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(54) THERAPEUTIC COMPOSITIONS AND METHODS OF USING SEROTONIN MODULATING MICROBIOME-BASED INTERVENTIONS TO TREAT SEROTONIN-RELATED DISEASES OR DISORDERS

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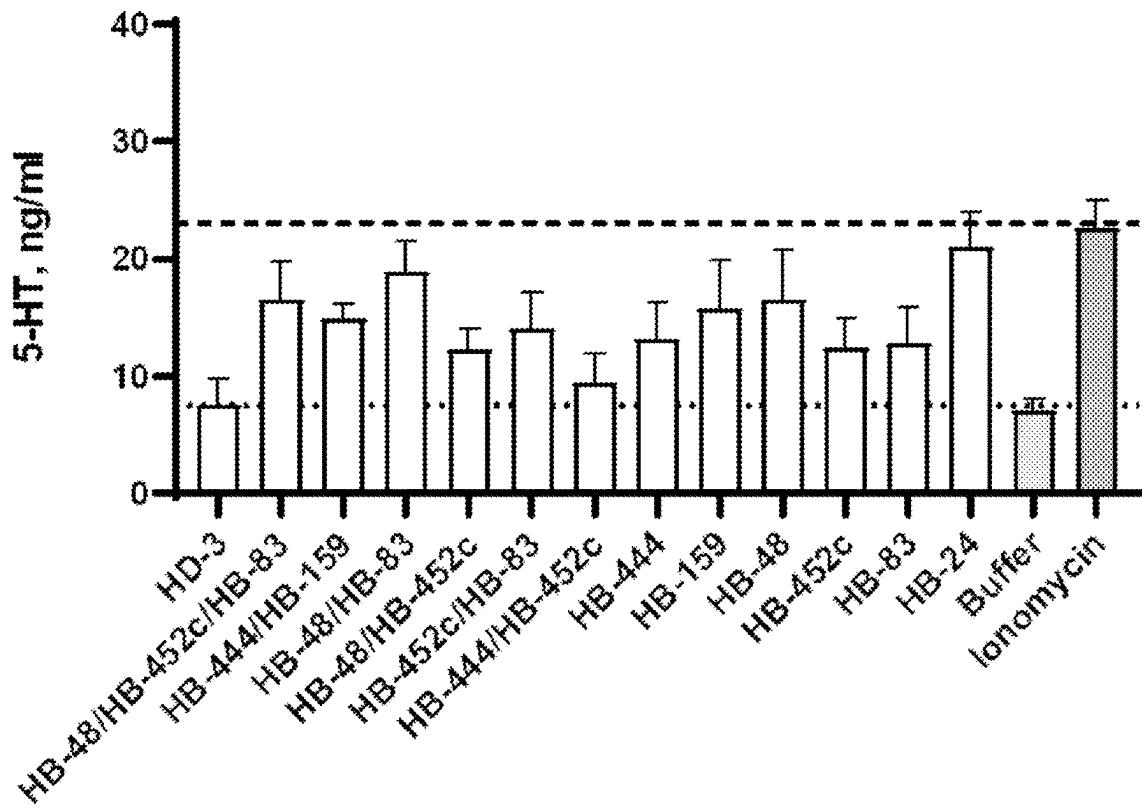
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ABSTRACT

The technology described herein is directed to compositions and methods for modulating serotonin in a subject. Described herein are compositions comprising viable or non-viable serotonin-modulating bacteria, conditioned medium(s) of serotonin-modulating bacteria, cell pellet(s) of serotonin-modulating bacteria, and/or metabolites and/or proteins derived from serotonin-modulating bacteria. Also described herein are methods of treating serotonin-related disease or disorders.

Specification includes a Sequence Listing.

Gut Simulator - Pellets



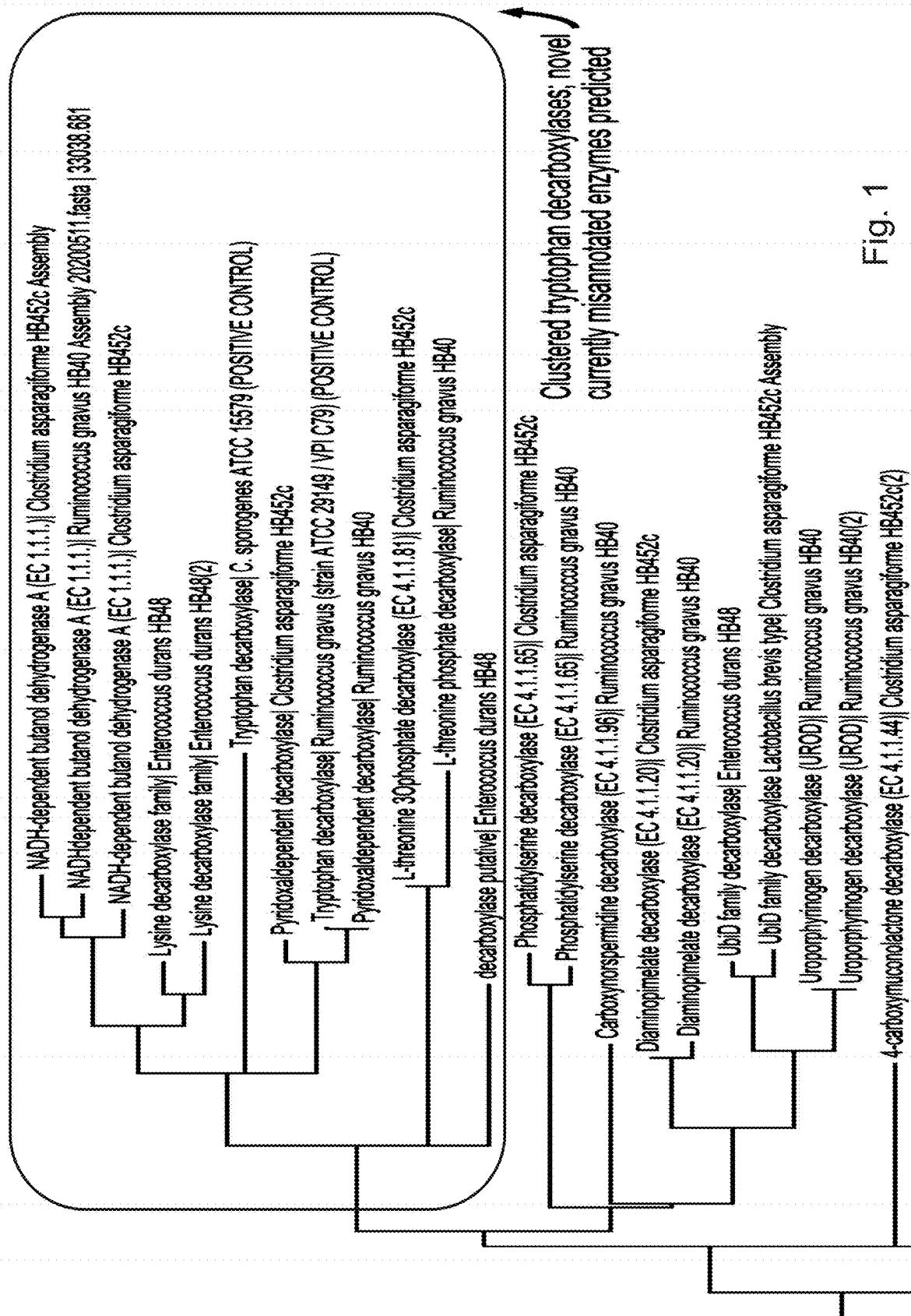
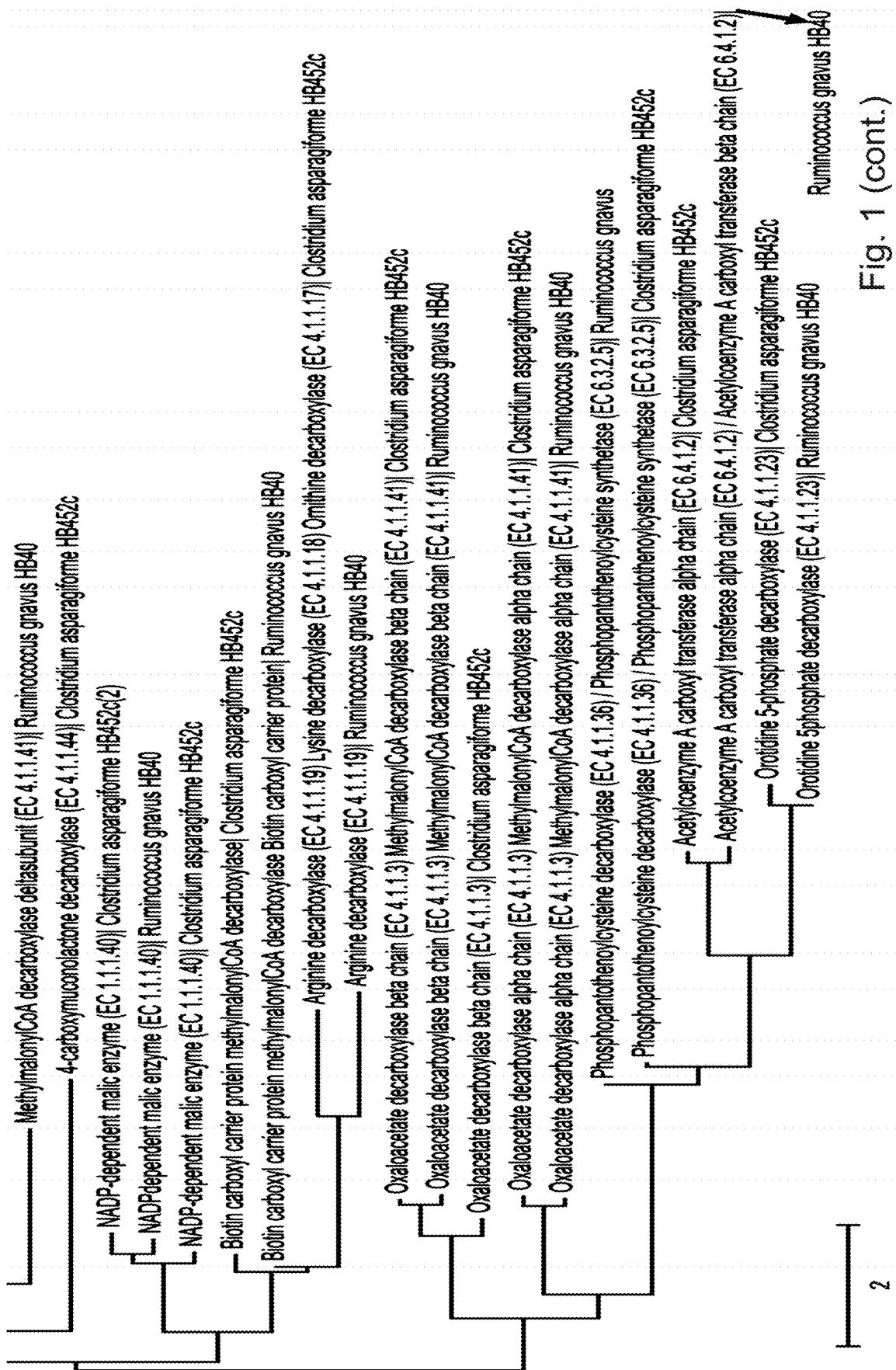
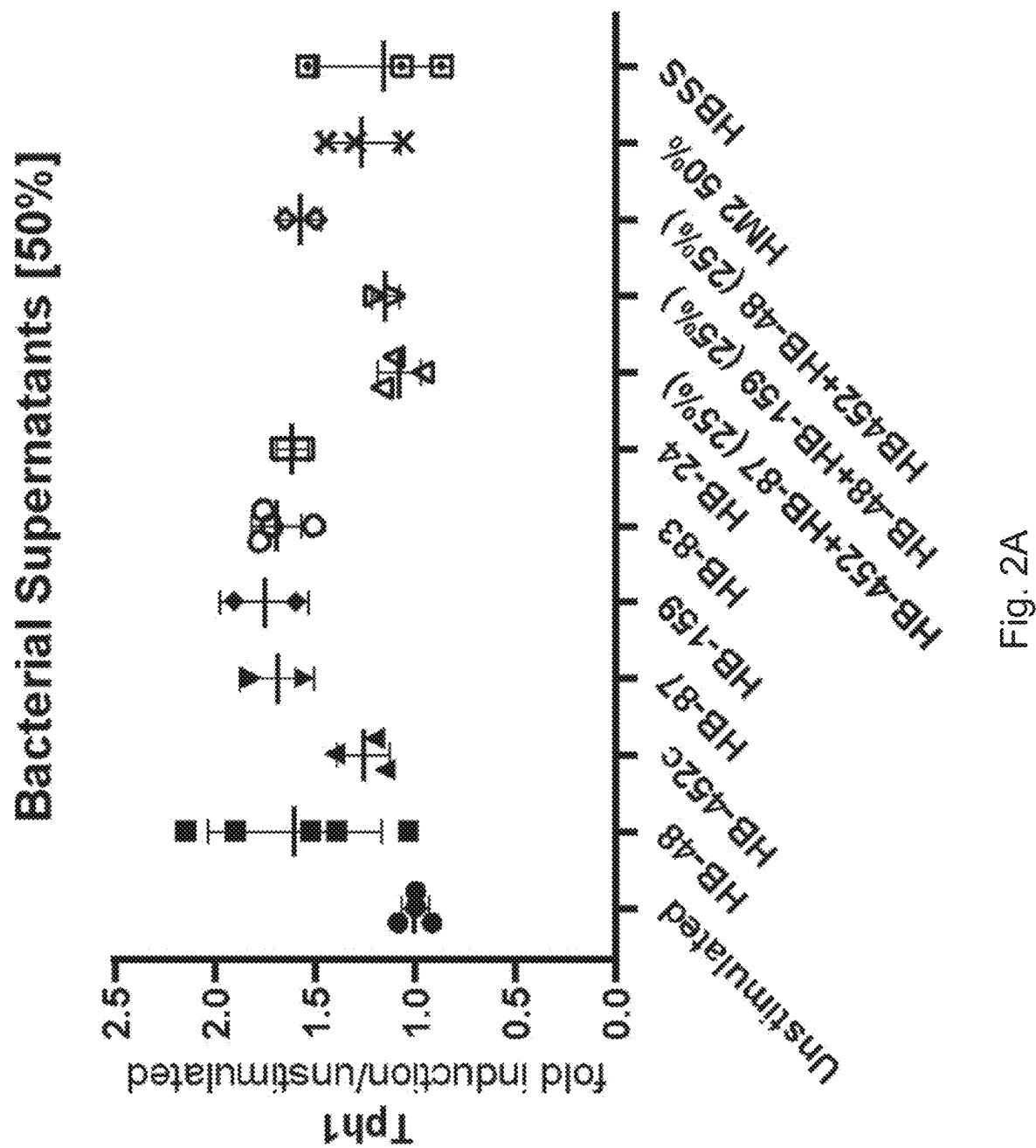
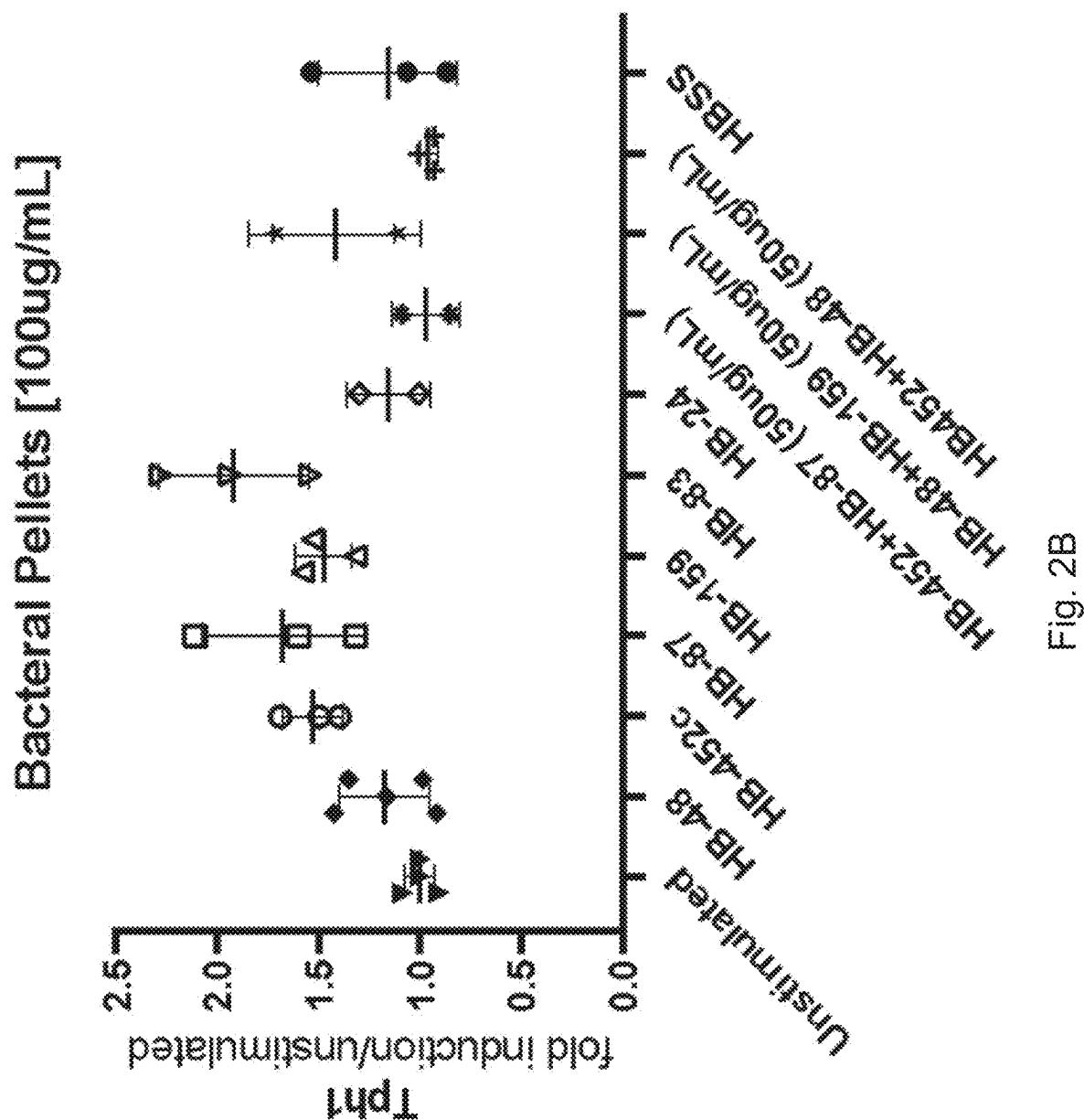


FIG. 1







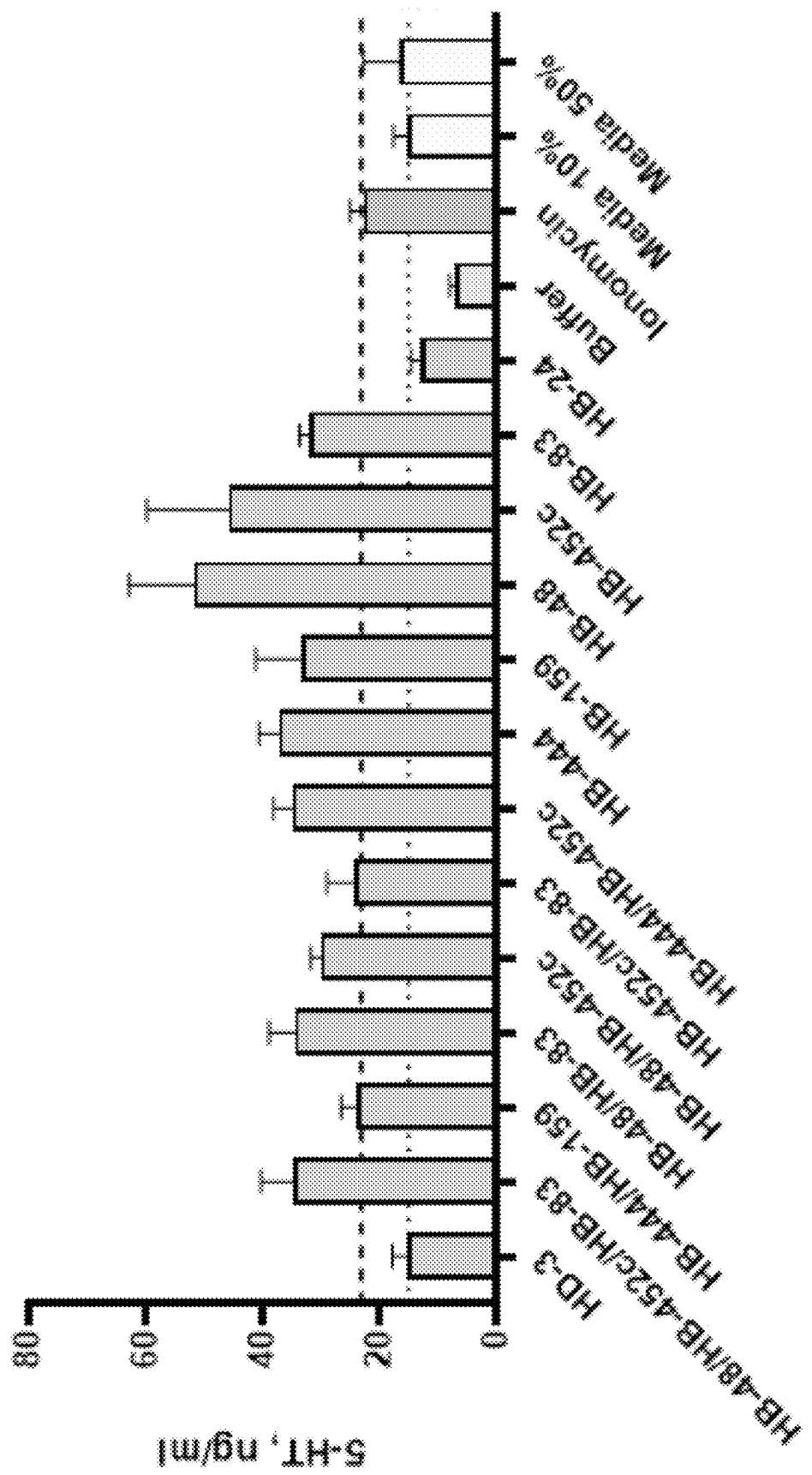
Gut Simulator - Supematant

Fig. 3

Gut Simulator - Pellets

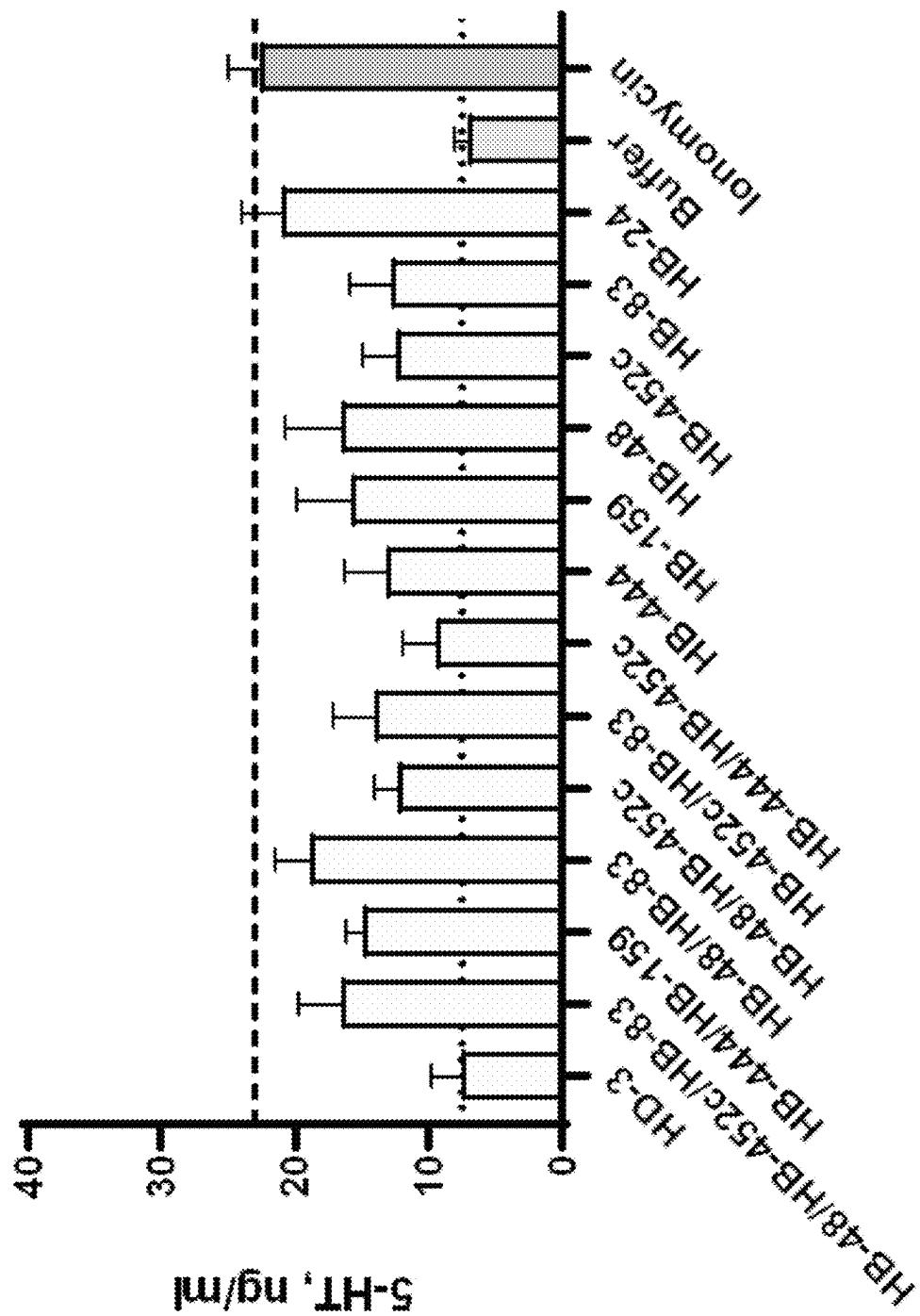


Fig. 4

**THERAPEUTIC COMPOSITIONS AND
METHODS OF USING SEROTONIN
MODULATING MICROBIOME-BASED
INTERVENTIONS TO TREAT
SEROTONIN-RELATED DISEASES OR
DISORDERS**

