

SIALYLATED GLYCOPROTEINSCROSS-REFERENCE TO RELATED APPLICATIONS

5 This application claims benefit to U.S. Provisional Application No. 61/818,563, filed May 2, 2013, which is hereby incorporated by reference.

FIELD OF THE INVENTION

10 The invention relates generally to glycobiology and glycoproteins.

BACKGROUND

15 Therapeutic glycoproteins are an important class of therapeutic biotechnology products, and therapeutic Fc containing glycoproteins, such as IVIG, Fc-receptor fusions, and antibodies (including murine, chimeric, humanized and human antibodies and fragments thereof) account for the majority of therapeutic biologic products.

SUMMARY

20 The invention encompasses the discovery of a novel mechanism of sialylation by a sialyltransferase (ST6 Gal-I), which sialylates a substrate (e.g., an Fc-containing glycoprotein comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm) in an ordered fashion. Specifically, under certain conditions, ST6 sialyltransferase catalyzes addition of a sialic acid on an α 1,3 arm, followed by addition of a second sialic acid on an α 1,6 arm, followed by removal of sialic acid from an α 1,3 arm. Accordingly, activity of ST6 sialyltransferase can be controlled using methods described herein to produce glycoproteins having particular branch sialylation patterns.

25 In one aspect, the invention features a method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and/or (ii) a target level of branched glycans having a sialic acid on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), the method comprising: providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; and contacting the glycoproteins with an ST6 sialyltransferase in the presence of a limited reaction condition, thereby producing a glycoprotein preparation having (i) the target level of branched glycans having a sialic acid on the α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and/or (ii) the target level of branched glycans having a sialic acid on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage).

35 In some embodiments, the ST6 sialyltransferase has at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity, or is 100% identical, to amino acid residues 95-416 of SEQ ID NO:1, to SEQ ID NO:2, or to SEQ ID NO:3.

40 In some embodiments, the limited reaction condition is sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm of a branched glycan and not sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,6 arm of a branched glycan.

 In some embodiments, the method further comprises isolating the glycoprotein preparation. In some embodiments, the method further comprises measuring a level of branched glycans comprising a

sialic acid on an α 1,3 arm and/or measuring a level of branched glycans having a sialic acid on an α 1,6 arm.

5 In some embodiments, level of branched glycans comprising a sialic acid on an α 1,3 arm and/or level of branched glycans having a sialic acid on an α 1,6 arm is measured by one or more of: releasing glycans (e.g., enzymatically releasing glycans) from glycoproteins and measuring the released glycans; measuring glycans on glycoproteins; derivatizing glycans and measuring derivatized glycans; measuring by fluorescence; measuring by mass spectrometry; and measuring by nuclear magnetic resonance.

10 In some embodiments, the target level of branched glycans having a sialic acid on an α 1,3 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of branched glycans having a sialic acid on an α 1,3 arm is less than 100%, 95%, 90%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% of glycans, branched glycans, or sialylated branched glycans.

15 In some embodiments, the target level of branched glycans having a sialic acid on an α 1,6 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of branched glycans having a sialic acid on an α 1,6 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans.

20 In some embodiments, target level is a mole percentage, mass percentage, and/or area percentage.

In some embodiments, the limited reaction condition is selected using a method comprising: a) contacting the glycoproteins with an ST6 sialyltransferase in the presence of a first reaction condition; b) measuring a first level of branched glycans comprising a sialic acid on an α 1,3 arm and/or branched glycans comprising a sialic acid on an α 1,6 arm after the first reaction condition; c) contacting the glycoproteins with the ST6 sialyltransferase in the presence of a second reaction condition; and d) measuring a second level of branched glycans comprising a sialic acid on an α 1,3 arm and/or branched glycans comprising a sialic acid on an α 1,6 arm after the second reaction condition; wherein the first reaction condition is selected as the limited reaction condition if the first level of branched glycans comprising a sialic acid on an α 1,3 arm is higher than the second level of branched glycans comprising a sialic acid on an α 1,3 arm; and/or the first level of branched glycans comprising a sialic acid on an α 1,6 arm is lower than the second level of branched glycans comprising a sialic acid on an α 1,6 arm. In some embodiments, the first reaction condition is selected from one or more of: a shorter reaction time relative to the second reaction condition; a lower ST6 sialyltransferase concentration and/or specific activity relative to the second reaction condition; a lower temperature relative to the second reaction condition; and a lower concentration of a sialic acid donor relative to the second reaction condition.

35 In some embodiments, the limited reaction condition is selected from one or more of: a shorter reaction time relative a control reaction condition; a lower ST6 sialyltransferase concentration and/or specific activity relative to a control reaction condition; a lower temperature relative to a control reaction condition; and a lower concentration of a sialic acid donor relative to a control reaction condition.

40 In another aspect, the invention features a method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the

preparation comprising (i) a target level of branched glycans having a sialic acid on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and/or (ii) a target level of branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), the method comprising: providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; and contacting the glycoproteins with an ST6 sialyltransferase in the presence of an extended reaction condition, thereby producing a glycoprotein preparation having (i) the target level of branched glycans having a sialic acid on the α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and/or (ii) the target level of branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage).

In some embodiments, the ST6 sialyltransferase has at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity, or is 100% identical, to amino acid residues 95-416 of SEQ ID NO:1, to SEQ ID NO:2, or to SEQ ID NO:3.

In some embodiments, the extended reaction condition is sufficient for the ST6 sialyltransferase substantially to remove a sialic acid from an α 1,3 arm of a disialylated branched glycan comprising a sialic acid on an α 1,3 arm and an α 1,6 arm.

In some embodiments, the method further comprises isolating the glycoprotein preparation. In some embodiments, the method further comprises measuring a level of branched glycans comprising a sialic acid on an α 1,6 arm and/or measuring a level of branched glycans having a sialic acid on an α 1,3 arm.

In some embodiments, level of branched glycans comprising a sialic acid on an α 1,6 arm and/or level of branched glycans having a sialic acid on an α 1,3 arm is measured by one or more of: releasing glycans (e.g., enzymatically releasing glycans) from glycoproteins and measuring the released glycans; measuring glycans on glycoproteins; derivatizing glycans and measuring derivatized glycans; measuring by fluorescence; measuring by mass spectrometry; and measuring by nuclear magnetic resonance. In some embodiments, target level is a mole percentage, mass percentage, and/or area percentage.

In some embodiments, the target level of branched glycans having a sialic acid on an α 1,6 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of branched glycans having a sialic acid on an α 1,6 arm is less than 100%, 95%, 90%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% of glycans, branched glycans, or sialylated branched glycans.

In some embodiments, the target level of branched glycans having a sialic acid on an α 1,3 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of branched glycans having a sialic acid on an α 1,3 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans.

In some embodiments, target level is a mole percentage, mass percentage, and/or area percentage.

In some embodiments, the extended reaction condition is selected using a method comprising: a) contacting the glycoproteins with an ST6 sialyltransferase in the presence of a first reaction condition; b) measuring a first level of branched glycans comprising a sialic acid on an α 1,6 arm and/or branched

glycans comprising a sialic acid on an α 1,3 arm after the first reaction condition; c) contacting the glycoproteins with the ST6 sialyltransferase in the presence of a second reaction condition; and d) measuring a second level of branched glycans comprising a sialic acid on an α 1,6 arm and/or branched glycans comprising a sialic acid on an α 1,3 arm after the second reaction condition; wherein the second reaction condition is selected as the extended reaction condition if the second level of branched glycans comprising a sialic acid on an α 1,6 arm is higher than the first level of branched glycans comprising a sialic acid on an α 1,6 arm; and/or the second level of branched glycans comprising a sialic acid on an α 1,3 arm is lower than the first level of branched glycans comprising a sialic acid on an α 1,3 arm. In some embodiments, the second reaction condition is selected from one or more of: a greater reaction time relative to the first reaction condition; a higher ST6 sialyltransferase concentration and/or specific activity relative to the first reaction condition; a higher temperature relative to the first reaction condition; and a higher concentration of a sialic acid donor relative to the first reaction condition.

In some embodiments, the extended reaction condition is selected from one or more of: a greater reaction time relative to a control reaction condition; a higher ST6 sialyltransferase concentration and/or specific activity relative to a control reaction condition; a higher temperature relative to a control reaction condition; and a higher concentration of a sialic acid donor relative to a control reaction condition.

In another aspect, the invention features a method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of disialylated branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), (ii) a target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and/or (iii) a target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), the method comprising: providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; and contacting the glycoproteins with an ST6 sialyltransferase in the presence of an intermediate reaction condition, thereby producing a glycoprotein preparation having (i) the target level of disialylated branched glycans having a sialic acid on the α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and on the α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), (ii) the target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), and/or (iii) the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage).

In some embodiments, the ST6 sialyltransferase has at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity, or is 100% identical, to amino acid residues 95-416 of SEQ ID NO:1, to SEQ ID NO:2, or to SEQ ID NO:3.

In some embodiments, the intermediate reaction condition is sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm and to an α 1,6 arm of a branched glycan, and not sufficient for the ST6 sialyltransferase substantially to remove a sialic acid from an α 1,3 arm of a branched glycan.

In some embodiments, the method further comprises isolating the glycoprotein preparation. In some embodiments, the method further comprises measuring a level of (i) disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) monosialylated branched glycans having a

sialic acid on an α 1,3 arm and/or (iii) monosialylated branched glycans having a sialic acid on an α 1,6 arm.

In some embodiments, level of (i) disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) monosialylated branched glycans having a sialic acid on an α 1,3 arm and/or (iii) monosialylated branched glycans having a sialic acid on an α 1,6 arm is measured by one or more of: releasing glycans (e.g., enzymatically releasing glycans) from glycoproteins and measuring the released glycans; measuring glycans on glycoproteins; derivatizing glycans and measuring derivatized glycans; measuring by fluorescence; measuring by mass spectrometry; and measuring by nuclear magnetic resonance.

In some embodiments, the target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm is less than 100%, 95%, 90%, 80%, 75%, 70%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% of glycans, branched glycans, or sialylated branched glycans.

In some embodiments, the target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans.

In some embodiments, the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of sialylated branched glycans. In some embodiments, the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans.

In some embodiments, target level is a mole percentage, mass percentage, and/or area percentage.

In another aspect, the invention features a method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of branched glycans having a sialic acid on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and/or (ii) a target level of branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), the method comprising: providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; and contacting the glycoproteins with an ST6 sialyltransferase in the presence of an initial reaction condition sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and to add a sialic acid to an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) of a branched glycan to produce a disialylated branched glycan; and contacting the disialylated branched glycan with the ST6 sialyltransferase in the presence of an extended reaction condition, thereby producing a glycoprotein preparation having (i) the target level of branched glycans

having a sialic acid on the α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and/or (ii) the target level of branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage).

5 In another aspect, the invention features a method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of disialylated branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), (ii) a target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and/or (iii) a target level of monosialylated branched
10 glycans having a sialic acid on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), the method comprising: providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; and contacting the glycoproteins with an ST6 sialyltransferase in the presence of an initial reaction condition sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) of a branched glycan to produce
15 a monosialylated branched glycan; and contacting the monosialylated branched glycan with the ST6 sialyltransferase in the presence of an extended reaction condition, thereby producing a glycoprotein preparation having (i) the target level of disialylated branched glycans having a sialic acid on an α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), (ii) the target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm (e.g.,
20 with a NeuAc- α 2,6-Gal terminal linkage) and/or (iii) the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage).

In another aspect, the invention features a method of removing a sialic acid from a branched glycan of an Fc region, the branched glycan comprising an α 1,3 arm and an α 1,6 arm, the method comprising: providing a branched glycan of an Fc region, the branched glycan comprising an α 1,3 arm and an α 1,6 arm and comprising a sialic acid on the α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage); contacting the branched glycan with an ST6 sialyltransferase in the presence of an initial
25 reaction condition sufficient for the ST6 sialyltransferase to add a sialic acid to the α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) to produce a disialylated branched glycan; and contacting the disialylated branched glycan with the ST6 sialyltransferase in the presence of an extended reaction
30 condition, thereby removing the sialic acid from the α 1,3 arm of the branched glycan.

In another aspect, the invention features a method of modulating sialylation of Fc region branched glycans comprising an α 1,3 arm and an α 1,6 arm, the method comprising: providing a reaction solution comprising (i) Fc region branched glycans comprising an α 1,3 arm and an α 1,6 arm, (ii) a ST6 sialyltransferase, and (iii) a sialic acid donor; and incubating the reaction solution under reaction
35 conditions sufficient for the ST6 sialyltransferase to catalyze transfer of a sialic acid primarily to the α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) only, primarily to the α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) only, or to both the α 1,3 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage) and the α 1,6 arm (e.g., with a NeuAc- α 2,6-Gal terminal linkage), wherein: a) incubating the reaction solution under reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid primarily
40 to the α 1,3 arm comprises controlling reaction kinetics such that: (i) the sialic acid addition rate for the α 1,3 arm ($R_a^{1,3}$) exceeds the sialic acid addition rate for the α 1,6 arm ($R_a^{1,6}$); or (ii) the sialic acid removal

rate for the $\alpha 1,6$ arm ($R_r^{1,6}$) exceeds $R_a^{1,6}$; b) incubating the reaction solution under reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid primarily to the $\alpha 1,6$ arm comprises controlling reaction kinetics such that: (i) $R_a^{1,6}$ exceeds $R_r^{1,6}$; and (ii) the sialic acid removal rate for the $\alpha 1,3$ arm ($R_r^{1,3}$) eventually exceeds $R_a^{1,3}$; or c) incubating the reaction solution under reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid to both the $\alpha 1,3$ and $\alpha 1,6$ arms comprises controlling reaction kinetics such that: (i) $R_a^{1,3}$ exceeds $R_r^{1,3}$; and (ii) $R_a^{1,6}$ exceeds $R_r^{1,6}$; thereby modulating sialylation of a branched glycan.

In some embodiments, controlling reaction kinetics comprises one or more of: modulating (e.g., increasing or decreasing) the time of the reaction; modulating (e.g., increasing or decreasing) level or activity of the sialyltransferase; and modulating (e.g., increasing or decreasing) the $R_r^{1,3}$ or $R_r^{1,6}$ rates by controlling or adjusting the ratio of the sialic acid donor to a sialic acid donor reaction product.

In some embodiments, the sialic acid donor is cytidine 5'-monophospho-N-acetyl neuraminic acid and the sialic acid donor reaction product is cytidine 5'-monophosphate.

In some embodiments, the reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid to both the $\alpha 1,3$ and $\alpha 1,6$ arms comprises supplementing the sialic donor at least once during the reaction. In some embodiments, the reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid to both the $\alpha 1,3$ and $\alpha 1,6$ arms comprises removing a sialic donor reaction product at least once during the reaction. In some embodiments, the reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid to both the $\alpha 1,3$ and $\alpha 1,6$ arms comprises supplementing the sialic donor reaction product at least once during the reaction.

