WHAT IS CLAIMED IS:

1. A live, recombinant commensal bacterium, wherein the bacterium is engineered to express a non-native protein or peptide, wherein the protein or peptide is associated with a host disease or condition, wherein upon administration of the bacterium to the host resulting in colonization of a native host niche by the bacterium, the host mounts an adaptive immune response to the non-native protein or peptide, wherein the adaptive immune response is a regulatory T-cell (Treg) response or an effector T-cell (Teffector) response.

2. The recombinant commensal bacterium of claim 1, wherein the colonization of the native host niche is persistent or transient.

3. The recombinant commensal bacterium of claim 2, wherein the native host niche is transiently colonized, and wherein colonization is for 1 day to 60 days.

4. The recombinant commensal bacterium of claim 2, wherein the native host niche is transiently colonized, and wherein colonization is for 3.5 days to 60 days.

5. The recombinant commensal bacterium of claim 3 or 4, wherein the native host niche is transiently colonized, and wherein colonization is for 7 days to 28 days.

6. The recombinant commensal bacterium of any one of claims 1 – 5, wherein colonization is determined by polymerase chain reaction or colony forming assay performed on a sample obtained from the host after 1 day, 3.5 days, 7 days, 14 days, 28 days, or 60 days after administration to the host.

7. The recombinant commensal bacterium of any one of claims 1 – 6, wherein the administration results in interaction of the bacterium with a native immune system partner cell.

8. The recombinant commensal bacterium of claim 7, wherein the native immune system partner cell is an antigen-presenting cell.

9. The recombinant commensal bacterium of claim 8, wherein the antigen-presenting cell is selected from the group consisting of a dendritic cell, a macrophage, a B-cell, and an intestinal epithelial cell.

10. The recombinant commensal bacterium of any one of claims 1 – 9, wherein the native host niche is selected from the group consisting of the gastrointestinal tract, respiratory tract, urogenital tract, and skin.

11. The recombinant commensal bacterium of any one of claims 1 – 10, wherein the non-native protein or peptide is a host protein or peptide.

12. The recombinant commensal bacterium of any one of claims 1 – 11, wherein the bacterium is a Gram-negative bacterium.

13. The recombinant commensal bacterium of claim 12, wherein the Gram-negative bacterium is selected from the group consisting of Bacteroides thetaiotaomicron, Helicobacter hepaticus and Parabacteroides sp.

14. The recombinant commensal bacterium of any one of claims 1 – 11, wherein the bacterium is a Gram-positive bacterium.

15. The recombinant commensal bacterium of claim 14, wherein the Gram-positive bacterium is selected from the group consisting of Staphylococcus epidermidis, Faecalibacterium sp. and Clostridium sp.

16. The recombinant commensal bacterium of any one of claims 1 – 11, wherein the administration is via a route selected from the group consisting of topical, enteral, parenteral and inhalation.

17. The recombinant commensal bacterium of claim 16, wherein the route is topical.

18. The recombinant commensal bacterium of claim 17, wherein the bacterium is S. epidermidis.

19. The recombinant commensal bacterium of claim 16, wherein the route is enteral.

20. The recombinant commensal bacterium of claim 19, wherein the bacterium is selected from the group consisting of Bacteroides spp., Clostridium spp., Helicobacter spp., Parabacteroides spp, and Prevotella spp.

21. The recombinant commensal bacterium of claim 20, wherein the bacterium is selected from the group consisting of Bacteroides thetaiotaomicron, Bacteroides vulgatus and Bacteroides finegoldii.

22. The recombinant commensal bacterium of any one of claims 1 – 11, wherein the adaptive immune response is a Treg response and the bacterium is selected from the group consisting of Bacteroides spp., Helicobacter spp., Parabacteroides spp., Clostridium spp., Staphylococcus spp., Lactobacillus spp., Fusobacterium spp., Enterococcus spp., Acenitobacter spp., Flavinofractor spp., Lachnospiraceae spp., Erysipelotrichaceae spp., Anaerostipes spp., Anaerotruncus spp., Coprococcus spp., Clostridiales spp., Odoribacter spp., Collinsella spp., Bifidobacterium spp., Streptococcus spp., and Prevotella spp.