**CROSS-REFERENCE TO RELATED
APPLICATIONS**

[0001] This application is a continuation under 35 U.S.C. § 120 of co-pending U.S. application Ser. No. 17/621,767, filed Dec. 22, 2021, which is a 35 U.S.C. § 371 National Phase Entry Application of International Patent Application No. PCT/US2020/039947 filed on Jun. 26, 2020, which designated the U.S., which claims benefit under 35 U.S.C. § 119(e) of U.S. Provisional Application No. 62/867,592 filed Jun. 27, 2019, the contents of which are incorporated herein by reference in their entireties.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted in XML format via Patent Center and is hereby incorporated by reference in its entirety. Said XML copy, created on Aug. 26, 2024, is named 083103-095640USC1_SL.xml and is 506,665 bytes in size.

TECHNICAL FIELD

[0003] The technology described herein relates to compositions and methods for modulating serotonin.

BACKGROUND

[0004] Recent work has connected the human microbiome—the trillions of bacteria that reside on or inside the body—to many components of health and disease. Of particular importance is the gut microbiome, the complex bacterial community located in the gastrointestinal tract. Incredibly, not only has the gut microbiome been found to be essential for maintaining metabolic and immune health, there is also amassing evidence that the gut microbiome interacts with the enteric and central nervous systems (ENS and CNS, respectively) via communication along the “gut-brain-axis”. Mechanistically, these interactions generally appear to be driven by direct production of metabolites that interact with these systems (e.g. neurotransmitters like GABA, or short-chain fatty acids like butyrate and acetate), modulation of dietary inputs which feed into these pathways (e.g. removal/alteration of the fate of tryptophan, which is an input for serotonin biosynthesis), or direct protein-protein or ligand-protein interactions (e.g. the sensing of microbial lipopolysaccharide (LPS) by toll-like receptors, which can induce inflammatory or anti-inflammatory cellular responses, depending on the LPS source organism). Of relevance is the link between serotonin (e.g., 5-hydroxytryptamine, 5-HT) and the microbiome.

[0005] More than 90% of the body's 5-HT is produced in the gastrointestinal (GI) tract. In many instances said 5-HT is produced by host gut cells under the influence of the gut microbiota, not produced by the microbiota itself. In the GI tract, 5-HT activates as many as 14 different 5-HT receptor subtypes, including those found on immune cells, enterocytes, and enteric nerves. In addition, circulating platelets sequester 5-HT from the GI tract, releasing it to promote hemostasis and distributing it to various body sites.

[0006] Serotonin generally has been shown to be involved in numerous physiological systems and disorders. This includes, as examples, intestinal movements, platelet activation/aggregation, stimulation of myenteric neurons and gut motility, mood, appetite, sleep, some cognitive functions such as memory and learning, bone metabolism and remodeling, reward seeking behavior, regulation of vascular tone, primary hemostasis, hemopoiesis, cell-mediated immune responses, tumor growth, angiogenesis, cancer cell differentiation, and cardiac functions. An abnormal level of serotonin can cause pathological conditions including, but not limited to, depression, anxiety, obsessive-compulsive disorder, irritable bowel syndrome, cardiovascular disease, osteoporosis, abnormal gastrointestinal motility, fibrosis, abnormal platelet aggregation, abnormal platelet activation, metabolic disease, and an abnormal immune response.

[0007] The microbiome plays a major role in influencing serotonergic neurotransmission. In germ free animals, there is a significant reduction of serotonin in the blood and colon of mice compared to controls.

[0008] Modulation of the gut microbiota, e.g., through microbiota-based therapeutics, has been shown to be an effective treatment for a number of diseases in mouse models, including, but not limited to obesity, colitis, colon cancer, and *Clostridium difficile* infection, giving proof of principle for microbiota-based therapeutics. These therapeutics could be in the form of live bacteria, dead bacteria, microbial metabolites or proteins, bacteria engineered to perform specific functions or produce certain metabolites/proteins, or means to alter the microbiome—e.g. diet, prebiotics, antibiotics, sorbents, or inhibitors of specific microbial/host functions.

SUMMARY

[0009] The present disclosure provides compositions and methods for decreasing at least one symptom of a serotonin-related disease or disorder in a subject in need thereof by altering the serotonin-modulating gut microbiota, serotonin-modulating gut-microbiota-derived metabolome, or serotonin-modulating gut-microbiota-derived proteome of the subject. The compositions can comprise one or more live serotonin-modulating bacteria, one or more dead-serotonin modulating bacteria, one or more conditioned medium(s) of serotonin-modulating bacteria, one or more cell pellet(s) of serotonin-modulating bacteria, and/or one or more 5-HT agonists, metabolites and/or proteins (derived from serotonin-modulating bacteria), and therapeutic compositions comprising the same. The method can comprise administering combinations of one or more live serotonin-modulating bacteria, one or more dead-serotonin modulating bacteria, one or more conditioned medium(s) of serotonin-modulating bacteria, one or more cell pellet(s) of serotonin-modulating bacteria, and/or one or more 5-HT agonists, metabolites and/or proteins (derived from serotonin-modulating bacteria).

[0010] The present technology has the advantage of alleviating the symptoms of serotonin-related disease or disorders without the aid of synthetic medications (e.g., serotonin-reuptake inhibitors), which can have unwanted side-effects, or in combination with existing medications. Additionally, the present technology can have the advantage of further improving other aspects of health of the subject, as the bacteria can perform multiple mechanisms (e.g. alter serotonin signaling but also alter the immune system).

Additional features and advantages of the present technology will be apparent to one of skill in the art.

[0011] In one aspect described herein is a therapeutic composition for increasing serotonin level in a mammalian subject in need thereof, the composition comprising an amount of a live isolated serotonin-increasing bacterial species, dead isolated serotonin-increasing bacterial species, conditioned medium from an isolated, cultured serotonin-increasing bacterial species, cell pellet of an isolated serotonin-increasing bacterial species, a purified metabolite produced by an isolated serotonin-increasing bacterial species, a purified protein produced by an isolated serotonin-increasing bacterial species, or a combination thereof sufficient to increase serotonin level in the subject, and an excipient or carrier suitable for delivery to the gut.

[0012] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species increases serotonin in at least one of the following ways: production of serotonin; production of secreted metabolites or secreted proteins that induce serotonin production; production of ligands that induce serotonin production; or production of an agonist of a serotonin receptor or the trace amine-associated receptor (TAAR).

[0013] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species is a serotonin-producing bacterial species.

[0014] In some embodiments of any of the aspects, the serotonin-producing bacterial species comprises one or more species selected from *Enterococcus durans*, *Clostridium lavalense*, *Clostridium asparagiforme*, *Ruminococcus gnatus*.

[0015] In some embodiments of any of the aspects, the serotonin-producing bacterial species comprises one or more species selected from *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnatus* HB-40, *Ruminococcus gnatus* HB-516.

[0016] In some embodiments of any of the aspects, the serotonin-producing bacterial species comprises a 16S sequence at least 95% identical to a 16S sequence selected from SEQ ID NOS: 1-4.

[0017] In some embodiments of any of the aspects, the serotonin-producing bacterial species produces serotonin under conditions found in the mammalian gut.

[0018] In some embodiments of any of the aspects, the mammalian subject is a human subject.

[0019] In some embodiments of any of the aspects, the isolated serotonin-producing bacterial species encodes and expresses a decarboxylase enzyme that catalyzes the production of tryptamine from tryptophan.

[0020] In some embodiments of any of the aspects, the decarboxylase enzyme is a tryptophan decarboxylase.

[0021] In some embodiments of any of the aspects, the decarboxylase enzyme belongs to the EC number 4.1.1.105.

[0022] In some embodiments of any of the aspects, the decarboxylase enzyme is at least 50% identical to an enzyme comprising an amino acid sequence selected from SEQ ID Nos: 115-119.

[0023] In some embodiments of any of the aspects, the isolated serotonin-producing bacterial species encodes and expresses an enzyme that hydroxylates tryptamine to produce serotonin.

[0024] In some embodiments of any of the aspects, the enzyme that hydroxylates tryptamine is a tryptamine 5-hydroxylase.

[0025] In some embodiments of any of the aspects, the enzyme that hydroxylates tryptamine is at least 50% identical to the enzyme of SEQ ID NO: 134.

[0026] In some embodiments of any of the aspects, the enzyme that hydroxylates tryptamine is an anaerobic hydroxylase.

[0027] In some embodiments of any of the aspects, the isolated serotonin-producing bacterial species encodes and expresses a decarboxylase enzyme that catalyzes the production of tryptamine from tryptophan and an enzyme that hydroxylates tryptamine to produce serotonin.

[0028] In some embodiments of any of the aspects, the live isolated serotonin-producing bacterial species, dead isolated serotonin producing bacterial species, conditioned medium from an isolated, cultured serotonin-producing bacterial species or cell pellet of an isolated serotonin-producing bacterial species comprises a first bacterial species that encodes and expresses a decarboxylase enzyme that catalyzes the production of tryptamine from tryptophan and a second bacterial species that encodes and expresses an enzyme that hydroxylates tryptamine to produce serotonin.

[0029] In some embodiments of any of the aspects, the decarboxylase is a lysine decarboxylase family enzyme.

[0030] In some embodiments of any of the aspects, the live isolated serotonin-producing bacterial species, dead isolated serotonin producing bacterial species, conditioned medium from an isolated, cultured serotonin-producing bacterial species or cell pellet of an isolated serotonin-producing bacterial species comprises one or more bacterial species that encode and express an enzyme that converts tryptophan to 5-hydroxy-L-tryptophan (5-HTP).

[0031] In some embodiments of any of the aspects, the enzyme that converts tryptophan to 5-hydroxy-L-tryptophan (5-HTP) has an amino acid sequence at least 50% identical to a sequence selected from SEQ ID Nos: 120-126.

[0032] In some embodiments of any of the aspects, the enzyme that converts tryptophan to 5-hydroxy-L-tryptophan (5-HTP) belongs to the EC number 1.14.16.4.

[0033] In some embodiments of any of the aspects, the live isolated serotonin-producing bacterial species, dead isolated serotonin producing bacterial species, conditioned medium from an isolated, cultured serotonin-producing bacterial species or cell pellet of an isolated serotonin-producing bacterial species comprises a bacterial species that encodes and expresses an enzyme that converts 5-hydroxy-L-tryptophan to serotonin.

[0034] In some embodiments of any of the aspects, the enzyme that converts 5-hydroxy-L-tryptophan to serotonin is an aromatic L-amino acid decarboxylase.

[0035] In some embodiments of any of the aspects, the enzyme that catalyzes the conversion of 5-hydroxy-L-tryptophan to serotonin belongs to the EC number 4.1.1.28.

[0036] In some embodiments of any of the aspects, the enzyme that converts 5-hydroxy-L-tryptophan to serotonin is at least 50% identical to a sequence selected from SEQ ID NOS: 127-133.

[0037] In some embodiments of any of the aspects, the isolated serotonin-producing bacterial species further encodes and expresses an enzyme that converts 5-hydroxy-L-tryptophan to serotonin.

[0038] In some embodiments of any of the aspects, the enzyme that converts 5-hydroxy-L-tryptophan to serotonin is an aromatic L-amino acid decarboxylase.

[0039] In some embodiments of any of the aspects, the enzyme that converts 5-hydroxy-L-tryptophan to serotonin is at least 50% identical to a sequence selected from SEQ ID NOS: 127-133.

[0040] In some embodiments of any of the aspects, the live isolated serotonin-producing bacterial species, dead isolated serotonin producing bacterial species, conditioned medium from an isolated, cultured serotonin-producing bacterial species or cell pellet of an isolated serotonin-producing bacterial species comprises a first bacterial species that encodes and expresses an enzyme that catalyzes the conversion of tryptophan to 5-hydroxy-L-tryptophan and a second bacterial species that encodes and expresses an enzyme that converts 5-hydroxy-L-tryptophan to serotonin.

[0041] In some embodiments of any of the aspects, the enzyme that catalyzes the conversion of tryptophan to 5-hydroxy-L-tryptophan is a tryptophan hydroxylase.

[0042] In some embodiments of any of the aspects, the enzyme that catalyzes the conversion of tryptophan to 5-hydroxy-L-tryptophan has an amino acid sequence at least 50% identical to a sequence selected from SEQ ID Nos: 120-126, and the enzyme that converts 5-hydroxy-L-tryptophan to serotonin is at least 50% identical to a sequence selected from SEQ ID NOS: 127-133.

[0043] In some embodiments of any of the aspects, the enzyme that catalyzes the conversion of tryptophan to 5-hydroxy-L-tryptophan is a phenylalanine hydroxylase.

[0044] In some embodiments of any of the aspects, the phenylalanine hydroxylase comprises an amino acid sequence comprising one or more of phenylalanine at the position corresponding to W192, isoleucine or leucine at the position corresponding to F197, and cysteine at the position corresponding to E219 of the phenylalanine hydroxylase of *Cupriavidus taiwanensis* (SEQ ID NO: 227).

[0045] In one aspect described herein is a pharmaceutical composition comprising a therapeutic composition as described herein and a pharmaceutically acceptable carrier.

[0046] In one aspect described herein is a method of increasing serotonin level in a mammalian subject in need thereof, the method comprising administering a composition as described herein to the subject, whereby a serotonin level is increased.

[0047] In some embodiments of any of the aspects, the administering is to the gut of the subject.

[0048] In some embodiments of any of the aspects, the level of serotonin in the gut is increased.

[0049] In some embodiments of any of the aspects, the level of serotonin in circulation is increased.

[0050] In one aspect described herein is a method of treating a disease or disorder involving or characterized by low serotonin in a subject in need thereof, the method comprising administering a composition as described herein to the subject, whereby the disease or disorder is treated.

[0051] In some embodiments of any of the aspects, the administering is to the gut of the subject.

[0052] In some embodiments of any of the aspects, the level of serotonin in the gut is increased.

[0053] In some embodiments of any of the aspects, the level of serotonin in circulation is increased.

[0054] In some embodiments of any of the aspects, the disease or disorder is selected from the group consisting of constipation, IBS-C, depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD),

memory loss (e.g. dementia), learning difficulties, osteoporosis, heartburn, dermatological conditions (eczema and itch), GERD, and pain disorders.

[0055] In some embodiments of any of the aspects, the disease or disorder is not a gut disease or disorder.

[0056] In some embodiments of any of the aspects, the disease or disorder is selected from the group consisting of depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, dermatological conditions (eczema and itch), and pain disorders.

[0057] In some embodiments of any of the aspects, the composition comprising an amount of a live isolated serotonin-increasing bacterial species, dead isolated serotonin increasing bacterial species, conditioned medium from an isolated, cultured serotonin-increasing bacterial species, cell pellet of an isolated serotonin-increasing bacterial species, a purified metabolite produced by an isolated serotonin-increasing bacterial species, a purified protein produced by an isolated serotonin-increasing bacterial species, or a combination thereof sufficient to increase serotonin level in the subject, and an excipient or carrier suitable for delivery to the gut promotes production of serotonin by cells of a subject in which the composition is delivered to their gut.

[0058] In some embodiments of any of the aspects, the composition promotes expression of tryptophan hydroxylase 1 in cells of the subject.

[0059] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species increases serotonin in at least one of the following ways: production of secreted metabolites or secreted proteins that induce serotonin production; production of ligands that induce serotonin production; or production of an agonist of a serotonin receptor or the trace amine-associated receptor (TAAR).

[0060] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species increases serotonin through production of secreted metabolites or secreted proteins that induce serotonin production.

[0061] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species comprises one or more species selected from the group consisting of: *Acidaminococcus intestini*, *Agathobacter rectalis*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis*, *Bacillus cereus*, *Bacteroides caccae*, *Bacteroides cellulosilyticus*, *Bacteroides dorei*, *Bacteroides inegoldii*, *Bacteroides fragilis*, *Bacteroides koreensis*, *Bacteroides ovatus*, *Bacteroides plebeius*, *Bacteroides salyersiae*, *Bacteroides stercoris*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylinosolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium breve*, *Bifidobacterium faecale*, *Bifidobacterium longum*, *Bilophila wadsworthia*, *Butyricimonas paraviriosa*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium clostridioforme*, *Clostridium hathewayi*, *Clostridium innoculum*, *Clostridium paraputrifcum*, *Clostridium saudense*, *Clostridium scindens*, *Clostridium tyrobutyricum*, *Clostridium hylemonae HB-73*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dysosmabacter welbionis*, *Eisenbergiella tayi*, *Enterococcus faecium*, *Erysipelatoclostridium ramosum*, *Eubacterium eligens*, *Faecalitalea cylindroides*, *Flavonifractor plautii*, *Flintibacter butyricus*, *Gemmiger formicilis*, *Gordonibacter pamelaeae*, *Hungatella effluvii*, *Hungatella hathewayi*,

Intestinimonas butyriciproducens, *Lactobacillus brevis*, *Mediterraneibacter faecis*, *Oscillibacter* sp., *Parabacteroides distasonis*, *Parabacteroides johnsonii*, *Parabacteroides merdae*, *Parasutterella excrementihominis*, *Ruminococcus bicirculans*, *Ruminococcus gnavus*, *Streptococcus gordonii*, and *Turicibacter sanguinis*.

[0062] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species comprises one or more species selected from the group consisting of *Acidaminococcus intestini* HB-95, *Agathobacter rectalis* HB-257, *Alistipes onderdonkii* HB-311, *Alistipes putredinis* HB-324, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellulolyticus* HB-227, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris* HB-33, *Bacteroides uniformis* HB-13, *Bacteroides vulgatus* HB-10, *Bacteroides xylanisolvens* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium breve* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium longum* HB-71, *Bilophila wadsworthia* HB-693, *Butyricimonas paravirosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium clostridioforme* HB-642, *Clostridium hathewayi* HB-152, *Clostridium innoculum* HB-82, *Clostridium paraputrificum* HB-27, *Clostridium saudiense* HB-142, *Clostridium scindens* HB-444, *Clostridium tyrobutyricum* HB-469, *Clostridium hylemonae* HB-73, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus eutactus* HB-155, *Dysosmobacter welbionis* HB-45, *Eisenbergiella tayi* HB-437, *Eisenbergiella tayi* HB-612, *Enterococcus faecium* HB-640, *Enterococcus faecium* HB-85, *Erysipelatoclostridium ramosum* HB-24, *Eubacterium eligens* HB-252, *Faecalitalea cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter butyricus* HB-344, *Gemmiger formicilis* HB-325, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Lactobacillus brevis* HB-87, *Mediterraneibacter faecis* HB-364, *Oscillibacter* sp. HB-28, *Parabacteroides distasonis* HB-20, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella excrementihominis* HB-330, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Streptococcus gordonii* HB-62, *Streptococcus gordonii* HB-98, and *Turicibacter sanguinis* HB-147.

[0063] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species comprises a 16S sequence at least 95% identical to a sequence selected from SEQ ID Nos 1, 2, and 5-69.

[0064] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species increases serotonin through production of an agonist of a serotonin receptor or the trace amine-associated receptor (TAAR).

[0065] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species encodes and expresses enzymes sufficient for the production of an agonist of a serotonin receptor or the trace amine-associated receptor (TAAR).

[0066] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from the group consisting of: *Akkermansia muciniphila*, *Adlercreutzia equolifaciens*, *Clostridium sporogenes*,

Clostridium lavalense, *Clostridium asparagiforme*, *Coprococcus eutactus*, *Coprococcus comes*, *Enterococcus durans*, *Enterorhabdus muris*, *Enterorhabdus caecimuris*, *Mycolicibacterium smegmatis*, *Peptostreptococcus russelii*, and *Ruminococcus gnavus*.

[0067] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from the group consisting of: *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516. In some embodiments, the 5-HT agonist-producing bacteria are greater than 95% similar by 16S sequencing to *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Clostridium sporogenes* JCM 7836, *Akkermansia muciniphila* BAA-835, *Clostridium sporogenes* McClung 2004, *Peptostreptococcus russelii* RT-10B, *Mycolicibacterium smegmatis* ATCC 19420, *Enterorhabdus muris* WCA-131-CoC-2, *Adlercreutzia equolifaciens* FJC-B9, *Enterorhabdus caecimuris* B7, *Coprococcus eutactus* ATCC 27759, and *Coprococcus comes* ATCC 27758.