In some embodiments, the method further comprises detecting reaction kinetics.

In some embodiments, the method further comprises measuring a level of sialylated glycans (e.g., a level of disialylated branched glycans having a sialic acid on an $\alpha 1,3$ arm and on an $\alpha 1,6$ arm, (ii) a level of monosialylated branched glycans having a sialic acid on an $\alpha 1,3$ arm and/or (iii) a level of monosialylated branched glycans having a sialic acid on an $\alpha 1,6$ arm). In some embodiments, level of sialylated glycans is measured by one or more of: releasing glycans (e.g., enzymatically releasing glycans) from glycoproteins and measuring the released glycans; measuring glycans on glycoproteins; derivatizing glycans and measuring derivatized glycans; measuring by fluorescence; measuring by mass spectrometry; and measuring by nuclear magnetic resonance.

In some embodiments, the Fc region branched glycans are on, or are derived from, a glycoprotein preparation. In some embodiments, the method further comprises formulating the preparation into a drug product if the preparation meets a target level, e.g., a target level described herein.

In another aspect, the invention features a method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an $\alpha 1,3$ arm and an $\alpha 1,6$ arm, the preparation comprising (i) a target level of branched glycans having a sialic acid on an $\alpha 1,3$ arm and/or (ii) a target level of branched glycans having a sialic acid on an $\alpha 1,6$ arm, the method comprising: providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an $\alpha 1,3$ arm and an $\alpha 1,6$ arm; contacting the glycoproteins with an ST6 sialyltransferase in the presence of a limited reaction condition sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an $\alpha 1,3$ arm of a branched glycan and not sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an

α 1,6 arm of a branched glycan, thereby producing a preparation of sialylated glycoproteins; and processing (e.g., one or more of formulating, filling into a container, labeling, packaging) the preparation into a drug product if the preparation meets the target level of branched glycans having a sialic acid on the α 1,3 arm and/or the target level of branched glycans having a sialic acid on an α 1,6 arm.

5 In some embodiments, the ST6 sialyltransferase has at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity, or is 100% identical, to amino acid residues 95-416 of SEQ ID NO:1, to SEQ ID NO:2, or to SEQ ID NO:3.

In some embodiments, the method further comprises isolating the glycoprotein preparation. In some embodiments, the method further comprises measuring a level of branched glycans comprising a sialic acid on an α 1,3 arm and/or measuring a level of branched glycans having a sialic acid on an α 1,6 arm.

10 In some embodiments, level of branched glycans comprising a sialic acid on an α 1,3 arm and/or level of branched glycans having a sialic acid on an α 1,6 arm is measured by one or more of: releasing glycans (e.g., enzymatically releasing glycans) from glycoproteins and measuring the released glycans; measuring glycans on glycoproteins; derivatizing glycans and measuring derivatized glycans; measuring by fluorescence; measuring by mass spectrometry; and measuring by nuclear magnetic resonance.

15 In some embodiments, the target level of branched glycans having a sialic acid on an α 1,3 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of branched glycans having a sialic acid on an α 1,3 arm is less than 100%, 95%, 90%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% of glycans, branched glycans, or sialylated branched glycans.

20 In some embodiments, the target level of branched glycans having a sialic acid on an α 1,6 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of branched glycans having a sialic acid on an α 1,6 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans.

In some embodiments, target level is a mole percentage, mass percentage, and/or area percentage.

30 In another aspect, the invention features a method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of branched glycans having a sialic acid on an α 1,6 arm and/or (ii) a target level of branched glycans having a sialic acid on an α 1,3 arm, the method comprising: providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; contacting the glycoproteins with an ST6 sialyltransferase in the presence of an extended reaction condition sufficient for the ST6 sialyltransferase substantially to remove a sialic acid from an α 1,3 arm of a disialylated branched glycan comprising a sialic acid on an α 1,3 arm and an α 1,6 arm, thereby producing a preparation of sialylated glycoproteins; and processing (e.g., one or more of formulating, filling into a container, labeling, packaging) the preparation into a drug product if the preparation meets the target level of branched glycans having a sialic acid on the α 1,6 arm and/or the target level of branched glycans having a sialic acid on an α 1,3 arm.

In some embodiments, the ST6 sialyltransferase has at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity, or is 100% identical, to amino acid residues 95-416 of SEQ ID NO:1, to SEQ ID NO:2, or to SEQ ID NO:3.

5 In some embodiments, the method further comprises isolating the glycoprotein preparation. In some embodiments, the method further comprises measuring a level of branched glycans comprising a sialic acid on an α 1,6 arm and/or measuring a level of branched glycans having a sialic acid on an α 1,3 arm.

10 In some embodiments, level of branched glycans comprising a sialic acid on an α 1,6 arm and/or level of branched glycans having a sialic acid on an α 1,3 arm is measured by one or more of: releasing glycans (e.g., enzymatically releasing glycans) from glycoproteins and measuring the released glycans; measuring glycans on glycoproteins; derivatizing glycans and measuring derivatized glycans; measuring by fluorescence; measuring by mass spectrometry; and measuring by nuclear magnetic resonance. In some embodiments, target level is a mole percentage, mass percentage, and/or area percentage.

15 In some embodiments, the target level of branched glycans having a sialic acid on an α 1,6 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of branched glycans having a sialic acid on an α 1,6 arm is less than 100%, 95%, 90%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% of glycans, branched glycans, or sialylated branched glycans.

20 In some embodiments, the target level of branched glycans having a sialic acid on an α 1,3 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of branched glycans having a sialic acid on an α 1,3 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans.

25 In some embodiments, target level is a mole percentage, mass percentage, and/or area percentage.

In another aspect, the invention features a method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) a target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm and/or (iii) a target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm, the method comprising: providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; contacting the glycoproteins with an ST6 sialyltransferase in the presence of an intermediate reaction condition sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm and to an α 1,6 arm of a branched glycan, and not sufficient for the ST6 sialyltransferase substantially to remove a sialic acid from an α 1,3 arm of a branched glycan, thereby producing a preparation of sialylated glycoproteins; and processing (e.g., one or more of formulating, filling into a container, labeling, packaging) the preparation into a drug product if the preparation meets (i) the target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) the target level of monosialylated branched glycans having a sialic

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acid on an α 1,3 arm and/or (iii) the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm.

In some embodiments, the ST6 sialyltransferase has at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity, or is 100% identical, to amino acid residues 95-416 of SEQ ID NO:1, to SEQ ID NO:2, or to SEQ ID NO:3.

In some embodiments, the method further comprises isolating the glycoprotein preparation. In some embodiments, the method further comprises measuring a level of (i) disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) monosialylated branched glycans having a sialic acid on an α 1,3 arm and/or (iii) monosialylated branched glycans having a sialic acid on an α 1,6 arm.

In some embodiments, level of (i) disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) monosialylated branched glycans having a sialic acid on an α 1,3 arm and/or (iii) monosialylated branched glycans having a sialic acid on an α 1,6 arm is measured by one or more of: releasing glycans (e.g., enzymatically releasing glycans) from glycoproteins and measuring the released glycans; measuring glycans on glycoproteins; derivatizing glycans and measuring derivatized glycans; measuring by fluorescence; measuring by mass spectrometry; and measuring by nuclear magnetic resonance.

In some embodiments, the target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm is less than 100%, 95%, 90%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% of glycans, branched glycans, or sialylated branched glycans.

In some embodiments, the target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of glycans, branched glycans, or sialylated branched glycans. In some embodiments, the target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans.

In some embodiments, the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of sialylated branched glycans. In some embodiments, the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of glycans, branched glycans, or sialylated branched glycans.

In some embodiments, target level is a mole percentage, mass percentage, and/or area percentage.

In any of the aspects described herein, in some embodiments, the target level of sialylated branched glycans (e.g., level of branched glycans having a sialic acid on an α 1,3 arm, level of branched glycans having a sialic acid on an α 1,6 arm, and/or level of branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm) is a level of sialylated branched glycans in a reference therapeutic product.

In some embodiments, the target level of sialylated branched glycans is a level in a reference therapeutic antibody product. In some embodiments, the target level of sialylated glycans is a pharmaceutical product specification or a quality control criterion for a pharmaceutical preparation, e.g., a Certificate of Analysis (CofA), a Certificate of Testing (CofT), or a Master Batch Record. In some embodiments, the product specification is a product description in an FDA label, a Physician's Insert, a USP monograph, or an EP monograph.

In some embodiments, the reference therapeutic product is selected from the group consisting of: abatacept, abciximab, adalimumab, aflibercept, alefacept, alemtuzumab, basiliximab, bevacizumab, belatacept, certolizumab, cetuximab, daclizumab, eculizumab, efalizumab, entanercept, gemtuzumab, ibritumomab, infliximab, muromonab-CD3, natalizumab, omalizumab, palivizumab; panitumumab, ranibizumab, rilonacept, rituximab, tositumomab, and trastuzumab.

In any of the aspects described herein, in some embodiments, the preparation is an IVIG preparation. In some embodiments, the preparation is a recombinant Fc containing glycoprotein preparation. In some embodiments, the recombinant glycoprotein is a recombinant antibody or Fc fusion protein.

In another aspect, the invention features a glycoprotein preparation produced by any of the methods described herein.

BRIEF DESCRIPTION OF THE DRAWINGS

The present teachings described herein will be more fully understood from the following description of various illustrative embodiments, when read together with the accompanying drawings. It should be understood that the drawings described below are for illustration purposes only and are not intended to limit the scope of the present teachings in any way.

FIG. 1 is a schematic illustration of a common core pentasaccharide $(\text{Man})_3(\text{GlcNAc})(\text{GlcNAc})$ of N-glycans.

FIG. 2 is a schematic illustration of an IgG antibody molecule.

FIG. 3 is a graphic representation of relative abundance of glycans at various times during a sialylation reaction with ST6 sialyltransferase.

FIG. 4 is a schematic illustration of a reaction scheme for ST6 sialyltransferase (fucose: triangles, N-acetylglucosamine: squares, mannose: dark circles, galactose: light circles, sialic acid: diamonds).

FIG. 5A depicts an exemplary ST6 sialyltransferase amino acid sequence (SEQ ID NO:1). FIG. 5B depicts an exemplary ST6 sialyltransferase amino acid sequence (SEQ ID NO:2). FIG. 5C depicts an exemplary ST6 sialyltransferase amino acid sequence (SEQ ID NO:3).

DETAILED DESCRIPTION

Antibodies are glycosylated at conserved positions in the constant regions of their heavy chain. For example, IgG antibodies have a single N-linked glycosylation site at Asn297 of the CH2 domain. Each antibody isotype has a distinct variety of N-linked carbohydrate structures in the constant regions. For human IgG, the core oligosaccharide normally consists of $\text{GlcNAc}_2\text{Man}_3\text{GlcNAc}$, with differing numbers of outer residues. Variation among individual IgG's can occur via attachment of galactose and/or galactose-sialic acid at one or both terminal GlcNAc or via attachment of a third GlcNAc arm (bisecting GlcNAc).

The present disclosure encompasses glycoprotein preparations (e.g., Fc region-containing glycoprotein preparations (e.g., IVIG, Fc or IgG antibodies)) having particular levels of branched glycans that are sialylated on an α 1,3 arm, an α 1,6 arm, or both, of the branched glycans in the Fc region (e.g., with a NeuAc- α 2,6-Gal terminal linkage). The levels can be measured on an individual Fc region (e.g., the number of branched glycans that are sialylated on an α 1,3 arm, an α 1,6 arm, or both, of the branched glycans in the Fc region), or on the overall composition of a preparation of glycoproteins (e.g., the number or percentage of branched glycans that are sialylated on an α 1,3 arm, an α 1,6 arm, or both, of the branched glycans in the Fc region in a preparation of glycoproteins).

10 Definitions

As used herein, "glycan" is a sugar, which can be monomers or polymers of sugar residues, such as at least three sugars, and can be linear or branched. A "glycan" can include natural sugar residues (e.g., glucose, N-acetylglucosamine, N-acetyl neuraminic acid, galactose, mannose, fucose, hexose, arabinose, ribose, xylose, etc.) and/or modified sugars (e.g., 2'-fluororibose, 2'-deoxyribose, phosphomannose, 6'sulfo N-acetylglucosamine, etc.). The term "glycan" includes homo and heteropolymers of sugar residues. The term "glycan" also encompasses a glycan component of a glycoconjugate (e.g., of a glycoprotein, glycolipid, proteoglycan, etc.). The term also encompasses free glycans, including glycans that have been cleaved or otherwise released from a glycoconjugate.

As used herein, the term "glycoprotein" refers to a protein that contains a peptide backbone covalently linked to one or more sugar moieties (i.e., glycans). The sugar moiety(ies) may be in the form of monosaccharides, disaccharides, oligosaccharides, and/or polysaccharides. The sugar moiety(ies) may comprise a single unbranched chain of sugar residues or may comprise one or more branched chains. Glycoproteins can contain O-linked sugar moieties and/or N-linked sugar moieties.

As used herein, the term "glycoprotein preparation" refers to a set of individual glycoprotein molecules, each of which comprises a polypeptide having a particular amino acid sequence (which amino acid sequence includes at least one glycosylation site) and at least one glycan covalently attached to the at least one glycosylation site. Individual molecules of a particular glycoprotein within a glycoprotein preparation typically have identical amino acid sequences but may differ in the occupancy of the at least one glycosylation sites and/or in the identity of the glycans linked to the at least one glycosylation sites. That is, a glycoprotein preparation may contain only a single glycoform of a particular glycoprotein, but more typically contains a plurality of glycoforms. Different preparations of the same glycoprotein may differ in the identity of glycoforms present (e.g., a glycoform that is present in one preparation may be absent from another) and/or in the relative amounts of different glycoforms.

The term "glycoform" is used herein to refer to a particular form of a glycoprotein. That is, when a glycoprotein includes a particular polypeptide that has the potential to be linked to different glycans or sets of glycans, then each different version of the glycoprotein (i.e., where the polypeptide is linked to a particular glycan or set of glycans) is referred to as a "glycoform".

"Reference glycoprotein", as used herein, refers to a glycoprotein having substantially the same amino acid sequence as (e.g., having about 95-100% identical amino acids of) a glycoprotein described herein, e.g., a glycoprotein to which it is compared. In some embodiments, a reference glycoprotein is a therapeutic glycoprotein described herein, e.g., an FDA approved therapeutic glycoprotein.

As used herein, the term "antibody" refers to a polypeptide that includes at least one immunoglobulin variable region, e.g., an amino acid sequence that provides an immunoglobulin variable domain or immunoglobulin variable domain sequence. For example, an antibody can include a heavy (H) chain variable region (abbreviated herein as VH), and a light (L) chain variable region (abbreviated herein as VL). In another example, an antibody includes two heavy (H) chain variable regions and two light (L) chain variable regions. The term "antibody" encompasses antigen-binding fragments of antibodies (e.g., single chain antibodies, Fab, F(ab')₂, Fd, Fv, and dAb fragments) as well as complete antibodies, e.g., intact immunoglobulins of types IgA, IgG, IgE, IgD, IgM (as well as subtypes thereof). The light chains of the immunoglobulin can be of types kappa or lambda.

