What is Claimed is:

1. An engineered Gram-negative bacterium for the production of a polysaccharide, wherein the Gram-negative bacterium comprises a regulatory gene of a capsular polysaccharide gene cluster of ~~a Gram-positive bacterium~~ *S. pneumoniae* CPS1, CPS2, CPS3, CPS4, CPS5, CPS6 (A and B), CPS7 (A,B, C), CPS8, CPS9 (A, L,N, V), CPS10 (A,B,C,F), CPS11 (A, B,C,D,F), CPS12(A,B,F), CPS13, CPS14 CPS15(A,B,C,F), CPS16(A,F), CPS17(A,F), CPS18(A,B,C,F), CPS19(A,B,C,F), CPS20,CPS21, CPS22(A,F), CPS23(A,B,F), CPS24(A,B,F), CPS25(A,F), CPS26, CPS27,CPS28(A,F), CPS29, CPS31, CPS32(A,F), CPS33(A,B,C,D,F), CPS34, CPS35(A,B,C,D,F), CPS36, CPS37, CPS38, CPS39, CPS40, CPS41(A,F), CPS42, CPS43, CPS44, CPS45, CPS46, CPS47(A,F), or CPS48; or *Staphylococcus aureus* CPS5, or CPS8; *Streptococcus agalactiae* (group B, GBS) CPSIa, CPSIb, CPSII, CPSIII, CPSIV, CPSV, CPSVI, CPSVII, or CPSVIII; or *Enterococcus faecalis* CPSA, CPSB, CPSC, or CPSD.

2. The Gram-negative bacterium of claim 1, wherein the Gram-negative bacterium comprises at least 25%, 50%, 75%, 85%, 90%, or at least 95% of the open reading frames of the capsular polysaccharide gene cluster.

3. The Gram-negative bacterium of claim 1, wherein said Gram-negative bacterium is selected from the group consisting of *Escherichia* species, *E. coli*, *Shigella* species, *Klebsiella* species, *Salmonella* species, *Yersinia* species, *Neisseria* species, *Vibrio* species and *Pseudomonas* species.

4. The Gram-negative bacterium of any one of the preceding claims, wherein said regulatory gene is a *Streptococcus pneumoniae* regulatory gene~~, optionally from *S. pneumoniae* Type 1 or *S. pneumoniae* Type 4~~.

5. The Gram-negative bacterium of claim 4, wherein said regulatory gene is from *S. pneumoniae* Type 1 or *S. pneumoniae* Type 4.

~~5.~~6. The Gram-negative bacterium of any one of ~~the preceding~~ claims 1-3, wherein said regulatory gene is a *Staphylococcus aureus* regulatory gene.

~~6.~~7. The Gram-negative bacterium of any one of ~~the preceding~~ claims 1-3, wherein said regulatory gene is a *Staphylococcus agalactiae* regulatory gene.

~~7.~~8. The Gram-negative bacterium of any one of ~~the preceding~~ claims 1-3, wherein said regulatory gene is an *Enterococcus faecalis* regulatory gene.

~~8.~~9. The Gram-negative bacterium of any one of the preceding claims, further comprising an oligosaccharyl transferase~~, optionally said oligosaccharyl transferase is herologous to the Gram-negative bacterium~~.

10. The Gram-negative bacterium of claim 9, wherein said oligosaccharyl transferase is heterologous to the Gram-negative bacterium.

~~9.~~11. The Gram-negative bacterium of any one of the preceding claims, wherein one or more genes native to the Gram-negative bacterium have been deleted or inactivated~~, optionally wherein said one or more deleted genes comprise the *waaL* gene or wherein said~~

~~one or more deleted genes comprise all genes associated with O antigen biosynthesis in the Gram-negative bacterium~~.

12. The Gram-negative bacterium of claim 11, wherein said one or more deleted genes comprise the *waaL* gene.

13. The Gram-negative bacterium of claim 12, wherein said one or more deleted genes comprise all genes associated with O antigen biosynthesis in the Gram-negative bacterium.

~~10.~~14. The Gram-negative bacterium of any one of the preceding claims, wherein said regulatory gene is *wzg*, *wzh*, *wzd*, *wze*, *capA*, *capB*, or *capC*.

~~11.~~15. The Gram-negative bacterium of any one of the preceding claims, further comprising a nucleic acid encoding a carrier protein comprising a consensus sequence for glycosylation~~, which is optionally heterologous to the Gram-negative bacterium or is optionally detoxified exotoxin A from *P. aeruginosa*, CRM197, Diphtheria toxoid, tetanus toxoid, detoxified hemolysin A of *S. aureus*, clumping factor A, clumping factor B, *E. coli* FimH, *E. coli* FimHC, *E. coli* heat labile enterotoxin, detoxified variants of *E. coli* heat labile enterotoxin, Cholera toxin B subunit (CTB), cholera toxin, detoxified variants of cholera toxin, *E. coli* sat protein, the passenger domain of *E. coli* sat protein, *C. jejuni* AcrA, *C. jejuni* natural glycoproteins, *S. pneumoniae* pneumolysin, *S. pneumoniae* NOX, *S. pneumoniae* PspA, *S. pneumoniae* PcpA, *S. pneumoniae* PhtD, *S. pneumoniae* PhtE, *S. pneumoniae* Ply, or *S. pneumoniae* LytB~~.