23. The recombinant commensal bacterium of claim 22, wherein the adaptive immune response is a Treg response and the bacterium is selected from the group consisting of Clostridium ramosum, Staphylococcus saprophyticus, Bacteroides thetaiotaomicron, Clostridium histolyticum, Lactobacillus rhamnosus, Parabacteroides johnsonii, Fusobacterium nucleatum, Enterococcus faecium, Lactobacillus casei, Acenitobacter lwofii, Bacteroides ovatus, ,Bacteroides vulgatus, Bacteroides uniformis, Bacteroides finegoldii, Clostridium spiroforme, Flavonifractor plautii, Clostridium hathewayi, Lachnospiraceae bacterium, Clostridium bolteae, Erysipelotrichaceae bacterium, Anaerostipes caccae, Anaerotruncus colihominis, Coprococcus comes , Clostridium asparagiforme, Clostridium symbiosum, Clostridium ramosum, Clostridium sp. D5, Clostridium scindens , Lachnospiraceae bacterium , Clostridiales bacterium , Bacteroides intestinalis, Bacteroides caccae, Bacteroides massiliensis, Parabacteroides distasonis, Odoribacter splanchnicus, Collinsella aerofaciens, Acinetobacter lwoffii, Bifidobacterium breve, Bacteroides finegoldii, Bacteroides fragilis, Bacteroides massiliensis, Bacteroides ovatus, Bifidobacterium bifidum, Lactobacillus acidofilus, Lactobacillus casei, Lactobacillus reuteri, Streptococcus thermophilus, and Prevotella histicola.

24. The recombinant commensal bacterium of claim 23, wherein the bacterium is selected from the group consisting of Bacteroides thetaiotaomicron, Bacteroides vulgatus, Bacteroides finegoldii and Helicobacter hepaticus.

25. The recombinant commensal bacterium of any one of claims 22 – 24, wherein the disease or condition is an autoimmune disorder.

26. The recombinant commensal bacterium of claim 25, wherein the autoimmune disorder is selected from the group consisting of multiple sclerosis, diabetes mellitus Type I, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, celiac disease, Graves' disease, Hashimoto's autoimmune thyroiditis, vitiligo, rheumatic fever, pernicious anemia/atrophic gastritis, alopecia areata, immune thrombocytopenic purpura, temporal arteritis,

ulcerative colitis, Crohn's disease, scleroderma, antiphospholipid syndrome, autoimmune hepatitis type 1, primary biliary cirrhosis, Sjogren's syndrome, Addison's disease, dermatitis herpetiformis, Kawasaki disease, sympathetic ophthalmia, HLA-B27 associated acute anterior uveitis, primary sclerosing cholangitis, discoid lupus erythematosus, polyarteritis nodosa, CREST Syndrome, myasthenia gravis, polymyositis/dermatomyositis, Still's disease, autoimmune hepatitis type 2, Wegener's granulomatosis, mixed Connective tissue disease, microscopic polyangiitis, autoimmune polyglandular syndrome, Felty's syndrome, autoimmune hemolytic anemia, chronic inflammatory demyelinating polyneuropathy, Guillain-Barre Syndrome, Behcet disease, autoimmune neutropenia, bullous pemphigoid, essential mixed cryoglobulinemia, linear morphea, autoimmune polyglandular syndrome 1 (APECED), acquired hemophilia A, Batten disease/neuronal ceroid lipofuscinoses, autoimmune pancreatitis, Hashimoto's encephalopathy, Goodpasture's disease, pemphigus vulgaris, autoimmune disseminated encephalomyelitis, relapsing polychondritis, Takayasu arteritis, Churg-Strauss syndrome, epidermolysis bullosa acquisita, cicatricial pemphigoid, pemphigus foliaceus, autoimmune hypoparathyroidism, autoimmune hypophysitis, autoimmune inner ear disease, autoimmune lymphoproliferative syndrome, autoimmune oophoritis, autoimmune orchitis, autoimmune polyglandular syndrome, Cogan's syndrome, encephalitis lethartica, erythema elevatum diutinum, Evans syndrome, immunodysregulation polyendocrinopathy enteropathy X-linked (IPEX), Issac's syndrome/acquired neuromyotonia, Miller Fisher syndrome, Morvan's syndrome, PANDAS, POEMS syndrome, Rasmussen's encephalitis, stiff-person syndrome, Vogt-Koyanagi-Harada syndrome, neuromyelitis optica, graft vs host disease, and autoimmune uveitis.