As used herein, the term "Fc region" refers to a dimer of two "Fc polypeptides", each "Fc polypeptide" comprising the constant region of an antibody excluding the first constant region immunoglobulin domain. In some embodiments, an "Fc region" includes two Fc polypeptides linked by one or more disulfide bonds, chemical linkers, or peptide linkers. "Fc polypeptide" refers to the last two constant region immunoglobulin domains of IgA, IgD, and IgG, and the last three constant region immunoglobulin domains of IgE and IgM, and may also include part or all of the flexible hinge N-terminal to these domains. For IgG, "Fc polypeptide" comprises immunoglobulin domains Cgamma2 (Cγ2) and Cgamma3 (Cγ3) and the lower part of the hinge between Cgamma1 (Cγ1) and Cγ2. Although the boundaries of the Fc polypeptide may vary, the human IgG heavy chain Fc polypeptide is usually defined to comprise residues starting at T223 or C226 or P230, to its carboxyl-terminus, wherein the numbering is according to the EU index as in Kabat et al. (1991, NIH Publication 91-3242, National Technical Information Services, Springfield, VA). For IgA, Fc polypeptide comprises immunoglobulin domains Calpha2 (Cα2) and Calpha3 (Cα3) and the lower part of the hinge between Calpha1 (Cα1) and Cα2. An Fc region can be synthetic, recombinant, or generated from natural sources such as IVIG.

As used herein, an "N-glycosylation site of an Fc region" refers to an amino acid residue within an Fc region to which a glycan is N-linked.

"Predetermined level" or "target level" as used herein, refers to a pre-specified particular level of one or more particular glycans, e.g., branched glycans having a sialic acid on an α1,3 arm, and/or branched glycans having a sialic acid on an α1,6 arm, and/or branched glycans having a sialic acid on an α1,3 arm and on an α1,6 arm. In some embodiments, a predetermined or target level is an absolute value or range. In some embodiments, a predetermined or target level is a relative value. In some embodiments, a predetermined level is the same as or different (e.g., higher or lower than) a level of one or more particular glycans (e.g., branched glycans having a sialic acid on an α1,3 arm, and/or branched glycans having a sialic acid on an α1,6 arm, and/or branched glycans having a sialic acid on an α1,3 arm and on an α1,6 arm) in a reference, e.g., a reference glycoprotein product, or a reference document such as a specification, alert limit, or master batch record for a pharmaceutical product.

In some embodiments, a predetermined or target level is an absolute level or range of (e.g., number of moles of) one or more glycans (e.g., branched glycans having a sialic acid on an α1,3 arm, and/or branched glycans having a sialic acid on an α1,6 arm, and/or branched glycans having a sialic acid on an α1,3 arm and on an α1,6 arm) in a glycoprotein preparation. In some embodiments, a predetermined or target level is a level or range of one or more glycans (e.g., branched glycans having a sialic acid on an α1,3 arm, and/or branched glycans having a sialic acid on an α1,6 arm, and/or branched

glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm) in a glycoprotein preparation relative to total level of glycans in the glycoprotein preparation. In some embodiments, a predetermined or target level is a level or range of one or more glycans (e.g., branched glycans having a sialic acid on an α 1,3 arm, and/or branched glycans having a sialic acid on an α 1,6 arm, and/or branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm) in a glycoprotein preparation relative to total level of sialylated glycans in the glycoprotein preparation. In some embodiments, a predetermined or target level is expressed as a percent.

For any given parameter, in some embodiments, "percent" refers to the number of moles of a particular glycan (glycan X) relative to total moles of glycans of a preparation. In some embodiments, "percent" refers to the number of moles of PNGase F-released Fc glycan X relative to total moles of PNGase F-released Fc glycans detected.

By "purified" (or "isolated") refers to a nucleic acid sequence (e.g., a polynucleotide) or an amino acid sequence (e.g., a polypeptide) that is removed or separated from other components present in its natural environment. For example, an isolated polypeptide is one that is separated from other components of a cell in which it was produced (e.g., the endoplasmic reticulum or cytoplasmic proteins and RNA). An isolated polynucleotide is one that is separated from other nuclear components (e.g., histones) and/or from upstream or downstream nucleic acid sequences. An isolated nucleic acid sequence or amino acid sequence can be at least 60% free, or at least 75% free, or at least 90% free, or at least 95% free from other components present in natural environment of the indicated nucleic acid sequence or amino acid sequence.

As used herein, "polynucleotide" (or "nucleotide sequence" or "nucleic acid molecule") refers to an oligonucleotide, nucleotide, or polynucleotide, and fragments or portions thereof, and to DNA or RNA of genomic or synthetic origin, which may be single- or double- stranded, and represent the sense or anti-sense strand.

As used herein, "polypeptide" (or "amino acid sequence" or "protein") refers to an oligopeptide, peptide, polypeptide, or protein sequence, and fragments or portions thereof, and to naturally occurring or synthetic molecules. "Amino acid sequence" and like terms, such as "polypeptide" or "protein", are not meant to limit the indicated amino acid sequence to the complete, native amino acid sequence associated with the recited protein molecule.

The term "pharmaceutically effective amount" or "therapeutically effective amount" refers to an amount (e.g., dose) effective in treating a patient, having a disorder or condition described herein. It is also to be understood herein that a "pharmaceutically effective amount" may be interpreted as an amount giving a desired therapeutic effect, either taken in one dose or in any dosage or route, taken alone or in combination with other therapeutic agents.

The term "treatment" or "treating", as used herein, refers to administering a therapy in an amount, manner, and/or mode effective to improve a condition, symptom, or parameter associated with a disorder or condition or to prevent or reduce progression of a disorder or condition, to a degree detectable to one skilled in the art. An effective amount, manner, or mode can vary depending on the subject and may be tailored to the subject.

As used herein, a "characteristic sequence" is a sequence that is found in all members of a family of polypeptides or nucleic acids, and therefore can be used by those of ordinary skill in the art to define members of the family.

As used herein, the term "homology" refers to the overall relatedness between polymeric molecules, *e.g.*, between nucleic acid molecules (*e.g.*, DNA molecules and/or RNA molecules) and/or between polypeptide molecules. In some embodiments, polymeric molecules are considered to be "homologous" to one another if their sequences are at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% identical. In some embodiments, polymeric molecules are considered to be "homologous" to one another if their sequences are at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% similar.

As used herein, the term "identity" refers to the overall relatedness between polymeric molecules, *e.g.*, between nucleic acid molecules (*e.g.*, DNA molecules and/or RNA molecules) and/or between polypeptide molecules. Calculation of the percent identity of two nucleic acid sequences, for example, can be performed by aligning the two sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in one or both of a first and a second nucleic acid sequences for optimal alignment and non-identical sequences can be disregarded for comparison purposes). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or substantially 100% of the length of the reference sequence. The nucleotides at corresponding nucleotide positions are then compared. When a position in the first sequence is occupied by the same nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which needs to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. For example, the percent identity between two nucleotide sequences can be determined using the algorithm of Meyers and Miller (CABIOS, 1989, 4:11-17), which has been incorporated into the ALIGN program (version 2.0) using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. The percent identity between two nucleotide sequences can, alternatively, be determined using the GAP program in the GCG software package using an NWSgapdna.CMP matrix.

As used herein, the term "ST6 sialyltransferase" refers to a polypeptide whose amino acid sequence includes at least one characteristic sequence of and/or shows at least 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80%, 79%, 78%, 77%, 76%, 75%, 74%, 73%, 72%, 71% or 70% identity with a protein involved in transfer of a sialic acid to a terminal galactose of a glycan through an α 2,6 linkage (*e.g.*, ST6 Gal-I). A wide variety of ST6 sialyltransferase sequences are known in the art, such as those described herein; in some embodiments, an ST6 sialyltransferase shares at least one characteristic sequence of and/or shows the specified degree of overall sequence identity with one of the ST6 sialyltransferases set forth herein (each of which may be considered a "reference" ST6 sialyltransferase). In some embodiments, an ST6 sialyltransferase as described herein shares at least one biological activity with a reference ST6 sialyltransferase as set

forth herein. In some such embodiment, the shared biological activity relates to transfer of a sialic acid to a glycan.

Glycoproteins

5 Described herein are preparations (e.g., therapeutic preparations) of polypeptides (e.g., glycoproteins), and methods of making and using such preparations, having particular levels of branched glycans having sialylation on an α 1,3 arm, an α 1,6 arm, and/or on both arms. Glycoproteins include, for example, any of a variety of hematologic agents (including, for instance, erythropoietin, blood-clotting factors, etc.), interferons, colony stimulating factors, antibodies, enzymes, and hormones. The identity of
10 a particular glycoprotein is not intended to limit the present disclosure, and a preparation described herein can include any glycoprotein of interest, e.g., a glycoprotein having an Fc region.

A glycoprotein described herein can include a target-binding domain that binds to a target of interest (e.g., binds to an antigen). For example, a glycoprotein, such as an antibody, can bind to a transmembrane polypeptide (e.g., receptor) or ligand (e.g., a growth factor). Exemplary molecular targets
15 (e.g., antigens) for glycoproteins described herein (e.g., antibodies) include CD proteins such as CD2, CD3, CD4, CD8, CD11, CD19, CD20, CD22, CD25, CD33, CD34, CD40, CD52; members of the ErbB receptor family such as the EGF receptor (EGFR, HER1, ErbB1), HER2 (ErbB2), HER3 (ErbB3) or HER4 (ErbB4) receptor; macrophage receptors such as CR1g; tumor necrosis factors such as TNF α or TRAIL/Apo-2; cell adhesion molecules such as LFA-1, Mac1, p150,95, VLA-4, ICAM-1, VCAM and α v β 3
20 integrin including either α or β subunits thereof (e.g., anti-CD11a, anti-CD18 or anti-CD11b antibodies); growth factors and receptors such as EGF, FGFR (e.g., FGFR3) and VEGF; IgE; cytokines such as IL1; cytokine receptors such as IL2 receptor; blood group antigens; flk2/flt3 receptor; obesity (OB) receptor; mpl receptor; CTLA-4; protein C; neutropilins; ephrins and receptors; netrins and receptors; slit and receptors; chemokines and chemokine receptors such as CCL5, CCR4, CCR5; amyloid beta;
25 complement factors, such as complement factor D; lipoproteins, such as oxidized LDL (oxLDL); lymphotoxins, such as lymphotoxin alpha (LTa). Other molecular targets include Tweak, B7RP-1, proprotein convertase subtilisin/kexin type 9 (PCSK9), sclerostin, c-kit, Tie-2, c-fms, and anti-M1.

Reference Polypeptides

30 In some embodiments, methods described herein are useful for controlling the sialylation of a reference polypeptide (e.g., a reference glycoprotein). In some embodiments, polypeptide (e.g., glycoprotein) preparations described herein have predetermined or target levels of glycans (e.g., branched glycans having a sialic acid on an α 1,3 arm, and/or branched glycans having a sialic acid on an α 1,6 arm, and/or branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm), where the
35 predetermined levels are substantially similar to or different from (e.g., higher or lower than) levels of glycans (e.g., branched glycans having a sialic acid on an α 1,3 arm, and/or branched glycans having a sialic acid on an α 1,6 arm, and/or branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm) in a reference polypeptide product (e.g., glycoprotein product). Nonlimiting, exemplary reference glycoprotein products can include abatacept (Orencia®, Bristol-Myers Squibb), abciximab (ReoPro®,
40 Roche), adalimumab (Humira®, Bristol-Myers Squibb), aflibercept (Eylea®, Regeneron Pharmaceuticals),

alefacept (Amevive®, Astellas Pharma), alemtuzumab (Campath®, Genzyme/Bayer), basiliximab (Simulect®, Novartis), belatacept (Nulojix®, Bristol-Myers Squibb), belimumab (Benlysta®, GlaxoSmithKline), bevacizumab (Avastin®, Roche), canakinumab (Ilaris®, Novartis), brentuximab vedotin (Adcetris®, Seattle Genetics), certolizumab (CIMZIA®, UCB, Brussels, Belgium), cetuximab (Erbix®, Merck-Serono), daclizumab (Zenapax®, Hoffmann-La Roche), denileukin diftitox (Ontak®, Eisai), denosumab (Prolia®, Amgen; Xgeva®, Amgen), eculizumab (Soliris®, Alexion Pharmaceuticals), efalizumab (Raptiva®, Genentech), etanercept (Enbrel®, Amgen-Pfizer), gemtuzumab (Mylotarg®, Pfizer), golimumab (Simponi®, Janssen), ibritumomab (Zevalin®, Spectrum Pharmaceuticals), infliximab (Remicade®, Centocor), ipilimumab (Yervoy™, Bristol-Myers Squibb), muromonab (Orthoclone OKT3®, Janssen-Cilag), natalizumab (Tysabri®, Biogen Idec, Elan), ofatumumab (Arzerra®, GlaxoSmithKline), omalizumab (Xolair®, Novartis), palivizumab (Synagis®, MedImmune), panitumumab (Vectibix®, Amgen), ranibizumab (Lucentis®, Genentech), rilonacept (Arcalyst®, Regeneron Pharmaceuticals), rituximab (MabThera®, Roche), tocilizumab (Actemra®, Genentech; RoActemra, Hoffman-La Roche) tositumomab (Bexxar®, GlaxoSmithKline), and trastuzumab (Herceptin®, Roche).

In some embodiments, a level of one or more glycans (e.g., branched glycans having a sialic acid on an α 1,3 arm, and/or branched glycans having a sialic acid on an α 1,6 arm, and/or branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm) in a reference polypeptide product is determined by analyzing one or more preparations (e.g., one or more lots) of the reference polypeptide. In some embodiments, a level of one or more glycans (e.g., branched glycans having a sialic acid on an α 1,3 arm, and/or branched glycans having a sialic acid on an α 1,6 arm, and/or branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm) in a reference polypeptide product is a range of the one or more glycans in two or more preparations of the reference polypeptide (e.g., two or more lots of the reference polypeptide product). In some embodiments, a level of one or more glycans is a range (e.g., spanning a lowest level of the one or more glycans to a highest level of the one or more glycans) in two or more lots of the reference polypeptide product.

N-Linked Glycosylation

N-linked oligosaccharide chains are added to a protein in the lumen of the endoplasmic reticulum (see Molecular Biology of the Cell, Garland Publishing, Inc. (Alberts et al., 1994)). Specifically, an initial oligosaccharide (typically 14-sugar) is added to the amino group on the side chain of an asparagine residue contained within the target consensus sequence of Asn-X-Ser/Thr, where X may be any amino acid except proline. The structure of this initial oligosaccharide is common to most eukaryotes, and contains 3 glucose, 9 mannose, and 2 N-acetylglucosamine residues. This initial oligosaccharide chain can be trimmed by specific glycosidase enzymes in the endoplasmic reticulum, resulting in a short, branched core oligosaccharide composed of two N-acetylglucosamine and three mannose residues (depicted in Figure 1, linked to an asparagine residue). One of the branches is referred to in the art as the " α 1,3 arm", and the second branch is referred to as the " α 1,6 arm", as denoted in Figure 1.

