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.

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 the Gram-negative bacterium comprises the complete capsular polysaccharide gene cluster.

4. The Gram-negative bacterium of claim 1, wherein the polysaccharide comprises an epitope of the capsular polysaccharide.

5. 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.

6. The Gram-negative bacterium of claim 5, wherein said Gram-negative bacterium is *E. coli*.

7. The Gram-negative bacterium of any one of the preceding claims, wherein said regulatory gene is a *Streptococcus pneumoniae* regulatory gene.

8. The Gram-negative bacterium of claim 7, wherein said *S. pneumoniae* regulatory gene is from *S. pneumoniae* Type 1.

9. The Gram-negative bacterium of claim 7, wherein said *S. pneumoniae* regulatory gene is from *S. pneumoniae* Type 4.

10. The Gram-negative bacterium of any one of the preceding claims, wherein said regulatory gene is a *Staphylococcus aureus* regulatory gene.

11. The Gram-negative bacterium of any one of the preceding claims, wherein said regulatory gene is a *Staphylococcus agalactiae* regulatory gene.

12. The Gram-negative bacterium of any one of the preceding claims, wherein said regulatory gene is an *Enterococcus faecalis* regulatory gene.

13. The Gram-negative bacterium of any one of the preceding claims, further comprising an oligosaccharyl transferase.

14. The Gram-negative bacterium of claim 13, wherein said oligosaccharyl transferase is heterologous to the Gram-negative bacterium.

15. The Gram-negative bacterium of any one of the preceding claims, further comprising at least one heterologous glycosyltransferase.

16. The Gram-negative bacterium of claim 15, wherein said heterologous glycosyltransferase is a prokaryotic glycosyltransferase.

17. The Gram-negative bacterium of claim 16, wherein the glycosyltransferase is obtained from the same Gram-positive bacterium as the regulatory gene.

18. 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.

19. The Gram-negative bacterium of claim 18, wherein said one or more deleted genes comprise the *waaL* gene.

20. The Gram-negative bacterium of claim 18, wherein said one or more deleted genes comprise all genes associated with O antigen biosynthesis in the Gram-negative bacterium.

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

22. 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.

23. The Gram-negative bacterium of claim 22, wherein the nucleic acid encoding the carrier protein is heterologous to the Gram-negative bacterium.

24. The Gram-negative bacterium of claim 22, wherein said carrier protein 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.

25. The Gram-negative bacterium of claim 22, wherein said carrier protein is an *S. pneumoniae* protein.

26. The Gram-negative bacterium of claim 22 or 24, wherein said carrier protein is conjugated to the polysaccharide by an oligosaccharyl transferase.

27. 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.

28. A vector capable of replication in a Gram-negative bacterium, wherein said vector comprises a regulatory gene associated with capsular polysaccharide biosynthesis in a Gram-positive bacterium.

29. The Gram-negative bacterium of any one of claims 1 to 27, wherein the expression and activity of UDP-glucose:undecaprenyl phosphate glucose-phosphate transferase activity is increased.

30. The Gram-negative bacterium of any one of claims 1 to 27, wherein the Gram-negative bacterium expresses WcaJ encoded by colanic acid wca operon of an enterocommonbacteriae (e.g., *E. coli* W3110).

31. An engineered Gram-negative bacterium for the production of a polysaccharide, wherein a gene encoding a Gtr enzyme of the Gram-negative bacterium is functionally inactivated.

32. The Gram-negative bacterium of claim 31 wherein the functional inactivation of the gene encoding a Gtr enzyme results in elimination of Und-P linked glucose.

33. The Gram-negative bacterium of claim 31 wherein the gene encoding a Gtr enzyme of the Gram-negative bacterium is deleted.

34. The Gram-negative bacterium of claim 31 or 33 wherein the genes encoding GtrA, GtrB, and/or GtrS are functionally inactivated.

35. The Gram-negative bacterium of claim 34 wherein the genes encoding GtrA, GtrB, and/or GtrS are deleted.

36. The Gram-negative bacterium of any one of claims 1 to 27 wherein the gene encoding a Gtr enzyme of the Gram-negative bacterium is functionally inactivated.

37. The Gram-negative bacterium of claim 36 wherein the gene encoding a Gtr enzyme of the Gram-negative bacterium is deleted.

38. The Gram-negative bacterium of claim 36 or 37 wherein the genes encoding GtrA, GtrB, and/or GtrS are functionally inactivated.

39. The Gram-negative bacterium of claim 38 wherein the genes encoding GtrA, GtrB, and/or GtrS are deleted.

40. The Gram-negative bacterium of claim 31, wherein said Gram-negative bacterium is selected from the group consisting of *Escherichia* species, *E. coli*, *Shigella* species, *Klebsiella* species, *Salmonella* species, *Yersinia* species, and *Pseudomonas* species.

41. The Gram-negative bacterium of any one of claims 31 to 40, further comprising an oligosaccharyl transferase.

42. The Gram-negative bacterium of claim 41, wherein said oligosaccharyl transferase is heterologous to the Gram-negative bacterium.

43. The Gram-negative bacterium of any one of claims 31 to 40, further comprising at least one glycosyltransferase that is heterologous to the Gram-negative bacterium.