[0068] In some embodiments of any of the aspects, the isolated bacterial species comprises a 16S sequence at least 95% identical to a sequence selected from SEQ ID Nos 1-4 and 105-114.

[0069] In some embodiments of any of the aspects, the agonist of the serotonin receptor or TAAR is selected from the group consisting of N-methyltryptamine, N,N-dimethyltryptamine, N-methylserotonin, and N,N-dimethylserotonin.

[0070] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species encodes and expresses one or more enzymes that catalyze the methylation of tryptamine by a mechanism corresponding to that of human indolethylamine N-methyltransferase, or one or more enzymes at least 50% identical to the radical S-adenosyl-L-methionine-dependent, ergothioneine biosynthetic enzyme egtD, or one or more phosphatidylethanolamine N-methyltransferase enzymes (e.g., SEQ ID NOs: 228 or 229).

[0071] In some embodiments of any of the aspects, culture supernatant of the isolated bacterial species increases expression of tryptophan hydroxylase 1 (TPH-1) in cells of the host.

[0072] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from the group consisting of *Enterococcus durans*, *Clostridium lavalense*, *Lactobacillus brevis*, *Bifidobacterium faecale*, *Anaerotruncus colihominis*, and *Clostridium ramosum*.

[0073] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from the group consisting of *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Lactobacillus brevis* HB-87, *Bifidobacterium faecale* HB-159, *Anaerotruncus colihominis* HB-83, and *Clostridium ramosum* HB-24 or a combination thereof.

[0074] In some embodiments of any of the aspects, the isolated bacterial species comprises a 16S sequence at least 95% identical to a sequence selected from the group consisting of SEQ ID Nos: 3, 4, 11, 28, 30 and 39.

[0075] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from the group consisting of *Clostridium scindens*,

Bifidobacterium faecale, *Enterococcus durans*, *Clostridium lavalense*, *Anaerotruncus colihominis*, and *Erysipelatoclostridium ramosum*.

[0076] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from the group consisting of *Clostridium scindens* HB-444, *Bifidobacterium faecale* HB-159, *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Anaerotruncus colihominis* HB-83, and *Erysipelatoclostridium ramosum* HB-24.

[0077] In some embodiments of any of the aspects, the isolated bacterial species comprises a 16S sequence that is at least 95% identical to one of SEQ ID NOS: 3, 4, 11, 23, 28 and 39.

[0078] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species increases serotonin through production of ligands that induce serotonin production.

[0079] In some embodiments of any of the aspects, a cell pellet from the isolated serotonin increasing bacterial species modulates serotonin when administered to a subject.

[0080] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from the group consisting of *Anaerotruncus colihominis*, *Bacteroides caccae*, *Bacteroides clarus*, *Bacteroides dorei*, *Bacteroides finegoldii*, *Bacteroides ovatus*, *Bacteroides salyersiae*, *Bacteroides thetaiotaomicron*, *Bacteroides xylanisolvans*, *Bifidobacterium adolescentis*, *Bifidobacterium faecale*, *Bittarella massiliensis*, *Blautia wexlerae*, *Clostridium aldenese*, *Clostridium bolteae*, *Clostridium hathewayi*, *Clostridium saudiense*, *Clostridium scindens*, *Clostridium tyrobutyricum*, *Dialister invisus*, *Eisenbergiella tayi*, *Enterococcus durans*, *Enterococcus faecium*, *Eubacterium eligens*, *Gemmiger formicilis*, *Gordonibacter pamelaeae*, *Hungatella effluvii*, *Lactobacillus brevis*, *Longibaculum muris*, *Mediterraneibacter faecis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Parasutterella exrementihominis*, *Prevotella copri*, *Prevotella* sp., *Prevotella* sp., *Romboutsia lituseburensis*, *Ruminococcus* sp., *Ruminococcus gnarus*, *Sellimonas intestinalis*, and *Sutterella wadsworthensis*.

[0081] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from the group consisting of *Anaerotruncus colihominis* HB-83, *Bacteroides caccae* HB-11, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides ovatus* HB-70, *Bacteroides salyersiae* HB-32, *Bacteroides thetaiotaomicron* HB-34, *Bacteroides xylanisolvans* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium faecale* HB-159, *Bittarella massiliensis* HB-477, *Blautia wexlerae* HB-16, *Clostridium aldenese* HB-440, *Clostridium bolteae* HB-442, *Clostridium hathewayi* HB-152, *Clostridium saudiense* HB-142, *Clostridium scindens* HB-444, *Clostridium tyrobutyricum* HB-469, *Dialister invisus* HB-387, *Eisenbergiella tayi* HB-612, *Enterococcus durans* HB-48, *Enterococcus faecium* HB-85, *Eubacterium eligens* HB-252, *Gemmiger formicilis* HB-325, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Lactobacillus brevis* HB-87, *Longibaculum muris* HB-79, *Mediterraneibacter faecis* HB-364, *Parabacteroides distasonis* HB-20, *Parabacteroides merdae* HB-63, *Parasutterella exrementihominis* HB-330, *Prevotella copri* HB-373, *Prevotella* sp HB-649, *Prevotella* sp. HB-333, *Romboutsia lituseburensis* HB-102,

Ruminococcus sp. HB-626, *Ruminococcus gnarus* HB-40, *Ruminococcus gnarus* HB-516, *Sellimonas intestinalis* HB-443, and *Sutterella wadsworthensis* HB-259.

[0082] In some embodiments of any of the aspects, the isolated bacterial species comprises a 16S sequence at least 95% identical to a sequence selected from the group consisting of SEQ ID Nos 1-3, 5-30 and 70-82.

[0083] In some embodiments of any of the aspects, the cell pellet increases expression of TPH-1 in cells of the subject.

[0084] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from *Clostridium lavalense*, *Lactobacillus brevis*, *Bifidobacterium faecale*, *Anaerotruncus colihominis*, and *Clostridium ramosum*.

[0085] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from *Clostridium lavalense* HB-452c, *Lactobacillus brevis* HB-87, *Bifidobacterium faecale* HB-159, *Anaerotruncus colihominis* HB-83, and *Clostridium ramosum* HB-24.

[0086] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species that comprise a 16S sequence at least 95% identical to a sequence selected from SEQ ID Nos 4, 11, 28, 30, and 39.

[0087] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from *Clostridium scindens*, *Bifidobacterium faecale*, *Enterococcus durans*, *Clostridium lavalense*, *Anaerotruncus colihominis*, and *Erysipelatoclostridium ramosum*.

[0088] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species selected from *Clostridium scindens* HB-444, *Bifidobacterium faecale* HB-159, *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Anaerotruncus colihominis* HB-83, and *Erysipelatoclostridium ramosum* HB-24.

[0089] In some embodiments of any of the aspects, the isolated bacterial species comprises one or more species that comprise a 16S sequence at least 95% identical to a sequence selected from SEQ ID Nos 3, 4, 11, 23, 28 and 39.

[0090] In some embodiments of any of the aspects, the isolated bacterial species are grown in medium containing one or more nutrients selected from the group consisting of conditioned medium from other bacteria, N-Acetyl-D-Galactosamine, N-Acetyl-D-Glucosamine, N-Acetyl- β -D-Mannosamine, Adonitol, Amygdalin, D-Arabitol, Arbutin, D-Cellobiose, α -Cyclodextrin, O-Cyclodextrin, Dextrin, Dulcitol, i-Erythritol, D-Fructose, L-Fucose, D-Galactose, D-Galacturonic Acid, Gentibiose, D-Gluconic Acid, D-Glucosaminic Acid, α -D-Glucose, α -D-Glucose 1-Phosphate, D-Glucose6-Phosphate, Glycerol, D,L- α -Glycerol Phosphate, m-Inositol, α -D-Lactose, Lactulose, Maltose, Maltotriose, D-Mannitol, D-Mannose, D-Melezitose, D-Melibiose, β -Methyl-DGlucose, α -Methyl-DGalactoside, β -Methyl-D-Galactoside, α -Methyl-D-Glucoside, β -Methyl-D-Glucoside, Mucin, Palatinose, D-Raffinose, L-Rhamnose, Salicin, D-Sorbitol, Stachyose, Sucrose, D-Trehalose, Turanose, Acetic Acid, Formic Acid, Fumaric Acid, Glyoxylic Acid, α -Hydroxybutyric Acid, β -Hydroxybutyric Acid, Itaconic Acid, α -Ketobutyric Acid, α -Ketovaleric Acid, D,L-Lactic Acid, L-Lactic Acid, D-Lactic Acid Methyl Ester, D-Malic Acid, L-Malic Acid, Propionic Acid, Pyruvic Acid, Pyruvic Acid Methyl Ester, D-Saccharic Acid, Succinamic Acid, Succinic Acid, Succinic Acid Mono-

Methyl Ester, m-Tartaric Acid, Urocanic Acid, Alaninamide, L-Alanine, L-Alanyl-LGlutamine, L-Alanyl-LHistidine, L-Alanyl-LThreonine, L-Asparagine, L-Glutamic Acid, L-Glutamine, Glycyl-LAspartic Acid, Glycyl-LGlutamine, Glycyl-LMethionine, Glycyl-LProline, L-Methionine, L-Phenylalanine, L-Serine, L-Threonine, L-Valine, L-Valine plus L-Aspartic Acid, 2'-Deoxy Adenosine, Inosine, Thymidine, Uridine, Thymidine-5'-Mono-phosphate, and Uridine-5'-Monophosphate.

[0091] In some embodiments of any of the aspects, an isolated serotonin-increasing bacterial species in the composition produces tryptophan.

[0092] In some embodiments of any of the aspects, an isolated serotonin-increasing bacterial species in the composition encodes or expresses at least one enzyme involved in tryptophan production.

[0093] In some embodiments of any of the aspects, the enzyme involved in tryptophan production is selected from the group consisting of: Tryptophan synthase; Indole-3-glycerol phosphate synthase; Anthranilate phosphoribosyl-transferase; Anthranilate synthase; and N-(5'-phosphoribosyl)anthranilate isomerase; 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase.

[0094] In some embodiments of any of the aspects, the enzyme involved in tryptophan production belongs to an EC number selected from the group consisting of: EC 4.2.1.20, EC 4.1.1.48, EC 2.4.2.18, EC 4.1.3.27, EC 5.3.1.24, and EC 5.3.1.36.

[0095] In some embodiments of any of the aspects, the enzyme involved in tryptophan production has an amino acid sequence at least 50% identical to a sequence selected from SEQ ID Nos 135-163.

[0096] In some embodiments of any of the aspects, an isolated serotonin-increasing bacterial species in the composition produces a metabolite of phenylalanine selected from phenethylamine, tyramine or N-methylated derivatives thereof that activate the TAAR system.

[0097] In some embodiments of any of the aspects, the isolated serotonin-increasing bacterial species in the composition produces one or more indole-3-carboxylic acid derivatives of tryptophan.

[0098] In some embodiments of any of the aspects, the indole-3-carboxylic acid derivative of tryptophan is one or more of indole-3-propionic acid, indole-3-acrylic acid, indole-3-lactic acid, indole-3-pyruvic acid, or indole-3-acetic acid.

[0099] In some embodiments of any of the aspects, the isolated bacterial species comprises and expresses genes of the fldAIBC gene cluster.

[0100] In some embodiments of any of the aspects, the isolated bacterial species encodes and expresses acyl-CoA dehydrogenase.

[0101] In some embodiments of any of the aspects, the acyl-CoA dehydrogenase belongs to EC 1.3.99.3; EC 1.3.8.7; EC 1.3.8.8; or EC 1.3.8.9.

[0102] In some embodiments of any of the aspects, the acyl-CoA dehydrogenase has an amino acid sequence at least 50% identical to a sequence selected from SEQ ID Nos 164-171.

[0103] In some embodiments of any of the aspects, the isolated bacterial species encodes and expresses an enzyme with a sequence at least 50% identical to an enzyme having an amino acid sequence of any one of SEQ ID Nos 172-184.

[0104] In some embodiments of any of the aspects, the isolated bacterial species encodes and expresses an enzyme belonging to an EC group selected from: EC 4.1.99.1; EC 2.8.3.17; EC 4.2.1.175; EC 5.6.1.9; and EC 2.1.1.

[0105] In one aspect described herein is a pharmaceutical composition comprising the therapeutic composition as described herein, and a pharmaceutically acceptable carrier.

[0106] In one aspect described herein is a method of increasing serotonin level in a mammalian subject in need thereof, the method comprising administering a composition as described herein to the subject, whereby a serotonin level is increased.

[0107] In some embodiments of any of the aspects, the administering is to the gut of the subject.

[0108] In some embodiments of any of the aspects, the level of serotonin in the gut is increased.

[0109] In some embodiments of any of the aspects, the level of serotonin in circulation is increased.

[0110] In one aspect described herein is a method of treating a disease or disorder involving or characterized by low serotonin in a subject in need thereof, the method comprising administering a composition as described herein to the subject, whereby the disease or disorder is treated.

[0111] In some embodiments of any of the aspects, the administering is to the gut of the subject.

[0112] In some embodiments of any of the aspects, the level of serotonin in the gut is increased.

[0113] In some embodiments of any of the aspects, the level of serotonin in circulation is increased.

[0114] In some embodiments of any of the aspects, the disease or disorder is selected from the group consisting of constipation, IBS-C, depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, heartburn, dermatological conditions (eczema and itch), GERD, and pain disorders.

[0115] In some embodiments of any of the aspects, the disease or disorder is not a gut disease or disorder.

[0116] In some embodiments of any of the aspects, the disease or disorder is selected from the group consisting of depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, dermatological conditions (eczema and itch), and pain disorders.

[0117] In one aspect described herein is a therapeutic composition for decreasing serotonin level in a mammalian subject in need thereof, the composition comprising an amount of a live isolated bacterial species, dead isolated bacterial species, conditioned medium from an isolated, cultured bacterial species, cell pellet of an isolated bacterial species, a purified metabolite produced by an isolated bacterial species, a purified protein produced by an isolated bacterial species, or a combination thereof sufficient to decrease serotonin level in the subject, and an excipient or carrier suitable for delivery to the gut.

[0118] In some embodiments of any of the aspects, bacterial species consumes serotonin and/or reduces host biosynthesis of serotonin.

[0119] In some embodiments of any of the aspects, the bacterial species is selected from one or more of *Bifidobacterium longum*, *Blautia coccoides*, *Blautia obeum*,

Clostridium butyricum, *Coprococcus comes*, *Dorea longicatena*, *Eubacterium rectale*, *Lachnoclostridium* sp., and *Slackia isoflavoniconvertens*.

[0120] In some embodiments of any of the aspects, the bacterial species is selected from one or more of: *Bifidobacterium longum* HB-234, *Blautia coccoides* HB-23, *Blautia obeum* HB-14, *Clostridium butyricum* HB-88, *Coprococcus comes* HB-80, *Dorea longicatena* HB-17, *Eubacterium rectale* HB-22, *Lachnoclostridium* sp. HB-698, and *Slackia isoflavoniconvertens* HB-326.

[0121] In some embodiments of any of the aspects, the isolated bacterial species comprises a 16S sequence at least 95% identical to a sequence selected from SEQ ID Nos 96-104.

[0122] In one aspect described herein is a method of decreasing serotonin in a mammalian subject in need thereof, the method comprising administering a composition as described herein to the subject, whereby a serotonin level is decreased.

[0123] In some embodiments of any of the aspects, the administering is to the gut of the subject.

[0124] In some embodiments of any of the aspects, the level of serotonin in the gut is decreased.

[0125] In some embodiments of any of the aspects, the level of serotonin in circulation is decreased.

[0126] In one aspect described herein is a method of treating a disease or disorder involving or characterized by high or elevated serotonin in a subject in need thereof, the method comprising administering a composition as described herein to the subject, whereby the disease or disorder is treated.

[0127] In some embodiments of any of the aspects, the administering is to the gut of the subject.

[0128] In some embodiments of any of the aspects, the level of serotonin in the gut is decreased.

[0129] In some embodiments of any of the aspects, the level of serotonin in circulation is decreased.

[0130] In some embodiments of any of the aspects, the disease or disorder is selected from the group consisting of diarrhea, IBS-D, inflammatory bowel disease, anxiety, social phobia, sleep disorders, schizophrenia, cancer, obesity, diabetes, coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or platelet disorders (e.g. essential thrombocytosis).

[0131] In some embodiments of any of the aspects, the disease or disorder is not a gut disease or disorder.

[0132] In some embodiments of any of the aspects, the disease or disorder is selected from the group consisting of anxiety, social phobia, sleep disorders, schizophrenia, cancer, obesity, diabetes, coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or platelet disorders (e.g. essential thrombocytosis).

[0133] In one aspect described herein is a therapeutic composition comprising one or more live isolated serotonin-modulating bacteria, dead isolated serotonin-modulating bacteria, conditioned medium(s) from an isolated, cultured serotonin-modulating bacteria, cell pellet(s) of isolated serotonin-modulating bacteria, purified metabolite(s) produced by isolated serotonin-modulating bacteria, purified protein(s) produced by an isolated serotonin-modulating bacteria, or a combination thereof, which alter serotonin signaling or biosynthesis in a subject in need thereof.

[0134] In some embodiments of any of the aspects, the at least one isolated serotonin-modulating bacteria belongs to

a genus selected from the group consisting of: *Acidaminococcus*, *Agathobacter*, *Adlercreutzia*, *Akkermansia*, *Alistipes*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Bilophila*, *Blattarella*, *Blautia*, *Blautia*, *Butyricimonas*, *Clostridium*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dialister*, *Dorea*, *Dysosmabacter*, *Eisenbergiella*, *Enterococcus*, *Enterorhabdus*, *Erysipelatoclostridium*, *Escherichia*, *Eubacterium*, *Faecalitalea*, *Flavonifractor*, *Flintibacter*, *Gemmiger*, *Gordonibacter*, *Hungatella*, *Intestinimonas*, *Lachnoclostridium*, *Lactobacillus*, *Lawsonibacter*, *Longibaculum*, *Mediterraneibacter*, *Mycolicibacterium*, *Oscillibacter*, *Parabacteroides*, *Parasutterella*, *Peptostreptococcus*, *Prevotella*, *Romboutsia*, *Ruminococcus*, *Sellimonas*, *Slackia*, *Streptococcus*, *Sutterella*, *Turicibacter*, and *Veillonella*.

[0135] In some embodiments of any of the aspects, the at least one isolated serotonin-modulating bacteria are species selected from the group consisting of: *Acidaminococcus intestini*, *Agathobacter rectalis*, *Akkermansia muciniphila*, *Adlercreutzia equolifaciens*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis*, *Bacillus cereus*, *Bacteroides caccae*, *Bacteroides cellulosilyticus*, *Bacteroides clarus*, *Bacteroides dorei*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides koreensis*, *Bacteroides ovatus*, *Bacteroides plebeius*, *Bacteroides salyersiae*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgaris*, *Bacteroides xylinisolvans*, *Bifidobacterium adolescentis*, *Bifidobacterium breve*, *Bifidobacterium faecale*, *Bifidobacterium longum*, *Bilophila wadsworthia*, *Blattarella massiliensis*, *Blautia coccoides*, *Blautia obeum*, *Blautia wexlerae*, *Butyricimonas paravirrosa*, *Clostridium asparagiforme*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium butyricum*, *Clostridium clostridioforme*, *Clostridium hathewayi*, *Clostridium innocuum*, *Clostridium lavalense*, *Clostridium paraputrificum*, *Clostridium saudience*, *Clostridium scindens*, *Clostridium* sp., *Clostridium sporogenes*, *Clostridium sphenoides*, *Clostridium symbiosum*, *Clostridium tyrobutyricum*, *Clostridium hylemonae*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dorea longicatena*, *Dysosmabacter welbionis*, *Eisenbergiella tayi*, *Enterococcus durans*, *Enterococcus faecium*, *Enterorhabdus caecimuris*, *Enterorhabdus muris*, *Erysipelatoclostridium ramosum*, *Escherichia coli*, *Eubacterium callanderi*, *Eubacterium eligens*, *Eubacterium rectale*, *Faecalitalea cylindroides*, *Flavonifractorplautii*, *Flintibacter butyricus*, *Gemmiger formicilis*, *Gemmiger* sp., *Gordonibacter pamelaeae*, *Hungatella effluvii*, *Hungatella hathewayi*, *Intestinimonas butyriciproducens*, *Intestinimonas massiliensis*, *Lachnoclostridium* sp., *Lactobacillus brevis*, *Lawsonibacter asaccharolyticus*, *Longibaculum muris*, *Longibaculum* sp., *Mediterraneibacter faecis*, *Mycolicibacterium smegmatis*, *Oscillibacter* sp., *Parabacteroides distasonis*, *Parabacteroides goldsteinii*, *Parabacteroides johnsonii*, *Parabacteroides merdae*, *Parasutterella excrementihominis*, *Peptostreptococcus russellii*, *Prevotella copri*, *Prevotella* sp., *Prevotella* sp., *Romboutsia lituseburensis*, *Ruminococcus bicirculans*, *Ruminococcus gnavus*, *Ruminococcus* sp., *Sellimonas intestinalis*, *Slackia isoflavoniconvertens*, *Streptococcus gordonii*, *Sutterella wadsworthensis*, *Turicibacter sanguinis*, and *Veillonella atypica*.

