Claims

1. Use of a pharmaceutical composition comprising a plurality of bacterial isolates in manufacture of a medicament for ~~A method of~~ treating or preventing inflammatory bowel disease (IBD) in a subject in need thereof, ~~the method comprising administering to the subject a plurality of bacterial isolates,~~ wherein the plurality of bacterial isolates comprises *Bacteroides stercoris* *and Bacteroides cellulosilyticus*, and at least ~~two~~ one of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Suboligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*, wherein the *Bacteroides stercoris* comprises a 16S ribosomal ribonucleic acid (rRNA) sequence that has at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with the nucleotide sequence of SEQ ID NO: 13~~at least two of the plurality of bacterial isolates are isolated from a stool of different human donors~~.

2. The ~~method~~ use of claim 1, wherein at least two of the plurality of bacterial isolates are isolated from a stool of different human donors ~~the *Bacteroides stercoris* comprises a 16S ribosomal ribonucleic acid (rRNA) sequence that has at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with the nucleotide sequence of SEQ ID NO: 13.~~

3. The ~~method~~ use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least ~~three~~ two of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

4. The ~~method~~ use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least ~~four~~ three of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

5. The ~~method~~ use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least ~~five~~ four of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

6. The ~~method~~ use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least ~~six~~ five of ~~*Bacteroides cellulosilyticus,*~~ *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

7. The ~~method~~ use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least ~~seven~~ six of ~~*Bacteroides cellulosilyticus,*~~ *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

8. The ~~method~~ use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least ~~eight~~ seven of ~~*Bacteroides cellulosilyticus,*~~ *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

9. The ~~method~~ use of any one of claims 1-8, wherein the plurality of bacterial isolates comprises a 16S rRNA sequence that has at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequences selected from SEQ ID NOs: 1, 2, 3, 7, 8, 11, 14, 18, 19, 20, 22 and 23.

10. The ~~method~~ use of any one of claims 1-9, wherein the plurality of bacterial isolates comprises:

(a) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NOs: 1 and/or 7,

(b) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 2,

(c) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 3.

(d) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 8,

(e) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 11

~~(f) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 13,~~

(~~g~~f) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 14,

(~~h~~g) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 18,

(~~i~~h) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 19,

(~~j~~i) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 20, and/or

(~~k~~j) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NOs: 22 and/or 23.

11. The ~~method~~ use of any one of claims 1-10, wherein the plurality of bacterial isolates comprises at least two bacterial isolates comprising *Faecalibacterium prausnitzii*, wherein the at least two bacterial isolates comprise different 16S rRNA sequences.

12. The ~~method~~ use of claim 11, wherein the at least two bacterial isolates comprising *Faecalibacterium prausnitzii* comprise 16S rRNA sequences that are at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% identity sequence identity with nucleotide sequences of SEQ ID NOs: 1 and/or 7.

13. The use ~~method~~ of claim 11 or 12, wherein the at least two bacterial isolates comprising Faecalib*acterim prausnitzii* are isolated from a stool of different human donors.

14. The use ~~method~~ of any one of claims 1-13, wherein the plurality of bacterial isolates comprises lyophilized bacteria.

15. The use ~~method~~ of any one of claims 1-14, wherein the plurality of bacterial isolates does not include *Escherichia coli*.

16. A pharmaceutical composition comprising a plurality of bacterial isolates, wherein the plurality of bacterial isolates comprise *Bacteroides stercoris* and *Bacteroides cellulosilyticus*,, and at least ~~two~~ one of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Subodligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*, wherein the *Bacteroides stercoris* comprises a 16S ribosomal ribonucleic acid (rRNA) sequence that has at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with the nucleotide sequence of SEQ ID NO: 13, and optionally wherein at least two of the plurality of bacterial isolates are isolated from a stool of different human donors.

17. The pharmaceutical composition of claim 16, wherein the plurality of bacterial isolates comprises at least ~~three~~ two of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Subo*d*ligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

18. The pharmaceutical composition of claim 16 or 17, wherein the plurality of bacterial isolates comprises at least ~~four~~ three of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Subo*d*ligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

19. The pharmaceutical composition of any one of claims 16-18, wherein the plurality of bacterial isolates comprises at least ~~five~~ four of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Sub*d*oligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

~~20. The pharmaceutical composition of any one of claims 16-19, wherein the plurality of bacterial isolates comprises at least five of *Bacteroides cellulosilyticus*, *Bacteroides uniformis*, *Suboligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.~~

~~21~~20. The pharmaceutical composition of any one of claims 16-~~20~~19, wherein the plurality of bacterial isolates comprises at least ~~six~~ five of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Sub*d*oligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

~~22~~21. The pharmaceutical composition of any one of claims 16-~~21~~20, wherein the plurality of bacterial isolates comprises at least ~~seven~~ six of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Sub*d*oligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

~~23~~22. The pharmaceutical composition of any one of claims 16-~~22~~21, wherein the plurality of bacterial isolates comprises at least ~~eight~~ seven of ~~*Bacteroides cellulosilyticus*,~~ *Bacteroides uniformis*, *Sub*d*oligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

~~24~~23. The pharmaceutical composition of any one of claims 16-~~23~~22, wherein the composition comprises a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequences selected from SEQ ID NOs: 1, 2, 3, 7, 8, 11, 14, 18, 19, 20, 22 and 23.

~~25~~24. The pharmaceutical composition of any one of claims 16-~~24~~23, wherein the pharmaceutical composition comprises at least two bacterial isolates comprising *Faecalibacterium prausnitzii*, wherein the at least two bacterial isolates comprise different 16S rRNA sequences.

~~26~~25. The pharmaceutical composition of claim ~~25~~24, wherein the pharmaceutical composition comprises 16S rRNA sequences that are at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% identity sequence identity with nucleotide sequences of SEQ ID NOs: 1 and 7.

~~27~~26. The pharmaceutical composition of any one of claims 16-~~26~~25, wherein the plurality of bacterial isolates comprises lyophilized bacteria.

~~28~~27. The pharmaceutical composition of any one of claims 16-~~27~~26, wherein the plurality of bacterial isolates does not include *Escherichia coli*.