Claims

1. A method for identifying a potential component for the oligosaccharyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation selected from the group consisting of

   (a) a potential oligosaccharide donor, preferably a lipid-linked oligosaccharide (LLO) or an undecaprenyl pyrophosphate bound oligosaccharide donor,

   (b) a potential oligosaccharyltransferase (OST),

   (c) a potential consensus sequence motif polypeptide, and

   (d) a potential glycosylation inhibitor,

   comprising the steps of

   (i) using the atomic coordinates of Table 1, preferably ±2, more preferably ±1.5, most preferably ±1.0 Å root mean square deviation (rmsd) from the backbone atoms, for generating a three-dimensional model of the catalytic domain of the oligosaccharyltransferase (OST) of *Campylobacter lari*, comprising at least three, preferably at least four, more preferably at least six, most preferably all of amino acids D56, R147, D154, D156, E319, R375, Y468, and H485, and/or, preferably and

   (ii) using the atomic coordinates of Table 1, preferably ±2, more preferably ±1.5, most preferably ±1.0 Å root mean square deviation (rmsd) from the backbone atoms, for generating a three-dimensional model of the polypeptide binding site of the oligosaccharyltransferase (OST) of *Campylobacter lari*, comprising at least two, preferably at least three, more preferably at least four, most preferably all of amino acids M318, R331, W463, W464, D465, and I572,

   (iii) preferably performing whole body translations and/or rotations on the coordinates of the amino acids of the three-dimensional models of (i) and/or (ii),

   (iv) using said three-dimensional model(s) of (i), (ii) and/or (iii) for designing or selecting at least one of potential components (a) to (d),

   (v) providing at least one of said potential components (a) to (d), and

   (vi) contacting at least one of said potential components (a) to (d) with the further functional components necessary for an oligosaccharyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation,

   (vii) identifying a functional component selected from the group consisting of

(A) a functional oligosaccharide donor, preferably a functional lipid-linked oligosaccharide (LLO) or an undecaprenyl pyrophosphate bound oligosaccharide donor,
(B) a functional oligosaccharyltransferase (OST),
(C) a functional consensus sequence motif polypeptide, and
(D) a functional glycosylation inhibitor.

2. The method of claim 1, wherein in step (ii) the three-dimensional model of the polypeptide binding site of the oligosaccharyltransferase (OST) of *Campylobacter lari* comprises at least two, preferably at least three, more preferably at least four, most preferably all of amino acids M318, A331, W463, W464, D465 and I572.

3. A method for designing a potential component for the oligosyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation selected from the group consisting of
(a) a potential oligosaccharide donor, preferably a lipid-linked oligosaccharide (LLO) or an undecaprenyl pyrophosphate bound oligosaccharide donor,
(b) a potential oligosaccharyltransferase (OST),
(c) a potential consensus sequence motif polypeptide, and
(d) a potential glycosylation inhibitor,
comprising the steps of
(i) using the atomic coordinates of Table 1, preferably ±2, more preferably ±1.5, most preferably ±1.0 Å root mean square deviation (rmsd) from the backbone atoms, for generating a three-dimensional model of the catalytic domain of the oligosaccharyltransferase (OST) of *Campylobacter lari*, comprising at least three, preferably at least four, more preferably at least six, most preferably all of amino acids D56, R147, D154, D156, E319, R375, Y468, and H485, and/or, preferably and
(ii) using the atomic coordinates of Table 1, preferably ±2, more preferably ±1.5, most preferably ±1.0 Å root mean square deviation (rmsd) from the backbone atoms, for generating a three-dimensional model of the polypeptide binding site of the oligosaccharyltransferase (OST) of Campylobacter lari, comprising at least two, preferably at least three, more preferably at least four, most preferably all of amino acids M318, R331, W463, W464, D465, and I572,

(iii) preferably performing whole body translations and/or rotations on the coordinates of the amino acids of the three-dimensional models of (i) and/or (ii),

(iii.1) using said three-dimensional model of (i), (ii) and/or (iii) for assessing the stereochemical complementarity between said three-dimensional model(s) (i), (ii) and/or (iii) and a known or potential component for the oligosaccharyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation selected from an oligosaccharide donor, preferably a lipid-linked oligosaccharide (LLO) or an undecaprenyl pyrophosphate bound oligosaccharide donor, a consensus sequence motif polypeptide, and a potential glycosylation inhibitor, or