N-glycans can be subdivided into three distinct groups called "high mannose type", "hybrid type", and "complex type", with a common pentasaccharide core (Man (α 1,6)-(Man(α 1,3))-Man(β 1,4)-GlcNAc(β 1,4)-GlcNAc(β 1,N)-Asn) occurring in all three groups.

After initial processing in the endoplasmic reticulum, the glycoprotein is transported to the Golgi where further processing may take place. If the glycan is transferred to the Golgi before it is completely trimmed to the core pentasaccharide structure, it results in a "high-mannose glycan".

5 Additionally or alternatively, one or more monosaccharides units of N-acetylglucosamine may be added to core mannose subunits to form a "complex glycan". Galactose may be added to N-acetylglucosamine subunits, and sialic acid subunits may be added to galactose subunits, resulting in chains that terminate with any of a sialic acid, a galactose or an N-acetylglucosamine residue. Additionally, a fucose residue may be added to an N-acetylglucosamine residue of the core oligosaccharide. Each of these additions is catalyzed by specific glycosyl transferases, known in the art.

10 Sialic acids are a family of 9-carbon monosaccharides with heterocyclic ring structures. They bear a negative charge via a carboxylic acid group attached to the ring as well as other chemical decorations including N-acetyl and N-glycolyl groups. The two main types of sialyl residues found in glycoproteins produced in mammalian expression systems are N-acetyl-neuraminic acid (NeuAc) and N-glycolylneuraminic acid (NeuGc). These usually occur as terminal structures attached to galactose (Gal) residues at the non-reducing termini of both N- and O-linked glycans. The glycosidic linkage configurations for these sialyl groups can be either α 2,3 or α 2,6.

"Hybrid glycans" comprise characteristics of both high-mannose and complex glycans. For example, one branch of a hybrid glycan may comprise primarily or exclusively mannose residues, while another branch may comprise N-acetylglucosamine, sialic acid, and/or galactose sugars.

20 *N-linked Glycosylation in Antibodies*

Antibodies are glycosylated at conserved, N-linked glycosylation sites in the Fc regions of immunoglobulin heavy chains. For example, each heavy chain of an IgG antibody has a single N-linked glycosylation site at Asn297 of the CH2 domain (see Jefferis, Nature Reviews 8:226-234 (2009)). IgA antibodies have N-linked glycosylation sites within the CH2 and CH3 domains, IgE antibodies have N-linked glycosylation sites within the CH3 domain, and IgM antibodies have N-linked glycosylation sites within the CH1, CH2, CH3, and CH4 domains (see Arnold et al., J. Biol. Chem. 280:29080-29087 (2005); Mattu et al., J. Biol. Chem. 273:2260-2272 (1998); Nettleton et al., Int. Arch. Allergy Immunol. 107:328-329 (1995)).

Each antibody isotype has a distinct variety of N-linked carbohydrate structures in the constant regions. For example, IgG has a single N-linked biantennary carbohydrate at Asn297 of the CH2 domain in each Fc polypeptide of the Fc region, which also contains the binding sites for C1q and Fc γ R (see Jefferis et al., Immunol. Rev. 163:59-76 (1998); and Wright et al., Trends Biotech 15:26-32 (1997)). For human IgG, the core oligosaccharide normally consists of GlcNAc₂Man₃GlcNAc, with differing numbers of outer residues. Variation among individual IgG can occur via attachment of galactose and/or galactose-sialic acid at one or both terminal GlcNAc or via attachment of a third GlcNAc arm (bisecting GlcNAc), and/or attachment of fucose.

Antibodies

The basic structure of an IgG antibody is illustrated in Figure 2. As shown in Figure 2, an IgG antibody consists of two identical light polypeptide chains and two identical heavy polypeptide chains linked together by disulphide bonds. The first domain located at the amino terminus of each chain is variable in amino acid sequence, providing antibody binding specificities found in each individual antibody. These are known as variable heavy (VH) and variable light (VL) regions. The other domains of each chain are relatively invariant in amino acid sequence and are known as constant heavy (CH) and constant light (CL) regions. As shown in Figure 2, for an IgG antibody, the light chain includes one variable region (VL) and one constant region (CL). An IgG heavy chain includes a variable region (VH), a first constant region (CH1), a hinge region, a second constant region (CH2), and a third constant region (CH3). In IgE and IgM antibodies, the heavy chain includes an additional constant region (CH4).

Antibodies described herein can include, for example, monoclonal antibodies, polyclonal antibodies (e.g., IVIG), multispecific antibodies, human antibodies, humanized antibodies, camelized antibodies, chimeric antibodies, single-chain Fvs (scFv), disulfide-linked Fvs (sdFv), and anti-idiotypic (anti-Id) antibodies, and antigen-binding fragments of any of the above. Antibodies can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass.

The term "Fc fragment", as used herein, refers to one or more fragments of an Fc region that retains an Fc function and/or activity described herein, such as binding to an Fc receptor. Examples of such fragments include fragments that include an N-linked glycosylation site of an Fc region (e.g., an Asn297 of an IgG heavy chain or homologous sites of other antibody isotypes), such as a CH2 domain. The term "antigen binding fragment" of an antibody, as used herein, refers to one or more fragments of an antibody that retain the ability to specifically bind to an antigen. Examples of binding fragments encompassed within the term "antigen binding fragment" of an antibody include a Fab fragment, a F(ab')₂ fragment, a Fd fragment, a Fv fragment, a scFv fragment, a dAb fragment (Ward et al., (1989) Nature 341:544-546), and an isolated complementarity determining region (CDR). These antibody fragments can be obtained using conventional techniques known to those with skill in the art, and fragments can be screened for utility in the same manner as are intact antibodies.

Glycoproteins (e.g., antibodies), or fragments thereof, for use as substrates for an ST6 sialyltransferase described herein, can be produced by any method known in the art for synthesizing glycoproteins (e.g., antibodies) (see, e.g., Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Brinkman et al., 1995, *J. Immunol. Methods* 182:41-50; WO 92/22324; WO 98/46645). Chimeric antibodies can be produced using methods described in, e.g., Morrison, 1985, *Science* 229:1202, and humanized antibodies by methods described in, e.g., U.S. Pat. No. 6,180,370.

Additional reference antibodies described herein are bispecific antibodies and multivalent antibodies, as described in, e.g., Segal et al., *J. Immunol. Methods* 248:1-6 (2001); and Tutt et al., *J. Immunol.* 147: 60 (1991).

Glycoprotein Conjugates

The disclosure includes glycoproteins (or Fc regions or Fc fragments containing one or more N-glycosylation sites thereof) that are conjugated or fused to one or more heterologous moieties.

Heterologous moieties include, but are not limited to, peptides, polypeptides, proteins, fusion proteins, nucleic acid molecules, small molecules, mimetic agents, synthetic drugs, inorganic molecules, and organic molecules. In some instances, a glycoprotein conjugate is a fusion protein that comprises a peptide, polypeptide, protein scaffold, scFv, dsFv, diabody, Tandab, or an antibody mimetic fused to an Fc region, such as a glycosylated Fc region. A fusion protein can include a linker region connecting an Fc region to a heterologous moiety (see, e.g., Hallewell et al. (1989), *J. Biol. Chem.* 264, 5260-5268; Alfthan et al. (1995), *Protein Eng.* 8, 725-731; Robinson & Sauer (1996)).

Exemplary, nonlimiting reference glycoprotein conjugate products include abatacept (Orencia®, Bristol-Myers Squibb), aflibercept (Eylea®, Regeneron Pharmaceuticals), alefacept (Amevive®, Astellas Pharma), belatacept (Nulojix®, Bristol-Myers Squibb), denileukin diftitox (Ontak®, Eisai), etanercept (Enbrel®, Amgen-Pfizer), and rilonacept (Arcalyst®, Regeneron Pharmaceuticals).

In some instances, a glycoprotein conjugate includes an Fc region (or an Fc fragment containing one or more N-glycosylation sites thereof) conjugated to a heterologous polypeptide of at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90 or at least 100 amino acids.

In some instances, a glycoprotein conjugate includes an Fc region (or an Fc fragment containing one or more N-glycosylation sites thereof) conjugated to one or more marker sequences, such as a peptide to facilitate purification. A particular marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, Calif., 91311). Other peptide tags useful for purification include, but are not limited to, the hemagglutinin "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., 1984, *Cell* 37:767) and the "Flag" tag.

In other instances, a glycoprotein conjugate includes an Fc region (or Fc fragment containing one or more N-glycosylation sites thereof) conjugated to a diagnostic or detectable agent. Such fusion proteins can be useful for monitoring or prognosing development or progression of disease or disorder as part of a clinical testing procedure, such as determining efficacy of a particular therapy. Such diagnosis and detection can be accomplished by coupling a glycoprotein to detectable substances including, but not limited to, various enzymes, such as but not limited to horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; prosthetic groups, such as, but not limited to, streptavidin/biotin and avidin/biotin; fluorescent materials, such as, but not limited to, umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; luminescent materials, such as, but not limited to, luminol; bioluminescent materials, such as but not limited to, luciferase, luciferin, and aequorin; radioactive materials, such as but not limited to iodine (¹³¹I, ¹²⁵I, ¹²³I), carbon (¹⁴C), sulfur (³⁵S), tritium (³H), indium (¹¹⁵In, ¹¹³In, ¹¹²In, ¹¹¹In), technetium (⁹⁹Tc), thallium (²⁰¹Tl), gallium (⁶⁸Ga, ⁶⁷Ga), palladium (¹⁰³Pd), molybdenum (⁹⁹Mo), xenon (¹³³Xe), fluorine (¹⁸F), ¹⁵³Sm, ¹⁷⁷Lu, ¹⁵³Gd, ¹⁵⁹Gd, ¹⁴⁹Pm, ¹⁴⁰La, ¹⁶⁹Yb, ¹⁷⁵Yb, ¹⁶⁶Ho, ⁹⁰Y, ⁴⁷Sc, ¹⁸⁶Re, ¹⁸⁸Re, ¹⁴²Pr, ¹⁰⁵Rh, ⁹⁷Ru, ⁶⁸Ge, ⁵⁷Co, ⁶⁵Zn, ⁸⁵Sr, ³²P, ⁵¹Cr, ⁵⁴Mn, ⁷⁵Se, ¹¹³Sn, and ¹¹⁷Sn; positron emitting metals using various

positron emission tomographies, non-radioactive paramagnetic metal ions, and molecules that are radiolabelled or conjugated to specific radioisotopes.

Techniques for conjugating therapeutic moieties to antibodies are well known (see, e.g., Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al. (eds.), pp. 243-56. (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in *Controlled Drug Delivery (2nd Ed.)*, Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987)).

Sialyltransferase Polypeptides

Methods and compositions described herein include the use of a sialyltransferase enzyme, e.g., an α 2,6 sialyltransferase (e.g., ST6 Gal-I). A number of ST6 sialyltransferases are known in the art and are commercially available (see, e.g., Takashima, *Biosci. Biotechnol. Biochem.* 72:1155-1167 (2008); Weinstein et al., *J. Biol. Chem.* 262:17735-17743 (1987)). ST6 Gal-I catalyzes the transfer of sialic acid from a sialic acid donor (e.g., cytidine 5'-monophospho-N-acetyl neuraminic acid) to a terminal galactose residue of glycans through an α 2,6 linkage. The sialic acid donor reaction product is cytidine 5'-monophosphate. In some embodiments, an ST6 sialyltransferase has or includes an amino acid sequence set forth in SEQ ID NO:2, SEQ ID NO:3, or in amino acid residues 95-416 of SEQ ID NO:1, or a characteristic sequence element thereof or therein. In some embodiments, an ST6 sialyltransferase has at least 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80%, 79%, 78%, 77%, 76%, 75%, 74%, 73%, 72%, 71%, or 70% overall sequence identity with one or more of SEQ ID NO:2, SEQ ID NO:3, or amino acid residues 95-416 of SEQ ID NO:1. Alternatively or additionally, in some embodiments, an ST6 sialyltransferase includes at least about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, or 150 or more contiguous amino acid residues found in SEQ ID NO:2, SEQ ID NO:3, or amino acid residues 95-416 of SEQ ID NO:1.

In some embodiments, an ST6 sialyltransferase differs from an amino acid sequence as set forth in SEQ ID NO:2, SEQ ID NO:3, or in amino acid residues 95-416 of SEQ ID NO:1, or characteristic sequence elements thereof or therein, by one or more amino acid residues. For example, in some embodiments, the difference is a conservative or nonconservative substitution of one or more amino acid residues. Conservative substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of similar characteristics. Typical conservative substitutions are the following replacements: replacement of an aliphatic amino acid, such as alanine, valine, leucine, and isoleucine, with another aliphatic amino acid; replacement of a serine with a threonine or vice versa; replacement of an acidic residue, such as aspartic acid and glutamic acid, with another acidic residue; replacement of a residue bearing an amide group, such as asparagine and glutamine, with another residue bearing an amide group; exchange of a basic residue, such as lysine and arginine, with another basic residue; and replacement of an aromatic residue, such as phenylalanine and tyrosine, with another aromatic residue.

In some embodiments, an ST6 sialyltransferase polypeptide includes a substituent group on one or more amino acid residues. Still other useful polypeptides are associated with (e.g., fused, linked, or coupled to) another moiety (e.g., a peptide or molecule). For example, an ST6 sialyltransferase polypeptides can be fused, linked, or coupled to an amino acid sequence (e.g., a leader sequence, a

secretory sequence, a proprotein sequence, a second polypeptide, or a sequence that facilitates purification, enrichment, or stabilization of the polypeptide).

Methods of Sialylating Glycoproteins

5 ST6 Gal-I sialyltransferase catalyzes the transfer of sialic acid from a sialic acid donor (e.g., cytidine 5'-monophospho-N-acetyl neuraminic acid) to a terminal galactose residue of glycans through an α 2,6 linkage. The present disclosure exploits the discovery that ST6 sialyltransferase catalyzes the transfer of sialic acid to branched glycans (e.g., Fc branched glycans) comprising an α 1,3 arm and an α 1,6 arm in an ordered fashion. As shown in Figure 4, ST6 sialyltransferase transfers a sialic acid to an α 1,3 arm of a branched glycan, which can be followed by transfer of a second sialic acid to an α 1,6 arm (yielding a disialylated branched glycan), and can further be followed by removal of sialic acid from an α 1,3 arm (yielding a branched glycan having a sialic acid on an α 1,6 arm). Accordingly, by controlling and/or modulating activity (e.g., kinetics) of ST6 sialyltransferase, glycoproteins having particular sialylation patterns can be produced.