[0136] In some embodiments of any of the aspects, the one or more serotonin-modulating bacteria include a strain selected from the group consisting of: *Acidaminococcus*

intestini HB-95, *Agathobacter rectalis* HB-257, *Akkermansia muciniphila* BAA-835, *Adlercreutzia equolifaciens* FJC-B9, *Alistipes onderdonkii* HB-311, *Alistipes putredinis* HB-324, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellulosilyticus* HB-227, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris* HB-33, *Bacteroides thetaiotaomicron* HB-34, *Bacteroides uniformis* HB-13, *Bacteroides vulgatus* HB-10, *Bacteroides xylanisolvans* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium breve* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium longum* HB-234, *Bifidobacterium longum* HB-71, *Bilophila wadsworthia* HB-693, *Bittarella massiliensis* HB-477, *Blautia coccoides* HB-23, *Blautia obeum* HB-14, *Blautia wexlerae* HB-16, *Butyricimonas paraviriosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium butyricum* HB-88, *Clostridium clostridioforme* HB-642, *Clostridium hathewayi* HB-152, *Clostridium innoculum* HB-82, *Clostridium lavalense* HB-452c, *Clostridium paraputrificum* HB-27, *Clostridium saudense* HB-142, *Clostridium scindens* HB-444, *Clostridium* sp. HB-358, *Clostridium sphenoides* HB-470, *Clostridium sporogenes* JCM 7836, *Clostridium sporogenes* McClung 2004, *Clostridium symbiosum* HB-67, *Clostridium tyrobutyricum* HB-469, *Clostridium hylemonae* HB-73, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus comes* HB-80, *Coprococcus comes* ATCC 27758, *Coprococcus eutactus* HB-155, *Coprococcus eutactus* ATCC 27759, *Dialister invisus* HB-387, *Dorea longicatena* HB-17, *Dysosmobaacter welbionis* HB-45, *Eisenbergiella tayi* HB-437, *Eisenbergiella tayi* HB-612, *Enterococcus durans* HB-48, *Enterococcus faecium* HB-640, *Enterococcus faecium* HB-85, *Enterorhabdus caecimuris* B7, *Enterorhabdus muris* WCA-131-CoC-2, *Erysipelatoclostridium ramosum* HB-24, *Escherichia coli* HB-490, *Eubacterium callanderi* HB-59, *Eubacterium eligens* HB-252, *Eubacterium rectale* HB-22, *Faecalitalea cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter butyricus* HB-344, *Gemmiger formicilis* HB-325, *Gemmiger* sp. HB-567, *Gordoniabacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Intestinimonas massiliensis* HB-651, *Lachnolstridium* sp. HB-698, *Lactobacillus brevis* HB-87, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum muris* HB-79, *Longibaculum* sp. HB-681, *Mediterraneibacter faecis* HB-364, *Mycolicibacterium smegmatis* ATCC 19420, *Oscillibacter* sp. HB-28, *Parabacteroides distasonis* HB-20, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella excrementihominis* HB-330, *Peptostreptococcus russelii* RT-10B, *Prevotella copri* HB-373, *Prevotella* sp. HB-649, *Prevotella* sp. HB-333, *Romboutsia lituseburensis* HB-102, *Ruminococcus bicirculans* HB-105, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Ruminococcus* sp. HB-626, *Sellimonas intestinalis* HB-443, *Slackia isoflavoniconvertens* HB-326, *Streptococcus gordonii* HB-62, *Streptococcus gordonii* HB-98, *Sutterella wadsworthensis* HB-259, *Turicibacter sanguinis* HB-147, and *Veillonella atypica* HB-251.

[0137] In some embodiments of any of the aspects, the one or more serotonin-modulating bacteria consists of a bacteria comprising a 16S rDNA sequence at least about 95% identical to a 16S rDNA sequence selected from one of SEQ ID NOs: 1-114.

[0138] In some embodiments of any of the aspects, the serotonin-modulating bacteria encode genes in their genome, which when expressed, result in the production of one or more metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0139] In some embodiments of any of the aspects, the encoded genes are expressed at physiologically relevant conditions of the human gastrointestinal tract, resulting in the production of metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0140] In some embodiments of any of the aspects, the composition is in the form of a probiotic, prebiotic, a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powder, a granule, a medical food, a supplement, or a combination thereof.

[0141] In some embodiments of any of the aspects, the composition is formulated to be administered orally, intravenously, intramuscularly, intrathecally, subcutaneously, sublingually, buccally, rectally, vaginally, by the ocular route, by the otic route, nasally, via inhalation, by nebulization, cutaneously, transdermally, or a combination thereof.

[0142] In one aspect described herein is a pharmaceutical composition comprising the therapeutic composition as described herein, and a pharmaceutically acceptable carrier.

[0143] In one aspect described herein is a method of treating a disease or disorder in a subject in need thereof, the method comprising administering to the subject an effective amount of a therapeutic composition comprising one or more live isolated serotonin-modulating bacteria, dead isolated serotonin modulating bacteria, conditioned medium(s) derived from an isolated serotonin-modulating bacteria, cell pellet(s) of isolated serotonin-modulating bacteria, purified metabolite(s) produced by isolated serotonin-modulating bacteria, purified protein(s) produced by isolated serotonin-modulating bacteria, or a combination thereof, thereby altering serotonin signaling or biosynthesis in the subject to treat the disease or disorder.

[0144] In some embodiments of any of the aspects, the disease or disorder is a serotonin-related disease or disorder.

[0145] In some embodiments of any of the aspects, the serotonin-related disease or disorder is selected from the group consisting of intestinal motility disorders, irritable bowel syndrome, inflammatory bowel disease, depression (e.g. major depressive disorder, treatment resistant depression, post-partum depression), anxiety disorders, addiction, social phobia, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, sleep disorders, schizophrenia, bone disease (e.g. osteoporosis), cancer (e.g. polycythemia vera or myelosclerosis), metabolic disease (e.g. obesity or diabetes), a dysregulated immune system, cardiac disease (e.g. coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or aorta disease), heartburn, dermatological conditions (e.g. eczema and itch), GERD, platelet disorders (e.g. essential thrombocytosis), and pain disorders.

[0146] In some embodiments of any of the aspects, the disease or disorder is caused by high serotonin levels and is

selected from the group: diarrhea, IBS-D, inflammatory bowel disease, anxiety, social phobia, sleep disorders, schizophrenia, cancer, obesity, diabetes, coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or platelet disorders (e.g. essential thrombocytosis).

[0147] In some embodiments of any of the aspects, the disease or disorder is caused by low serotonin levels and is selected from the group: constipation, IBS-C, depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, heartburn, dermatological conditions (eczema and itch), GERD, or pain disorders.

[0148] In some embodiments of any of the aspects, treating a disease or disorder comprises decreasing at least one symptom of the disease or disorder, selected from: fatigue, insomnia, stress, persistent anxiety, persistent sadness, social withdrawal, substance withdrawal, irritability, thoughts of suicide, thoughts of self-harm, restlessness, low sex drive, lack of focus, loss of appetite, high blood pressure, low blood pressure, high heart rate, low heart rate, constipation, diarrhea, chronic pain, heartburn, fatigue, trouble breathing, stomach aches, nosebleeds, gum, stomach bleeding, headaches, weight gain, burning of the skin, altered inflammatory markers, neurodevelopmental deficits, and/or seizures.

[0149] In some embodiments of any of the aspects, the at least one isolated serotonin-modulating bacteria belongs to a genus selected from the group consisting of: *Acidaminococcus*, *Agathobacter*, *Adlercreutzia*, *Akkermansia*, *Alistipes*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Bilophila*, *Bittarella*, *Blautia*, *Blautia*, *Butyricimonas*, *Clostridium*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dialister*, *Dorea*, *Dysosmabacter*, *Eisenbergiella*, *Enterococcus*, *Enterorhabdus*, *Erysipelatoclostridium*, *Escherichia*, *Eubacterium*, *Faecalitalea*, *Flavonifractor*, *Flintibacter*, *Gemmiger*, *Gordonibacter*, *Hungatella*, *Intestinimonas*, *Lachnoclostridium*, *Lactobacillus*, *Lawsonibacter*, *Longibaculum*, *Mediterraneibacter*, *Mycolicibacterium*, *Oscillibacter*, *Parabacteroides*, *Parasutterella*, *Peptostreptococcus*, *Prevotella*, *Romboutsia*, *Ruminococcus*, *Sellimonas*, *Slackia*, *Streptococcus*, *Sutterella*, *Turicibacter*, and *Veillonella*.

[0150] In some embodiments of any of the aspects, the at least one isolated serotonin-modulating bacteria are species selected from the group consisting of: *Acidaminococcus intestini*, *Agathobacter rectalis*, *Akkermansia muciniphila*, *Adlercreutzia equolifaciens*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis*, *Bacillus cereus*, *Bacteroides caccae*, *Bacteroides cellulosilyticus*, *Bacteroides clarus*, *Bacteroides dorei*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides koreensis*, *Bacteroides ovatus*, *Bacteroides plebeius*, *Bacteroides salyersiae*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylinisolvans*, *Bifidobacterium adolescentis*, *Bifidobacterium breve*, *Bifidobacterium faecale*, *Bifidobacterium longum*, *Bilophila wadsworthia*, *Bittarella massiliensis*, *Blautia coccoides*, *Blautia obeum*, *Blautia wexlerae*, *Butyricimonas paravirosa*, *Clostridium asparagineforme*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium butyricum*, *Clostridium clostradioforme*, *Clostridium hathewayi*, *Clostridium innoculum*, *Clostridium lavalense*, *Clostridium paraputrificum*, *Clostridium saudicense*, *Clostridium scindens*, *Clostridium symbiosum*, *Clostridium tyrobutyricum*, *Clostridium hylemonae*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dorea longicatena*, *Dysosmabacter welbionis*, *Eisenbergiella tayi*, *Enterococcus durans*, *Enterococcus faecium*, *Enterorhabdus caecimuris*, *Enterorhabdus muris*, *Erysipelatoclostridium ramosum*, *Escherichia coli*, *Eubacterium callanderi*, *Eubacterium eligens*, *Eubacterium rectale*, *Faecalitalea cylindroides*, *Flavonifractorplautii*, *Flintibacter butyricus*, *Gemmiger formicilis*, *Gemmiger sp.*, *Gordonibacter pamelaeae*, *Hungatella effluvii*, *Hungatella hathewayi*, *Intestinimonas butyriciproducens*, *Intestinimonas massiliensis*, *Lachnoclostridium sp.*, *Lactobacillus brevis*, *Lawsonibacter asaccharolyticus*, *Longibaculum muris*, *Longibaculum sp.*, *Mediterraneibacter faecis*, *Mycolicibacterium smegmatis*, *Oscillibacter sp.*, *Parabacteroides distasonis*, *Parabacteroides goldsteinii*, *Parabacteroides johnsonii*, *Parabacteroides merdae*, *Parasutterella excrementihominis*, *Peptostreptococcus russellii*, *Prevotella copri*, *Prevotella sp.*, *Romboutsia lituseburensis*, *Ruminococcus bicirculans*, *Ruminococcus gnayus*, *Ruminococcus sp.*, *Sellimonas intestinalis*, *Slackia isoflavoniconvertens*, *Streptococcus gordoni*, *Sutterella wadsworthensis*, *Turicibacter sanguinis*, and *Veillonella atypica*.

[0151] In some embodiments of any of the aspects, the one or more serotonin-modulating bacteria include a strain selected from the group consisting of: *Acidaminococcus intestini* HB-95, *Agathobacter rectalis* HB-257, *Akkermansia muciniphila* BAA-835, *Adlercreutzia equolifaciens* FJC-B9, *Alistipes onderdonkii* HB-311, *Alistipes putredinis* HB-324, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellulosilyticus* HB-227, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris* HB-33, *Bacteroides thetaiotaomicron* HB-34, *Bacteroides uniformis* HB-13, *Bacteroides vulgatus* HB-10, *Bacteroides xylinisolvans* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium breve* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium longum* HB-234, *Bifidobacterium longum* HB-71, *Bilophila wadsworthia* HB-693, *Bittarella massiliensis* HB-477, *Blautia coccoides* HB-23, *Blautia obeum* HB-14, *Blautia wexlerae* HB-16, *Butyricimonas paravirosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium butyricum* HB-88, *Clostridium clostradioforme* HB-642, *Clostridium hathewayi* HB-152, *Clostridium innoculum* HB-82, *Clostridium lavalense* HB-452c, *Clostridium paraputrificum* HB-27, *Clostridium saudicense* HB-142, *Clostridium scindens* HB-444, *Clostridium sp.* HB-358, *Clostridium sphenoides* HB-470, *Clostridium sporogenes* JCM 7836, *Clostridium sporogenes* McClung 2004, *Clostridium symbiosum* HB-67, *Clostridium tyrobutyricum* HB-469, *Clostridium hylemonae* HB-73, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus comes* HB-80, *Coprococcus comes* ATCC 27758, *Coprococcus eutactus* HB-155, *Coprococcus eutactus* ATCC 27759, *Dialister invisus* HB-387, *Dorea longicatena* HB-17, *Dysosmabacter welbionis* HB-45, *Eisenbergiella tayi* HB-437, *Eisenbergiella tayi* HB-612, *Enterococcus durans*

HB-48, *Enterococcus faecium* HB-640, *Enterococcus faecium* HB-85, *Enterorhabdus caecimuris* B7, *Enterorhabdus muris* WCA-131-CoC-2, *Erysipelatoclostridium ramosum* HB-24, *Escherichia coli* HB-490, *Eubacterium callanderi* HB-59, *Eubacterium eligens* HB-252, *Eubacterium rectale* HB-22, *Faecalitalea cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter butyricus* HB-344, *Gemmiger formicilis* HB-325, *Gemmiger* sp. HB-567, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Intestinimonas massiliensis* HB-651, *Lachnoclostridium* sp. HB-698, *Lactobacillus brevis* HB-87, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum muris* HB-79, *Longibaculum* sp. HB-681, *Mediterraneibacter faecis* HB-364, *Mycolicibacterium smegmatis* ATCC 19420, *Oscillibacter* sp. HB-28, *Parabacteroides distasonis* HB-20, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella excrementihominis* HB-330, *Peptostreptococcus russellii* RT-10B, *Prevotella copri* HB-373, *Prevotella* sp. HB-649, *Prevotella* sp. HB-333, *Romboutsia lituseburensis* HB-102, *Ruminococcus bicirculans* HB-105, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Ruminococcus* sp. HB-626, *Sellimonas intestinalis* HB-443, *Slackia isoflavoniconvertens* HB-326, *Streptococcus gordonii* HB-62, *Streptococcus gordonii* HB-98, *Sutterella wadsworthensis* HB-259, *Turicibacter sanguinis* HB-147, and *Veillonella atypica* HB-251.

[0152] In some embodiments of any of the aspects, the one or more serotonin-modulating bacteria consists of a bacteria comprising a 16S rDNA sequence at least about 95% identical to a 16S rDNA sequence selected from one of SEQ ID NOs: 1-114.

[0153] In some embodiments of any of the aspects, the serotonin-modulating bacteria encode genes in their genome, which when expressed, result in the production of one or more metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0154] In some embodiments of any of the aspects, the encoded genes are expressed at physiologically relevant conditions of the human gastrointestinal tract, resulting in the production of metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0155] In some embodiments of any of the aspects, the composition is in the form of a probiotic, prebiotic, a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powders, a granule, a medical food, supplement or a combination thereof.

[0156] In some embodiments of any of the aspects, the composition is administered orally, intravenously, intramuscularly, intrathecally, subcutaneously, sublingually, buccally, rectally, vaginally, by the ocular route, by the otic route, nasally, via inhalation, by nebulization, cutaneously, transdermally, or a combination thereof.

[0157] In some embodiments of any of the aspects, the method further comprises identifying a subject in need of treatment by measuring a serotonin level in a sample from the subject, and comparing the level to a reference level.

[0158] In some embodiments of any of the aspects, the serotonin level is measured in stool, blood, or tissue of the subject.

[0159] In some embodiments of any of the aspects, a serotonin level less than the reference level identifies a subject in need of treatment.

[0160] In some embodiments of any of the aspects, the levels of serotonin in the stool, blood, or tissue of the subject are altered relative to their initial quantitated amounts, after administering the therapeutic composition.

[0161] In some embodiments of any of the aspects, the method further comprises identifying a subject in need of treatment by measuring levels of fecal serotonin modulating bacteria.

[0162] In some embodiments of any of the aspects, the level of fecal serotonin-modulating bacteria is measured by fecal 16S rDNA sequencing, fecal shotgun metagenomic sequencing, measurement of fecal genes involved in the production of microbiota-derived serotonin modulating metabolites, measurement of proteins by sequencing or proteomics or comparable methods, or levels of fecal, blood, or tissue serotonin-modulating metabolites via LC/MS or comparable methods.

[0163] In some embodiments of any of the aspects, the levels of serotonin modulating bacteria, genes involved in the production of microbiota-derived serotonin modulating metabolites or proteins, or levels of serotonin-modulating metabolites are altered relative to their initial quantitated amounts after administering the therapeutic composition.

BRIEF DESCRIPTION OF THE DRAWINGS

[0164] FIG. 1 is a schematic showing a phylogenetic tree generated to identify microbial enzymes and the microbes that produce them that can carry out the tryptophan decarboxylase function that generates tryptamine from tryptophan (see e.g., SEQ ID NOs: 185-226).

[0165] FIG. 2A-2B are a series of bar graphs showing that supernatants and cell pellets from 5-HT modulating bacterial strains increase mammalian Tryptophan Hydroxylase 1 (TPH-1) expression. (FIG. 2A) Supernatant and (FIG. 2B) cell pellets from 48-hour cultures of 5-HT modulating bacteria were introduced into cultures of RIN14B pancreas cells. Expression of Tryptophan Hydroxylase 1, a rate limiting step of 5-HT biosynthesis, was measured via qPCR. HM2 indicates the bacterial medium.

[0166] FIG. 3 is a bar graph showing that 5-HT modulating bacteria elevate 5-HT signaling in a human gut simulator complex background using bacterial supernatants. Human fecal samples were spiked into an in-house human gut simulator, creating a mock microbiome community. This community normalized for 48 hours, and then 10⁸ CFU of 5-HT modulating bacteria alone or in combination were spiked into the system. The supernatants of this system were then collected after 48 hours, spiked into RIN14B rat pancreas cell culture at 50% final volume, incubated at 37° C. in a CO₂ incubator for an hour, and 5-HT is measured via ELISA. HD-3=donor microbiome background spiked only with vehicle, buffer=HBSS, ionomycin=positive control, Media 10% and 50% are basal mediums used in the gut simulator.

[0167] FIG. 4 is a bar graph showing that 5-HT modulating bacteria elevate 5-HT signaling in a human gut simulator complex background using bacterial cell pellets. Human fecal samples were loaded into an in-house human gut simulator, creating a mock microbiome community. This community normalized for 48 hours, and then 10⁸ CFU of 5-HT modulating bacteria alone or in combination were

spiked into the system. The cell pellets of this system were then collected after 48 hours, spiked into RIN14B rat pancreas cell culture at 100 ng/mL, incubated at 37° C. in a CO₂ incubator for an hour, and 5-HT was measured via ELISA. HD-3=donor microbiome background spiked only with vehicle, buffer=HBSS, ionomycin=positive control, Media 10% and 50% are basal mediums used in the gut simulator.

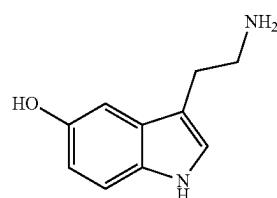
DETAILED DESCRIPTION

[0168] Embodiments of the technology described herein provide compositions and methods for decreasing at least one symptom of a serotonin-related disease or disorder in a subject in need thereof by altering the serotonin-modulating gut microbiota, serotonin-modulating gut-microbiota-derived metabolome, or serotonin-modulating gut-microbiota-derived proteome of the subject. The compositions can comprise one or more live serotonin-modulating bacteria, one or more dead-serotonin modulating bacteria, one or more conditioned medium(s) of serotonin-modulating bacteria, one or more cell pellet(s) of serotonin-modulating bacteria, and/or one or more 5-HT agonists, metabolites and/or proteins (derived from serotonin-modulating bacteria), or therapeutic or pharmaceutical compositions comprising the same. The method can comprise administering combinations of one or more live serotonin-modulating bacteria, one or more dead-serotonin modulating bacteria, one or more conditioned medium(s) of serotonin-modulating bacteria, one or more cell pellet(s) of serotonin-modulating bacteria, and/or one or more 5-HT agonists, metabolites and/or proteins (derived from serotonin-modulating bacteria).

[0169] The present technology has the advantage of alleviating the symptoms of serotonin-related disease or disorders without the aid of synthetic medications (e.g., serotonin-reuptake inhibitors), which can have unwanted side-effects, or in combination with existing medications. Additionally, the present technology can have the advantage of further improving other aspects of health of the subject, as the bacteria can perform multiple mechanisms (e.g. alter serotonin signaling but also alter the immune system). Additional features and advantages of the present technology will be apparent to one of ordinary skill in the art.

Serotonin

[0170] The term "Serotonin" should be understood as referring to 5-hydroxytryptamine, which has the below chemical structure:



[0171] Serotonin is a monoamine neurotransmitter involved in a wide range of physiological processes, including mood, anxiety, sleep, appetite, temperature, eating behavior, sexual behavior, movements and gastrointestinal motility. Serotonin is synthesized from the amino acid

L-tryptophan by two enzymes—tryptophan hydroxylase (TPH) and aromatic amino acid decarboxylase (DDC), which can be expressed by the host.

[0172] More than 90% of the body's 5-HT is produced in the gastrointestinal (GI) tract. In many instances said 5-HT is produced by host gut cells under the influence of the gut microbiota, not produced by the microbiota itself. In the GI tract, 5-HT activates as many as 14 different 5-HT receptor subtypes, including those found on immune cells, enterocytes, and enteric nerves. In addition, circulating platelets sequester 5-HT from the GI tract, releasing it to promote hemostasis and distributing it to various body sites. As such, gut-derived 5-HT regulates diverse functions, including the immune response and intestinal motility. Perhaps not surprising due to its function, a disrupted serotonergic system appears to be strongly associated with symptomologies of IBS, particularly for IBS-C.

Serotonin and the Microbiome

[0173] The microbiome plays a major role in influencing serotonergic neurotransmission. In germ free animals, there is a significant reduction of serotonin in the blood and colon of mice compared to controls, a feature which is associated with reduced intestinal motility. Both serotonin levels and normal GI transit motility can be restored via recolonization with a consortium of "spore-forming" bacteria. These general findings were repeated using a single species of bacteria, *Clostridium ramosum*, which when introduced into germ-free mice restored serotonin levels in the cecum and serum. Further supporting this microbiome-serotonin connection is a study wherein it was found that the disrupted intestinal motility and damaged GI barrier phenotype of chronic constipation could be transplanted from humans to rodents via fecal microbiome transplant (FMT). No effect was observed when the microbiome from healthy humans was transferred. This phenotype was associated with reduced serum levels of serotonin as well as increased expression of the serotonin transporter SERT.

[0174] The present disclosure provides compositions and methods for decreasing at least one symptom of a serotonin-related disease or disorder in a subject in need thereof by altering the serotonin-modulating gut microbiota, serotonin-modulating gut-microbiota-derived metabolome, or serotonin-modulating gut-microbiota-derived proteome of the subject. For more information concerning the microbiome and/or serotonin, see e.g., Mayer et al., Neuroscience 34, 15490-15496 (2014); Lynch & Pedersen, N Engl J Med 375, 2369-2379 (2016); Fung et al., Nat Neurosci 20, 145-155 (2017); Strandwitz, Brain Res 1693, 128-133 (2018); Agus et al., Cell host & microbe 23, 716-724 (2018); d'Hennezel et al., mSystems 2, e00046-17 (2017); Skelly et al., Nat Rev Immunol, 2019 May, 19(5):305-323; Gershon & Tack, Gastroenterology 132, 397-414 (2007); Amireault et al., ACS Chem Neurosci 4, 64-71 (2013); Matthes & Bader, Trends Pharmacol Sci 39, 560-572 (2018); Spohn & Mawe, Nat Rev Gastroenterol Hepatol 14, 412-420 (2017); Wikoff et al. Proc Natl Acad Sci USA 106, 3698-3703, (2009); Tumbaugh et al., Nature 444, 1027-1031 (2006); Rooks et al., ISME J 8, 1403-1417 (2014); Zackular et al., MBio 4, e00692-00613 (2013); Petrof et al., Microbiome 1, 3 (2013); Baganz & Blakely, ACS Chem Neurosci 4, 48-63 (2013); Sikander et al., Clin Chim Acta 403, 47-55 (2009); Yano et al., Cell 161, 264-276 (2015); Mandic et al., Sci Rep 9, 1177 (2019); Cao

et al. Sci Rep 7, 10322 (2017); the contents of each of which are incorporated by reference herein in their entireties.