(iii.2) varying at least one amino acid in said three-dimensional model of (i), (ii) and/or (iii) and using said varied three-dimensional model of (i), (ii) and/or (iii) for assessing the stereochemical complementarity between said three-dimensional models (i), (ii) and/or (iii) and a known or potential component for the oligosaccharyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation selected from an oligosaccharide (LLO) donor, preferably a lipid-linked oligosaccharide (LLO) donor or an undecaprenyl pyrophosphate bound oligosaccharide donor, a consensus sequence motif polypeptide, and a potential glycosylation inhibitor,

(iv) optimizing said stereochemical complementarity in an iterative approach by observing changes in the three-dimensional model of (iii.1), (iii.2) or the component for the oligosaccharyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation,

(v) designing a potential component selected from (a) to (d) which optimizes said stereochemical complementarity of said three-dimensional model(s) and potential component,

(vi.1) optionally providing the optimized potential component, and

(vi.2) contacting at least one of said potential components (a) to (d) with the further functional components necessary for an oligosaccharyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation,

(vi.3) identifying a functional component selected from the group consisting of

(A) a functional oligosaccharide donor, preferably a functional lipid-linked oligosaccharide (LLO) or an undecaprenyl pyrophosphate bound oligosaccharide donor,

(B) a functional oligosaccharyltransferase (OST),

(C) a functional consensus sequence motif polypeptide, and

(D) a functional glycosylation inhibitor.

4. The method of claim 3, wherein in step (ii) the three-dimensional model of the polypeptide binding site of the oligosaccharyltransferase (OST) of *Campylobacter lari* comprises at least two, preferably at least three, more preferably at least four, most preferably all of amino acids M318, A331, W463, W464, D465 and I572.

5. The method according to any of claims 1 to 4, wherein the specific three-dimensional catalytic site model of step (i) further comprises one or more, preferably all of the amino acids selected from the group having residues located within Van der Waals distance to the bound peptide of SEQ ID NO: 2, preferably selected from the group consisting of Thr53, Thr54, Asn55, Asp56, Asn146, Arg147, Tyr152, Glu315, Thr316, Ile317, Met318, Glu319, Val320, Asn321, Arg331, Leu374, Arg375, Tyr433, Ser435, Val438, Trp463, Trp464, Asp465, Gly482, His485, Ile572, Val575.

6. The method according to any of claims 1 to 4, wherein the specific three-dimensional catalytic site model of step (i) further comprises one or more, preferably all of the amino acids selected from the group having residues located within Van der Waals distance to the bound peptide of SEQ ID NO: 2, preferably selected from the group consisting of Thr53, Thr54, Asn55, Asp56, Asn146, Arg147, Tyr152, Glu315, Thr316, Ile317, Met318, Glu319, Val320, Asn321, Ala331, Leu374, Arg375, Tyr433, Ser435, Val438, Trp463, Trp464, Asp465, Gly482, His485, Ile572, Val575.

7. The method according to any one of claims 1 to 6, wherein the potential component is an oligosaccharide donor (a), preferably a lipid-linked oligosaccharide (LLO) or an undecaprenyl pyrophosphate bound oligosaccharide donor.

8. The method according to any one of claims 1 to 6, wherein the potential component is a oligosaccharyltransferase (OST) (b).

9. The method according to any one of claims 1 to 6, wherein the potential component is a potential consensus sequence motif polypeptide (c).

10. The method according to any one of claims 1 to 6, wherein the potential component is a glycosylation inhibitor (d).

11. Machine-readable medium comprising
(i) the atomic coordinates of Table 1, preferably ±2, more preferably ±1.5, most preferably ±1.0 Å root mean square deviation (rmsd) from the backbone atoms, preferably comprising at least one, two or three, preferably at least four or five, more preferably at least six or 7, most preferably all of amino acids D56, R147, D154, D156, E319, R357, Y468, and H485, and/or, preferably and
(ii) the atomic coordinates of Table 1, preferably ±2, more preferably ±1.5, most preferably ±1.0 Å root mean square deviation (rmd) from the backbone atoms, for generating a three-dimensional model of the polypeptide binding site of the oligosaccharyltransferase (OST) of *Campylobacter lari*, comprising at least one or two, preferably at least three, more preferably at least four or five, most preferably all of amino acids M318, R331, W463, W464, D465, and I572,
(iii) preferably the atomic coordinates of (i) or (ii) modified by performing whole body translations and/or rotations on said coordinates.

12. The machine-readable medium according to claim 11, comprising
(ii) the atomic coordinates of Table 1, preferably ±2, more preferably ±1.5, most preferably ±1.0 Å root mean square deviation (rmd) from the backbone atoms, for generating a three-dimensional model of the polypeptide binding site of the oligosaccharyltransferase (OST) of *Campylobacter lari*, comprising at least one or two, preferably at least three, more preferably at least four or five, most preferably all of amino acids M318, A331, W463, W464, D465, and I572.