15 Any parameter generally known to affect enzyme kinetics can be controlled and/or modulated to produce a glycoprotein preparation having a predetermined or target level of sialic acid on an α 1,3 arm of a branched glycan, on an α 1,6 arm of a branched glycan, and/or on an α 1,3 arm and an α 1,6 arm of a branched glycan. For example, reaction time, ST6 sialyltransferase concentration and/or specific activity, branched glycan concentration, sialic acid donor concentration, sialic acid donor reaction product concentration, pH, buffer composition, and/or temperature can be controlled and/or modulated to produce a glycoprotein preparation having a desired level of sialylation (e.g., α 1,3 arm and/or α 1,6 arm sialylation).

20 In some embodiments, to preferentially sialylate an α 1,3 arm of branched glycans (e.g., having an α 1,3 arm and an α 1,6 arm), branched glycans are contacted in vitro with an ST6 sialyltransferase under limited reaction conditions. Such limited reaction conditions are selected such that addition of a sialic acid to an α 1,3 arm is enhanced relative to addition of a sialic acid to an α 1,6 arm (e.g., rate of transfer of a sialic acid to an α 1,3 arm (" $R_a^{1,3}$ ") exceeds rate of transfer of a sialic acid to an α 1,6 arm (" $R_a^{1,6}$ "). In some embodiments, limited reaction conditions are further selected such that removal of a sialic acid from an α 1,6 arm is enhanced relative to addition of a sialic acid to an α 1,6 arm (e.g., rate of removal of a sialic acid from an α 1,6 arm (" $R_r^{1,6}$ ") exceeds rate of transfer of a sialic acid to an α 1,6 arm (" $R_a^{1,6}$ "). Limited reaction conditions can include, for example, reduced reaction time, reduced enzyme concentration and/or activity, reduced amount of branched glycans, reduced level of sialic acid donor, and/or reduced temperature.

25 In some embodiments, to preferentially sialylate an α 1,6 arm of branched glycans (e.g., having an α 1,3 arm and an α 1,6 arm), branched glycans can be contacted in vitro with an ST6 sialyltransferase under extended reaction conditions. Such extended reaction conditions are selected such that addition of a sialic acid to an α 1,6 arm is enhanced relative to removal of a sialic acid from an α 1,6 arm (e.g., rate of transfer of a sialic acid to an α 1,6 arm (" $R_a^{1,6}$ ") exceeds rate of removal of a sialic acid from an α 1,6 arm (" $R_r^{1,6}$ "). In some embodiments, extended reaction conditions are further selected such that, after initial conditions that enhance addition of sialic acid to an α 1,3 arm, conditions are extended such that removal of a sialic acid from an α 1,3 arm is eventually enhanced relative to addition of a sialic acid to an α 1,3 arm (e.g., rate of removal of a sialic acid from an α 1,3 arm (" $R_r^{1,3}$ ") exceeds rate of transfer of a sialic acid to

an α 1,3 arm ("R_a^{1,3}"). Extended reaction conditions can include, for example, increased reaction time, increased enzyme concentration and/or activity, increased amount of branched glycans, increased level of sialic acid donor, and/or increased temperature.

5 In some embodiments, to preferentially sialylate both an α 1,3 arm and an α 1,6 arm of branched glycans (e.g., having an α 1,3 arm and an α 1,6 arm), branched glycans are contacted in vitro with an ST6 sialyltransferase under intermediate reaction conditions. Such intermediate reaction conditions are selected such that addition of a sialic acid to an α 1,3 arm is enhanced relative to removal of a sialic acid from an α 1,3 arm (e.g., rate of transfer of a sialic acid to an α 1,3 arm ("R_a^{1,3}") exceeds rate of removal of a sialic acid from an α 1,3 arm ("R_r^{1,3}"). In some embodiments, intermediate reaction conditions are further
10 selected such that addition of a sialic acid to an α 1,6 arm is enhanced relative to removal of a sialic acid from an α 1,6 arm (e.g., rate of addition of a sialic acid to an α 1,6 arm ("R_a^{1,6}") exceeds rate of removal of a sialic acid from an α 1,6 arm ("R_r^{1,6}"). Intermediate reaction conditions can include, for example, intermediate reaction time, intermediate enzyme concentration and/or activity, intermediate amount of branched glycans, intermediate level of sialic acid donor, and/or intermediate temperature. In some
15 embodiments, intermediate reaction conditions further include supplementing the sialic acid donor at least once during the reaction. In some embodiments, intermediate reaction conditions further include removing a sialic acid donor reaction product at least once during the reaction. In some embodiments, intermediate reaction conditions further include supplementing the sialic acid donor reaction product at least once during the reaction.

20 In some embodiments, a glycoprotein, e.g., a glycosylated antibody, is sialylated after the glycoprotein is produced. For example, a glycoprotein can be recombinantly expressed in a host cell (as described herein) and purified using standard methods. The purified glycoprotein is then contacted with an ST6 sialyltransferase (e.g., a recombinantly expressed and purified ST6 sialyltransferase) in the presence of reaction conditions as described herein. In certain embodiments, the conditions include
25 contacting the purified glycoprotein with an ST6 sialyltransferase in the presence of a sialic acid donor, e.g., cytidine 5'-monophospho-N-acetyl neuraminic acid, manganese, and/or other divalent metal ions. In some embodiments, IVIG is used in a sialylation method described herein.

In some embodiments, chemoenzymatic sialylation is used to sialylate glycoproteins. Briefly, this method involves sialylation of a purified branched glycan, followed by incorporation of the sialylated
30 branched glycan en bloc onto a polypeptide to produce a sialylated glycoprotein.

A branched glycan can be synthesized de novo using standard techniques or can be obtained from a glycoprotein preparation (e.g., a recombinant glycoprotein, Fc, or IVIG) using an appropriate enzyme, such as an endoglycosidase (e.g., EndoH or EndoF). After sialylation of the branched glycan, the sialylated branched glycan can be conjugated to a polypeptide using an appropriate enzyme, such as
35 a transglycosidase, to produce a sialylated glycoprotein.

In one exemplary method, a purified branched N-glycan is obtained from a glycoprotein (e.g., a glycoprotein preparation, e.g., IVIG) using an endoglycosidase. The purified branched N-glycan is then chemically activated on the reducing end to form a chemically active intermediate. The branched N-glycan is then further processed, trimmed, and/or glycosylated using appropriate known glycosidases.
40 The branched glycan is then sialylated using an ST6 sialylation as described herein. After engineering,

the desired branched N-glycan is transferred onto a glycoprotein using a transglycosidase (such as a transglycosidase in which glycosidic activity has been attenuated using genetically engineering).

5 In some embodiments, a branched glycan used in methods described herein is a galactosylated branched glycan (e.g., includes a terminal galactose residue). In some embodiments, a branched glycan is galactosylated before being sialylated using a method described herein. In some embodiments, a branched glycan is first contacted with a galactosyltransferase (e.g., a beta-1,3-galactosyltransferase) and subsequently contacted with an ST6 sialyltransferase as described herein. In some embodiments, a galactosylated glycan is purified before being contacted with an ST6
10 sialyltransferase. In some embodiments, a branched glycan is contacted with a galactosyltransferase and an ST6 sialyltransferase in a single step.

In some embodiments, a host cell is genetically engineered to express a glycoprotein described herein and one or more sialyltransferase enzymes, e.g., an ST6 sialyltransferase. In some embodiments, the host cell is genetically engineered to further express a galactosyltransferase. The genetically
15 engineered host cell can be cultured under conditions sufficient to produce a particular sialylated glycoprotein. For example, to produce glycoproteins preferentially sialylated on α 1,3 arms of branched glycans, a host cell can be genetically engineered to express a relatively low level of ST6 sialyltransferase, whereas to produce glycoproteins preferentially sialylated on α 1,6 arms of branched glycans, a host cell can be genetically engineered to express a relatively high level of ST6
20 sialyltransferase. In some embodiments, to produce glycoproteins preferentially sialylated on α 1,3 arms of branched glycans, a genetically engineered host cell can be cultured in a relatively low level of sialic acid donor, whereas to produce glycoproteins preferentially sialylated on α 1,6 arms of branched glycans, a genetically engineered host cell can be cultured in a relatively high level of sialic acid donor.

25 Recombinant Gene Expression

In accordance with the present disclosure, there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are described in the literature (see, e.g., Green & Sambrook, *Molecular Cloning: A Laboratory Manual*, Fourth Edition (2012) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.; *DNA Cloning: A Practical
30 Approach*, Volumes I-IV (D. N. Glover ed. 1995; 1996); *Oligonucleotide Synthesis* (M. J. Gait ed. 1984); *Nucleic Acid Hybridisation* (B. D. Hames & S. J. Higgins eds. (1985)); *Transcription And Translation* (B. D. Hames & S. J. Higgins, eds. (1984)); *Culture of Animal Cells*, Sixth Edition (R. I. Freshney, ed. (2010)); *Immobilized Cells and Enzymes* (IRL Press, (1986)); B. Perbal, *A Practical Guide To Molecular Cloning*, Second Edition (1988); F. M. Ausubel et al. (eds.), *Current Protocols in Molecular Biology*, John Wiley &
35 Sons, Inc. (1995).

Recombinant expression of a gene, such as a gene encoding a polypeptide, such as an antibody or a sialyltransferase described herein, can include construction of an expression vector containing a polynucleotide that encodes the polypeptide. Once a polynucleotide has been obtained, a vector for the production of the polypeptide can be produced by recombinant DNA technology using techniques known
40 in the art. Known methods can be used to construct expression vectors containing polypeptide coding

sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination.

An expression vector can be transferred to a host cell by conventional techniques, and the transfected cells can then be cultured by conventional techniques to produce polypeptide.

5 A variety of host expression vector systems can be used (see, e.g., U.S. Pat. No. 5,807,715). Such host-expression systems can be used to produce polypeptides and, where desired, subsequently purified. Such host expression systems include microorganisms such as bacteria (e.g., *E. coli* and *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing polypeptide coding sequences; yeast (e.g., *Saccharomyces* and *Pichia*) transformed
10 with recombinant yeast expression vectors containing polypeptide coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing polypeptide coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g. Ti plasmid) containing polypeptide coding sequences; or mammalian cell systems (e.g.,
15 COS, CHO, BHK, 293, NS0, and 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter).

For bacterial systems, a number of expression vectors can be used, including, but not limited to, the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO 12:1791); pIN vectors (Inouye & Inouye,
20 1985, Nucleic Acids Res. 13:3101-3109; Van Heeke & Schuster, 1989, J. Biol. Chem. 24:5503-5509); and the like. pGEX vectors can also be used to express foreign polypeptides as fusion proteins with glutathione 5-transferase (GST).

For expression in mammalian host cells, viral-based expression systems can be utilized (see, e.g., Logan & Shenk, 1984, Proc. Natl. Acad. Sci. USA 81:355-359). The efficiency of expression can be
25 enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see, e.g., Bittner et al., 1987, Methods in Enzymol. 153:516-544).

In addition, a host cell strain can be chosen that modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification
30 of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the polypeptide expressed. Such cells include, for example, established mammalian cell lines and insect cell lines, animal cells, fungal cells, and yeast cells. Mammalian host cells include, but are not limited to, CHO, VERY, BHK, HeLa, COS, MDCK, 293, 3T3, W138, BT483, Hs578T, HTB2, BT20 and T47D, NS0 (a murine myeloma cell line that does not
35 endogenously produce any immunoglobulin chains), CRL7030 and HsS78Bst cells.

For long-term, high-yield production of recombinant proteins, host cells are engineered to stably express a polypeptide. Host cells can be transformed with DNA controlled by appropriate expression control elements known in the art, including promoter, enhancer, sequences, transcription terminators, polyadenylation sites, and selectable markers. Methods commonly known in the art of recombinant DNA
40 technology can be used to select a desired recombinant clone.

Once a glycoprotein described herein been produced by recombinant expression, it may be purified by any method known in the art for purification, for example, by chromatography (e.g., ion exchange, affinity, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. For example, an antibody can be isolated and purified by appropriately selecting and combining affinity columns such as Protein A column with chromatography columns, filtration, ultra filtration, salting-out and dialysis procedures (see *Antibodies: A Laboratory Manual*, Ed Harlow, David Lane, Cold Spring Harbor Laboratory, 1988). Further, as described herein, a glycoprotein can be fused to heterologous polypeptide sequences to facilitate purification. Glycoproteins having desired sugar chains can be separated with a lectin column by methods known in the art (see, e.g., WO 02/30954).

Glycan Evaluation

Glycans of glycoproteins can be evaluated using any methods known in the art. For example, sialylation of glycan compositions (e.g., level of branched glycans that are sialylated on an α 1,3 arm and/or an α 1,6 arm) can be characterized using methods described in, e.g., Barb, *Biochemistry* 48:9705–9707 (2009); Anumula, *J. Immunol. Methods* 382:167–176 (2012); Gilar et al., *Analytical Biochem.* 417:80-88 (2011); Wuhler et al., *J. Chromatogr. B.* 849:115-128 (2007). In some embodiments, in addition to evaluation of sialylation of glycans, one or more parameters described in Table 1 are evaluated.

In some instances, glycan structure and composition as described herein are analyzed, for example, by one or more, enzymatic, chromatographic, mass spectrometry (MS), chromatographic followed by MS, electrophoretic methods, electrophoretic methods followed by MS, nuclear magnetic resonance (NMR) methods, and combinations thereof. Exemplary enzymatic methods include contacting a glycoprotein preparation with one or more enzymes under conditions and for a time sufficient to release one or more glycan(s) (e.g., one or more exposed glycan(s)). In some instances, the one or more enzymes include(s) PNGase F. Exemplary chromatographic methods include, but are not limited to, Strong Anion Exchange chromatography using Pulsed Amperometric Detection (SAX-PAD), liquid chromatography (LC), high performance liquid chromatography (HPLC), ultra performance liquid chromatography (UPLC), thin layer chromatography (TLC), amide column chromatography, and combinations thereof. Exemplary mass spectrometry (MS) include, but are not limited to, tandem MS, LC-MS, LC-MS/MS, matrix assisted laser desorption ionisation mass spectrometry (MALDI-MS), Fourier transform mass spectrometry (FTMS), ion mobility separation with mass spectrometry (IMS-MS), electron transfer dissociation (ETD-MS), and combinations thereof. Exemplary electrophoretic methods include, but are not limited to, capillary electrophoresis (CE), CE-MS, gel electrophoresis, agarose gel electrophoresis, acrylamide gel electrophoresis, SDS-polyacrylamide gel electrophoresis (SDS-PAGE) followed by Western blotting using antibodies that recognize specific glycan structures, and combinations thereof. Exemplary nuclear magnetic resonance (NMR) include, but are not limited to, one-dimensional NMR (1D-NMR), two-dimensional NMR (2D-NMR), correlation spectroscopy magnetic-angle spinning NMR (COSY-NMR), total correlated spectroscopy NMR (TOCSY-NMR), heteronuclear single-quantum coherence NMR (HSQC-NMR), heteronuclear multiple quantum coherence (HMQC-NMR), rotational

nuclear overhauser effect spectroscopy NMR (ROESY-NMR), nuclear overhauser effect spectroscopy (NOESY-NMR), and combinations thereof.