16. The Gram-negative bacterium of claim 15 wherein the carrier protein comprising a consensus sequence for glycosylation is heterologous to the Gram-negative bacterium.

17. The Gram-negative bacterium of claim 15 wherein the carrier protein comprising a consensus sequence for glycosylation is detoxified exotoxin A from *P. aeruginosa*, CRM197, Diphtheria toxoid, tetanus toxoid, detoxified hemolysin A of *S. aureus*, clumping factor A, clumping factor B, *E. coli* FimH, *E. coli* FimHC, *E. coli* heat labile enterotoxin, detoxified variants of *E. coli* heat labile enterotoxin, Cholera toxin B subunit (CTB), cholera toxin, detoxified variants of cholera toxin, *E. coli* sat protein, the passenger domain of *E. coli* sat protein, *C. jejuni* AcrA, *C. jejuni* natural glycoproteins, *S. pneumoniae* pneumolysin, *S.*

pneumoniae NOX, *S. pneumoniae* PspA, *S. pneumoniae* PcpA, *S. pneumoniae* PhtD, *S. pneumoniae* PhtE, *S. pneumoniae* Ply, or *S. pneumoniae* LytB.

~~12. The Gram-negative bacterium of any one of the preceding claims, wherein the capsular polysaccharide is *S. pneumoniae* CPS1, CPS2, CPS3, CP4, CPS5, CPS6 (A and B), CPS7 (A,B, C), CPS8, CPS9 (A, L,N, V), CPS10 (A,B,C,F), CPS11 (A, B,C,D,F), CPS12(A,B,F), CPS13, CPS14 CPS15(A,B,C,F), CPS16(A,F), CPS17(A,F), CPS18(A,B,C,F), CPS19(A,B,C,F), CPS20,CPS21, CPS22(A,F), CPS23(A,B,F), CPS24(A,B,F), CPS25(A,F), CPS26, CPS27,CPS28(A,F), CPS29, CPS31, CPS32(A,F), CPS33(A,B,C,D,F), CPS34, CPS35(A,B,C,D,F), CPS36, CPS37, CPS38, CPS39, CPS40, CPS41(A,F), CPS42, CPS43, CPS44, CPS45, CPS46, CPS47(A,F), or CPS48; or *Staphylococcus aureus* CPS5, or CPS8; *Streptococcus agalactiae* (group B, GBS) CPSIa, CPSIb, CPSII, CPSIII, CPSIV, CPSV, CPSVI, CPSVII, or CPSVIII; or *Enterococcus faecalis* CPSA, CPSB, CPSC, or CPSD.~~

~~13.~~18. A recombinant glycoprotein produced by the Gram-negative bacterium of any one of claims ~~1-12~~ 1-17.

~~14.~~19. A method of producing a recombinant glycoprotein comprising culturing the Gram-negative bacterium of any one of claims ~~1-12~~ 1-17 under conditions suitable for the production of proteins~~, optionally further comprising purifying the recombinant glycoprotein~~.

20. A method of producing a recombinant glycoprotein according to claim 19, further comprising purifying the recombinant glycoprotein.

21. A method of producing a glycoconjugate vaccine which comprises pneumococcal polysaccharides, comprising producing recombinant glycoproteins by culturing the Gram-negative bacterium of any one of claims 1-17 under conditions suitable for the production of recombinant glycoproteins, wherein the recombinant glycoproteins comprise capsular polysaccharides selected from *S. pneumoniae* CPS1, CPS2, CPS3, CPS4, CPS5, CPS6 (A and B), CPS7 (A,B,C), CPS8, CPS9 (A,L,N,V), CPS10 (A,B,C,F), CPS11 (A,B,C,D,F), CPS12 (A,B,F), CPS13, CPS14, CPS15 (A,B,C,F), CPS16 (A,F), CPS17 (A,F), CPS18 (A,B,C,F), CPS19 (A,B,C,F), CPS20, CPS21, CPS22 (A,F), CPS23 (A,B,F), CPS24 (A,B,F), CPS25 (A,F), CPS26, CPS27, CPS28 (A,F), CPS29, CPS31, CPS32 (A,F), CPS33 (A,B,C,D,F), CPS34, CPS35 (A,B,C,D,F), CPS36, CPS37, CPS38, CPS39, CPS40, CPS41 (A,F), CPS42, CPS43, CPS44, CPS45, CPS46, CPS47 (A,F), or CPS48.

22. A method of producing a glycoconjugate vaccine according to claim 21 further comprising purifying the recombinant glycoproteins.

23. The method of producing a glycoconjugate vaccine of claim 21 or claim 22 wherein the recombinant glycoproteins comprise capsular polysaccharides selected from *S. pneumoniae* CPS1, CPS4 and CPS14.

~~15. An engineered *E. coli* cell comprising a *Plesiomonas shigelloides* O antigen gene cluster wherein the *wbgW* gene of the O antigen gene cluster is inactivated and wherein the *E. coli* cell produces Und-PP-D-FucNAc4N.~~

~~16. An engineered *E. coli* cell comprising a *Shigella sonnei* or *Plesiomonas shigelloides* O17 O antigen gene cluster wherein the *wbgW* gene of the O antigen gene cluster is inactivated and wherein the *E. coli* cell produces Und-PP-D-FucNAc4N.~~