27. The recombinant commensal bacterium of claim 25 or 26, wherein the autoimmune disorder is selected from the group consisting of multiple sclerosis and diabetes mellitus Type I.

28. The recombinant commensal bacterium of claim 25 or 26, wherein the non-native protein or peptide is selected from the group consisting of ovalbumin, myelin oligodendrocyte glycoprotein, insulin, chromogranin A, hybrid insulin peptides, proteolipid protein, myelin basic protein, villin, epithelial cellular adhesion molecule, collagen alpha-1, aggrecan core protein, 60kDa chaperonin 2, vimentin, alpha-enolase, fibrinogen alpha chain, fibrinogen beta chain, chitinase-3-like protein, 60kDa mitochondrial heat shock protein, matrix metalloproteinase-16, thyroid peroxidase, thyrotropin receptor, thyroglobulin, gluten, TSHR protein, glutamate decarboxylase 2, receptor-type tyrosine-protein phosphatase-like N, glucose-6-phosphatase 2, insulin isoform 2, zinc transporter 8, glutamate decarboxylase 1, GAD65, UniProt:A2RGM0,

integrin alpha-Iib, integrin beta-3, EBV DNA polymerase catalytic subunit, 2’3’-cyclic-nucleotide 3’ phosphodiesterase, myelin associated oligodendrocyte basic protein, small nuclear ribonucleoprotein, U1 small nuclear ribonucleoprotein, histone H2B, histone H2A, histone H3.2, beta-2-glycoprotein, histone H4, 60S ribosomal protein L7, TNF-alpha, myeloperoxidase, Cbir1, MS4A12, DNA topoisomerase, CYP2D6, O-phosphoseryl-tRNA selenium transferase, pyruvate dehydrogenase complex, spectrin alpha chain, steroid 21-hydroxylase, acetylcholine receptor, MMP-16, keratin associated proteins. Chondroitin sulfate proteoglycan 4, myeloblastin, U1 small nuclear ribonucleoprotein 70 kDa, blood group Rh(D), blood group Rh(CE), myelin P2 protein, peripheral myelin protein 22, myelin protein P0, S-arrestin, collagen Alpha-1, coagulation factor VIII, collagen alpha-3(IV), desmoglein-3, desmoglein-1, Insulin-2, major DNA-binding protein, tyrosinase, 5,6-dihydroxyindole-2-carboxylic acid oxidase, HLA-A2, aquaporin-4, myelin proteolipid protein, ABC transporter, HLA I B-27 alpha chain, HLA I B-7 alpha chain, and retinol-binding protein 3.

29. The recombinant commensal bacterial of claim 28, wherein the non-native protein or peptide is selected from the group consisting of ovalbumin, myelin oligodendrocyte glycoprotein, insulin, chromogranin A, hybrid insulin peptides, proteolipid protein, myelin basic protein, villin, epithelial cellular adhesion molecule,

30. The recombinant commensal bacterium of any one of claims 22 – 29, wherein the bacterium is engineered to secrete the expressed protein or peptide.

31. The recombinant commensal bacterium of any one of claims 22 – 29, wherein the bacterium is engineered to express a fusion protein comprising the protein or peptide and a native bacterial protein or portion thereof.

32. The recombinant commensal bacterium of claim 31, wherein the protein or peptide is fused to the N-terminus or the C-terminus of the native bacterial protein or portion thereof.

33. The recombinant commensal bacterium of claim 31 or 32, wherein the native bacterial protein is selected from the group consisting of sialidase, endonuclease, secreted endoglycosidase, anti-sigma factor, thiol peroxidase, hypothetical protein BT_2621, hypothetical protein BT_3223, peptidase, Icc family phosphohydrolase, exo-poly-alpha-D-galacturonosidase, and hypothetical protein BT_4428.