In some instances, techniques described herein may be combined with one or more other technologies for the detection, analysis, and or isolation of glycans or glycoproteins. For example, in certain instances, glycans are analyzed in accordance with the present disclosure using one or more available methods (to give but a few examples, see Anumula, *Anal. Biochem.*, 350(1):1, 2006; Klein et al., *Anal. Biochem.*, 179:162, 1989; and/or Townsend, R.R. *Carbohydrate Analysis" High Performance Liquid Chromatography and Capillary Electrophoresis.*, Ed. Z. El Rassi, pp 181-209, 1995; WO2008/128216; WO2008/128220; WO2008/128218; WO2008/130926; WO2008/128225; WO2008/130924; WO2008/128221; WO2008/128228; WO2008/128227; WO2008/128230; WO2008/128219; WO2008/128222; WO2010/071817; WO2010/071824; WO2010/085251; WO2011/069056; and WO2011/127322, each of which is incorporated herein by reference in its entirety). For example, in some instances, glycans are characterized using one or more of chromatographic methods, electrophoretic methods, nuclear magnetic resonance methods, and combinations thereof. In some instances, methods for evaluating one or more target protein specific parameters, e.g., in a glycoprotein preparation, e.g., one or more of the parameters disclosed herein, can be performed by one or more of following methods.

In some instances, methods for evaluating one or more target protein specific parameters, e.g., in a glycoprotein preparation, e.g., one or more of the parameters disclosed herein, can be performed by one or more of following methods.

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Table 1: Exemplary methods of evaluating parameters:

Method(s)	Relevant literature	Parameter
C18 UPLC Mass Spec.*	Chen and Flynn, <i>Anal. Biochem.</i> , 370:147-161 (2007) Chen and Flynn, <i>J. Am. Soc. Mass Spectrom.</i> , 20:1821-1833 (2009)	Glycan(s) (e.g., N-linked glycan, exposed N-linked glycan, glycan detection, glycan identification, and characterization; site specific glycation; glycoform detection (e.g., parameters 1-7); percent glycosylation; and/or aglycosyl)

Peptide LC-MS (reducing/non-reducing)	Dick et al., Biotechnol. Bioeng., 100:1132-1143 (2008) Yan et al., J. Chrom. A., 1164:153-161 (2007) Chelius et al., Anal. Chem., 78:2370- 2376 (2006) Miller et al., J. Pharm. Sci., 100:2543- 2550 (2011)	C-terminal lysine
LC-MS (reducing/non- reducing/alkylated)	Dick et al., Biotechnol. Bioeng., 100:1132-1143 (2008) Goetze et al., Glycobiol., 21:949-959 (2011)	
Weak cation exchange (WCX) chromatography	Dick et al., Biotechnol. Bioeng., 100:1132-1143 (2008)	
LC-MS (reducing/non- reducing/alkylated)	Dick et al., Biotechnol. Bioeng., 100:1132-1143 (2008) Goetze et al., Glycobiol., 21:949-959 (2011)	
Peptide LC-MS (reducing/non-reducing)	Yan et al., J. Chrom. A., 1164:153-161 (2007) Chelius et al., Anal. Chem., 78:2370- 2376 (2006) Miller et al., J. Pharm. Sci., 100:2543- 2550 (2011)	N-terminal pyroglu
Peptide LC-MS (reducing/non-reducing)	Yan et al., J. Chrom. A., 1164:153-161 (2007); Xie et al., mAbs, 2:379-394 (2010)	Methionine oxidation
Peptide LC-MS (reducing/non-reducing)	Miller et al., J. Pharm. Sci., 100:2543- 2550 (2011)	Site specific glycation
Peptide LC-MS (reducing/non-reducing)	Wang et al., Anal. Chem., 83:3133-3140 (2011); Chumsae et al., Anal. Chem., 81:6449- 6457 (2009)	Free cysteine
Bioanalyzer (reducing/non-reducing)*	Forrer et al., Anal. Biochem., 334:81-88 (2004)	Glycan (e.g., N-linked glycan, exposed N-linked glycan)

		(including, for example, glycan detection, identification, and characterization; site specific glycation; glycoform detection; percent glycosylation; and/or aglycosyl)
LC-MS (reducing/non-reducing/alkylated)* * Methods include removal (e.g., enzymatic, chemical, and physical) of glycans	Dick et al., <i>Biotechnol. Bioeng.</i> , 100:1132-1143 (2008) Goetze et al., <i>Glycobiol.</i> , 21:949-959 (2011) Xie et al., <i>mAbs</i> , 2:379-394 (2010)	Glycan (e.g., N-linked glycan, exposed N-linked glycan) (including, for example, glycan detection, identification, and characterization; site specific glycation; glycoform detection; percent glycosylation; and/or aglycosyl)
Bioanalyzer (reducing/non-reducing)	Forrer et al., <i>Anal. Biochem.</i> , 334:81-88 (2004)	Light chain : Heavy chain
Peptide LC-MS (reducing/non-reducing)	Yan et al., <i>J. Chrom. A.</i> , 1164:153-161 (2007) Chelius et al., <i>Anal. Chem.</i> , 78:2370-2376 (2006) Miller et al., <i>J. Pharm. Sci.</i> , 100:2543-2550 (2011)	Non-glycosylation-related peptide modifications (including, for example, sequence analysis and identification of sequence variants; oxidation; succinimide; aspartic acid; and/or site-specific aspartic acid)
Weak cation exchange (WCX) chromatography	Dick et al., <i>Biotechnol. Bioeng.</i> , 100:1132-1143 (2008)	Isoforms (including, for example, charge variants (acidic variants and basic variants); and/or deamidated variants)
Anion-exchange chromatography	Ahn et al., <i>J. Chrom. B</i> , 878:403-408 (2010)	Sialylated glycan
Anion-exchange chromatography	Ahn et al., <i>J. Chrom. B</i> , 878:403-408 (2010)	Sulfated glycan
1,2-diamino-4,5- methylenedioxybenzene (DMB) labeling method	Hokke et al., <i>FEBS Lett.</i> , 275:9-14 (1990)	Sialic acid
LC-MS	Johnson et al., <i>Anal. Biochem.</i> , 360:75-83 (2007)	C-terminal amidation
LC-MS	Johnson et al., <i>Anal. Biochem.</i> , 360:75-83 (2007)	N-terminal fragmentation

Circular dichroism spectroscopy	Harn et al., Current Trends in Monoclonal Antibody Development and Manufacturing, S. J. Shire et al., eds, 229-246 (2010)	Secondary structure (including, for example, alpha helix content and/or beta sheet content)
Intrinsic and/or ANS dye fluorescence	Harn et al., Current Trends in Monoclonal Antibody Development and Manufacturing, S. J. Shire et al., eds, 229-246 (2010)	Tertiary structure (including, for example, extent of protein folding)
Hydrogen-deuterium exchange-MS	Houde et al., Anal. Chem., 81:2644-2651 (2009)	Tertiary structure and dynamics (including, for example, accessibility of amide protons to solvent water)
Size-exclusion chromatography	Carpenter et al., J. Pharm. Sci., 99:2200-2208 (2010)	Extent of aggregation
Analytical ultracentrifugation	Pekar and Sukumar, Anal. Biochem., 367:225-237 (2007)	

The literature recited above are hereby incorporated by reference in their entirety or, in the alternative, to the extent that they pertain to one or more of the methods for determining a parameter described herein.

5 Glycoprotein Properties

Sialylation patterns of glycoproteins can affect their anti-inflammatory properties. Accordingly, in some embodiments, methods described herein are useful for producing glycoproteins with particular levels of anti-inflammatory properties. In some embodiments, methods described herein are used to produce Fc region-containing glycoproteins containing sialic acid on α 1,3 arms of branched glycans with a NeuAc- α 2,6-Gal terminal linkages and that exhibit increased anti-inflammatory activity relative to a reference glycoprotein, e.g., a level of anti-inflammatory activity that is at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, at least 125%, at least 150%, at least 175%, at least 200%, at least 250%, at least 300%, or higher, relative to a reference glycoprotein.

15 In some embodiments, methods described herein are used to produce Fc region-containing glycoproteins having sialic acids on α 1,6 arms or on both α 1,3 and α 1,6 arms of branched glycans that have the same or alternate properties or biological activities in different disease states.

Pharmaceutical Compositions and Administration

20 A glycoprotein of the present disclosure (e.g., an Fc region-containing glycoprotein comprising branched glycans that are sialylated on an α 1,3 arm, an α 1,6 arm, or both, of the branched glycan in the Fc region, e.g., with a NeuAc- α 2,6-Gal terminal linkage), can be incorporated into a pharmaceutical composition. In some embodiments, such a pharmaceutical composition is useful as an improved composition for the prevention and/or treatment of diseases relative to the corresponding reference

glycoprotein. Pharmaceutical compositions comprising a glycoprotein can be formulated by methods known to those skilled in the art. The pharmaceutical composition can be administered parenterally in the form of an injectable formulation comprising a sterile solution or suspension in water or another pharmaceutically acceptable liquid. For example, the pharmaceutical composition can be formulated by suitably combining the sialylated glycoprotein with pharmaceutically acceptable vehicles or media, such as sterile water and physiological saline, vegetable oil, emulsifier, suspension agent, surfactant, stabilizer, flavoring excipient, diluent, vehicle, preservative, binder, followed by mixing in a unit dose form required for generally accepted pharmaceutical practices. The amount of active ingredient included in the pharmaceutical preparations is such that a suitable dose within the designated range is provided.

The sterile composition for injection can be formulated in accordance with conventional pharmaceutical practices using distilled water for injection as a vehicle. For example, physiological saline or an isotonic solution containing glucose and other supplements such as D-sorbitol, D-mannose, D-mannitol, and sodium chloride may be used as an aqueous solution for injection, optionally in combination with a suitable solubilizing agent, for example, alcohol such as ethanol and polyalcohol such as propylene glycol or polyethylene glycol, and a nonionic surfactant such as polysorbate 80™, HCO-50 and the like.

Nonlimiting examples of oily liquid include sesame oil and soybean oil, and it may be combined with benzyl benzoate or benzyl alcohol as a solubilizing agent. Other items that may be included are a buffer such as a phosphate buffer, or sodium acetate buffer, a soothing agent such as procaine hydrochloride, a stabilizer such as benzyl alcohol or phenol, and an antioxidant. The formulated injection can be packaged in a suitable ampule.

In some instances, the level of sialylated glycans (e.g., branched glycans that are sialylated on an α 1,3 arm, an α 1,6 arm, or both, of the branched glycan in the Fc region, e.g., with a NeuAc- α 2,6-Gal terminal linkage) in a preparation of antibodies or Fc-containing polypeptides, produced using a method described herein can be compared to a predetermined or target level (e.g., a level in a reference standard or pharmaceutical specification), e.g., to make a decision regarding the composition of the polypeptide preparation, e.g., a decision to classify, select, accept or discard, release or withhold, process into a drug product, ship, move to a different location, formulate, label, package, release into commerce, or sell or offer for sale the polypeptide, e.g., a recombinant antibody. In other instances, the decision can be to accept, modify or reject a production parameter or parameters used to make the polypeptide, e.g., an antibody. Particular, nonlimiting examples of reference standards include a control level (e.g., a polypeptide produced by a different method) or a range or value in a product specification (e.g., a master batch record, a release specification, an FDA label or Physician's Insert) or quality or identity criterion for a pharmaceutical preparation containing the polypeptide preparation.

In some instances, methods (i.e., evaluation, identification, and production methods) include taking action (e.g., physical action) in response to the methods disclosed herein. For example, a polypeptide preparation is classified, selected, accepted or discarded, released or withheld, processed into a drug product, shipped, moved to a different location, formulated, labeled, packaged, released into commerce, or sold or offered for sale, depending on whether the preselected or target value is met. In some instances, processing may include formulating (e.g., combining with pharmaceutical excipients), packaging (e.g., in a syringe or vial), labeling, or shipping at least a portion of the polypeptide preparation. In some instances, processing includes formulating (e.g., combining with pharmaceutical excipients),

packaging (e.g., in a syringe or vial), and labeling at least a portion of the preparation as a drug product described herein. Processing can include directing and/or contracting another party to process as described herein.

5 In some instances, a biological activity of a polypeptide preparation (e.g., an antibody preparation) is assessed. Biological activity of the preparation can be analyzed by any known method. In some embodiments, a binding activity of a polypeptide is assessed (e.g., binding to a receptor). In some
10 embodiments, a therapeutic activity of a polypeptide is assessed (e.g., an activity of a polypeptide in decreasing severity or symptom of a disease or condition, or in delaying appearance of a symptom of a disease or condition). In some embodiments, a pharmacologic activity of a polypeptide is assessed (e.g., bioavailability, pharmacokinetics, pharmacodynamics). For methods of analyzing bioavailability,
15 pharmacokinetics, and pharmacodynamics of glycoprotein therapeutics, see, e.g., Weiner et al., J. Pharm. Biomed. Anal. 15(5):571-9, 1997; Srinivas et al., J. Pharm. Sci. 85(1):1-4, 1996; and Srinivas et al., Pharm. Res. 14(7):911-6, 1997.

15 The particular biological activity or therapeutic activity that can be tested will vary depending on the particular polypeptide (e.g., antibody). The potential adverse activity or toxicity (e.g., propensity to cause hypertension, allergic reactions, thrombotic events, seizures, or other adverse events) of polypeptide preparations can be analyzed by any available method. In some embodiments, immunogenicity of a polypeptide preparation is assessed, e.g., by determining whether the preparation elicits an antibody response in a subject.

20 Route of administration can be parenteral, for example, administration by injection, transnasal administration, transpulmonary administration, or transcutaneous administration. Administration can be systemic or local by intravenous injection, intramuscular injection, intraperitoneal injection, subcutaneous injection.

25 A suitable means of administration can be selected based on the age and condition of the patient. A single dose of the pharmaceutical composition containing a modified glycoprotein can be selected from a range of 0.001 to 1000 mg/kg of body weight. On the other hand, a dose can be selected in the range of 0.001 to 100000 mg/body weight, but the present disclosure is not limited to such ranges. The dose and method of administration varies depending on the weight, age, condition, and the like of the patient, and can be suitably selected as needed by those skilled in the art.

30 All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting. 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
35 herein can be used in the practice or testing of the present invention, suitable methods and materials are described herein.

EXAMPLES

40 Example 1 – Galactosylation and sialylation of IVIG

The sialylation of IVIG by the sialyltransferase ST6 was analyzed. IVIG was first galactosylated and then sialylated. The reactions were performed sequentially. There was no purification between galactosylation and sialylation reactions. The relative abundance of glycoforms was analyzed following the sialylation reactions.

