

CLAIMS

1. A bacterium comprising the *E. coli* Nissle (ECOLIN) Phage 3 genome, in which the *E. coli* Nissle Phage 3 genome comprises a complete or partial deletion of *E. coli* Nissle Phage 3 gene 10110 (ECOLIN_10110), ECOLIN_10115, ECOLIN_10120, ECOLIN_10125,
5 ECOLIN_10130, ECOLIN_10135, ECOLIN_10140, ECOLIN_10145, ECOLIN_10150, ECOLIN_10160, ECOLIN_10165, ECOLIN_10170, and ECOLIN_10175, in which the bacterium is *Escherichia coli* Nissle.
2. A bacterium according to Claim 1, in which the deletion is a complete deletion of ECOLIN_10110, ECOLIN_10115, ECOLIN_10120, ECOLIN_10125, ECOLIN_10130,
10 ECOLIN_10135, ECOLIN_10140, ECOLIN_10145, ECOLIN_10150, ECOLIN_10160, ECOLIN_10165, and ECOLIN_10170, and a partial deletion of ECOLIN_10175.
3. A bacterium according to Claim 2, in which the deletion comprises SEQ ID NO: 130.
4. A bacterium according to Claim 2, in which the deletion consists of SEQ ID NO: 130.
5. A bacterium according to any preceding claim, comprising one or more additional
15 genetic modifications.
6. A bacterium according to Claim 5, in which the one or more additional genetic modifications comprise one or more mutations in one or more endogenous genes.
7. A bacterium according to Claim 6, in which the one or more mutations in one or more endogenous genes are point mutations.
- 20 8. A bacterium according to Claim 6, in which the one or more mutations in one or more endogenous genes are deletions.
9. A bacterium according to any of Claims 5 to 8, in which the one or more additional genetic modifications comprise the addition of one or more non-native genes.
10. A bacterium according to Claim 9, in which the one or more non-native genes are
25 present on a chromosome.
11. A bacterium according to Claim 9, in which the one or more non-native genes are present on a plasmid.

12. A bacterium according to Claim 9, 10 or 11, in which the one or more non-native genes encode one or more biosynthetic enzymes for the production of one or more effector molecules.
13. A bacterium according to Claim 9, 10 or 11, in which the one or more non-native genes
5 encode one or more effector molecules.
14. A bacterium according to Claim 9, 10 or 11, in which the one or more non-native genes encode one or more enzymes for the consumption of one or more toxic metabolites.
15. A bacterium according to Claim 9, 10 or 11, in which the one or more non-native genes encode one or more transporters for the uptake of toxic metabolites.
- 10 16. A bacterium according to Claims 9, 10 or 11, in which the one or more non-native genes encode one or more exporters for the export of metabolites.
17. A bacterium according to any preceding claim, in which the bacterium is an auxotroph in a gene that is complemented when the bacterium is present in a mammalian gut.
18. A bacterium according to Claim 17, in which the mammalian gut is a human gut.
- 15 19. A bacterium according to Claim 17 or 18, in which the bacterium is an auxotroph in diaminopimelic acid or an enzyme in the thymidine biosynthetic pathway.
20. A bacterium according to any preceding claim, in which the bacterium further comprises antibiotic resistance.
21. A pharmaceutically acceptable composition comprising a bacterium according to any
20 preceding claim and a pharmaceutically acceptable carrier.
22. A composition according to Claim 21 formulated for oral administration.