WHAT IS CLAIMED IS:

1. A method for preventing or treating an alcohol hangover, comprising administering to the gut of a subject in need thereof an effective amount of a composition comprising a recombinant bacterium recombinantly engineered to constitutively express an aldehyde dehydrogenase.

2. The method of claim **1**, wherein the recombinant bacteria comprises:

a) a polynucleotide comprising an expression construct comprising a flagellin gene promoter operatively linked with a heterologous nucleotide sequence encoding an aldehyde dehydrogenase, wherein the flagellin gene promoter comprises one or more genetic modifications that reduce CsrA repression of translation of an mRNA transcribed from the flagellin gene promoter; and

b) a genetic modification of a sigma factor repressor, wherein the modification reduces inhibition of sigma factor initiation of transcription from the flagellin gene promoter.

3. The method of claim **2**, wherein the bacterium belongs to a genus selected from *Bacillus, Bifidobacterium, Enterococcus, Escherichia, Lactobacillus, Leuconostoc, Pediococcus, Pediococcus* and *Streptococcus*.

4. The method of claim **2**, wherein (1) the bacterium belongs to genus *Bacillus*, (2) the flagellin gene promoter is a modified Bacillus hag promoter comprising one or more genetic modifications of the CsrA BS1 binding site and/or the CsrA BS2 binding site, (3) the sigma factor is SigD and (4) the SigD repressor is *FlgM*.

5. The method of claim **4**, wherein the *hag* promoter comprises one or more genetic modifications in the 12-base-pair BS1 binding site or in the surrounding bases on either side of the binding site that form the stem of the stem-loop secondary structure of BS1.

6. The method of claim **4**, wherein the *hag* promoter comprises a modification of the CsrA BS1 recognition sequence, AGGA.

7. The method of claim **4**, wherein the *hag* promoter comprises the nucleotide sequence GCACAAGAACGT [SEQ ID NO:2].

8. The method of claim **4**, wherein the one or more genetic modifications comprise one or more point mutations to the CsrA BS2 binding site.

9. The method of claim **4**, wherein the *hag* promoter comprises one or more genetic modifications that disrupt the stem and loop structure of BS2 by eliminating complementarity that allows hydrogen bonding.

10. The method of claim **4**, wherein the *hag* promoter comprises a modification of the BS2 binding site, wherein the modification comprises the nucleotide sequence ATTTAGGGAGGAA [SEQ ID NO:3].

11. The method of claim **1**, wherein the aldehyde dehydrogenase is a bacterial aldehyde dehydrogenase.

12. The method of claim **4**, wherein the aldehyde dehydrogenase is selected from (1) AcoD from *Cupriavidus necator* and (2) AldB from *E. coli*.

13. The method of claim **4**, wherein the genetic modification in a *flgM* gene comprises deletion of all or part of the *flgM* gene.

14. The method of claim **4**, wherein the genetic modification in a *flgM* gene disrupts secondary or tertiary structure.

15. The method of claim **4**, wherein the expression construct is located in a bacterial chromosome.

16. The method of claim **1**, comprising administering the composition to the subject during consumption of alcohol.

17. The method of claim **1**, comprising administering the composition to the subject up to 24 hours before commencement of consumption of alcohol.

18. The method of claim **1**, wherein the composition is administered orally.

19. The method of claim **1**, wherein the composition further comprises a physiologically acceptable carrier selected from lactic acid fermented foods, fermented dairy products, resistant starch, dietary fibers, carbohydrates, proteins and glycosylated proteins, water, capsule filler, and a gummy material.

20. The method of claim **1**, wherein the composition comprises about 10^4 to about 10^{12} colony forming units of the recombinant bacteria.

21. A recombinant microorganism comprising:

a) a polynucleotide comprising an expression construct comprising a flagellin gene promoter operatively linked with a heterologous nucleotide sequence encoding a subject polypeptide, wherein the flagellin gene promoter comprises one or more genetic modifications that reduce CsrA repression of translation of an mRNA transcribed from the flagellin gene promoter; and

b) a genetic modification of a *flgM* gene that reduces inhibition of SigD initiation of transcription.

22. The recombinant microorganism of claim **21**, which constitutively expresses the polypeptide.

23. The recombinant microorganism of claim **21**, wherein the microorganism is probiotic.

24. The recombinant microorganism of claim **21**, wherein the microorganism belongs to genus selected from *Bacillus, Bifidobacterium, Enterococcus, Escherichia coli, Lactobacillus, Leuconostoc, Pediococcus, Pediococcus* and *Streptococcus*.