34. The recombinant commensal bacterium of claim 33, wherein the native bacterial protein is sialidase or anti-sigma factor.

35. The recombinant commensal bacterium of any one of claims 1-11, wherein the adaptive immune response is a Teffector response and the bacterium is selected from the group consisting of S. epidermidis, Corynebacterium spp., Parabacteroides distasonis, Parabacteroides gordonii, Alistipes senegalensis, Parabacteroides johnsonii, Paraprevotella xylaniphila, Bacteroides dorei, Bacteroides uniformis JCM 5828, Eubacterium limosum, Ruminococcaceae bacterium cv2, Phascolarctobacterium faecium, Fusobacterium ulcerans, Klebsiella pneumoniae , Clostridium bolteae 90B3, Clostridium cf. saccharolyticum K10, Clostridium symbiosum WAL-14673, Clostridium hathewayi 12489931, Ruminococcus obeum A2-162, Ruminococcus gnavus AGR2154, Butyrate-producing bacterium SSC/2, Clostridium sp. ASF356, Coprobacillus sp. D6 cont1.1 , Eubacterium sp. 3_1_31 cont1.1, Erysipelotrichaceae bacterium 21_3 , Subdoligranulum sp. 4_3_54A2FAA, Ruminococcus bromii L2-63, Firmicutes bacterium ASF500, Firmicutes bacterium ASF500, Bacteroides dorei 5_1_36/D4 supercont2.3, Bifidobacterium animalis subsp. Lactis ATCC 27673, and Bifidobacterium breve UCC2003.

36. The recombinant commensal bacterium of claim 35, wherein the bacterium is selected from the group consisting of S. epidermidis LM087 and Corynebacterium spp.

37. The recombinant commensal bacterium of claim 35 or 36, wherein the disease or condition is a proliferative disorder.

38. The recombinant commensal bacterium of claim 37, wherein the proliferative disorder is cancer.

39. The recombinant commensal bacterium of claim 38, wherein the cancer is selected from melanoma, basal cell carcinoma, squamous cell carcinoma, and testicular cancer.

40. The recombinant commensal bacterium of claim 38, wherein the cancer is melanoma.

41. The recombinant commensal bacterium of any one of claims 35 – 37 wherein the non-native protein or peptide is selected from the group consisting of PMEL, TRP2, MART-1, NY-ESO, MAGE-A, and a neoantigen.

42. The recombinant commensal bacterium of claim 41, wherein the non-native protein or peptide is PMEL.

43. The recombinant commensal bacterium of any one of claims 35 – 42, wherein the bacterium is engineered to secrete the expressed protein or peptide.

44. The recombinant commensal bacterium of any one of claims 35 – 42, wherein the bacterium is engineered to express a fusion protein comprising the protein or peptide and a native bacterial protein or portion thereof.

45. The recombinant commensal bacterium of claim 44, wherein the protein or peptide is fused to the N-terminus or the C-terminus of the native bacterial protein or portion thereof.

46. The recombinant commensal bacterium of any one of claims 35 – 45, wherein the native bacterial protein is selected from the group consisting of sialidase, endonuclease, secreted endoglycosidase, anti-sigma factor, thiol peroxidase, hypothetical protein BT_2621, hypothetical protein BT_3223, peptidase, Icc family phosphohydrolase, exo-poly-alpha-D-galacturonosidase, and hypothetical protein BT_4428.

47. The recombinant commensal bacterium of claim 46, wherein the native bacterial protein is sialidase or anti-sigma factor.

48. The recombinant commensal bacterium of any one of claims 1 – 47, wherein the bacterium is to be administered in combination with a high-complexity defined microbial community.