Serotonin Modulation by Bacteria

[0175] The microbiota can modulate a subject's serotonin signaling and/or biosynthesis by producing specific metabolites which are sensed by a subject's cells resulting in alterations in host gene expression, protein activity, or metabolic output/requirements, influencing serotonin biosynthesis and salvage pathways. In some embodiments, a bacterial species can produce a co-factor or nutrient that is used in these pathways, stimulating activity of host serotonin biosynthesis. In other embodiments, the microbiota can alternatively remove nutrients from the host, via consumption or secretion of secondary metabolites that bind to nutrients (e.g. siderophores, which bind soluble iron, an essential nutrient), preventing or reducing biosynthesis of serotonin.

[0176] The microbiota can also produce proteins including agonist or other proteins that interact with host receptors that sense microbial components. In some embodiments, these proteins are sensed by Toll-like receptors (TLRs), which signal to the host to produce or restrict production of serotonin.

[0177] The microbiota can also modulate pharmacological agents, which are intended to interact with a subject's serotonin signaling/biosynthesis pathways. In some embodiments, these can be agonists or antagonists of Tph1 and Tph2, SERT, 5-HT_{1A}, 5-HT_{1B}, 5-HT_{1D}, 5-HT_{1E}, 5-HT_{1F}, 5-HT_{2A}, 5-HT_{2B}, 5-HT_{2C}, 5-HT₃, 5-HT₄, 5-HT_{5A}, 5-HT_{5B}, 5-HT₆, 5-HT₇, among others. In some embodiments, compositions, described below, can be employed to alter these biotransformations.

Serotonin-Modulating Bacterial Compositions

[0178] In some embodiments, described herein are therapeutic compositions comprising live serotonin-modulating bacteria, dead or inactivated serotonin-modulating bacteria, conditioned medium(s) of cultured serotonin-modulating bacteria, cell pellet(s) of serotonin-modulating bacteria, and/or metabolites and/or proteins derived from serotonin-modulating bacteria, that are delivered to the gastrointestinal tract of the subject to modulate serotonin signaling and/or biosynthesis of the subject, either directly or by altering native microbial (e.g., bacterial, archaeal, fungal, protist, or viral) community composition or gene expression, resulting in increased or reduced levels of serotonin-modulating bacteria, or alterations in the microbiota-derived metabolome and/or microbiota-derived proteome to a more serotonin-stimulating or serotonin-inhibitory state.

[0179] In some embodiments, the serotonin-modulating gut microbiota, serotonin-modulating gut-microbiota-derived metabolome, or serotonin-modulating gut-microbiota-derived proteome of the subject is altered by increasing/decreasing the number of at least one serotonin-modulating bacteria by administering an effective amount of a microbiota modulator selected from: serotonin-modulating bacteria, probiotics, antimicrobials, species-specific antimicrobials, prebiotics, bacteriophages, genetic elements (e.g. CRISPR) or any combination thereof.

[0180] In some embodiments, the serotonin-modulating bacteria encode one or more genes in their genome, which when expressed, result in the production of one or more

metabolites or proteins that influence subject serotonin signaling/biosynthesis. In some embodiments, these genes are expressed at physiologically relevant conditions of the human gastrointestinal tract. Non-limiting examples of such enzymes, and the species that encode and express them, are described further herein and specifically indicated in the sequence listing.

[0181] In some embodiments, the serotonin-modulating bacterial species are serotonin-increasing bacterial species. In some embodiments, the serotonin-increasing bacterial species increases serotonin in at least one of the following ways: production of serotonin; production of secreted metabolites or secreted proteins that induce serotonin production; production of ligands that induce serotonin production; production of an agonist (e.g., of a serotonin receptor or the trace amine-associated receptor (TAAR)); or any combination thereof.

Bacterial Compositions

[0182] In some embodiments, described herein are therapeutic compositions comprising one or more bacteria (e.g. purified bacteria) that are capable of increasing or decreasing subject serotonin levels in a subject in need thereof, when delivered to the intestinal tract. The bacteria can be capable of producing metabolites or proteins at physiologically relevant conditions, such as those conditions found in the human gut, that modulate subject serotonin signaling/biosynthesis in the body (e.g. the gastrointestinal tract, the circulatory system, or the brain). The bacteria can also be capable of altering native microbial (e.g., bacterial, archaeal, fungal, protist, or viral) community composition or gene expression, resulting in increased or reduced levels of serotonin-modulating bacteria, or alterations in the microbiota-derived metabolome and/or microbiota-derived proteome to a more serotonin-stimulating or serotonin-inhibitory state. In some embodiments, the one or more bacteria are not viable, or the one or more bacteria comprise a combination of viable and non-viable bacteria. In some embodiments, the bacterial composition comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, or more, types of isolated bacteria. Where non-viable bacteria or a component thereof can modulate serotonin, it is likely that a factor, e.g., a protein or other factor comprised by the bacteria, or a collection of such factors is involved in the serotonin-inducing effects, rather than simply a metabolite produced by the bacteria.

[0183] In some embodiments, the composition comprises a consortium of serotonin-modulating bacteria. As a non-limiting example, the consortium can comprise at least 2 species or strains, at least 3 species or strains, at least 4 species or strains, at least 5 species or strains, at least 6 species or strains, at least 7 species or strains, at least 8 species or strains, at least 9 species or strains, at least 10 species or strains, at least 11 species or strains, at least 12 species or strains, at least 13 species or strains, at least 14 species or strains, at least 15 species or strains, at least 16 species or strains, at least 17 species or strains, at least 18 species or strains, at least 19 species or strains, or at least 20 species or strains of serotonin-modulating bacteria. In some embodiments, a consortium comprises fewer than 50 species or strains of serotonin-modulating bacteria, fewer than 40 species or strains, fewer than 30 species or strains, fewer than 25 species or strains, fewer than 20 species or strains, fewer than 19 species or strains, fewer than 18 species or strains, fewer than 17 species or strains, fewer than 16

species or strains, fewer than 15 species or strains, fewer than 14 species or strains, fewer than 13 species or strains, fewer than 12 species or strains, fewer than 11 species or strains, fewer than 10 species or strains, fewer than 9 species or strains, fewer than 8 species or strains, fewer than 7 species or strains, fewer than 6 species or strains, fewer than 5 species or strains, fewer than 4 species or strains, or fewer than 3 species or strains of serotonin-modulating bacteria. In one embodiment, a consortium comprises species that modulate serotonin production via different mechanisms. Such consortia can provide additive or synergistic effects on serotonin levels. As a non-limiting example, in one embodiment, a consortium comprises a species that encodes and expresses one or more enzymes that generate serotonin from one or more biosynthetic precursor substrates and a species that stimulates host serotonin production. As another non-limiting example, in one embodiment, a consortium comprises a first species that encodes and expresses one or more enzymes for the production of a biosynthetic serotonin precursor, and a second species that encodes and expresses one or more enzymes that convert the biosynthetic serotonin precursor to serotonin.

[0184] In some embodiments, combinations of bacteria are selected for therapeutics, food, medical foods, or any other product for synergistic effects on host 5-HT signaling. In a non-limiting example, combinations of bacteria can be selected to capture multiple mechanisms involved in modulating host 5-HT signaling. As a non-limiting example, a strain with only the ability to elevate 5-HT signaling via its cell pellet can be combined with a separate bacterium, wherein said second bacterium has a supernatant that elicits an effect, produces 5-HT, and/or produces 5-HT agonists. In some embodiments, by combining mechanisms or adding redundancy of any mechanism (e.g., multiple organisms with the capability to produce 5-HT) within a product, one can to elicit a stronger or more consistent effect on host 5-HT signaling, and thus a more favorable impact in the target indications and/or symptoms. In a non-limiting example, *Clostridium lavalense* HB-452C, which produces 5-HT and the 5-HT agonist tryptamine, can be combined with *Bifidobacterium adolescentis* HB-179, which has a strong cell pellet and supernatant induction phenotype.

[0185] In some embodiments, the one or more serotonin-modulating bacteria belong to a genus selected from the group consisting of: *Acidaminococcus*, *Agathobacter*, *Adlercreutzia*, *Akkermansia*, *Alistipes*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Bilophila*, *Bittarella*, *Blautia*, *Butyricimonas*, *Clostridium*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dialister*, *Dorea*, *Dysosmabacter*, *Eisenbergiella*, *Enterococcus*, *Enterorhabdus*, *Erysipelatoclostridium*, *Escherichia*, *Eubacterium*, *Faecalitalea*, *Flavonifractor*, *Flintibacter*, *Gemmiger*, *Gordonibacter*, *Hungatella*, *Intestinimonas*, *Lachnoclostridium*, *Lactobacillus*, *Lawsonibacter*, *Longibaculum*, *Mediterraneibacter*, *Mycolicibacterium*, *Oscillibacter*, *Parabacteroides*, *Parasutterella*, *Peptostreptococcus*, *Prevotella*, *Romboutsia*, *Ruminococcus*, *Sellimonas*, *Slackia*, *Streptococcus*, *Sutterella*, *Turicibacter*, and *Veillonella*.

[0186] In some embodiments, the one or more serotonin-modulating bacteria are species selected from the group consisting of: *Acidaminococcus intestini*, *Agathobacter rectalis*, *Akkermansia muciniphila*, *Adlercreutzia equolifaciens*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis*, *Bacillus cereus*, *Bacteroides caccae*, *Bacteroides cellulosilyticus*, *Bacteroides clarus*, *Bacteroides dorei*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides koreensis*, *Bacteroides ovatus*, *Bacteroides plebeius*, *Bacteroides salyersiae*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium breve*, *Bifidobacterium faecale*, *Bifidobacterium longum*, *Bilophila wadsworthia*, *Bittarella massiliensis*, *Blautia coccoides*, *Blautia obeum*, *Blautia wexlerae*, *Butyricimonas paravirosa*, *Clostridium asparagineforme*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium butyricum*, *Clostridium clostridioforme*, *Clostridium hathewayi*, *Clostridium innoculum*, *Clostridium lavalense*, *Clostridium paraputrificum*, *Clostridium saudense*, *Clostridium scindens*, *Clostridium* sp., *Clostridium sporogenes*, *Clostridium sphenoides*, *Clostridium symbiosum*, *Clostridium tyrobutyricum*, *Clostridium hylemonae*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dorea longicatena*, *Dysosmabacter welbionis*, *Eisenbergiella tayi*, *Enterococcus durans*, *Enterococcus faecium*, *Enterorhabdus caecimuris*, *Enterorhabdus muris*, *Erysipelatoclostridium ramosum*, *Escherichia coli*, *Eubacterium callanderi*, *Eubacterium eligens*, *Eubacterium rectale*, *Faecalitalea cylindroides*, *Flavonifractor plautii*, *Flintibacter butyricus*, *Gemmiger formicilis*, *Gemmiger* sp., *Gordonibacter pamelaeae*, *Hungatella effluvii*, *Hungatella hathewayi*, *Intestinimonas butyriciproducens*, *Intestinimonas massiliensis*, *Lachnoclostridium* sp., *Lactobacillus brevis*, *Lawsonibacter asaccharolyticus*, *Longibaculum muris*, *Longibaculum* sp., *Mediterraneibacter faecis*, *Mycolicibacterium smegmatis*, *Oscillibacter* sp., *Parabacteroides distasonis*, *Parabacteroides goldsteinii*, *Parabacteroides johnsonii*, *Parabacteroides merdae*, *Parasutterella excrementihominis*, *Peptostreptococcus russelli*, *Prevotella copri*, *Prevotella* sp., *Prevotella* sp., *Romboutsia lituseburensis*, *Ruminococcus bicirculans*, *Ruminococcus gnavus*, *Ruminococcus* sp., *Sellimonas intestinalis*, *Slackia isoflavoniconvertens*, *Streptococcus gordonii*, *Sutterella wadsworthensis*, *Turicibacter sanguinis*, and *Veillonella atypica*.

[0187] In some embodiments, the one or more serotonin-modulating bacteria include a strain selected from the group consisting of: *Acidaminococcus intestini* HB-95, *Agathobacter rectalis* HB-257, *Akkermansia muciniphila* BAA-835, *Adlercreutzia equolifaciens* FJC-B9, *Alistipes onderdonkii* HB-311, *Alistipes putredinis* HB-324, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellulosilyticus* HB-227, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris* HB-33, *Bacteroides thetaiotaomicron* HB-34, *Bacteroides uniformis* HB-13, *Bacteroides vulgatus* HB-10, *Bacteroides xylanisolvens* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium breve* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium longum* HB-234, *Bifidobacterium longum* HB-71, *Bilophila wadsworthia* HB-693, *Bittarella massiliensis* HB-477, *Blautia coccoides* HB-23, *Blautia obeum* HB-14, *Blautia wexlerae* HB-16, *Butyricimonas paravirosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium butyricum* HB-88, *Clostridium clostridioforme* HB-642, *Clostridium hathewayi* HB-152,

Clostridium innoculum HB-82, *Clostridium lavalense* HB-452c, *Clostridium paraputreficum* HB-27, *Clostridium saudiense* HB-142, *Clostridium scindens* HB-444, *Clostridium* sp. HB-358, *Clostridium sphenoides* HB-470, *Clostridium sporogenes* JCM 7836, *Clostridium sporogenes* McClung 2004, *Clostridium symbiosum* HB-67, *Clostridium tyrobutyricum* HB-469, *Clostridium hylemonae* HB-73, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus comes* HB-80, *Coprococcus comes* ATCC 27758, *Coprococcus eutactus* HB-155, *Coprococcus eutactus* ATCC 27759, *Dialister invisus* HB-387, *Dorea longicatena* HB-17, *Dysosmobacter welbionis* HB-45, *Eisenbergiella tayi* HB-437, *Eisenbergiella tayi* HB-612, *Enterococcus durans* HB-48, *Enterococcus faecium* HB-640, *Enterococcus faecium* HB-85, *Enterorhabdus caecimuris* B7, *Enterorhabdus muris* WCA-131-CoC-2, *Erysipelatoclostridium ramosum* HB-24, *Escherichia coli* HB-490, *Eubacterium callanderi* HB-59, *Eubacterium eligens* HB-252, *Eubacterium rectale* HB-22, *Faecalitalea cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter butyricus* HB-344, *Gemmiger formicilis* HB-325, *Gemmiger* sp. HB-567, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Intestinimonas massiliensis* HB-651, *Lachnoclostridium* sp. HB-698, *Lactobacillus brevis* HB-87, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum muris* HB-79, *Longibaculum* sp. HB-681, *Mediterraneibacter faecis* HB-364, *Mycolicibacterium smegmatis* ATCC 19420, *Oscillibacter* sp. HB-28, *Parabacteroides distasonis* HB-20, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella excrementihominis* HB-330, *Peptostreptococcus russellii* RT-10B, *Prevotella copri* HB-373, *Prevotella* sp HB-649, *Prevotella* sp. HB-333, *Romboutsia lituseurensis* HB-102, *Ruminococcus bicirculans* HB-105, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Ruminococcus* sp. HB-626, *Sellimonas intestinalis* HB-443, *Slackia isoflavoniconvertens* HB-326, *Streptococcus gordonii* HB-62, *Streptococcus gordonii* HB-98, *Sutterella wadsworthensis* HB-259, *Turicibacter sanguinis* HB-147, and *Veillonella atypica* HB-251.

[0188] In some embodiments, the one or more serotonin-modulating bacteria comprises a 16S rDNA sequence that is at least about 95% identical to a 16S rDNA sequence selected from one of SEQ ID NOS: 1-114. As a non-limiting example, a serotonin-modulating bacteria comprises a 16S rDNA sequence with at least 95% identity, at least 96% identity, at least 97% identity, at least 98% identity, at least 99% identity, at least 99.5% identity, at least 99.5% identity or 100% identity to a 16S rDNA sequence described herein (e.g., SEQ ID NOS: 1-114).

[0189] In some embodiments, a live bacteria, which directly produces metabolites or proteins which interact with the host, or modulates the native serotonin-modulating microbiota, serotonin-modulating metabolome, or serotonin-modulating proteome, can be superior to pharmacological interventions, as neurotransmission follows circadian rhythms, which are difficult to appropriately capture therapeutically with small molecules (while a serotonin-modulating bacteria or the native microbiota, which also has circadian rhythms, can capture this capability).

[0190] In some embodiments, a dead bacteria, which can serve as a source of metabolites or proteins to interact with the host, or modulates the native serotonin-modulating microbiota, serotonin-modulating metabolome, or serotonin-modulating proteome, can be superior to pharmacological interventions, as neurotransmission follows circadian rhythms, which are difficult to appropriately capture therapeutically with small molecules (while altering the native microbiota, which also has circadian rhythms, can capture this capability).

[0191] In some embodiments, a live or dead bacteria can be superior to pharmacological interventions, as they can capture multiple therapeutic mechanisms (e.g. the live or dead bacteria alter serotonin via small molecules as well as proteins).

[0192] In some embodiments, synergistic effects of serotonin modulation can be observed when using more than one live or dead bacteria, or by combining live or dead bacteria, or when combining single strains with the native microbiota.

[0193] In some embodiments, the serotonin-modulating bacteria described herein are exemplary in their serotonin-modulating characteristics, as compared to other bacterial strains.

[0194] In some embodiments, the serotonin-modulating bacteria produce serotonin-modulating metabolites or express genes found to elicit host serotonin release, at a physiologically relevant condition of the human gastrointestinal tract.

[0195] In some embodiments, the serotonin-modulating bacteria are engineered to produce serotonin-modulating metabolites and/or produce serotonin-modulating proteins. In some embodiments, these engineered serotonin-modulating bacteria produce the recombinant serotonin-modulating metabolites or proteins under physiologically relevant conditions of the human gastrointestinal tract.

[0196] In some embodiments, the serotonin-modulating bacteria can be delivered to the gastrointestinal tract in the form of a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powder, a granule, a medical food, supplement or a combination thereof. In some embodiments, the serotonin-modulating bacteria is administered as a fecal transplant or suppository.

[0197] In some embodiments, the viable serotonin-modulating bacteria is encapsulated, lyophilized, formulated in a food item, or is formulated in a liquid, gel, fluid-gel, or nanoparticles in a liquid. In some embodiments of any of the aspects, the composition further comprises a pre-biotic composition.

[0198] In some embodiments, serotonin-modulating bacteria described herein can be associated with negative health conditions. Without being bound by theory, commensal variants of these bacteria and/or therapeutics comprising bacterial products are free of virulence factors (e.g. exotoxins and endotoxins) and/or antimicrobial resistance. In some embodiments, commensal, non-pathogenic variants of *Bacteroides vulgatus*, *Bilophila wadsworthia*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium clostridioforme*, *Clostridium hathewayi*, *Clostridium innoculum*, *Eisenbergiella tayi*, *Enterococcus faecium*, *Hungatella effluvii*, *Hungatella hathewayi*, and/or *Parabacteroides distasonis* are used.

5-HT Producers

[0199] In some embodiments, described herein are therapeutic compositions comprising one or more bacteria (e.g., purified bacteria) that produce 5-HT. These bacteria were identified to produce 5-HT via a cell culture screen and then validated with liquid chromatography-mass spectrometry (LC/MS) (see e.g., Tables 1A-1D “5-HT producer”). In some embodiments, the 5-HT producing bacteria belong to the order Lactobacillales or Clostridia. In some embodiments, the 5-HT producing bacteria belong to the genus *Lactobacillus*, *Enterococcus*, *Clostridium*, or *Ruminococcus*. In some embodiments, the 5-HT producing bacteria are the species *Enterococcus durans*, *Clostridium lavalense*, *Clostridium asparagiforme*, or *Ruminococcus gnavus*. In some embodiments, the 5-HT producing bacteria are the strains *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnavus* HB-40, or *Ruminococcus gnavus* HB-516. In some embodiments, the 16S sequence of the 5-HT producing bacteria is at least 95% identical (e.g., at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% identical, or 100% identical) to a 16S sequence of a bacterial strain selected from the group consisting of: *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnavus* HB-40, and *Ruminococcus gnavus* HB-516. Thus, in some embodiments, bacteria that have a 16S sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5% or at least 99.9% identical to the 16S sequence of a bacterial strain selected from *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnavus* HB-40, and *Ruminococcus gnavus* HB-516 are identified as candidate 5-HT-producing bacteria. Such candidates can be confirmed as 5-HT producers via LC/MS analysis as described herein or as known in the art. In some embodiments, the 16S sequence of the 5-HT producing bacteria is at least 95% identical (e.g., at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% identical, or 100% identical) to one of SEQ ID NOS: 1-4. In some embodiments, 5-HT producing bacteria produce 5-HT at physiologically relevant conditions of the human gastrointestinal tract.

[0200] In some embodiments, the 5-HT producing bacteria have encoded in their genomes and express under the conditions in the human gastrointestinal tract: (1) a decarboxylase that catalyzes the production of tryptamine from tryptophan (e.g., a tryptophan decarboxylase); and/or (2) an enzyme to perform hydroxylation to form 5-HT from tryptamine. Tryptamine is a precursor to 5-HT, as well as a 5-HT agonist. In some embodiments, the decarboxylase that catalyzes the production of tryptamine from tryptophan is annotated under the Enzyme Commission Number (EC Number) of 4.1.1.105. In some embodiments, the decarboxylase that catalyzes the production of tryptamine from tryptophan is referred to as L-tryptophan decarboxylase or tryptophan decarboxylase. Given an EC number, one can readily identify bacterial species that encode such enzymes, thereby identifying candidate serotonin-modulating bacteria and, through their genomic sequences, structural information regarding the encoded enzymes themselves.

[0201] In some embodiments, the amino acid sequence of the decarboxylase that catalyzes the production of tryptamine from tryptophan is at least 50% similar (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least

91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% similar) to one of SEQ ID NOS: 115-119. In some embodiments, the amino acid sequence of the decarboxylase that catalyzes the production of tryptamine from tryptophan is at least 50% identical (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% identical) to one of SEQ ID NOS: 115-119.

[0202] In some embodiments, the decarboxylase is not annotated as a tryptophan decarboxylase, but is or can be identified by: (1) performing a neighbor-joining alignment of all decarboxylases identified in a given genome; (2) aligning those decarboxylases to positive control enzymes from other bacteria; and (3) identifying genes which cluster with those positive controls. As a non-limiting example, a decarboxylase capable of converting tryptophan to tryptamine was predicted by: (1) sequencing the complete genome of *Enterococcus durans* HB-48; (2) annotating all decarboxylases found within the genome using PROKKA or a similar tool; and (3) creating a phylogenetic alignment using MEGA5 (statistical method=maximum likelihood; model=Jones-Taylor Thornton; all other settings default) or a similar tool (see e.g., Seemann, Bioinformatics. 2014 Jul. 15; 30(14):2068-9; Tamura et al., Mol Biol Evol. 2011 October; 28(10):2731-9; the contents of each of which are incorporated herein by reference in their entireties). As a non-limiting example, “all decarboxylases found within the genome” can include decarboxylases annotated to the EC number 4.1.1. As a non-limiting example, “all decarboxylases” can include decarboxylases annotated to the following EC numbers: 1.1.1; 1.1.1.40; 4.1.1; 4.1.1.18; 4.1.1.17; 4.1.1.19; 4.1.1.20; 4.1.1.23; 4.1.1.3; 4.1.1.36; 4.1.1.41; 4.1.1.44; 4.1.1.65; 4.1.1.81; 4.1.1.96; 6.3.2.5; or 6.4.1.2.