44. The Gram-negative bacterium of claim 43, wherein said glycosyltransferase is a prokaryotic glycosyltransferase.

45. The Gram-negative bacterium of any one of claims 31 to 40, further comprising a nucleic acid encoding a carrier protein comprising a consensus sequence for glycosylation.

46. The Gram-negative bacterium of claim 45, wherein the nucleic acid encoding the carrier protein is heterologous to the Gram-negative bacterium.

47. The Gram-negative bacterium of claim 45, wherein said carrier protein is detoxified exotoxin A from *P. auruginosa*, 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, and *C. jejuni* natural glycoproteins.

48. The Gram-negative bacterium of claim 45, wherein said carrier protein is conjugated to the polysaccharide by the oligosaccharyl transferase.

49. The Gram-negative bacterium of claim 31 wherein the polysaccharide is a capsular polysaccharide of *Streptococcus pneumoniae*.

50. The Gram-negative bacterium of any one of claims 31 to 48, wherein the polysaccharide is an O antigen of *E. coli* (O1, O2, O3, O4, O5, O6, O7, O8, O9, O10, O11, O12, O13, O14, O15, O16, O17, O18, O19, O20, O21, O22, O23, O24, O25, O26, O27, O28, O29, O30, O32, O33, O34, O35, O36, O37, O38, O39, O40, O41, O42, O43, O44, O45, O46, O48, O49, O50, O51, O52, O53, O54, O55, O56, O57, O58, O59, O60, O61, O62, O63, O64, O65, O66, O68, O69, O70, O71, O73, O74, O75, O76, O77, O78, O79, O80, O81, O82, O83,

O84, O85, O86, O87, O88, O89, O90, O91, O92, O93, O95, O96, O97, O98, O99, O100, O101, O102, O103, O104, O105, O106, O107, O108, O109, O110, O111, O112, O113, O114, O115, O116, O117, O118, O119, O120, O121, O123, O124, O125, O126, O127, O128, O129, O130, O131, O132, O133, O134, O135, O136, O137, O138, O139, O140, O141, O142, O143, O144,O145, O146, O147, O148, O149, O150, O151, O152, O153, O154, O155, O156, O157, O158, O159, O160, O161, O162, O163, O164, O165, O166, O167, O168, O169, O170, O171, O172, O173, O174, O175, O176, O177, O178, O179, O180, O181, O182, O183, O184, O185, O186, O187), Salmonella sp (*S. enterica* subsp. Enterica, *S. enterica* subsp. Salamae, *S. enterica* subsp. arizonae, *S. enterica* subsp. Diarizonae, *S. enterica* subsp. Houtenae, *S. bongori*, and *S. enterica* subsp. Indica, and O types 1-67, Pseudomonas sp (*P. aeruginosa* O serotypes 1-20), Klebsiella sp. (particularly K. *pneumonia* serotypes O1, O2 (and subserotypes), O3, O4, O5, O6, O7, O8, O9, O10, O11, O12), Acinetobacter O antigens (in particular *A. baumannii* O antigens), *Chlamydia trachomatis* O antigens (serotypes A, B, C, D, E, F, G, H, I J, K, L1, L2, L3), *Vibrio cholera* O antigens O1 to 155, Listeria sp., in particular *L. monocytogenes* type 1, 2, 3, 4 and subserotypes thereof, *Legionella pneumophila* serotypes 1 to 15 O antigens, *Bordetella parapertussis* O antigens, *Burkholderia mallei and pseudomallei* O antigens, *Francisella tularensis*, Campylobacter sp. (C. jejuni); Capsular polysaccharides of *Clostridium difficile* (serotypes A, G, H, K, S1, S4, D, Cd-5, and *C. perfringens* serotypes A, B, C, D und E), *Staphylococcus aureus* type 5 and 8, *Streptococcus pyrogenes* (group B streptococcus capsular serotype polysaccharides), *E. coli*, *Streptococcus agalacticae* (group A streptococcal capsular polysaccharides), *Neisseria meningitidis* (serotypes A, B, C, W, Y, X), *Candida albicans*, *Haemophilus influenza*, *Enterococcus faecalis* capsular polysaccharides type I-V; and other surface polysaccharide structures, e.g. the *Borrelia burgdorferi* glycolipids), *Neisseria meningitidis* pilin O glycan and lipooligosaccharide (LOS), *Haemophilus influenza* LOS, Leishmania major lipophosphoglycan, tumor associated carbohydrate antigens, malaria glycosyl phosphatidylinositol, or mycobacterium tuberculosis arabinomannan.

51. A recombinant glycoprotein produced by the Gram-negative bacterium of any one of claims 1-27 and 29-50.

52. A method of producing a recombinant glycoprotein comprising culturing the Gram-negative bacterium of any one of claims 1-27 and 29-50 under conditions suitable for the production of proteins.

53. The method of claim 52 further comprising purifying the recombinant glycoprotein.

54. 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.

55. 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.

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.

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 any one of the preceding claims, wherein said regulatory gene is a *Staphylococcus aureus* regulatory gene.

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

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

8. 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.

9. 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.

10. 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. 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.

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

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

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.