49. The recombinant commensal bacterium of any one of claims 1 – 48, wherein the host is a mammal.

50. The recombinant commensal bacterium of claim 49, wherein the mammal is a human.

51. A polynucleotide used to engineer the recombinant commensal bacterium of any one of claims 1 - 50.

52. A method for generating an antigen-presenting cell displaying an antigen derived from a non-native protein or peptide, comprising: administering the recombinant commensal bacterium of any one of claims 1 – 50 to a subject, wherein the administration results in colonization of the native host niche by the bacterium, internalization of the bacterium by an antigen-presenting cell, and presentation of the antigen by the antigen-presenting cell.

53. The method of claim 52, wherein the colonization of the native host niche is persistent or transient.

54. The method of claim 53, wherein the native host niche is transiently colonized, and wherein colonization is for 1 day to 60 days.

55. The method of claim 54, wherein the native host niche is transiently colonized, and wherein colonization is for 3.5 days to 60 days.

56. The method of claim 54 or 55, wherein the native host niche is transiently colonized, and wherein colonization is for 7 days to 28 days.

57. The method of any one of claims 52 – 56, wherein colonization is determined by polymerase chain reaction or colony forming assay performed on a sample obtained from the host after 1 day, 3.5 days, 7 days, 14 days, 28 days, or 60 days after administration to the host.

58. The method of any one of claims 52 – 57, wherein the administration results in interaction of the bacterium with a native immune system partner cell.

59. The method of claim 58, wherein the native immune system partner cell is the antigen-presenting cell.

60. The method of claim 59, wherein the antigen-presenting cell is selected from the group consisting of a dendritic cell, a macrophage, a B-Cell, and an intestinal epithelial cell.

61. The method of any one of claims 52 – 60, wherein the native host niche is selected from the group consisting of the gastrointestinal tract, respiratory tract, urogenital tract, and skin.

62. The method of any one of claims 52 – 61, wherein the presentation is within an MHC II complex.

63. The method of any one of claims 52 – 61, wherein the presentation is within an MHC I complex.

64. The method of any one of claims 52 – 63, wherein the bacterium is a Gram-negative bacterium.

65. The method of claim 64, wherein the Gram-negative bacterium is selected from the group consisting of Bacteroides thetaiotaomicron, Helicobacter hepaticus, Parabacteroides sp., and Prevotella spp.

66. The method of any one of claims 52 – 63, wherein the bacterium is a Gram-positive bacterium.

67. The method of claim 66, wherein the Gram-positive bacterium is selected from the group consisting of Staphylococcus epidermidis, Faecalibacterium sp. and Clostridium sp.

68. The method of any one of claims 52 – 63, wherein the administration is via a route selected from the group consisting of topical, enteral, parenteral and inhalation.

69. The method of claim 68, wherein the route is topical.

70. The method of claim 69, wherein the bacterium is S. epidermidis.

71. The method of claim 68, wherein the route is enteral.

72. The method of claim 71, wherein the bacterium is selected from the group consisting of Bacteroides spp., Clostridium spp., Helicobacter spp., Parabacteroides spp, and Prevotella spp.

73. The method of claim 72, wherein the bacterium is selected from the group consisting of Bacteroides thetaiotaomicron, Bacteroides vulgatus and Bacteroides finegoldii.

74. The method of claim 73, wherein the native bacterial protein is selected from the group consisting of sialidase, endonuclease, secreted endoglycosidase, anti-sigma factor, thiol peroxidase, hypothetical protein BT_2621, hypothetical protein BT_3223, peptidase, Icc family phosphohydrolase, exo-poly-alpha-D-galacturonosidase, and hypothetical protein BT_4428.

75. The method of claim 74, wherein the native bacterial protein is sialidase or anti-sigma factor.

76. The method of claim 75, wherein the non-native protein or peptide is melanocyte oligodendrocyte glycoprotein.

77. The method of claim 76, wherein the disease or condition is multiple sclerosis.

78. Use of the recombinant commensal bacterium of any one of claims 1-50 in the manufacture of a medicament ~~A method~~ for generating a T-cell response in a subject~~,~~ ~~comprising: administering the recombinant commensal bacterium of any one of claims 1-50 to the subject~~, wherein the administration of the medicament results in colonization of a native host niche by the bacterium and generation of the T-cell response, wherein the T-cell response is to an antigen derived from the non-native protein or peptide.