5 A. Galactosylation

A reaction was set up that contained the following components at the concentrations indicated:

Constituent	Final concentration
MOPS (pH 7.4)	25 mM
MnCl ₂	10 mM
IVIG	12.5 mg/ml
B4GalT1 (90 u/ml)	400 mu/ml
UDP-Galactose	50 mM

The reaction was incubated for 72 hours at 37 °C.

B. Sialylation

10 To an aliquot of the galactosylation reaction were added CMP-NANA, MOPS buffer and ST6Gal1. The final volume was adjusted so that the final concentration of components in the reaction was as indicated.

Constituent	Final concentration
MOPS (pH 7.4)	50 mM
MnCl ₂	8 mM
IVIG	10 mg/ml
CMP-NANA	20 mM
ST6Gal1 (SEQ ID NO:1)	0.6 mg ST6 /mg IVIG

15 The reaction was incubated at 37 °C. Aliquots were extracted at the times indicated in Figure 2 and frozen at -20 °C for later analyses.

C. Results

20 As shown in Figure 3, the predominant glycoform changed over time from G2F to A1F (1,3) to A2F to A1F (1,6). The results are summarized in the reaction scheme depicted in Figure 4. As shown in Figure 4, the product glycoform can change between G2F, A1F (1,3), A2F, and A1F (1,6) during the course of a reaction due to competing addition (forward reaction) and removal (back reaction) steps.

The sialyltransferase ST6 can add sialic acid to either branch of a substrate's biantennary N-glycan. However, these results demonstrate that addition to each branch happens at different rates,

resulting in different end products depending on the reaction conditions. Addition of sialic acid to the α 1,3 branch is much faster than addition to the α 1,6 branch.

5 These data also demonstrate that sialyltransferase ST6 can also catalyze the removal of sialic acids from N-glycans. The removal of sialic acid from the α 1,3 branch is much faster than removal from the α 1,6 branch. This can surprisingly lead to the production of Fc glycans substantially or primarily monosialylated on the α 1,6 branch by modulating reaction conditions.

10 This Example demonstrates that reaction conditions can be controlled to produce a glycoprotein product having a predetermined or target sialylation levels. Such conditions can include time, ST6 sialyltransferase concentration, substrate concentration, donor sugar nucleotide concentration, product nucleotide concentration, pH, buffer composition, and/or temperature.

CLAIMS

1. A method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of branched glycans having a sialic acid on an α 1,3 arm and/or (ii) a target level of branched glycans having a sialic acid on an α 1,6 arm, the method comprising:
 - providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; and
 - contacting the glycoproteins with an ST6 sialyltransferase in the presence of a limited reaction condition, thereby producing a glycoprotein preparation having (i) the target level of branched glycans having a sialic acid on the α 1,3 arm and/or (ii) the target level of branched glycans having a sialic acid on an α 1,6 arm.
2. The method of claim 1, wherein the limited reaction condition is sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm of a branched glycan and not sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,6 arm of a branched glycan.
3. The method of claim 1, further comprising isolating the glycoprotein preparation.
4. The method of claim 3, further comprising measuring a level of branched glycans comprising a sialic acid on an α 1,3 arm and/or measuring a level of branched glycans having a sialic acid on an α 1,6 arm.
5. The method of claim 1, wherein the target level of branched glycans having a sialic acid on an α 1,3 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of sialylated branched glycans.
6. The method of claim 1, wherein the target level of branched glycans having a sialic acid on an α 1,6 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of sialylated branched glycans.
7. The method of claim 1, wherein the limited reaction condition is selected using a method comprising:
 - a) contacting the glycoproteins with an ST6 sialyltransferase in the presence of a first reaction condition;
 - b) measuring a first level of branched glycans comprising a sialic acid on an α 1,3 arm and/or branched glycans comprising a sialic acid on an α 1,6 arm after the first reaction condition;
 - c) contacting the glycoproteins with the ST6 sialyltransferase in the presence of a second reaction condition; and
 - d) measuring a second level of branched glycans comprising a sialic acid on an α 1,3 arm and/or branched glycans comprising a sialic acid on an α 1,6 arm after the second reaction condition;

wherein the first reaction condition is selected as the limited reaction condition if the first level of branched glycans comprising a sialic acid on an α 1,3 arm is higher than the second level of branched glycans comprising a sialic acid on an α 1,3 arm; and/or the first level of branched glycans comprising a sialic acid on an α 1,6 arm is lower than the second level of branched glycans comprising a sialic acid on an α 1,6 arm.

8. The method of claim 7, wherein the first reaction condition is selected from one or more of:
 - a shorter reaction time relative to the second reaction condition;
 - a lower ST6 sialyltransferase concentration and/or specific activity relative to the second reaction condition;
 - a lower temperature relative to the second reaction condition; and
 - a lower concentration of a sialic acid donor relative to the second reaction condition.
9. The method of claim 1, wherein the limited reaction condition is selected from one or more of:
 - a shorter reaction time relative a control reaction condition;
 - a lower ST6 sialyltransferase concentration and/or specific activity relative to a control reaction condition;
 - a lower temperature relative to a control reaction condition; and
 - a lower concentration of a sialic acid donor relative to a control reaction condition.
10. The method of claim 1, wherein the ST6 sialyltransferase has at least 90% identity to amino acid residues 95-416 of SEQ ID NO:1, at least 90% identity to SEQ ID NO:2, or at least 90% identity to SEQ ID NO:3.
11. A method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of branched glycans having a sialic acid on an α 1,6 arm and/or (ii) a target level of branched glycans having a sialic acid on an α 1,3 arm, the method comprising:
 - providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; and
 - contacting the glycoproteins with an ST6 sialyltransferase in the presence of an extended reaction condition, thereby producing a glycoprotein preparation having (i) the target level of branched glycans having a sialic acid on the α 1,6 arm and/or (ii) the target level of branched glycans having a sialic acid on an α 1,3 arm.
12. The method of claim 11, wherein the extended reaction condition is sufficient for the ST6 sialyltransferase substantially to remove a sialic acid from an α 1,3 arm of a disialylated branched glycan comprising a sialic acid on an α 1,3 arm and an α 1,6 arm.
13. The method of claim 11, further comprising isolating the glycoprotein preparation.

14. The method of claim 13, further comprising measuring a level of branched glycans comprising a sialic acid on an α 1,6 arm and/or a level of branched glycans having a sialic acid on an α 1,3 arm.
15. The method of claim 11, wherein the target level of branched glycans having a sialic acid on an α 1,6 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of sialylated branched glycans.
16. The method of claim 11, wherein the target level of branched glycans having a sialic acid on an α 1,3 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of sialylated branched glycans.
17. The method of claim 11, wherein the extended reaction condition is selected using a method comprising:
- contacting the glycoproteins with an ST6 sialyltransferase in the presence of a first reaction condition;
 - measuring a first level of branched glycans comprising a sialic acid on an α 1,6 arm and/or branched glycans comprising a sialic acid on an α 1,3 arm after the first reaction condition;
 - contacting the glycoproteins with the ST6 sialyltransferase in the presence of a second reaction condition; and
 - measuring a second level of branched glycans comprising a sialic acid on an α 1,6 arm and/or branched glycans comprising a sialic acid on an α 1,3 arm after the second reaction condition;
- wherein the second reaction condition is selected as the extended reaction condition if the second level of branched glycans comprising a sialic acid on an α 1,6 arm is higher than the first level of branched glycans comprising a sialic acid on an α 1,6 arm; and/or the second level of branched glycans comprising a sialic acid on an α 1,3 arm is lower than the first level of branched glycans comprising a sialic acid on an α 1,3 arm.
18. The method of claim 17, wherein the second reaction condition is selected from one or more of:
- a greater reaction time relative to the first reaction condition;
 - a higher ST6 sialyltransferase concentration and/or specific activity relative to the first reaction condition;
 - a higher temperature relative to the first reaction condition; and
 - a higher concentration of a sialic acid donor relative to the first reaction condition.
19. The method of claim 11, wherein the extended reaction condition is selected from one or more of:
- a greater reaction time relative a control reaction condition;
 - a higher ST6 sialyltransferase concentration and/or specific activity relative to a control reaction condition;
 - a higher temperature relative to a control reaction condition; and
 - a higher concentration of a sialic acid donor relative to a control reaction condition.

20. The method of claim 11, wherein the ST6 sialyltransferase has at least 90% identity to amino acid residues 95-416 of SEQ ID NO:1, at least 90% identity to SEQ ID NO:2, or at least 90% identity to SEQ ID NO:3.
21. A method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) a target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm and/or (iii) a target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm, the method comprising:
providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; and
contacting the glycoproteins with an ST6 sialyltransferase in the presence of an intermediate reaction condition, thereby producing a glycoprotein preparation having (i) the target level of disialylated branched glycans having a sialic acid on the α 1,3 arm and on the α 1,6 arm, (ii) the target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm, and/or (iii) the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm.
22. The method of claim 21, wherein the intermediate reaction condition is sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm and to an α 1,6 arm of a branched glycan, and not sufficient for the ST6 sialyltransferase substantially to remove a sialic acid from an α 1,3 arm of a branched glycan.
23. The method of claim 21, further comprising isolating the glycoprotein preparation.
24. The method of claim 23, further comprising measuring a level of (i) disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) monosialylated branched glycans having a sialic acid on an α 1,3 arm and/or (iii) monosialylated branched glycans having a sialic acid on an α 1,6 arm.
25. The method of claim 21, wherein the target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm is at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of sialylated branched glycans.
26. The method of claim 21, wherein the target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of sialylated branched glycans.
27. The method of claim 21, wherein the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm is less than 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5%, or less of sialylated branched glycans.

28. A method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of branched glycans having a sialic acid on an α 1,6 arm and/or (ii) a target level of branched glycans having a sialic acid on an α 1,3 arm, the method comprising:

providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; and

contacting the glycoproteins with an ST6 sialyltransferase in the presence of an initial reaction condition sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm and to add a sialic acid to an α 1,6 arm of a branched glycan to produce a disialylated branched glycan; and

contacting the disialylated branched glycan with the ST6 sialyltransferase in the presence of an extended reaction condition, thereby producing a glycoprotein preparation having (i) the target level of branched glycans having a sialic acid on the α 1,6 arm and/or (ii) the target level of branched glycans having a sialic acid on an α 1,3 arm.

29. A method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) a target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm and/or (iii) a target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm, the method comprising:

providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm; and

contacting the glycoproteins with an ST6 sialyltransferase in the presence of an initial reaction condition sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm of a branched glycan to produce a monosialylated branched glycan; and

contacting the monosialylated branched glycan with the ST6 sialyltransferase in the presence of an extended reaction condition, thereby producing a glycoprotein preparation having (i) the target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) the target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm and/or (iii) the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm.

30. A method of removing a sialic acid from a branched glycan of an Fc region, the branched glycan comprising an α 1,3 arm and an α 1,6 arm, the method comprising:

providing a branched glycan of an Fc region, the branched glycan comprising an α 1,3 arm and an α 1,6 arm and comprising a sialic acid on the α 1,3 arm;

contacting the branched glycan with an ST6 sialyltransferase in the presence of an initial reaction condition sufficient for the ST6 sialyltransferase to add a sialic acid to the α 1,6 arm to produce a disialylated branched glycan; and

contacting the disialylated branched glycan with the ST6 sialyltransferase in the presence of an extended reaction condition, thereby removing the sialic acid from the α 1,3 arm of the branched glycan.

31. A method of modulating sialylation of Fc region branched glycans comprising an α 1,3 arm and an α 1,6 arm, the method comprising:

providing a reaction solution comprising (i) Fc region branched glycans comprising an α 1,3 arm and an α 1,6 arm, (ii) a ST6 sialyltransferase, and (iii) a sialic acid donor; and

incubating the reaction solution under reaction conditions sufficient for the ST6 sialyltransferase to catalyze transfer of a sialic acid primarily to the α 1,3 arm only, primarily to the α 1,6 arm only, or to both the α 1,3 arm and the α 1,6 arm, wherein:

a) incubating the reaction solution under reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid primarily to the α 1,3 arm comprises controlling reaction kinetics such that: (i) the sialic acid addition rate for the α 1,3 arm ($R_a^{1,3}$) exceeds the sialic acid addition rate for the α 1,6 arm ($R_a^{1,6}$); or (ii) the sialic acid removal rate for the α 1,6 arm ($R_r^{1,6}$) exceeds $R_a^{1,6}$;

b) incubating the reaction solution under reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid primarily to the α 1,6 arm comprises controlling reaction kinetics such that: (i) $R_a^{1,6}$ exceeds $R_r^{1,6}$; and (ii) the sialic acid removal rate for the α 1,3 arm ($R_r^{1,3}$) eventually exceeds $R_a^{1,3}$; or

c) incubating the reaction solution under reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid to both the α 1,3 and α 1,6 arms comprises controlling reaction kinetics such that: (i) $R_a^{1,3}$ exceeds $R_r^{1,3}$; and (ii) $R_a^{1,6}$ exceeds $R_r^{1,6}$; thereby modulating sialylation of a branched glycan.

32. The method of claim 31, wherein controlling reaction kinetics comprises modulating the time of the reaction.

33. The method of claim 31 or 32, wherein controlling reaction kinetics comprises modulating the level or activity of the sialyltransferase.

34. The method of claim 31, comprising detecting reaction kinetics.

35. The method of claim 31, comprising measuring a level of sialylated glycans.

36. The method of claim 31 or 32, where controlling reaction kinetics comprises modulating the $R_r^{1,3}$ or $R_r^{1,6}$ rates by controlling or adjusting the ratio of the sialic acid donor to a sialic acid donor reaction product.

37. The method of claim 36, wherein the sialic acid donor is cytidine 5'-monophospho-N-acetylneuraminic acid and the sialic acid donor reaction product is cytidine 5'-monophosphate.

38. The method of claim 31, wherein the reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid to both the α 1,3 and α 1,6 arms comprises supplementing the sialic donor at least once during the reaction.

39. The method of claim 31, wherein the reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid to both the α 1,3 and α 1,6 arms comprises removing a sialic donor reaction product at least once during the reaction.
40. The method of claim 31, wherein the reaction conditions sufficient for the sialyltransferase to catalyze transfer of the sialic acid to both the α 1,3 and α 1,6 arms comprises supplementing the sialic donor reaction product at least once during the reaction.
41. The method of any one of claims 1-40, wherein the preparation is an IVIG preparation.
42. The method of any one of claims 1-40, wherein the preparation is a recombinant Fc containing glycoprotein preparation.
43. The method of claim 42, wherein the recombinant glycoprotein is a recombinant antibody or Fc fusion protein.
44. A glycoprotein preparation produced by the method of any one of claims 1-40.
45. A glycoprotein preparation produced by the method of any one of claims 11-16, wherein at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of sialylated branched glycans have a sialic acid on an α 1,6 arm.
46. A method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of branched glycans having a sialic acid on an α 1,3 arm and/or (ii) a target level of branched glycans having a sialic acid on an α 1,6 arm, the method comprising:
- providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm;
 - contacting the glycoproteins with an ST6 sialyltransferase in the presence of a limited reaction condition sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm of a branched glycan and not sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,6 arm of a branched glycan, thereby producing a preparation of sialylated glycoproteins; and
 - formulating the preparation into a drug product if the preparation meets the target level of branched glycans having a sialic acid on the α 1,3 arm and/or the target level of branched glycans having a sialic acid on an α 1,6 arm.
47. The method of claim 46, further comprising measuring the level of branched glycans having a sialic acid on the α 1,3 arm and/or the level of branched glycans having a sialic acid on an α 1,6 arm in the preparation.