[0203] In this non-limiting example, an enzyme previously identified as a “Lysine decarboxylase family” enzyme (e.g., EC 4.1.1.18) from *Enterococcus durans* HB48 was clustered with positive control tryptophan decarboxylase enzymes (see e.g., FIG. 1, SEQ ID NOS: 119, 188 and 226). Bacteria encoding and expressing this lysine decarboxylase family enzyme are thus identified as candidate 5-HT producing bacteria. LC/MS performed as described herein can demonstrate 5-HT production by such bacteria. A similar approach can be applied to identify and confirm bacterial enzymes, and thereby bacteria encoding such enzymes, that catalyze additional reactions that generate serotonin from one or more precursor substrates. In particular, this approach can be applied to the enzymes described in the following.

[0204] In some embodiments, the amino acid sequence of the decarboxylase that catalyzes the production of tryptamine from tryptophan (e.g., despite being annotated as a lysine decarboxylase) is at least 50% similar (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% similar) to one of SEQ ID NOS: 119, 188 or 226. In some embodiments, the amino acid sequence of the decarboxylase that catalyzes the production of tryptamine from tryptophan (e.g., despite being annotated as a lysine decarboxylase) is at least 50% identical (e.g., at least

50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% identical) to one of SEQ ID NOs: 119, 188 or 226.

[0205] In some embodiments, the enzyme capable of converting tryptamine to 5-HT is tryptamine 5-hydroxylase. A similar approach to that described above is applicable to identify additional bacterial enzymes, and thereby additional candidate bacteria encoding such enzymes, that catalyze the conversion of tryptamine to 5-HT. In some embodiments, the enzyme capable of converting tryptamine to 5-HT belongs to the EC Number 1.14 or 1.14.14. In some embodiments, the enzyme capable of converting tryptamine to 5-HT is an O₂-independent hydroxylating enzyme (e.g., a molybdoenzyme capable of performing an O₂-independent hydroxylation; e.g., SEQ ID NO: 134) as described further herein. In some embodiments, multiple enzymes convert tryptamine to 5-HT in a multi-step process.

[0206] In some embodiments, the 5-HT producing bacteria have encoded in their genomes and express under the conditions in the human gastrointestinal tract: (1) an enzyme to convert tryptophan to 5-hydroxy-L-tryptophan (5-HTP) (e.g., tryptophan hydroxylase); and/or (2) an enzyme to convert 5-hydroxy-L-tryptophan to serotonin (e.g., aromatic L-amino acid decarboxylase). In some embodiments, the hydroxylase capable of converting tryptophan to 5-hydroxy-L-tryptophan is annotated under the EC Number 1.14.16.4. In some embodiments, the hydroxylase capable of converting tryptophan to 5-hydroxy-L-tryptophan is referred to as: tryptophan 5-monooxygenase; L-tryptophan hydroxylase; indoleacetic acid-5-hydroxylase; tryptophan 5-hydroxylase; and/or tryptophan hydroxylase.

[0207] In some embodiments, the amino acid sequence of the hydroxylase capable of converting tryptophan to 5-hydroxy-L-tryptophan is at least 50% similar (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% similar) to one of SEQ ID NOs: 120-126. In some embodiments, the amino acid sequence of the hydroxylase capable of converting tryptophan to 5-hydroxy-L-tryptophan is at least 50% identical (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% identical) to one of SEQ ID NOs: 120-126. Bacteria that encode and express both an enzyme to convert tryptophan to 5-hydroxy-L-tryptophan (5-HTP) (e.g., tryptophan hydroxylase) and an enzyme to convert 5-hydroxy-L-tryptophan to serotonin (e.g., aromatic L-amino acid decarboxylase) can produce serotonin from tryptophan. It is specifically contemplated that one or more bacterial species that encode and express an enzyme that converts tryptophan to 5-hydroxy-L-tryptophan (5-HTP) (e.g., tryptophan hydroxylase) could be paired with one or more bacterial species that encode and express an enzyme that converts 5-hydroxy-L-tryptophan to serotonin (e.g., aromatic L-amino acid decarboxylase) such that together, the paired bacterial species can generate serotonin from tryptophan.

[0208] In some embodiments, the decarboxylase capable of converting 5-hydroxy-L-tryptophan to serotonin is annotated under the EC number 4.1.1.28. In some embodiments, the decarboxylase capable of converting 5-hydroxy-L-tryptophan to serotonin is referred to as: aromatic-L-amino-acid decarboxylase; DOPA decarboxylase; tryptophan decarboxylase; hydroxytryptophan decarboxylase; L-DOPA decarboxylase; aromatic amino acid decarboxylase; and/or 5-hydroxytryptophan decarboxylase. In some embodiments, the amino acid sequence of the decarboxylase capable of converting 5-hydroxy-L-tryptophan to serotonin is at least 50% similar (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% similar) to one of SEQ ID NOs: 127-133. In some embodiments, the amino acid sequence of the decarboxylase capable of converting 5-hydroxy-L-tryptophan to serotonin is at least 50% identical (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% identical) to one of SEQ ID NOs: 127-133.

[0209] In some embodiments, the enzyme capable of converting tryptophan to 5-hydroxy-L-tryptophan is annotated as a phenylalanine hydroxylase. In a non-limiting example, a single point mutation in a phenylalanine hydroxylase (e.g., W192F, F197I, F197L, E219C, or any combination thereof in a phenylalanine hydroxylase from *Cupriavidus taiwanensis* (*CtAAAH*); see e.g., SEQ ID NO: 227 NCBI Reference Sequence: WP_012354318.1; e.g., EC 1.14.16.1) permits conversion of tryptophan to 5-HTP (see e.g., Mora-Villalobos and Zeng, J Biol Eng. 2018 Mar. 15; 12:3, the content of which is incorporated herein by reference in its entirety).

[0210] In some embodiments, a tryptamine 5-hydroxylase and/or tryptophan hydroxylase is not expected to function because the known enzymes require oxygen and the mammalian gastrointestinal tract environment is anaerobic. In some embodiments, 5-HT producing bacteria can circumvent the oxygen requirements of these enzymes via activity of a molybdoenzyme capable of performing an O₂-independent hydroxylation. A non-limiting example of an O₂-independent hydroxylating enzyme can be observed in *Sterolibacterium denitrificans* (see e.g., Demer and Fuchs, J Biol Chem. 2012 Oct. 26; 287(44):36905-16, the content of which is incorporated herein by reference in its entirety).

[0211] In some embodiments, the amino acid sequence of the O₂-independent hydroxylating enzyme is at least 50% similar (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% similar) to SEQ ID NO: 134. In some embodiments, the amino acid sequence of the O₂-independent hydroxylating enzyme is at least 50% identical (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% identical) to SEQ ID NO: 134.

[0212] Without wishing to be bound by theory, such anaerobic hydrolases are thought to exist in the human gut microbiome and in 5-HT producing bacteria, permitting hydroxylation of tryptamine and/or 5-hydroxy-L-tryptophan. In some embodiments, bacteria can have one or more of the enzymes involved in 5-HT production, resulting in synergistic production of 5-HT. In a non-limiting example, a bacteria (native or exogenous) can possess (i.e., encode and express) a functional tryptophan decarboxylase that produces tryptamine, and another bacteria in the same environment (native or exogenous) encodes and expresses a hydroxylase that effectively converts tryptamine to 5-HT.

[0213] Bacteria with a particularly strong result in the RIN14B model were profiled for serotonin and tryptamine production via LC/MS. Using this method, four strains were identified as tryptamine and 5-HT producers—*Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnatus* HB-40, *Ruminococcus gnatus* HB-516 (see e.g., Tables 1A-1D; see e.g., SEQ ID NOS: 1-4).

[0214] In some embodiments, the genes involved in 5-HT production (e.g., from tryptamine or 5-HTP) can be identified by performing a genome similarity assessment. Without being bound by theory, closely related genomes of bacteria found to be 5-HT producing bacteria and non-5-HT producing bacteria can be compared to identify sequences found only in the 5-HT producers. Identification of such genes permits directed gene-deletion strategies, using methods like CRISPR-Cas, to determine which enzymes are responsible for 5-HT production. In some embodiments, keystone 5-HT producing bacteria can be identified by searching for expression of 5-HT producing genes, as identified herein, in human fecal and cecal transcriptomic cohorts.

Conditioned Medium

[0215] In some embodiments, described herein are therapeutic compositions comprising one or more conditioned medium or media derived from serotonin-modulating bacteria, that are delivered to the gastrointestinal tract of the subject to alter serotonin signaling/biosynthesis, either directly or by altering native microbial (e.g., bacterial, archaeal, fungal, protist, or viral) community composition or gene expression, resulting in increased or reduced levels of serotonin-modulating bacteria, or alterations in the microbiota-derived metabolome and/or microbiota-derived proteome to a more serotonin-stimulating or serotonin-inhibitory state. In some embodiments, the composition of conditioned medium or media are derived from at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, or more, types of isolated serotonin-modulating bacteria.

[0216] Described herein are organisms of which their supernatant modulates host 5-HT biosynthesis (see e.g., Tables 1A-1D “5-HT positive Supernatant”). In some embodiments, the 5-HT modulating bacteria can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT biosynthesis. In some embodiments, the 5-HT modulating bacterial species that can produce metabolites that influence host 5-HT biosynthesis belongs to a genus selected from the group consisting of: *Acidaminococcus*, *Agathobacter*, *Alistipes*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Bilophila*, *Butyricimonas*, *Clostridium*, *Clostridium hylemonae*, *Collinsella*, *Coprococcus*, *Dysosmabacter*, *Eisenbergiella*, *Enterococcus*, *Erysipelatoclostridium*, *Eubacterium*, *Faecalitalea*, *Flavonifractor*, *Flintibacter*,

Gemmiger, *Gordonibacter*, *Hungatella*, *Intestinimonas*, *Lactobacillus*, *Mediterraneibacter*, *Oscillibacter*, *Parabacteroides*, *Parasutterella*, *Ruminococcus*, *Streptococcus*, and *Turicibacter*.

[0217] In some embodiments, the 5-HT modulating bacterial species that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT biosynthesis is a species selected from the group consisting of: *Acidaminococcus intestini*, *Agathobacter rectalis*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis*, *Bacillus cereus*, *Bacteroides caccae*, *Bacteroides cellulosilyticus*, *Bacteroides dorei*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides koreensis*, *Bacteroides ovatus*, *Bacteroides plebeius*, *Bacteroides salyersiae*, *Bacteroides stercoris*, *Bacteroides uniformis*, *Bacteroides vulgaris*, *Bacteroides xylanisolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium breve*, *Bifidobacterium faecale*, *Bifidobacterium longum*, *Bilophila wadsworthia*, *Butyricimonas paravirosa*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium clostridioforme*, *Clostridium hathewayi*, *Clostridium innoculum*, *Clostridium paraputrificum*, *Clostridium saudience*, *Clostridium scindens*, *Clostridium tyrobutyricum*, *Clostridium hylemonae* HB-73, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dysosmabacter welbionis*, *Eisenbergiella tayi*, *Enterococcus faecium*, *Erysipelatoclostridium ramosum*, *Eubacterium eligens*, *Faecalitalea cylindroides*, *Flavonifractor plautii*, *Flintibacter butyricus*, *Gemmiger formicilis*, *Gordonibacter pamelaeae*, *Hungatella effluvii*, *Hungatella hathewayi*, *Intestinimonas butyriciproducens*, *Lactobacillus brevis*, *Mediterraneibacter faecis*, *Oscillibacter sp.*, *Parabacteroides distasonis*, *Parabacteroides johnsonii*, *Parabacteroides merdae*, *Parasutterella exrementihominis*, *Ruminococcus bicirculans*, *Ruminococcus gnatus*, *Streptococcus gordonii*, and *Turicibacter sanguinis*.

[0218] In some embodiments, the 5-HT modulating bacteria that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT biosynthesis is a strain selected from the group consisting of: *Acidaminococcus intestini* HB-95, *Agathobacter rectalis* HB-257, *Alistipes onderdonkii* HB-311, *Alistipes putredinis* HB-324, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellulosilyticus* HB-227, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris* HB-33, *Bacteroides uniformis* HB-13, *Bacteroides vulgaris* HB-10, *Bacteroides xylanisolvens* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium breve* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium longum* HB-71, *Bilophila wadsworthia* HB-693, *Butyricimonas paravirosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium clostridioforme* HB-642, *Clostridium hathewayi* HB-152, *Clostridium innoculum* HB-82, *Clostridium paraputrificum* HB-27, *Clostridium saudience* HB-142, *Clostridium scindens* HB-444, *Clostridium tyrobutyricum* HB-469, *Clostridium hylemonae* HB-73, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus eutactus* HB-155, *Dysosmabacter welbionis* HB-45, *Eisenbergiella tayi* HB-437, *Eisenbergiella tayi* HB-612, *Enterococcus faecium* HB-640, *Enterococcus faecium* HB-85,

Erysipelatoclostridium ramosum HB-24, *Eubacterium eligenes* HB-252, *Faecalitalea cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter butyricus* HB-344, *Gemmiger formicilis* HB-325, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Lactobacillus brevis* HB-87, *Mediterraneibacter faecis* HB-364, *Oscillibacter* sp. HB-28, *Parabacteroides distasonis* HB-20, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella excrementihominis* HB-330, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Streptococcus gordonii* HB-62, *Streptococcus gordonii* HB-98, and *Turicibacter sanguinis* HB-147.

[0219] In some embodiments, the 5-HT modulating bacteria that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT biosynthesis comprise a 16S sequence that is at 95% identical (e.g., at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% identical) to one of SEQ ID NOs: 1-2 and 5-69. In some embodiments, the 5-HT modulating bacteria that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT biosynthesis do so at physiologically relevant conditions of the human gastrointestinal tract.

[0220] In some embodiments, the metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT biosynthesis can be identified by leveraging metabolomics. Without being bound by theory, untargeted or targeted metabolomics can be performed on supernatant from bacteria identified to elevate host 5-HT biosynthesis, as well as supernatant from bacteria with supernatant with no effect. By comparing metabolites from these two pools of organisms, candidate 5-HT modulating metabolites can be identified. Similarly, as described above, a genome exclusion method can be applied. Here the genomes of bacteria with supernatant that elevate host 5-HT biosynthesis can be compared to those where their supernatant has no effect, to identify candidate genetic functions associated with altered 5-HT biosynthesis. Once genetic elements are identified, transcriptomics of human fecal and cecal cohorts can be leveraged to identify bacteria in humans that express these genes in the human gastrointestinal tract.

[0221] Non-limiting examples of bacterial supernatants that result in increased expression of host Tryptophan Hydroxylase 1 (TPH-1) are provided in FIG. 2A. In some embodiments, the 5-HT modulating bacterial species that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host TPH-1 expression belongs to a genus selected from the group consisting of: *Enterococcus*, *Clostridium*, *Lactobacillus*, *Bifidobacterium*, and *Anaerotruncus*. In some embodiments, the 5-HT modulating bacterial species that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host TPH-1 expression is a species selected from the group consisting of: *Enterococcus durans*, *Clostridium lavalense*, *Lactobacillus brevis*, *Bifidobacterium faecale*, *Anaerotruncus colihominis*, and *Clostridium ramosum*. In some embodiments, the 5-HT modulating bacterial species that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host TPH-1 expression is a strain selected from the group consisting of:

consisting of: *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Lactobacillus brevis* HB-87, *Bifidobacterium faecale* HB-159, *Anaerotruncus colihominis* HB-83, and *Clostridium ramosum* HB-24. In some embodiments, the 5-HT modulating bacteria that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host TPH-1 expression comprises a 16S sequence that is at 95% identical (e.g., at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% identical) to one of SEQ ID NOs: 3, 4, 11, 28, 30, and 39.

[0222] In some embodiments, a composition comprises at least two 5-HT modulating bacteria that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host TPH-1 expression. Non-limiting examples of such combinations include: a bacterium belonging to the genus *Clostridium* and a bacterium belonging to the genus *Lactobacillus*; a bacterium belonging to the genus *Enterococcus* and a bacterium belonging to the genus *Bifidobacterium*; a bacterium belonging to the genus *Clostridium* and a bacterium belonging to the genus *Enterococcus*; *Clostridium lavalense* and *Lactobacillus brevis*; *Enterococcus durans* and *Bifidobacterium faecale*; *Clostridium lavalense* and *Enterococcus durans*; *Clostridium lavalense* HB-452c and *Lactobacillus brevis* HB-87; *Enterococcus durans* HB-48 and *Bifidobacterium faecale* HB-159; and *Clostridium lavalense* HB-452c and *Enterococcus durans* HB-48.

[0223] Non-limiting examples of bacterial supernatants that result in increased expression of host 5-HT in a gut simulator are provided in FIG. 3. In some embodiments, the 5-HT modulating bacterial species that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT expression belongs to a genus selected from the group consisting of: *Clostridium*, *Bifidobacterium*, *Enterococcus*, *Anaerotruncus*, and *Erysipelatoclostridium*. In some embodiments, the 5-HT modulating bacterial species that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT expression is a species selected from the group consisting of: *Clostridium scindens*, *Bifidobacterium faecale*, *Enterococcus durans*, *Clostridium lavalense*, *Anaerotruncus colihominis*, and *Erysipelatoclostridium ramosum*. In some embodiments, the 5-HT modulating bacterial species that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT expression is a strain selected from the group consisting of: *Clostridium scindens* HB-444, *Bifidobacterium faecale* HB-159, *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Anaerotruncus colihominis* HB-83, and *Erysipelatoclostridium ramosum* HB-24. In some embodiments, the 5-HT modulating bacterial species that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT expression comprises a 16S sequence that is at 95% identical (e.g., at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% identical) to one of SEQ ID NOs: 3, 4, 11, 23, 28 and 39.

[0224] In some embodiments, a composition comprises at least two 5-HT modulating bacterial species that can produce metabolites or proteins (e.g., secreted metabolites or secreted proteins in the supernatant) that influence host 5-HT expression. Non-limiting examples of such combina-

tions include: a bacterial species belonging to the genus *Enterococcus*, a bacterial species belonging to the genus *Clostridium*, and a bacterial species belonging to the genus *Anaerotruncus*; a bacterial species belonging to the genus *Clostridium* and a bacterial species belonging to the genus *Bifidobacterium*; a bacterial species belonging to the genus *Enterococcus* and a bacterial species belonging to the genus *Anaerotruncus*; a bacterial species belonging to the genus *Enterococcus* and a bacterial species belonging to the genus *Clostridium*; a bacterial species belonging to the genus *Clostridium* and a bacterial species belonging to the genus *Anaerotruncus*; two bacterial species belonging to the genus *Clostridium*; *Enterococcus durans*, *Clostridium lavalense*, and *Anaerotruncus colihominis*; *Clostridium scindens* and *Bifidobacterium faecale*; *Enterococcus durans* and *Anaerotruncus colihominis*; *Enterococcus durans* and *Clostridium lavalense*; *Clostridium lavalense* and *Anaerotruncus colihominis*; *Clostridium scindens* and *Clostridium lavalense*; *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, and *Anaerotruncus colihominis* HB-83; *Clostridium scindens* HB-444 and *Bifidobacterium faecale* HB-159; *Enterococcus durans* HB-48 and *Anaerotruncus colihominis* HB-83; *Enterococcus durans* HB-48 and *Clostridium lavalense* HB-452c; *Clostridium lavalense* HB-452c and *Anaerotruncus colihominis* HB-83; and *Clostridium scindens* HB-444 and *Clostridium lavalense* HB-452c.

[0225] In some embodiments the conditioned medium is prepared by growing bacteria for a time period, ranging between 1 minute to 480 hours in medium containing one or more of the following nutrients: conditioned medium from other bacteria, N-Acetyl-D-Galactosamine, N-Acetyl-D-Glucosamine, N-Acetyl- β -D-Mannosamine, Adonitol, Amygdalin, D-Arabinotol, Arbutin, D-Cellobiose, α -Cyclodextrin, β -Cyclodextrin, Dextrin, Dulcitol, i-Erythritol, D-Fructose, L-Fucose, D-Galactose, D-Galacturonic Acid, Gentiobiose, D-Gluconic Acid, D-Glucosaminic Acid, α -D-Glucose, α -D-Glucose1-Phosphate, D-Glucose6-Phosphate, Glycerol, D,L- α -Glycerol Phosphate, m-Inositol, α -D-Lactose, Lactulose, Maltose, Maltotriose, D-Mannitol, D-Mannose, D-Melezitose, D-Melibiose, β -Methyl-D-Glucose, α -Methyl-DGalactoside, β -Methyl-D-Galactoside, α -Methyl-D-Glucoside, β -Methyl-D-Glucoside, Mucin, Palatinose, D-Raffinose, L-Rhamnose, Salicin, D-Sorbitol, Stachyose, Sucrose, D-Trehalose, Turanose, Acetic Acid, Formic Acid, Fumaric Acid, Glyoxylic Acid, α -Hydroxybutyric Acid, β -Hydroxybutyric Acid, Itaconic Acid, α -Keto-butyric Acid, α -Ketovaleric Acid, D,L-Lactic Acid, L-Lactic Acid, D-Lactic Acid Methyl Ester, D-Malic Acid, L-Malic Acid, Propionic Acid, Pyruvic Acid, Pyruvic Acid Methyl Ester, D-Saccharic Acid, Succinamic Acid, Succinic Acid, Succinic Acid Mono-Methyl Ester, m-Tartaric Acid, Uronic Acid, Alaninamide, L-Alanine, L-Alanyl-LGlutamine, L-Alanyl-LHistidine, L-Alanyl-LThreonine, L-Asparagine, L-Glutamic Acid, L-Glutamine, Glycyl-LAspartic Acid, Glycyl-LGlutamine, Glycyl-LMethionine, Glycyl-LProline, L-Methionine, L-Phenylalanine, L-Serine, L-Threonine, L-Valine, L-Valine plus L-Aspartic Acid, 2'-Deoxy Adenosine, Inosine, Thymidine, Uridine, Thymidine-5'-Monophosphate, or Uridine-5'-Monophosphate. In some embodiments of any of the aspects, the conditioned medium is prepared by growing bacteria in HM2 media.

[0226] In some embodiments, the conditioned medium is prepared by sterilize filtration. In some embodiments, the

conditioned medium is prepared by centrifugation. In some embodiments, conditioned medium is also referred to herein as a supernatant.

[0227] In some embodiments, conditioned medium from serotonin-modulating bacteria are superior to live or dead bacteria, as they can be simpler to manufacture and formulate, as long-term viability of the source organism is not necessary.

[0228] In some embodiments, conditioned medium from serotonin-modulating bacteria are superior to live or dead bacteria, or purified metabolites or proteins from serotonin-modulating bacteria, as they can capture a broader range of mechanisms. In some embodiments, this broader range of mechanisms includes serving as a prebiotic source for the native microbiota.

[0229] In some embodiments, conditioned medium from serotonin-modulating bacteria can be superior to pharmacological interventions, as they can capture multiple therapeutic mechanisms (e.g. the conditioned medium alter serotonin via small molecules or metabolites as well as proteins).