25. The recombinant microorganism of claim **21**, wherein the microorganism belongs to genus *Bacillus*.

26. The recombinant microorganism of claim **21**, wherein the microorganism is *B. subtilis*.

27. The recombinant microorganism of any of the foregoing claims, wherein the flagellin gene promoter is a *hag* promoter.

28. The recombinant microorganism of claim **27**, wherein the *hag* promoter comprises one or more genetic modifications that reduce CsrA repression of translation of an mRNA transcribed from the flagellin gene promoter, wherein the genetic modification comprises modification of the CsrA BS1 binding site and/or CsrA BS2 binding site (e.g., nucleotide substitution, insertion or deletion).

29. The recombinant microorganism of claim **28**, wherein the one or more genetic modifications comprise one or a plurality (e.g., two, three or four) of genetic modifications to the CsrA BS1 recognition sequence, AGGA, e.g., to the sequence AGAA.

30. The recombinant microorganism of claim **28**, wherein the one or more genetic modifications comprise one or more genetic modifications in the 12-base-pair BS1 binding

site or in the surrounding bases on either side of the binding site that form the stem of the stem-loop secondary structure of BS1.

31. The recombinant microorganism of claim **28**, wherein the one or more genetic modifications comprise one or a plurality (e.g., at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12) of genetic modifications in the BS1 binding site, gcacaaggacgt.

32. The recombinant microorganism of claim **28**, wherein the one or more genetic modifications disrupt the stem and loop structure of BS1 by eliminating complementarity that allows hydrogen bonding.

33. The recombinant microorganism of claim **28**, wherein the one or more genetic modifications comprise one or a plurality of genetic modifications in the sequence taagggcacaaggacgtgcctta [SEQ ID NO: 1] that are involved in hydrogen bonding, for example, to eliminate one, two, three, four or more hydrogen bond pairs.

34. The recombinant microorganism of claim **28**, wherein the modified BS1 has the nucleotide sequence GCACAAGAACGT [SEQ ID NO: 2].

35. The recombinant microorganism of claim **28**, wherein the one or more genetic modifications comprise one or more point mutations to the CsrA BS2 binding site.

36. The recombinant microorganism of claim **28**, wherein the one or more genetic modifications comprise one or a plurality (e.g., at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13) of genetic modification in the 13-base-pair BS2 binding site or in the surrounding bases on either side of the binding site that form the stem of the stem-loop secondary structure of BS2.

37. The recombinant microorganism of claim **28**, wherein the one or more genetic modifications disrupt the stem and loop structure of BS2 by eliminating complementarity that allows hydrogen bonding.

38. The recombinant microorganism of claim **28**, wherein the modified BS2 has the nucleotide sequence ATTTAGGGAGGAA [SEQ ID NO: 3].

39. The recombinant microorganism of claim **28**, wherein the one or more genetic modifications to the BS2 binding site does not include an alteration of nucleotides in the Shine-Dalgarno sequence agggagga.

40. The recombinant microorganism of any of the foregoing claims, wherein the flagellin gene promoter is located in a bacterial chromosome or in a plasmid.

41. The recombinant microorganism of any of the foregoing claims, wherein the subject polypeptide is an aldehyde dehydrogenase.

42. The recombinant microorganism of claim **41**, wherein the aldehyde dehydrogenase is AcoD from *Cupriavidus necator* and comprises an amino acid sequence identical to or substantially identical to:
MNMAEIAQLGVSNPYKQQYENYIGGAWVPPAGGEYFESTTPITGKPFTRVPRSGQQDVDA
ALDAAHAAKAAWARTSTTERANILNRIADRIEANLKLLAVAESIDNGKPVRETTAADLPLAVD
HFRYFAGCIRAQEGGISEIDADTIAYHFHEPLGVVGQIIPWNFPLLMATWKLAPALAAGNCVV
LKPAEQTPASILVLMEVIGDLLPPGVVNVINGFGLEAGKPLASSPRISKVAFTGETTTGRLIM
QYASQNLIPVTLELGGKSPNIFFEDVLAADDAFFDKALEGFAMFALNQGEVCTCPSRALIQE
SIYDRFMERALKRVAAIRQGHPLDTGTMIGAQASAEQLEKILSYIDLGRKEGAQCLTGGERN
VLDGDLAGGYYVKPTVFAGHNKMRIFQEEIFGPVVSVTTFKDEEEALAIANDTLYGLGAGV
WTRDGARAFRMGRGIQAGRVWTNCYHAYPAHAAFGGYKQSGIGRENHRMMLDHYQQTK
NLLVSYSPNALGFF [SEQ ID NO: 4].