CLAIMS

1. A method for identifying a potential component for the oligosaccharyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation selected from the group consisting of

(a) a potential oligosaccharide donor,

(b) a potential oligosaccharyltransferase (OST),

(c) a potential consensus sequence motif polypeptide, and

(d) a potential glycosylation inhibitor,

comprising the steps of

(i) using the atomic coordinates of Table 1, preferably ±2, more preferably ±1.5, most preferably ±1.0 Å root mean square deviation (rmsd) from the backbone atoms, for generating a three-dimensional model of the catalytic domain of the oligosaccharyltransferase (OST) of *Campylobacter lari*, wherein said three-dimensional model of the catalytic domain comprises eight amino acid residues, and wherein said amino acid residues comprise at least one, at least two, at least three, at least four, at least six, or all of amino acids D56, R147, D154, D156, E319, R375, Y468, and H485, and/or

(ii) using the atomic coordinates of Table 1, preferably ±2, more preferably ±1.5, most preferably ±1.0 A root mean square deviation (rmsd) from the backbone atoms, for generating a three-dimensional model of the polypeptide binding site of the oligosaccharyltransferase (OST) of *Campylobacter lari,* wherein said three-dimensional model of the polypeptide binding site comprises six amino acid residues, and wherein said amino acid residues comprise at least one, at least two, at least three, at least four, or all of amino acids M318, R331, W463, W464, D465, and I572,

(iii) performing whole body translations and/or rotations on the coordinates of the amino acids of the three-dimensional models of (i) and/or (ii),

(iv) using said three-dimensional model(s) of (i), (ii) and/or (iii) for designing or selecting at least one of potential components (a) to (d),

(v) providing at least one of said potential components (a) to (d), and

(vi) contacting at least one of said potential components (a) to (d) with the further functional components necessary for an oligosaccharyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation,

(vii) identifying a functional component selected from the group consisting of

(A) a functional oligosaccharide donor,

(B) a functional oligosaccharyltransferase (OST),

(C) a functional consensus sequence motif polypeptide, and

(D) a functional glycosylation inhibitor.

2. The method of claim 1, wherein in step (ii) the three-dimensional model of the polypeptide binding site of the oligosaccharyltransferase (OST) of *Campylobacter lari* comprises at least two, at least three, at least four, or all of amino acids M318, A331, W463, W464, D465 and I572.

3. A method for designing a potential component for the oligosaccharyltransferase (OST)catalysed asparagine-linked ("N-linked") glycosylation selected from the group consisting of

(a) a potential oligosaccharide donor,

(b) a potential oligosaccharyltransferase (OST),

(c) a potential consensus sequence motif polypeptide, and

(d) a potential glycosylation inhibitor,

comprising the steps of

(i) using the atomic coordinates of Table 1, preferably $\pm$2, more preferably

$\pm$1.5, most preferably $\pm$1.0 Å root mean square deviation (rmsd) from the backbone atoms, for generating a three-dimensional model of the catalytic domain of the oligosaccharyltransferase (OST) of *Campylobacter lari*, wherein said three-dimensional model of the catalytic domain comprises eight amino acid residues, and wherein said amino acid residues comprise at least one, at least two, at least three, at least four, at least six, or all of amino acids D56, R147, D154, D156, E319, R375, Y468, and H485, and/or

(ii) using the atomic coordinates of Table 1, preferably $\pm$2 more preferably

$\pm$1.5, most preferably $\pm$ 1.0 Å root mean square deviation (rmsd) from the backbone atoms, for generating a three-dimensional model of the

polypeptide binding site of the oligosaccharyltransferase (OST) *of Campylobacter lari*, wherein said three-dimensional model of the polypeptide binding site comprises six amino acid residues, and wherein said amino acid residues comprise at least one, at least two, at least three, at least four, or all of amino acids M318, R331, W463, W464, D465, and I572,

(iii) performing whole body translations and/or rotations on the coordinates of the amino acids of the three-dimensional models of (i) and/or (ii),

(iii.1) using said three-dimensional model of (i), (ii) and/or (iii) for assessing the stereochemical complementarity between said three-dimensional model(s) (i), (ii) and/or (iii) and a known or potential component for the oligosac charyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation selected from an oligosaccharide donor, a consensus sequence motif polypeptide, and a potential glycosylation inhibitor, or

(iii.2) varying at least one amino acid in said three-dimensional model of (i), (ii) and/or (iii) and using said varied three-dimensional model of (i), (ii) and/or (iii) for assessing the stereochemical complementarity between said three dimensional models (i), (ii) and/or (iii) and a known or potential component for the oligosaccharyltransferase (OST)-catalysed asparagine-linked ("N linked") glycosylation selected from an oligosaccharide (LLO) donor, a consensus sequence motif polypeptide, and a potential glycosylation inhibitor,