79. The use~~method~~ of claim 78, wherein the colonization of the native host niche is persistent or transient.

80. The use~~method~~ of claim 79, wherein the native host niche is transiently colonized, and wherein colonization is for 1 day to 60 days.

81. The use~~method~~ of claim 80, wherein the native host niche is transiently colonized, and wherein colonization is for 3.5 days to 60 days.

82. The use~~method~~ of claim 80 or 81, wherein the native host niche is transiently colonized, and wherein colonization is for 7 days to 28 days.

83. The use~~method~~ of any one of claims 78 – 82, wherein colonization is determined by polymerase chain reaction or colony forming assay performed on a sample obtained from the host after 1 day, 3.5 days, 7 days, 14 days, 28 days, or 60 days after administration to the host.

84. The use~~method~~ of any one of claims 78 - 83, wherein the administration is via a route selected from the group consisting of topical, enteral, parenteral and inhalation.

85. The use~~method~~ of claim 84, wherein the route is topical.

86. The use~~method~~ of claim 84, wherein the route is enteral.

87. ~~.~~The use~~method~~ of any one of claims 84 - 86, wherein the bacterium is selected from the group consisting of Bacteroides spp., Clostridium spp., Helicobacter spp., Parabacteroides spp, Prevotella spp., and Staphylococcus epidermidis.

88. The use~~method~~ of any one of claims 84-87, wherein the T-cell response is a Treg or a Teffector response.

89. The use~~method~~ of claim 88, wherein the route is enteral and the T-cell response is a Treg response.

90. The use~~method~~ of claim 89, wherein the bacterium is selected from the group consisting of Bacteroides spp., Clostridium spp., Helicobacter spp., Parabacteroides spp, and Prevotella spp.

91. The use~~method~~ of claim 90, wherein the bacterium is selected from the group consisting of Bacteroides thetaiotaomicron, Bacteroides vulgatus, and Bacteroides finegoldii.

92. The usemethod of claim 91, wherein the native bacterial protein is selected from the group consisting of sialidase, endonuclease, secreted endoglycosidase, anti-sigma factor, thiol peroxidase, hypothetical protein BT_2621, hypothetical protein BT_3223, peptidase, Icc family phosphohydrolase, exo-poly-alpha-D-galacturonosidase, and hypothetical protein BT_4428.

93. The usemethod of claim 92, wherein the native bacterial protein is sialidase or anti-sigma factor.

94. The usemethod of claim 93, wherein the non-native protein or peptide is myelin oligodendrocyte glycoprotein.

95. The usemethod of claim 94, wherein the disease or condition is multiple sclerosis.

96. The usemethod of claim 88, wherein the route is topical and the T-cell response is a Teffector response.

97. The usemethod of claim 96, wherein the bacterium is S. epidermidis.

98. Use of the recombinant commensal bacterium of any one of claims 1-50 in the manufacture of a medicamentA method of for treating a disease or condition in a subject, comprising: administering the recombinant commensal bacterium of any one of claims 1-50 to the subject, wherein the administration of the medicament results in colonization of a native host niche by the bacterium and generation of a T-cell response, wherein the T-cell response is to an antigen derived from the non-native protein or peptide, and wherein the T-cell response treats the disease or condition in the subject.

99. The usemethod of claim 98, wherein the colonization of the native host niche is persistent or transient.

100. The usemethod of claim 99, wherein the native host niche is transiently colonized, and wherein colonization is for 1 day to 60 days.

101. The usemethod of claim 100, wherein the native host niche is transiently colonized, and wherein colonization is for 3.5 days to 60 days.

102. The usemethod of claim 100 or 101, wherein the native host niche is transiently colonized, and wherein colonization is for 7 days to 28 days.

103. The use~~method~~ of any one of claims 98 – 102, wherein colonization is determined by polymerase chain reaction or colony forming assay performed on a sample obtained from the host after 1 day, 3.5 days, 7 days, 14 days, 28 days, or 60 days after administration to the host.

104. The use~~method~~ of claim any one of claims 98 - 104, wherein the disease or condition is selected from the group consisting of an autoimmune disorder and a proliferative disorder.