[0230] In some embodiments, the conditioned medium from serotonin-modulating bacteria described herein are exemplary in their serotonin-modulating characteristics, as compared to other bacterial strains or as compared to conditioned medium from other bacterial strains.

[0231] In some embodiments, the conditioned medium from serotonin-modulating bacteria can be delivered to the gastrointestinal tract in the form of a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powder, a granule, a medical food, supplement or a combination thereof. In some embodiments, the conditioned medium is administered rectally or via suppository.

Cell Pellets

[0232] In some embodiments, described herein are therapeutic compositions comprising one or more cell pellets derived from serotonin-modulating bacteria, that are delivered to the gastrointestinal tract of the subject to alter serotonin signaling/biosynthesis, either directly or by altering native microbial (e.g., bacterial, archaeal, fungal, protist, or viral) community composition or gene expression, resulting in increased or reduced levels of serotonin-modulating bacteria, or alterations in the microbiota-derived metabolome and/or microbiota-derived proteome to a more serotonin-stimulating or serotonin-inhibitory state. In some embodiments, the cell pellet composition is derived from at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, or more, types of isolated serotonin-modulating bacteria.

[0233] Described herein are organisms that modulate 5-HT signaling via production of ligands present in the cell pellet (see e.g., Tables 1A-1D “5-HT Positive Cell Pellet”). In some embodiments, the ligand in the pellet is a polypeptide. In some embodiments, bacteria and/or bacterial ligand modulate serotonin through a Toll-like receptor (TLR)-mediated mechanism. Non-limiting examples of TLRs related to bacterial sensing include TLR1, TLR2, TLR4, TLR5, TLR6, and/or TLR9. As a non-limiting example, microbial proteins can influence host 5-HT signaling via interactions with toll-like receptor 2 (TLR2). TLR2 is a key component of the host innate immune system for maintenance of intestinal homeostasis and detection of various microbial-associated molecular patterns. Both Gram-positive and Gram-negative bacteria possess TLR2 agonists, which are generally cell-wall components, such as lipopro-

teins, glycoproteins and lipids, peptidoglycan, and atypical LPS molecules. Together with TLR1 and TLR4, TLR2 is expressed in human and murine Enterochromaffin (EC) cells. TLR2 has been identified as a target for host 5-HT modulation. Microbiota-dependent TLR2 signaling was found necessary to sustain EC cell number and biology in the mouse intestine, to regulate TPH1 expression and 5-HT production, and restore EC cell function in germ-free and antibiotic-treated animals. See e.g., Wang et al., *J Immunol.* 2019 May 15; 202(10):3041-3052; Akira & Takeda, *Nat Rev Immunol.* 4, 499-511, (2004); Bogunovic, et al. Enterocrine cells express functional Toll-like receptors. *Am J Physiol Gastrointest Liver Physiol.* 292 (2007); the contents of each of which are incorporated herein by reference in their entirities.

[0234] In some embodiments, the 5-HT modulating bacteria have cell pellets that can increase host 5-HT biosynthesis. In some embodiments, the 5-HT modulating bacteria that have cell pellets that can increase host 5-HT biosynthesis belong to a genus selected from the group consisting of: *Anaerotruncus*, *Bacteroides*, *Bifidobacterium*, *Bittarella*, *Blautia*, *Clostridium*, *Dialister*, *Eisenbergiella*, *Enterococcus*, *Eubacterium*, *Gemmiger*, *Gordonibacter*, *Hungatella*, *Lactobacillus*, *Longibaculum*, *Mediterraneibacter*, *Parabacteroides*, *Parasutterella*, *Prevotella*, *Romboutsia*, *Ruminococcus*, *Sellimonas*, and *Sutterella*.

[0235] In some embodiments, the 5-HT modulating bacteria that have cell pellets that can increase host 5-HT biosynthesis are a species selected from the group consisting of: *Anaerotruncus colihominis*, *Bacteroides caccae*, *Bacteroides clarus*, *Bacteroides dorei*, *Bacteroides finegoldii*, *Bacteroides ovatus*, *Bacteroides salyersiae*, *Bacteroides thetaiotaomicron*, *Bacteroides xylinosolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium faecale*, *Bittarella massiliensis*, *Blautia wexlerae*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium hathewayi*, *Clostridium saudicense*, *Clostridium scindens*, *Clostridium tyrobutyricum*, *Dialister invisus*, *Eisenbergiella tayi*, *Enterococcus durans*, *Enterococcus faecium*, *Eubacterium eligens*, *Gemmiger formicilis*, *Gordonibacter pamelaeae*, *Hungatella effluvii*, *Lactobacillus brevis*, *Longibaculum muris*, *Mediterraneibacter faecis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Parasutterella exrementihominis*, *Prevotella copri*, *Prevotella sp.*, *Romboutsia lituseburensis*, *Ruminococcus sp.*, *Ruminococcus gnarus*, *Sellimonas intestinalis*, and *Sutterella wadsworthensis*.

[0236] In some embodiments, the 5-HT modulating bacterial species that have cell pellets that can increase host 5-HT biosynthesis include a strain selected from the group consisting of: *Anaerotruncus colihominis* HB-83, *Bacteroides caccae* HB-11, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides ovatus* HB-70, *Bacteroides salyersiae* HB-32, *Bacteroides thetaiotaomicron* HB-34, *Bacteroides xylinosolvens* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium faecale* HB-159, *Bittarella massiliensis* HB-477, *Blautia wexlerae* HB-16, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium hathewayi* HB-152, *Clostridium saudicense* HB-142, *Clostridium scindens* HB-444, *Clostridium tyrobutyricum* HB-469, *Dialister invisus* HB-387, *Eisenbergiella tayi* HB-612, *Enterococcus durans* HB-48, *Enterococcus faecium* HB-85, *Eubacterium eligens* HB-252, *Gemmiger formicilis* HB-325, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Lac-*

tobacillus brevis HB-87, *Longibaculum muris* HB-79, *Mediterraneibacter faecis* HB-364, *Parabacteroides distasonis* HB-20, *Parabacteroides merdae* HB-63, *Parasutterella exrementihominis* HB-330, *Prevotella copri* HB-373, *Prevotella sp.* HB-649, *Prevotella sp.* HB-333, *Romboutsia lituseburensis* HB-102, *Ruminococcus sp.* HB-626, *Ruminococcus gnarus* HB-40, *Ruminococcus gnarus* HB-516, *Sellimonas intestinalis* HB-443, and *Sutterella wadsworthensis* HB-259.

[0237] In some embodiments, the 5-HT modulating bacterial species that have cell pellets that can increase host 5-HT biosynthesis comprise a 16S sequences that is at least 95% identical (e.g., at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% identical) to one of SEQ ID NOs: 1-3, 5-30, and 70-82. In some embodiments, the 5-HT modulating bacterial species that have cell pellets that can increase host 5-HT biosynthesis do so at physiologically relevant conditions of the human gastrointestinal tract. In some embodiments, the proteins or cell pellet ligands that influence host 5-HT biosynthesis can be identified by leveraging proteomics. Without being bound by theory, proteomics can be performed on cell pellets from bacteria identified to elevate host 5-HT biosynthesis, as well as cell pellets from bacteria with no effect. By comparing proteins from these two pools of organisms, candidate 5-HT modulating proteins or ligands can be identified. Similarly, as described above, a genome exclusion method can be applied. Here the genomes of bacteria with cell pellets that elevate host 5-HT biosynthesis can be compared to those where their cell pellet has no effect, to identify candidate genetic functions associated with altered 5-HT biosynthesis. Once genetic elements are identified, transcriptomics of human fecal and cecal cohorts can be leveraged to identify bacteria in humans that express these genes in the human gastrointestinal tract.

[0238] Non-limiting examples of bacterial pellets that result in increased expression of host Tryptophan Hydroxylase 1 (TPH-1) are provided in FIG. 2B. In some embodiments, the 5-HT modulating bacterial species that have cell pellets that influence host TPH-1 expression belongs to a genus selected from the group consisting of: *Clostridium*, *Lactobacillus*, *Bifidobacterium*, and *Anaerotruncus*. In some embodiments, the 5-HT modulating bacterial species that have cell pellets that influence host TPH-1 expression is a species selected from the group consisting of: *Clostridium lavalense*, *Lactobacillus brevis*, *Bifidobacterium faecale*, *Anaerotruncus colihominis*, and *Clostridium ramosum*. In some embodiments, the 5-HT modulating bacterial species that have cell pellets that influence host TPH-1 expression is a strain selected from the group consisting of: *Clostridium lavalense* HB-452c, *Lactobacillus brevis* HB-87, *Bifidobacterium faecale* HB-159, *Anaerotruncus colihominis* HB-83, and *Clostridium ramosum* HB-24. In some embodiments, the 5-HT modulating bacterial species that have cell pellets that influence host TPH-1 expression comprises a 16S sequence that is at 95% identical (e.g., at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% identical) to one of SEQ ID NOs: 4, 11, 28, 30, and 39.

[0239] In some embodiments, a composition comprises at least two 5-HT modulating bacteria that have cell pellets that influence host TPH-1 expression. Non-limiting examples of such combinations include: a bacterial species belonging to the genus *Clostridium* and a bacterial species belonging to

the genus *Lactobacillus*; a bacterial species belonging to the genus *Enterococcus* and a bacterial species belonging to the genus *Bifidobacterium*; a bacterial species belonging to the genus *Clostridium* and a bacterial species belonging to the genus *Enterococcus*; *Clostridium lavalense* and *Lactobacillus brevis*; *Enterococcus durans* and *Bifidobacterium faecale*; *Clostridium lavalense* and *Enterococcus durans*; *Clostridium lavalense* HB-452c and *Lactobacillus brevis* HB-87; *Enterococcus durans* HB-48 and *Bifidobacterium faecale* HB-159; and *Clostridium lavalense* HB-452c and *Enterococcus durans* HB-48.

[0240] Non-limiting examples of bacterial pellets that result in increased expression of host 5-HT in a gut simulator are provided in FIG. 4. In some embodiments, the 5-HT modulating bacterial species that have cell pellets that influence host 5-HT expression belongs to a genus selected from the group consisting of: *Clostridium*, *Bifidobacterium*, *Enterococcus*, *Anaerotruncus*, and *Erysipelatoclostridium*. In some embodiments, the 5-HT modulating bacterial species that has a cell pellet that influences host 5-HT expression is a species selected from the group consisting of: *Clostridium scindens*, *Bifidobacterium faecale*, *Enterococcus durans*, *Clostridium lavalense*, *Anaerotruncus colihominis*, and *Erysipelatoclostridium ramosum*. In some embodiments, the 5-HT modulating bacterial species that has a cell pellet that influences host 5-HT expression is a strain selected from the group consisting of: *Clostridium scindens* HB-444, *Bifidobacterium faecale* HB-159, *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Anaerotruncus colihominis* HB-83, and *Erysipelatoclostridium ramosum* HB-24. In some embodiments, the 5-HT modulating bacterial species that have cell pellets that influence host 5-HT expression comprises a 16S sequence that is at 95% identical (e.g., at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% identical) to one of SEQ ID NOs: 3, 4, 11, 23, 28 and 39.

[0241] In some embodiments, a composition comprises at least two 5-HT modulating bacteria that have cell pellets that influence host 5-HT expression. Non-limiting examples of such combinations include: a bacterial species belonging to the genus *Enterococcus*, a bacterial species belonging to the genus *Clostridium*, and a bacterial species belonging to the genus *Anaerotruncus*; a bacterial species belonging to the genus *Clostridium* and a bacterial species belonging to the genus *Bifidobacterium*; a bacterial species belonging to the genus *Enterococcus* and a bacterial species belonging to the genus *Anaerotruncus*; a bacterial species belonging to the genus *Enterococcus* and a bacterial species belonging to the genus *Clostridium*; a bacterial species belonging to the genus *Clostridium* and a bacterial species belonging to the genus *Anaerotruncus*; two bacterial species belonging to the genus *Clostridium*; *Enterococcus durans*, *Clostridium lavalense*, and *Anaerotruncus colihominis*; *Clostridium scindens* and *Bifidobacterium faecale*; *Enterococcus durans* and *Anaerotruncus colihominis*; *Enterococcus durans* and *Clostridium lavalense*; *Clostridium lavalense* and *Anaerotruncus colihominis*; *Clostridium scindens* and *Clostridium lavalense*; *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, and *Anaerotruncus colihominis* HB-83; *Clostridium scindens* HB-444 and *Bifidobacterium faecale* HB-159; *Enterococcus durans* HB-48 and *Anaerotruncus colihominis* HB-83; *Enterococcus durans* HB-48 and *Clostridium lavalense* HB-452c; *Clostridium*

lavalense HB-452c and *Anaerotruncus colihominis* HB-83; and *Clostridium scindens* HB-444 and *Clostridium lavalense* HB-452c.

[0242] In some embodiments the cell pellets are prepared by growing bacteria for a time period, ranging between 1 minute to 480 hours in medium containing one or more of the following nutrients: conditioned medium from other bacteria, N-Acetyl-D-Galactosamine, N-Acetyl-D-Glucosamine, N-Acetyl- β -D-Mannosamine, Adonitol, Amygdalin, D-Arabitol, Arbutin, D-Cellobiose, α -Cyclodextrin, (3-Cyclodextrin, Dextrin, Dulcitol, i-Erythritol, D-Fructose, L-Fucose, D-Galactose, D-Galacturonic Acid, Gentibiose, D-Gluconic Acid, D-Glucosaminic Acid, α -D-Glucose, α -D-Glucose 1-Phosphate, D-Glucose6-Phosphate, Glycerol, D,L- α -Glycerol Phosphate, m-Inositol, α -D-Lactose, Lactulose, Maltose, Maltotriose, D-Mannitol, D-Mannose, D-Melezitose, D-Melibiose, β -Methyl-DGlucose, α -Methyl-DGalactoside, β -Methyl-D-Galactoside, α -Methyl-D-Glucoside, β -Methyl-D-Glucoside, Mucin, Palatinose, D-Raffinose, L-Rhamnose, Salicin, D-Sorbitol, Stachyose, Sucrose, D-Trehalose, Turanose, Acetic Acid, Formic Acid, Fumaric Acid, Glyoxylic Acid, α -Hydroxybutyric Acid, β -Hydroxybutyric Acid, Itaconic Acid, α -Keto- β Butyric Acid, α -Ketovaleric Acid, D,L-Lactic Acid, L-Lactic Acid, D-Lactic Acid Methyl Ester, D-Malic Acid, L-Malic Acid, Propionic Acid, Pyruvic Acid, Pyruvic Acid Methyl Ester, D-Saccharic Acid, Succinamic Acid, Succinic Acid, Succinic Acid Mono-Methyl Ester, m-Tartaric Acid, Urocanic Acid, Alaninamide, L-Alanine, L-Alanyl-LGlutamine, L-Alanyl-LHistidine, L-Alanyl-LThreonine, L-Asparagine, L-Glutamic Acid, L-Glutamine, Glycyl-LAspartic Acid, Glycyl-LGlutamine, Glycyl-LMethionine, Glycyl-LProline, L-Methionine, L-Phenylalanine, L-Serine, L-Threonine, L-Valine, L-Valine plus L-Aspartic Acid, 2'-Deoxy Adenosine, Inosine, Thymidine, Uridine, Thymidine-5'-Monophosphate, or Uridine-5'-Monophosphate. In some embodiments of any of the aspects, the cell pellets are prepared by growing bacteria in HM2 media.

[0243] In some embodiments, the cell pellets are prepared by killing viable bacteria using high temperatures, freeze-thaw cycles, chloroform treatment, irradiation, or other appropriate means known to those skilled in the art, optionally followed by centrifugation (or other concentrating step) and/or at least one wash step using phosphate buffered saline or another liquid.

[0244] In some embodiments, cell pellets from serotonin-modulating bacteria are superior to live or dead bacteria, as they can be simpler to manufacture and formulate, as long-term viability of the source organism is not necessary.

[0245] In some embodiments, cell pellets from serotonin-modulating bacteria are superior to live or dead bacteria, or purified metabolites or proteins from serotonin-modulating bacteria, as they can capture a broader range of mechanisms. In some embodiments, this broader range of mechanisms includes serving as a prebiotic source for the native microbiota.

[0246] In some embodiments, cell pellets from serotonin-modulating bacteria can be superior to pharmacological interventions, as they can capture multiple therapeutic mechanisms (e.g. the cell pellets alter serotonin via small molecules as well as proteins).

[0247] In some embodiments, the cell pellets from serotonin-modulating bacteria described herein are exemplary in

their serotonin-modulating characteristics, as compared to other bacterial strains or as compared to cell pellets from other bacterial strains.

[0248] In some embodiments, the cell pellets from serotonin-modulating bacteria can be delivered to the gastrointestinal tract in the form of a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powders, a granule, a medical food, supplement or a combination thereof. In some embodiments, the cell pellets are administered rectally or via suppository.

5-HT Agonists, Purified Metabolites or Proteins

[0249] In some embodiments, described herein are therapeutic compositions comprising one or more purified 5-HT agonists, metabolites and/or proteins, derived from serotonin-modulating bacteria, that are delivered to the gastrointestinal tract to alter subject serotonin signaling/biosynthesis, either directly or by altering native microbial (e.g., bacterial, archaeal, fungal, protist, or viral) community composition or gene expression, resulting in increased or reduced levels of serotonin-modulating bacteria, or alterations in the microbiota-derived metabolome and/or microbiota-derived proteome to a more serotonin-stimulating or serotonin-inhibitory state. In some embodiments, the composition comprises purified 5-HT agonists, metabolites and/or proteins derived from at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, or more, types of isolated serotonin-modulating bacteria.

[0250] In some embodiments, described herein are therapeutic compositions comprising one or more bacterial species (e.g. purified bacteria) that can modulate 5-HT signaling by producing agonists of 5-HT receptors (see e.g., Tables 1A-1D “Agonist Producer”). In some embodiments, described herein are therapeutic compositions comprising purified 5-HT agonists from serotonin-modulating bacteria described herein.

[0251] There are a range of serotonin receptors, each responsible for eliciting release of a range of neurotransmitters and hormones. Likely the most relevant for enteric 5-HT signaling is the 5-HT₄ receptor, which is a known pro-kinetic pharmacological target. Interestingly, the 5-HT₄ receptor is widely distributed throughout the gastrointestinal tract and has been shown to sense and respond to lumen-derived metabolites. A non-limiting example of a 5-HT agonist is the tryptophan metabolite tryptamine, which is sensed in the same manner as the receptor's natural agonist 5-HT. Of note, tryptamine is produced by bacterial decarboxylation of dietary tryptophan, and microbiota-derived tryptamine has been shown to accelerate GI transit in a mouse model. This indicates it is possible to elicit a 5-HT-like effect, mediated via TLR-4, without serotonin. Tryptamine also activates the human Trace Amine Associated Receptor (TAAR) system, modulating serotonin by promoting its release into the synaptic cleft. See e.g., Manabe et al. Expert Opin Investig Drugs 19, 765-775, (2010); Bhattacharai et al., Cell host & microbe 23, 775-785 e775, (2018); the contents of which are incorporated herein by reference in their entireties.

[0252] In some embodiments, the 5-HT modulating bacterial species that produces a 5-HT agonist (e.g., tryptamine) is used to treat a serotonin-related disease or disorder or its symptom(s) caused by low serotonin levels that is not a gut disease or disorder. In some embodiments, the serotonin-related disease or disorder or its symptom(s) caused by low serotonin levels is selected from the group consisting of depression, anxiety, addiction, neurodegenerative disorders,

autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, dermatological conditions (eczema and itch), and pain disorders.

[0253] In some embodiments, the 5-HT modulating bacterial species can elicit an elevation of host 5-HT signaling via production of 5-HT agonists or TAAR agonists. In some embodiments, the 5-HT agonist-producing bacterial species belongs to a genus selected from the group consisting of: *Adlercreutzia*, *Akkermansia*, *Clostridium*, *Coprococcus*, *Enterococcus*, *Enterorhabdus*, *Mycolicibacterium*, *Pepto-streptococcus*, and *Ruminococcus*. In some embodiments, the 5-HT agonist-producing bacterial species is a species selected from the group consisting of: *Akkermansia muciniphila*, *Adlercreutzia equolifaciens*, *Clostridium sporogenes*, *Clostridium lavalense*, *Clostridium asparagiforme*, *Coprococcus eutactus*, *Coprococcus comes*, *Enterococcus durans*, *Enterorhabdus muris*, *Enterorhabdus caecimuris*, *Mycolicibacterium smegmatis*, *Peptostreptococcus russelii*, and *Ruminococcus gnavus*. In some embodiments, the 5-HT agonist-producing bacterial species is a strain selected from the group consisting of: *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516. In some embodiments, the 5-HT agonist-producing bacteria are greater than 95% similar by 16S sequencing to *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Clostridium sporogenes* JCM 7836, *Akkermansia muciniphila* BAA-835, *Clostridium sporogenes* McClung 2004, *Peptostreptococcus russelii* RT-10B, *Mycolicibacterium smegmatis* ATCC 19420, *Enterorhabdus muris* WCA-131-CoC-2, *Adlercreutzia equolifaciens* FJC-B9, *Enterorhabdus caecimuris* B7, *Coprococcus eutactus* ATCC 27759, and *Coprococcus comes* ATCC 27758.

[0254] In some embodiments, the 5-HT agonist-producing bacterial species comprises a 16S sequence that is at least 95% identical (e.g., at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% identical) to one of SEQ ID NOs: 1-4 and 105-114. In some embodiments, the 5-HT agonist-producing bacterial species produces the 5-HT agonist at physiologically relevant conditions of the human gastrointestinal tract.

[0255] Metabolites and derivatives of tryptophan which are known to have agonist properties at various 5-HT receptors and TAAR include, but are not limited to, N-methyltryptamine, N,N-dimethyltryptamine, N-methylserotonin, and N,N-dimethylserotonin. These compounds can be synthesized either by methylation of tryptamine by bacterial enzymes functionally homologous to human indolethylamine N-methyltransferase (e.g., GenBank Reference No: AAF18306.1; e.g., EC 2.1.1.49), or by human (or microbial as described further herein) tryptophan decarboxylase and hydroxylase enzymes (e.g., EC 4.1.1.105, EC 1.14.16.4) acting upon bacterially synthesized N-methylated derivatives of tryptophan including, but not limited to, L-abrine, N,N-alpha-dimethyltryptophan, and hypaphorine (also known as tryptophan betaine). These N-methylated tryptophan derivatives can be biosynthesized by radical S-adenosyl-L-methionine (SAM)-dependent enzymes with greater than 50% sequence homology to the ergothioneine biosynthetic enzyme egtID (e.g., UniProt AOR5M8 or NCBI Reference Sequence: WP_058127191.1; e.g., EC 2.1.1.44; see e.g., SEQ ID NO: 228), or by phosphatidylethanolamine

N-methyltransferase enzymes similar to those used to biosynthesize phosphatidylcholine (e.g., EC 2.1.1.- or EC 2.1.1.17; e.g., SEQ ID NO: 229). Bacteria, particularly those in the genera *Akkermansia*, *Eubacterium*, *Bacteroides*, *Coprococcus*, or *Enterorhabdus*, which produce these compounds and their metabolites can be delivered to exert 5-HT agonist effects, or to indirectly modulate 5-HT activity via inhibition of 5-HT reuptake by the serotonin uptake transporter (SERT) or the vesicular monoamine transporters (VMAT), or by inhibition of the monoamine oxidase enzyme.