48. A method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of branched glycans having a sialic acid on an α 1,6 arm and/or (ii) a target level of branched glycans having a sialic acid on an α 1,3 arm, the method comprising:

providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm;

contacting the glycoproteins with an ST6 sialyltransferase in the presence of an extended reaction condition sufficient for the ST6 sialyltransferase substantially to remove a sialic acid from an α 1,3 arm of a disialylated branched glycan comprising a sialic acid on an α 1,3 arm and an α 1,6 arm, thereby producing a preparation of sialylated glycoproteins; and

formulating the preparation into a drug product if the preparation meets the target level of branched glycans having a sialic acid on the α 1,6 arm and/or the target level of branched glycans having a sialic acid on an α 1,3 arm.

49. The method of claim 48, further comprising measuring the level of branched glycans having a sialic acid on the α 1,6 arm and/or the level of branched glycans having a sialic acid on an α 1,3 arm in the preparation.

50. A method of producing a preparation of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm, the preparation comprising (i) a target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) a target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm and/or (iii) a target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm, the method comprising:

providing a plurality of glycoproteins comprising Fc regions comprising branched glycans comprising an α 1,3 arm and an α 1,6 arm;

contacting the glycoproteins with an ST6 sialyltransferase in the presence of an intermediate reaction condition sufficient for the ST6 sialyltransferase substantially to add a sialic acid to an α 1,3 arm and to an α 1,6 arm of a branched glycan, and not sufficient for the ST6 sialyltransferase substantially to remove a sialic acid from an α 1,3 arm of a branched glycan, thereby producing a preparation of sialylated glycoproteins; and

formulating the preparation into a drug product if the preparation meets (i) the target level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, (ii) the target level of monosialylated branched glycans having a sialic acid on an α 1,3 arm and/or (iii) the target level of monosialylated branched glycans having a sialic acid on an α 1,6 arm.

51. The method of claim 50, further comprising measuring the level of disialylated branched glycans having a sialic acid on an α 1,3 arm and on an α 1,6 arm, the level of monosialylated branched glycans having a sialic acid on an α 1,3 arm, and/or the level of monosialylated branched glycans having a sialic acid on an α 1,6 arm in the preparation.

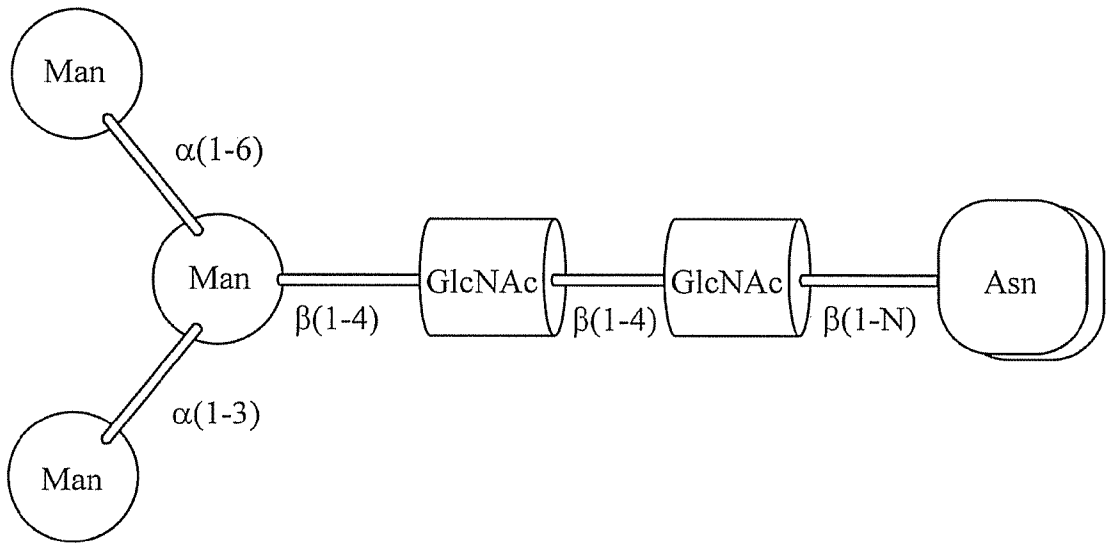


FIG. 1

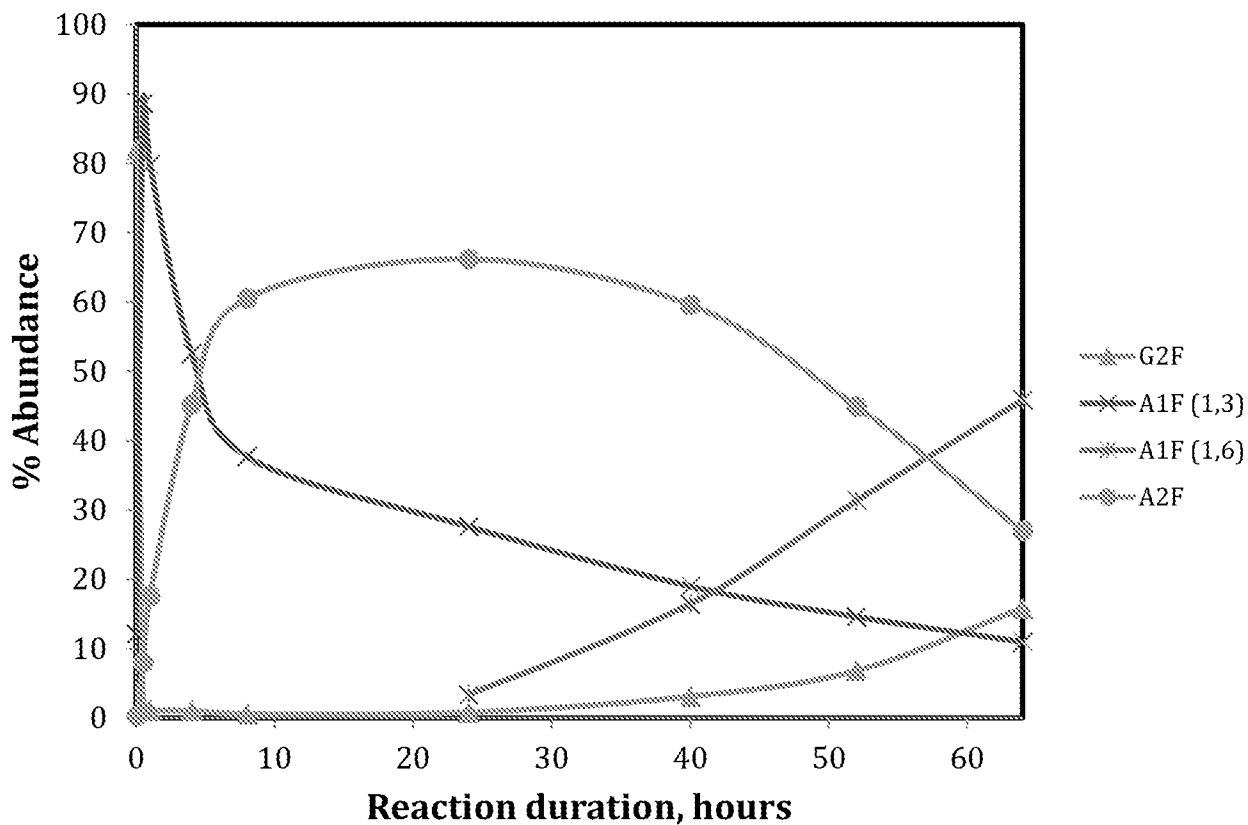


FIG. 3

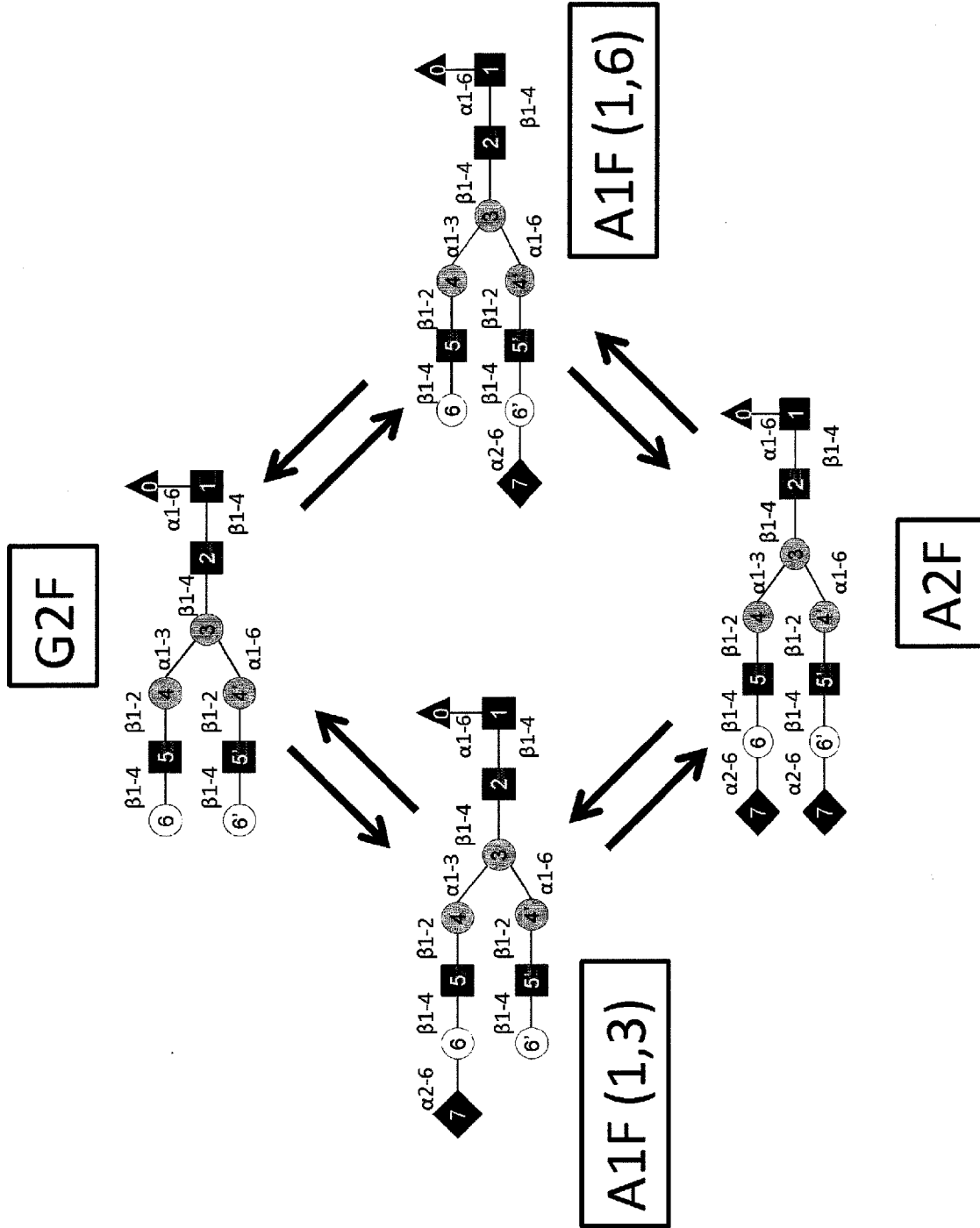


FIG. 4

SEQ ID NO:1

MTRLTVLALLAGLLASSRAGSSPLLAMEWSHPQFEKLEGGGSGGGSGGSWSHPQFEKHAHAHSR
KDHLIHNHVHKEEHAHAHNKELGTAVFQGPMPRAIRGRSFQVWVKDSSSKNLI PRLQKIWKNYLS
MNKYKVSYKGP GPGIKFSAEALRCHLRDHVNVSMVEVTDFFPNTSEWEGYLPKESIRTKAGPWG
RCAVVSSAGSLKSSQLGREIDDHDAVLRFN GAPTANFQQDVGTKTTIRLMNSQLVTTEKRFKLD
SLYNEGILIVWDPSVYHSDIPK WYQNP DY NFFN NYKTYRKLHPNQPFYILKPQMPWELWDILQE
ISPEEI QPNPPSSGMLGIIIMM TLCDQVDIYEF LPSKRKTDVCY YYYQKFFDSACTMGAYHPLLY
EKNLVKHLNQGTDEDIYLLGKATLPGFRTIHC PG

FIG. 5A

SEQ ID NO:2

GSYYDSFKLQTKEFQVLKSLGK LAMGSDS QSVSSSSTQDPHRGRQTLGSLRGLAKAKPEASFQV
WVKDSSSKNLI PRLQKIWKNYLSMNKYKVSYKGP GPGIKFSAEALRCHLRDHVNVSMVEVTDFF
PNTSEWEGYLPKESIRTKAGPWGRCAVVSSAGSLKSSQLGREIDDHDAVLRFN GAPTANFQQDV
GKTTIRLMNSQLVTTEKRFKDSL YNEGILIVWDPSVYHSDIPK WYQNP DY NFFN NYKTYRKL
HPNQPFYILKPQMPWELWDILQEISPEEI QPNPPSSGMLGIIIMM TLCDQVDIYEF LPSKRKTD
VCY YYYQKFFDSACTMGAYHPLLYEKNLVKHLNQGTDEDIYLLGKATLPGFRTIHC

FIG. 5B

SEQ ID NO:3

MIHTNLKKKFSYFILAFLLFALICVWKKGSYEALKLQAKEFQVTKSLEKLAIGSGSQSTSASIK
QDSKPGSQVLSHLRVTAKVKPQSPYQVWDKNSSSKNLPRLQKILKNYLSMNKYKVSYKGP GPG
VKFSVEALRCHLRDRVNVSMIEATDFFPNTTEWEGYLPKENFR TKAGPWHRCAVVSSAGSLKSS
HLGKEIDSHDAVLRFN GAPVADEFQDVG MKTTIRLMNSQLITTEKQFLKDSL YNEGILIVWDPS
LYHADIPNWKKPDY NFFETYKSYRKLYPSQPFYILRPQMPWELWDIIQE IAPDRIQPNPPSSG
MLGIIIMM TLCDQVDVYEF LPSKRKTDVCY YHQQKFFDSACTMGAYHPLLYEKNMVKQLNEG TDE
DIYIFGKATLSGFRTIHC

FIG. 5C