105. The use~~method~~ of claim 104, wherein the autoimmune disorder is selected from the group consisting of multiple sclerosis, diabetes mellitus Type I, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, celiac disease, Graves' disease, Hashimoto's autoimmune thyroiditis, vitiligo, rheumatic fever, pernicious anemia/atrophic gastritis, alopecia areata, immune thrombocytopenic purpura, temporal arteritis, ulcerative colitis, Crohn's disease, scleroderma, antiphospholipid syndrome, autoimmune hepatitis type 1, primary biliary cirrhosis, Sjogren's syndrome, Addison's disease, dermatitis herpetiformis, Kawasaki disease, sympathetic ophthalmia, HLA-B27 associated acute anterior uveitis, primary sclerosing cholangitis, discoid lupus erythematosus, polyarteritis nodosa, CREST Syndrome, myasthenia gravis, polymyositis/dermatomyositis, Still's disease, autoimmune hepatitis type 2, Wegener's granulomatosis, mixed Connective tissue disease, microscopic polyangiitis, autoimmune polyglandular syndrome, Felty's syndrome, autoimmune hemolytic anemia, chronic inflammatory demyelinating polyneuropathy, Guillain-Barre Syndrome, Behcet disease, autoimmune neutropenia, bullous pemphigoid, essential mixed cryoglobulinemia, linear morphea, autoimmune polyglandular syndrome 1 (APECED), acquired hemophilia A, Batten disease/neuronal ceroid lipofuscinoses, autoimmune pancreatitis, Hashimoto's encephalopathy, Goodpasture's disease, pemphigus vulgaris, autoimmune disseminated encephalomyelitis, relapsing polychondritis, Takayasu arteritis, Churg-Strauss syndrome, epidermolysis bullosa acquisita, cicatricial pemphigoid, pemphigus foliaceus, autoimmune hypoparathyroidism, autoimmune hypophysitis, autoimmune inner ear disease, autoimmune lymphoproliferative syndrome, autoimmune oophoritis, autoimmune orchitis, autoimmune polyglandular syndrome, Cogan's syndrome, encephalitis lethartica, erythema elevatum diutinum, Evans syndrome, immunodysregulation polyendocrinopathy enteropathy X-linked (IPEX), Issac's syndrome/acquired neuromyotonia, Miller Fisher syndrome, Morvan's syndrome, PANDAS, POEMS syndrome, Rasmussen's encephalitis, stiff-person syndrome, Vogt-Koyanagi-Harada syndrome, neuromyelitis optica, graft vs host disease, and autoimmune uveitis.

106. The use~~method~~ of claim 105, wherein the autoimmune disorder is selected from the group consisting of multiple sclerosis, and diabetes mellitus Type I.

107. The use~~method~~ of claim 104, wherein the proliferative disorder is cancer.

108. The use~~method~~ of claim 107, wherein the cancer is selected from melanoma, basal cell carcinoma, squamous cell carcinoma, and testicular cancer.

109. The use~~method~~ of claim 107, wherein the cancer is melanoma.

110. The use~~method~~ of any one of claims 98 - 109, wherein the administration is via a route selected from the group consisting of topical, enteral, parenteral and inhalation.

111. The use~~method~~ of claim 110, wherein the route is topical.

112. The use~~method~~ of claim 111, wherein the bacterium is S. epidermidis.

113. The use~~method~~ of claim 112, wherein the disease is cancer.

114. The use~~method~~ of claim 113, wherein the cancer is melanoma.

115. The use~~method~~ of claim 113, wherein the non-native protein or peptide is selected from the group consisting of a melanocyte-specific antigen and a testis cancer antigen.

116. The use~~method~~ of claim 115, wherein the melanocyte-specific antigen is selected from the group consisting of PMEL, TRP2 and MART-1.

117. The use~~method~~ of claim 115, wherein the testis cancer antigen is selected from the group consisting of NY-ESO and MAGE-A.

118. The use~~method~~ of claim 110, wherein the route is enteral.

119. The use~~method~~ of claim 118, wherein the bacterium is selected from the group consisting of Bacteroides spp., Clostridium spp., Helicobacter spp., Parabacteroides spp, and Prevotella spp.