43. The recombinant microorganism of claim **41**, wherein the aldehyde dehydrogenase is a human aldehyde dehydrogenase, e.g., having an amino acid sequence identical to or substantially identical to
MLRAAARFGPRLGRRLLSAAATQAVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPS
TGEVICQVAEGDKEDVDKAVKAARAAFQLGSPWRRMDASHRGRLLNRLADLIERDRTYLA
ALETLDNGKPYVISYLVDLDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCG
QIIPWNFPLLMQAWKLGPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPG
FGPTAGAAIASHEDVDKVAFTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADM
DWAVEQAHFALFFNQGQCCCAGSRTFVQEDIYDEFVERSVARAKSRVVGNPFDSKTEQG
P
QVDETQFKKILGYINTGKQEGAKLLCGGGIAADRGYFIQPTVFGDVQDGMTIAKEEIFGP
VMQILKFKTIEEVVGRANNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQS
PFGGYKMSGSGRELGEYGLQAYTEVKTVTVKVPQKNS [SEQ ID NO: 5].

44. The recombinant microorganism of claim **21**, wherein the genetic modification in a *flgM* gene comprises deletion of all or part of the *flgM* gene.

45. The recombinant microorganism of claim **21**, wherein the genetic modification in a *flgM* gene comprises a single mutation or series of mutations in the sequence encoding active sites of *flgM*.

46. The recombinant microorganism of claim **21**, wherein the genetic modification in a *flgM* gene disrupts secondary or tertiary structure, such as in one of the helices that defines FlgM secondary structure.

47. The recombinant microorganism of claim **21**, wherein the genetic modification in a *flgM* gene comprises altering an amino acid in the 3rd or 4th helix at the C-terminal end of the FlgM protein, e.g., selected from I-58, K-62, I-65, G-68, D-73, A-78 of the B. subtilis FlgM.

48. The recombinant microorganism of claim **21**, wherein the genetic modification in a *flgM* gene comprises altering one or more amino acids predicted to participate in FlgM binding to SigD, e.g., selected from I-3, G-7, S-10, V-11, A-40, K-41, M43, I-58, L-61, K-62, I-65, Y-70, K-71, V-72, D-73, A-74, H-76, I-77, A-78, N-80, M-81, I-82, N-83, F-84, Y-85, and K-86 of the B. subtilis FlgM.

49. A recombinant probiotic microorganism that constitutively expresses an aldehyde dehydrogenase.

50. The recombinant probiotic microorganism of claim **49**, wherein the microorganism comprises:

a) a polynucleotide comprising an expression construct comprising a flagellin gene promoter operatively linked with a heterologous nucleotide sequence encoding a subject polypeptide; and

b) a genetic modification in a FlgM gene that reduces inhibition of SigD expression.

51. The recombinant probiotic microorganism of claim **50**, wherein the flagellin gene promoter comprises one or more genetic modifications that reduce CsrA repression of translation of an mRNA transcribed from the promoter.

52. A polynucleotide comprising an expression construct comprising a flagellin gene promoter operatively linked with a heterologous nucleotide sequence encoding a subject polypeptide, wherein the flagellin gene promoter comprises one or more genetic modifications that reduce CsrA repression of translation an mRNA transcribed from the flagellin gene promoter.

53. A method of making a polypeptide comprising culturing a recombinant microorganism of claim **21**, or claim **49**.

54. The method of claim **53**, further comprising isolating the polypeptide.

55. A composition comprising a physiologically acceptable carrier and a recombinant probiotic microorganism, wherein the recombinant probiotic microorganism comprises:

a) a polynucleotide comprising an expression construct comprising a flagellin gene promoter operatively linked with a heterologous nucleotide sequence encoding a subject polypeptide; and

b) a genetic modification of a FlgM gene that reduces inhibition of SigD initiation of transcription.

56. The composition of claim **55**, wherein the flagellin gene promoter comprises one or more genetic modifications that reduce CsrA repression of translation of an mRNA transcribed from the flagellin gene promoter.

57. The composition of claim **55**, wherein the subject polypeptide is an aldehyde dehydrogenase.

58. The composition of claim **55**, wherein the physiologically acceptable carrier is selected from lactic acid fermented foods, fermented dairy products, resistant starch, dietary fibers, carbohydrates, proteins and glycosylated proteins, water, capsule filler, and a gummy material.

