CLAIMS

1. A genetically engineered bacterium comprising an arginine regulon,

wherein the bacterium comprises a gene encoding an arginine feedback resistant N-acetylglutamate synthetase ($ArgA^{fbr}$), wherein the $ArgA^{fbr}$ has reduced arginine feedback inhibition as compared to a wild-type N-acetylglutamate synthetase from the same bacterial subtype under the same conditions and wherein expression of the gene encoding $ArgA^{fbr}$ is controlled by a promoter that is induced by low-oxygen or anaerobic conditions; and

wherein the bacterium has been genetically engineered to lack a functional ArgR.

2. The bacterium of claim 1, wherein each copy of a functional argR gene normally present in a corresponding wild-type bacterium has been deleted.

3. The bacterium of claim 1, wherein each copy of a functional argG gene normally present in a corresponding wild-type bacterium has been independently deleted or rendered inactive by one or more nucleotide deletions, insertions or substitutions.

4. The bacterium of claim 3, wherein each copy of the functional argG gene normally present in a corresponding wild-type bacterium has been deleted.

5. The bacterium of claim 1, wherein under low-oxygen or anaerobic conditions, the transcription of each gene that is present in an operon comprising a functional ARG box and which encodes an arginine biosynthesis enzyme is increased as compared to a corresponding gene in a wild-type bacterium under the same conditions.

6. The bacterium of claim 1, wherein the promoter that is induced under low-oxygen or anaerobic conditions is an FNR promoter.

7. The bacterium of claim 1, wherein the arginine feedback resistant N-acetylglutamate synthetase gene has a DNA sequence selected from:

a) SEQ ID NO:28, and

b) a DNA sequence that, but for the redundancy of the genetic code, encodes the same polypeptide as encoded by SEQ ID NO:28.

8. The bacterium of claim 1, wherein the bacterium is a non-pathogenic bacterium.

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

10. The bacterium of claim 1, wherein the bacterium is selected from the group consisting of *Bacteroides, Bifidobacterium, Clostridium, Escherichia, Lactobacillus,* and *Lactococcus.*

11. The bacterium of claim 1, wherein the bacterium is *Escherichia coli* strain Nissle.

12. The bacterium of claim 1, wherein the gene encoding the arginine feedback resistant N-acetylglutamate synthetase ($ArgA^{fbr}$) is present on a plasmid in the bacterium and operably linked on the plasmid to the promoter that is induced under low-oxygen or anaerobic conditions.

13. The bacterium of claim 1, wherein the gene encoding the arginine feedback resistant N-acetylglutamate synthetase ($ArgA^{fbr}$) is present in the bacterial chromosome and is operably linked in the chromosome to the promoter that is induced under low-oxygen or anaerobic conditions.

14. The bacterium of claim 1, wherein the bacterium is an auxotroph in a gene that is complemented when the bacterium is present in a mammalian gut.

15. The bacterium of claim 14, wherein the mammalian gut is a human gut.

16. A pharmaceutically acceptable composition comprising a genetically engineered bacterium comprising an arginine regulon, wherein the bacterium comprises a gene encoding an arginine feedback resistant N-acetylglutamate synthetase ($ArgA^{fbr}$), wherein the $ArgA^{fbr}$ has reduced arginine feedback inhibition as compared to a wild-type N-acetylglutamate synthetase from the same bacterial subtype under the same conditions, wherein expression of the gene encoding $ArgA^{fbr}$ is controlled by a promoter that is induced by low-oxygen or anaerobic conditions; and wherein the bacterium has been genetically engineered to lack a functional ArgR; and a pharmaceutically acceptable carrier.

17. The bacterium of claim 14, wherein the bacterium is a thyA or dapB auxotroph.

18. The bacterium of claim 1, wherein the bacterium comprises an antibiotic resistance gene.