120. The use~~method~~ of claim 119, wherein the bacterium is selected from the group consisting of Bacteroides thetaiotaomicron, Bacteroides vulgatus, and Bacteroides finegoldii.

121. The use~~method~~ of claim 120, wherein the native bacterial protein is selected from the group consisting of sialidase, endonuclease, secreted endoglycosidase, anti-sigma factor, thiol peroxidase, hypothetical protein BT_2621, hypothetical protein BT_3223, peptidase, Icc family phosphohydrolase, exo-poly-alpha-D-galacturonosidase, and hypothetical protein BT_4428.

122. The use~~method~~ of claim 121, wherein the native bacterial protein is sialidase or anti-sigma factor.

123. The use~~method~~ of any one of claims 118 - 122, wherein the autoimmune disorder is selected from the group consisting of multiple sclerosis, diabetes mellitus Type I, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, celiac disease, Graves' disease, Hashimoto's autoimmune thyroiditis, vitiligo, rheumatic fever, pernicious anemia/atrophic gastritis, alopecia areata, immune thrombocytopenic purpura, temporal arteritis, ulcerative colitis, Crohn's disease, scleroderma, antiphospholipid syndrome, autoimmune hepatitis type 1, primary biliary cirrhosis, Sjogren's syndrome, Addison's disease, dermatitis herpetiformis, Kawasaki disease, sympathetic ophthalmia, HLA-B27 associated acute anterior uveitis, primary sclerosing cholangitis, discoid lupus erythematosus, polyarteritis nodosa, CREST Syndrome, myasthenia gravis, polymyositis/dermatomyositis, Still's disease, autoimmune hepatitis type 2, Wegener's granulomatosis, mixed Connective tissue disease, microscopic polyangiitis, autoimmune polyglandular syndrome, Felty's syndrome, autoimmune hemolytic anemia, chronic inflammatory demyelinating polyneuropathy, Guillain-Barre Syndrome, Behcet disease, autoimmune neutropenia, bullous pemphigoid, essential mixed cryoglobulinemia, linear morphea, autoimmune polyglandular syndrome 1 (APECED), acquired hemophilia A, Batten disease/neuronal ceroid lipofuscinoses, autoimmune pancreatitis, Hashimoto's encephalopathy, Goodpasture's disease, pemphigus vulgaris, autoimmune disseminated encephalomyelitis, relapsing polychondritis, Takayasu arteritis, Churg-Strauss syndrome, epidermolysis bullosa acquisita, cicatricial pemphigoid, pemphigus foliaceus, autoimmune hypoparathyroidism, autoimmune hypophysitis, autoimmune inner ear disease, autoimmune lymphoproliferative syndrome, autoimmune oophoritis, autoimmune orchitis, autoimmune polyglandular syndrome, Cogan's syndrome, encephalitis lethartica, erythema elevatum diutinum, Evans syndrome, immunodysregulation polyendocrinopathy enteropathy X-linked (IPEX), Issac's syndrome/acquired neuromyotonia, Miller Fisher syndrome, Morvan's syndrome, PANDAS, POEMS syndrome, Rasmussen's encephalitis, stiff-person syndrome, Vogt-Koyanagi-Harada syndrome, neuromyelitis optica, graft vs host disease, and autoimmune uveitis.

124. The use~~method~~ of claim 123, wherein the autoimmune disorder is multiple sclerosis.

125. The use~~method~~ of claim 124, wherein the bacterium is selected from the group consisting of Bacteroides thetaiotaomicron, Bacteroides vulgatus, and Bacteroides finegoldii.

126. The use~~method~~ of claim 125, wherein the non-native protein is myelin oligodendrocyte glycoprotein.

127. The use~~method~~ of any one of claims 52 - 126, wherein the bacterium is to be administered in combination with a high-complexity defined microbial community.

128. The use~~method~~ of any one of claims 52 - 127, wherein the host is a mammal.

129. The use~~method~~ of claim 128, wherein the mammal is a human.