59. A unit dose of a composition of claim **55**, comprising about 10^4 to about 10^{12} colony forming units of the recombinant probiotic microorganisms.

60. A method of metabolizing an analyte in a gut or in circulation in a subject comprising administering to the subject an effective amount of a composition comprising microorganisms that constitutively express an enzyme that metabolizes the analyte.

61. A method of producing a target compound comprising:

a) contacting a culture comprising a recombinant microorganism of claim 1 with an analyte, wherein the subject polypeptide is an enzyme for which the analyte is a substrate, and

b) culturing the microorganism, wherein the enzyme catalyzes the conversion of the analyte into the target compound.

62. The method of claim **61**, wherein the enzyme is selected from an amylase, a lipase and a protease.

WHAT IS CLAIMED IS:

1. A composition formulated for oral administration to humans, the composition comprising:

a recombinant bacterium, wherein the recombinant bacterium constitutively expresses an expression product encoded by a heterologous nucleic acid sequence operatively linked with a flagellin gene promoter,

wherein the expression product is an aldehyde dehydrogenase (ALDH) enzyme that oxidizes acetaldehyde to acetate,

wherein the recombinant bacterium is present in the composition in an amount sufficient that, when the composition is orally administered to a human, it metabolizes acetaldehyde in the presence of alcohol.

2. The composition of claim 1, wherein the recombinant bacterium does not express an alcohol dehydrogenase.

3. The composition of claim 1, wherein the ALDH is the only enzyme encoded by a heterologous nucleic acid sequence in the recombinant bacterium.

4. The composition of claim 1, wherein the bacterium is a probiotic bacterium.

5. The composition of claim 1, wherein the bacterium is of a genus selected from *Bacillus*, *Bifidobacterium*, *Enterococcus*, *Escherichia*, *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Pediococcus*, and *Streptococcus*.

6. The composition of claim 1, wherein the bacterium is of the genus *Bacillus*.

7. The composition of claim 1, wherein the bacterium is of the species *B. subtilis*.

8. The composition of claim 1, wherein the bacterium is a spore-forming bacterium.

9. The composition of claim 8, wherein the bacterium is in a spore form.

10. The composition of claim 1, wherein the composition comprises about 10^4 to about 10^{12} colony forming units of the recombinant bacterium.

11. The composition of claim 1, wherein the recombinant bacterium is present as a bacterial cell culture in the composition.

12. The composition of claim 1,

wherein the flagellin gene promoter comprises a mutation in a CsrA binding site,

wherein the mutation in the CsrA binding site inhibits binding of CsrA to mRNA transcripts encoding the ALDH enzyme but does not preclude expression of the ALDH enzyme, and

wherein the recombinant bacterium comprises a mutation of an endogenous *flgM* gene that reduces inhibition of a sigma factor.

13. The composition of claim 12, which composition comprises a preparation of the recombinant bacterium characterized in that the expression product is expressed in the preparation at a level determined to be at least about 4 times greater than that observed under comparable conditions when the expression product is expressed under control of a pHyspank promoter.

14. The composition of claim 12, wherein the flagellin gene promoter is a *B. subtilis hag* promoter.

15. The composition of claim 12, wherein the mutation in the CsrA binding site is a mutation in a *B. subtilis hag* promoter CsrA binding site selected from binding site 1 (BS1) and binding site 2 (BS2).

16. The composition of claim 12 wherein the sigma factor is SigD.

17. The composition of claim 1, wherein the composition comprises a physiologically acceptable carrier.

18. The composition of claim 17, wherein the physiologically acceptable carrier is selected from a lactic acid fermented food, fermented dairy product, resistant starch, dietary fiber, carbohydrate, protein, glycosylated protein, water, capsule filler, and gummy material.

19. The composition of claim 1, wherein metabolism of acetaldehyde in the presence of alcohol is detected as reduction in one or more effects of an alcohol hangover.

20. The composition of claim 19, wherein the one or more effects of an alcohol hangover are selected from the group consisting of dehydration, poor sleep, grogginess, nausea, vomiting, headache, malaise, dry mouth, sensitivity to light and sound, sweating, muscle pain, diarrhea, stomach pain, gastrointestinal distress, vertigo, anxiety, depression, irritability, elevated acetaldehyde concentration in the body, and combinations thereof.