(iv) optimizing said stereochemical complementarity in an iterative approach

by observing changes in the three-dimensional model of (iii.1), (iii.2) or the component for the oligosaccharyltransferase (OST)-catalysed asparagine linked ("N-linked") glycosylation,

(v) designing a potential component selected from (a) to (d) which optimizes said stereochemical complementarity of said three-dimensional model(s) and potential component,

(vi.1) optionally providing the optimized potential component, and

(vi.2) contacting at least one of said potential components (a) to (d) with the further functional components necessary for an oligosaccharyltransferase (OST)-catalysed asparagine-linked ("N-linked") glycosylation,

(vi.3) identifying a functional component selected from the group consisting of

(A) a functional oligosaccharide donor,

(B) a functional oligosaccharyltransferase (OST),

(C) a functional consensus sequence motif polypeptide, and

(D) a functional glycosylation inhibitor.

4. The method of claim 3, wherein in step (ii) the three-dimensional model of the polypeptide binding site of the oligosaccharyltransferase (OST) of *Campylobacter lari* comprises at least two, at least three, at least four, or all of amino acids M318, A331, W463, W464, D465 and I572.

5. The method according to any of claims 1 to 4, wherein the specific three-dimensional catalytic site model of step (i) further comprises one or more or all of the amino acids selected from the group having residues located within Van der Waals distance to the bound peptide of SEQ ID NO: 2, selected from the group consisting of Thr53, Thr54, Asn55, Asp56, Asn146, Arg147, Tyr152, Glu315, Thr316, Ile317, Met318, Glu319, Val320, Asn321, Arg331, Leu374, Arg375, Tyr433, Ser435, Val438, Trp463, Trp464, Asp465, Gly482, His485, Ile572, Val575.

6. The method according to any of claims 1 to 4, wherein the specific three-dimensional catalytic site model of step (i) further comprises one or more or all of the amino acids selected from the group having residues located within Vander Waals distance to the bound peptide of SEQ ID NO: 2, selected from the group consisting of Thr53, Thr54, Asn55, Asp56, Asn146, Arg147, Tyr152, Glu315, Thr316, Ile317, Met318, Glu319, Val320, Asn321, Ala331, Leu374, Arg375, Tyr433, Ser435, Val438, Trp463, Trp464, Asp465, Gly482, His485, Ile572, Val575.

7. The method according to any one of claims 1 to 4, wherein the potential component is an oligosaccharide donor (a).

8. The method according to any one of claims 1 to 4, wherein the potential component is an oligosaccharyltransferase (OST) (b).

9. The method according to any one of claims 1 to 4, wherein the potential component is a potential consensus sequence motif polypeptide (c).

10. The method according to any one of claims 1 to 4, wherein the potential component is a glycosylation inhibitor (d).

11. The method according to claim 5, wherein the potential component is an oligosaccharide donor (a).

12. The method according to claim 5, wherein the potential component is an oligosaccharyltransferase (OST) (b).

13. The method according to claim 5, wherein the potential component is a potential consensus sequence motif polypeptide (c).

14. The method according to claim 5, wherein the potential component is a glycosylation inhibitor (d).

15. The method according to claim 6, wherein the potential component is an oligosaccharide donor (a).

16. The method according to claim 6, wherein the potential component is an oligosaccharyltransferase (OST) (b).

17. The method according to claim 6, wherein the potential component is a potential consensus sequence motif polypeptide (c).

18. The method according to claim 6, wherein the potential component is a glycosylation inhibitor (d).

19. The method according to claim 1 or 3, wherein the potential oligosaccharide donor is a lipid-linked oligosaccharide (LLO) or an undecaprenyl pyrophosphate bound oligosaccharide donor.

20. The method according to claim 1 or 3, wherein the atomic coordinates of Table 1 of step (i) or step (ii) comprise ±2, ±1.5, or ±1.0 Å root mean square deviation (rmsd) from a backbone atom.

21. The method according to claim 7, wherein the potential oligosaccharide donor is a lipid-linked oligosaccharide (LLO) or an undecaprenyl pyrophosphate bound oligosaccharide donor.

22. The method according to claim 11, wherein the potential oligosaccharide donor is a lipid-linked oligosaccharide (LLO) or an undecaprenyl pyrophosphate bound oligosaccharide donor.

23. The method according to claim 15, wherein the potential oligosaccharide donor is a lipid-linked oligosaccharide (LLO) or an undecaprenyl pyrophosphate bound oligosaccharide donor.