[0256] In some embodiments, the amino acid sequence of an enzyme involved in N-methylated tryptophan derivative production is at least 50% similar (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% similar) to one of SEQ ID NOs: 228-229. In some embodiments, the amino acid sequence of an enzyme involved in N-methylated tryptophan derivative production is at least 50% identical (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% identical) to one of SEQ ID NOs: 228-229.

[0257] In some embodiments, the serotonin-modulating bacteria can produce tryptophan itself, which feeds into production pathways of 5-HT, 5-HT agonists, and TAAR agonists. In some embodiments, the serotonin-modulating bacterial species encodes or expresses at least one functional enzyme involved in tryptophan biosynthesis. In some embodiments, the enzyme involved in tryptophan production is selected from the group consisting of: Tryptophan synthase (SEQ ID NOs: 135-144; EC 4.2.1.20); Indole-3-glycerol phosphate synthase (SEQ ID NOs: 145-148; EC 4.1.1.48); Anthranilate phosphoribosyltransferase (e.g., SEQ ID NOs: 149-153; EC 2.4.2.18); Anthranilate synthase (e.g., SEQ ID NO: 154-158; EC 4.1.3.27); N-(5'-phosphoribosyl)anthranilate isomerase (e.g., SEQ ID NO: 159-162, EC 5.3.1.24); 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase (e.g., SEQ ID NO: 163; EC 5.3.1.36). In some embodiments, the enzyme involved in tryptophan production belongs to an EC number selected from the group consisting of: EC 4.2.1.20, EC 4.1.1.48, EC 2.4.2.18, EC 4.1.3.27, EC 5.3.1.24, and EC 5.3.1.36.

[0258] In some embodiments, the amino acid sequence of enzyme involved in tryptophan production is at least 50% similar (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% similar) to one of SEQ ID NOs: 135-163. In some embodiments, the amino acid sequence of enzyme involved in tryptophan production is at least 50% identical (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% identical) to one of SEQ ID NOs: 135-163.

[0259] Metabolites of phenylalanine including, but not limited to, phenethylamine, tyramine, and N-methylated derivatives thereof can also activate the TAAR system, modulating serotonin release and reuptake. These metabolites can be biosynthesized in a similar manner to those described above by administered bacteria, particularly those in the genera *Akkermansia*, *Eubacterium*, *Bacteroides*, *Coprococcus*, or *Enterorhabdus*.

[0260] Indole-3-carboxylic acid derivatives of tryptophan include indole-3-propionic acid (I3PA), synthesized by the fldAIBC gene cluster, and the related compounds, indole-3-acrylic acid (I3A), indole-3-lactic acid (I3LA), indole-3-pyruvic acid (I3PyA) and indole-3-acetic acid (I3Ac). In some embodiments, bacteria in the genera *Clostridium* or *Peptostreptococcus* that produce I3PA can be used alone or in combination with other bacteria and their metabolites to modulate serotonergic tone either via direct action by I3PA and related metabolites at 5-HT receptors (projected based on structural similarity of I3PA to tryptamine and 5-HT) or via transporter and reuptake inhibition (projected based on pharmacodynamic similarity of I3PA and the known monoamine reuptake inhibitor hyperforin at the pregnane X receptor).

[0261] In some embodiments, combinations of bacteria may be used to capture combined functional production of I3PA or other indole-3-carboxylic acid derivatives of tryptophan, whereas single strains do not have complete functional capabilities of producing I3PA. In some embodiments, a key enzyme in production of I3PA is acyl-CoA dehydrogenase, which is found in the 5-HT modulating genera *Acidaminococcus*, *Agathobacter*, *Alistipes*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Butyrimonas*, *Clostridium*, *Coprococcus*, *Eisenbergiella*, *Enterococcus*, *Erysipielatostridium*, *Eubacterium*, *Faecalitalea*, *Flavonifractor*, *Gemmiger*, *Gordonibacter*, *Hungatella*, *Lachnospirillum*, *Lactobacillus*, *Oscillibacter*, *Parabacteroides*, *Ruminococcus*, and/or *Streptococcus*. In some embodiments, acyl-CoA dehydrogenase is not found in members of the genera *Bilophila*, *Collinsella*, *Intestinimonas*, *Parasutterella*, and/or *Turicibacter*.

[0262] In some embodiments, the acyl-CoA dehydrogenase belongs to EC 1.3.99.3; EC 1.3.8.7; EC 1.3.8.8; or EC 1.3.8.9. In some embodiments, the amino acid sequence of the acyl-CoA dehydrogenase is at least 50% similar (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% similar) to one of SEQ ID NOs: 164-171. In some embodiments, the amino acid sequence of the acyl-CoA dehydrogenase is at least 50% identical (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% identical) to one of SEQ ID NOs: 164-171.

[0263] Indole-3-alcohol and -aldehyde derivatives of tryptophan include but are not limited to indole-3-carbinol and indole-3-carboxaldehyde, and can exert serotonergic effects by the mechanisms described above.

[0264] In some embodiments, the bacterial enzymes involved in production of metabolites capable of acting as 5-HT agonists or signaling modifiers are selected from the

group consisting of: Tryptophanase (EC 4.1.99.1; e.g., SEQ ID NO: 172); Indole-3-propionate biosynthesis enzymes (e.g., SEQ ID NO: 173-180); Cinnamoyl-CoA:phenyllactate CoA-transferase (EC 2.8.3.17; e.g., SEQ ID NOs: 173 or 177); (R)-3-(aryl)lactoyl-CoA dehydratase, alpha or beta subunit (EC 4.2.1.175; e.g., SEQ ID NOs: 174, 175, 178, 179); archerase (EC 5.6.1.9; e.g., SEQ ID NOs: 176 or 180); Tryptophan/aromatic amino acid N-methyltransferase (EC 2.1.1.—e.g., SEQ ID NOs: 181-184); see e.g., Table 3.

TABLE 3

| Exemplary bacterial enzymes involved in 5-HT agonist or modifier production | | | |
|---|---|-----------|---|
| Enzyme | EC | SEQ ID NO | Example Bacteria |
| Tryptophanase (indole production) | EC 4.1.99.1 | 172 | <i>Enterocloster lavalensis</i> HB-452c |
| Indole-3-propionate biosynthesis enzymes | EC 2.8.3.17, EC 4.2.1.175, EC 5.6.1.9 | 173-180 | <i>Clostridium sporogenes</i> ; <i>Peptostreptococcus russellii</i> |
| Tryptophan/aromatic amino acid N-methyltransferase | EC 2.1.1.— | 181-184 | <i>Escherichia coli</i> ; <i>Mycobacterium smegmatis</i> ; <i>Mycobacterium vaccae</i> ; <i>Akkermansia muciniphila</i> ; <i>Adlercreutzia equolifaciens</i> ; <i>Enterorhabdus</i> spp. |

[0265] In some embodiments, the amino acid sequences of the bacterial enzymes involved in production of metabolites capable of acting as 5-HT agonists or signaling modifiers, including those named above, are at least 50% similar (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% similar) to one of SEQ ID NOs: 172-184. In some embodiments, the amino acid sequences of the bacterial enzymes involved in production of metabolites capable of acting as 5-HT agonists or signaling modifiers, including those named above, are at least 50% identical (e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9%, or 100% identical) to one of SEQ ID NOs: 172-184.

[0266] In some embodiments, one or more 5-HT agonists, purified metabolites and/or proteins, derived from serotonin-modulating bacteria, are superior to live or dead serotonin-modulating bacteria or conditioned medium or cell pellets of serotonin-modulating bacteria. In some embodiments, superiority is observed through increased potency of the one or more 5-HT agonists, purified metabolites and/or proteins. In some embodiments, superiority is observed through ease of manufacturing and development.

[0267] In some embodiments, combinations of purified 5-HT agonists, metabolites and/or proteins, derived from serotonin-modulating bacteria, are synergistic in their capacity to modulate a serotonin signaling or biosynthesis in a subject.

[0268] In some embodiments, the one or more purified 5-HT agonists, metabolites and/or proteins, derived from serotonin-modulating bacteria described herein, are exemplary in their serotonin-modulating characteristics, as com-

pared to purified 5-HT agonists, metabolites and/or proteins derived from other bacterial strains.

[0269] In some embodiments, the purified 5-HT agonists, metabolites and/or proteins, derived from serotonin-modulating bacteria, can be delivered to the gastrointestinal tract in the form of a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powders, a granule, a medical food, supplement or a combination thereof. In some embodiments, the 5-HT

agonists, purified metabolites and/or proteins are administered rectally or via suppository.

5-HT Reducers

[0270] In some embodiments, described herein are therapeutic compositions comprising one or more bacteria (e.g. purified bacteria) that consume 5-HT and/or reduce host biosynthesis of 5-HT (see e.g., Tables 1A-1D “5-HT Reducer”). In some embodiments, the composition of serotonin reducers are derived from at least 2, 3, 4, 5, 6, 7, 8, 9, or 10, or more, types of isolated serotonin-modulating bacteria.

[0271] In some embodiments, a bacterial negative modulator of 5-HT signaling belongs to a genus selected from the group consisting of: *Bifidobacterium*, *Blautia*, *Clostridium*, *Coprococcus*, *Dorea*, *Eubacterium*, *Lachnoclostridium*, and *Slackia*. In some embodiments a bacterial negative modulator of 5-HT signaling is a species selected from the group consisting of: *Bifidobacterium longum*, *Blautia coccoides*, *Blautia obeum*, *Clostridium butyricum*, *Coprococcus comes*, *Dorea longicatena*, *Eubacterium rectale*, *Lachnoclostridium* sp., and *Slackia isoflavoniconvertens*. In some embodiments, the bacterial negative modulator of 5-HT signaling is a strain selected from the group consisting of: *Bifidobacterium longum* HB-234, *Blautia coccoides* HB-23, *Blautia obeum* HB-14, *Clostridium butyricum* HB-88, *Coprococcus comes* HB-80, *Dorea longicatena* HB-17, *Eubacterium rectale* HB-22, *Lachnoclostridium* sp. HB-698, and *Slackia isoflavoniconvertens* HB-326.

[0272] In some embodiments, a bacterial negative modulator of 5-HT signaling comprises a 16S sequence that is at least 95% identical (e.g., at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, at least 99.9% identical) to one of SEQ ID NOs: 96-104. In some embodiments, the bacterial negative modulators of 5-HT signaling consume tryptophan, preventing access from the host. In some embodiments, the bacterial negative modulators of 5-HT signaling consume 5-HT agonists or 5-HT potentiating

metabolites. In some embodiments the bacterial negative modulators of 5-HT signaling out-compete positive 5-HT modulating bacteria in the human gastrointestinal tract.

Minimal 5-HT-Impact

[0273] In some embodiments, described herein are bacteria with little to no effect on 5-HT (see e.g., Tables 1A-1D “No or Low 5-HT Impact”). In some embodiments, the 5-HT modulating bacteria genus is not selected from the group consisting of: *Clostridium*, *Escherichia*, *Eubacterium*, *Gemmiger*, *Intestinimonas*, *Lawsonibacter*, *Longibaculum*, *Parabacteroides*, *Ruminococcus*, and *Veillonella*, wherein the bacteria does not encode or express one or more, up to all of the enzymes described herein for 5-HT production, or for 5-HT modulation.

[0274] In some embodiments, the 5-HT modulating bacteria species is not selected the group consisting of: *Clostridium* sp., *Clostridium sphenoides*, *Clostridium symbiosum*, *Escherichia coli*, *Eubacterium callanderi*, *Gemmiger* sp., *Intestinimonas massiliensis*, *Lawsonibacter asaccharolyticus*, *Longibaculum* sp., *Parabacteroides distasonis*, *Parabacteroides goldsteinii*, *Ruminococcus bicirculans*, and *Veillonella atypica*, wherein the bacteria does not encode or express one or more, up to all of the enzymes described herein for 5-HT production, or for 5-HT modulation.

[0275] In some embodiments, the 5-HT modulating bacteria strain is not a bacterium selected from the group consisting of: *Clostridium* sp. HB-358, *Clostridium sphenoides* HB-470, *Clostridium symbiosum* HB-67, *Escherichia coli* HB-490, *Eubacterium callanderi* HB-59, *Gemmiger* sp. HB-567, *Intestinimonas massiliensis* HB-651, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum* sp. HB-681, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Ruminococcus bicirculans* HB-105, and *Veillonella atypica* HB-251, wherein the bacteria does not encode or express one or more, up to all of the enzymes described herein for 5-HT production, or for 5-HT modulation.

Combined Compositions

[0276] It is noted that the individual bacterial species or strain described herein can modulate serotonin as individual species or strain. It is also contemplated that consortia of these species, either with other members of the species or strains described herein, or with other species or strains, that, for example, express one or more genes, or produce one or more metabolites that modulate serotonin levels, can provide additional benefits regarding serotonin modulation.

[0277] In some embodiments, described herein are therapeutic compositions comprising combinations of one or more live serotonin-modulating bacteria, one or more dead or inactivated serotonin-modulating bacteria, one or more conditioned medium(s) of serotonin-modulating bacteria, one or more cell pellet(s) of serotonin-modulating bacteria, and/or one or more metabolites and/or proteins (derived from serotonin-modulating bacteria), that are delivered to the gastrointestinal tract of the subject to modulate serotonin signaling and/or biosynthesis of the subject, either directly or by altering native microbial (e.g., bacterial, archaeal, fungal, protist, or viral) community composition or gene expression, resulting in increased or reduced levels of serotonin-modulating bacteria, or alterations in the microbiota-derived metabolome and/or microbiota-derived proteome to

a more serotonin-stimulating or serotonin-inhibitory state. In some embodiments, the composition of live bacteria, dead bacteria, conditioned medium(s), cell pellet(s), purified 5-HT agonists, metabolites, or proteins are derived from at least 2, 3, 4, 5, 6, 7, 8, 9, or 10, or more, types of isolated serotonin-modulating bacteria.

[0278] In some embodiments, combinations of one or more live serotonin-modulating bacteria, one or more dead-serotonin modulating bacteria, one or more conditioned medium(s) of serotonin-modulating bacteria, one or more cell pellet(s) of serotonin-modulating bacteria, and/or one or more metabolites and/or proteins (derived from serotonin-modulating bacteria) are superior to alternative formulations, through activation of multiple mechanisms. For example, metabolites produced by serotonin-modulating bacteria can elevate serotonin biosynthesis by the host via TPH-1, while proteins derived from serotonin-modulating bacteria can elevate serotonin biosynthesis by the host via TPH-2. In some embodiments, combinations of one or more live serotonin-modulating bacteria, one or more dead-serotonin modulating bacteria, one or more conditioned medium(s) of serotonin-modulating bacteria, one or more cell pellet(s) of serotonin-modulating bacteria, and/or one or more metabolites and/or proteins (derived from serotonin-modulating bacteria) are synergistic in their capacity to modulate a subject's serotonin signaling or biosynthesis.

[0279] In some embodiments, combinations of one or more live serotonin-modulating bacteria, one or more dead-serotonin modulating bacteria, one or more conditioned medium(s) of serotonin-modulating bacteria, one or more cell pellet(s) of serotonin-modulating bacteria, and/or one or more metabolites and/or proteins (derived from serotonin-modulating bacteria) are exemplary in their serotonin-modulating characteristics, as compared to purified metabolites and/or proteins derived from bacteria bacterial strains.

[0280] In some embodiments, the combinations of one or more live serotonin-modulating bacteria, one or more dead-serotonin modulating bacteria, one or more conditioned medium(s) of serotonin-modulating bacteria, one or more cell pellet(s) of serotonin-modulating bacteria, and/or one or more metabolites and/or proteins (derived from serotonin-modulating bacteria) can be delivered to the gastrointestinal tract in the form of a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powders, a granule, a medical food, supplement or a combination thereof. In some embodiments, the composition is administered as a fecal transplant (in embodiments comprising live bacteria), rectally or via suppository.

[0281] In some embodiments, combinations of bacteria are selected for therapeutics, food, medical foods, or any other product for synergistic effects on host 5-HT signaling. In a non-limiting example, combinations of bacteria can be selected to capture multiple mechanisms involved in modulating host 5-HT signaling. As a non-limiting example, a strain with only the ability to elevate 5-HT signaling via its cell pellet can be combined with a separate bacterium, wherein said second bacterium has a supernatant that elicits an effect, produces 5-HT, and/or produces 5-HT agonists. In some embodiments, by combining mechanisms or adding redundancy of any mechanism (e.g., multiple organisms with the capability to produce 5-HT) within a product, one can to elicit a stronger or more consistent effect on host 5-HT signaling, and thus a more favorable impact in the target indications and/or symptoms. In a non-limiting

example, *Clostridium lavalense* HB-452C, which produces 5-HT and the 5-HT agonist tryptamine, can be combined with *Bifidobacterium adolescentis* HB-179, which has a strong cell pellet and supernatant induction phenotype.

Therapeutic Compositions

[0282] Bacteria, their components, proteins, metabolites, or conditioned medium-derived products can be formulated and/or used as therapeutic compositions, e.g., to alter serotonin levels in an individual in need thereof. Such therapeutic compositions can also be pharmaceutical compositions, formulated with a pharmaceutically acceptable carrier. Thus, as used herein, the term "pharmaceutical composition" refers to the active therapeutic agent in combination with a pharmaceutically acceptable carrier e.g. a carrier commonly used in the pharmaceutical industry. The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio. In some embodiments of any of the aspects, a pharmaceutically acceptable carrier can be a carrier other than water. In some embodiments of any of the aspects, a pharmaceutically acceptable carrier can be a cream, emulsion, gel, liposome, nanoparticle, and/or ointment. In some embodiments of any of the aspects, a pharmaceutically acceptable carrier can be an artificial or engineered carrier, e.g., a carrier that the active ingredient would not be found to occur in nature.

[0283] Any of the serotonin-modulating bacteria described herein (e.g., live or dead bacteria, natural bacteria or engineered bacteria), conditioned medium(s) of serotonin-modulating bacteria, cell pellet(s) of serotonin-modulating bacteria, and/or metabolites and/or proteins (derived from serotonin-modulating bacteria) can be incorporated into a therapeutic composition. For instance, the therapeutic compositions can be administered to a patient in need thereof to treat or alleviate the symptom of a serotonin-related disease or disorder.

[0284] In some embodiments, bacteria, conditioned medium, cell pellets, proteins, and/or metabolites are purified prior to incorporation into a therapeutic composition. For instance, bacteria can be purified so that the population of bacteria is substantially free of other bacteria (e.g., contains at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, or at least 98%, at least 99% of the specific bacterial strain or strains desired in the composition).

[0285] In some embodiments, the therapeutic composition is a probiotic or a medical food comprising at least one serotonin-modulating bacterial strain, conditioned medium, cell pellets, purified metabolites, and/or proteins from one or more serotonin-modulating bacteria, or any combinations thereof. The therapeutic composition can be administered, for instance, as a probiotic, a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powder, granules, or any combination thereof. The composition can also be formulated as a medical food. The composition can also be administered as a fecal transplant or suppository.

[0286] In some embodiments, the composition is formulated for oral administration. In some embodiments the composition is formulated for rectal or colorectal adminis-

tration. In some embodiments, the composition is administered orally, intravenously, intramuscularly, intrathecally, subcutaneously, sublingually, buccally, rectally, vaginally, by the ocular route, by the otic route, nasally, via inhalation, by nebulization, cutaneously, or transdermally. In some embodiments, the composition is administered via multiple methods or routes to increase potency or take advantage of synergistic effects.

[0287] In some embodiments, the dose of the therapeutic can comprise e.g., at least 1×10^3 CFUs, 1×10^4 CFUs, 1×10^5 CFUs, 1×10^6 CFUs, 1×10^7 CFUs, 1×10^8 CFUs, 1×10^9 CFUs, 1×10^{10} CFUs, 1×10^{11} CFUs, 1×10^{12} CFUs, or greater than 1×10^{12} CFUs of the desired bacterial species. In some embodiments, wherein the desired bacterial species are inactivated or not viable, CFUs correspond to the CFUs of an equivalent preparation of live bacterial species, or to the CFUs of the preparation prior to killing or inactivation of the bacterial species. In some embodiments, the dose of the therapeutic can contain the conditioned medium or cell pellet from e.g., at least 1×10^3 CFUs, 1×10^4 CFUs, 1×10^5 CFUs, 1×10^6 CFUs, 1×10^7 CFUs, 1×10^8 CFUs, 1×10^9 CFUs, 1×10^{10} CFUs, 1×10^{11} CFUs, 1×10^{12} CFUs, 1×10^{13} CFUs, 1×10^{14} CFUs, or greater than 1×10^{12} CFUs of the desired bacterial species. In some embodiments, the purified metabolite or protein can be derived from e.g., at least 1×10^3 CFUs, 1×10^4 CFUs, 1×10^5 CFUs, 1×10^6 CFUs, 1×10^7 CFUs, 1×10^8 CFUs, 1×10^9 CFUs, 1×10^{10} CFUs, 1×10^{11} CFUs, or greater than 1×10^{12} CFUs of the desired bacterial species.

[0288] In some embodiments, the therapeutic composition or dose unit comprises a pharmaceutically acceptable formulation, including an enteric coating or similar to survive the acidity of the stomach and permit delivery into the small or large intestine, a prebiotic (such as, but not limited to, amino acids (e.g., arginine, glutarate, and ornithine), biotin, fructooligosaccharide, galactooligosaccharides, hemi celluloses (e.g., arabinoxylan, xylan, xyloglucan, and glucomannan), inulin, chitin, lactulose, mannan oligosaccharides, oligofructose-enriched inulin, gums (e.g., guar gum, gum arabic and carrageenan), oligofructose, oligodextrose, tagatose, resistant maltodextrins (e.g., resistant starch), transgalactooligosaccharide, pectins (e.g., xylogalacturonan, citrus pectin, apple pectin, and rhamnogalacturonan-I), dietary fibers (e.g., soy fiber, sugarbeet fiber, pea fiber, corn bran, and oat fiber) xylooligosaccharides, polyamines (such as but not limited to spermidine and putrescine), an effective amount of an anti-bacterial agent, anti-fungal agent, anti-viral agent, or anti-parasitic agent, or any combinations of the above. As a non-limiting example, the therapeutic composition can also be in the form of a yogurt containing one or more purified strains of serotonin-modulating bacteria, conditioned medium, cell pellet(s), and/or purified metabolite(s) and/or protein(s) from one or more serotonin-modulating bacteria.

Serotonin-Related Diseases or Disorders

[0289] In one or more embodiments of any of the above aspects, a serotonin-related disease or disorder that can be treated by administration of a therapeutic composition described herein is selected from the group consisting of intestinal motility disorders (e.g., diarrhea or constipation), irritable bowel syndrome (e.g., IBS-D, IBS-C, IBS-M), inflammatory bowel disease, depression (e.g., major depressive disorder, treatment resistant depression, post-partum

depression), anxiety, anxiety disorders, addiction, social phobia, major depressive disorder (MDD), neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, sleep disorders, schizophrenia, bone disease (e.g. osteoporosis), cancer (e.g. polycythemia vera or myelosclerosis), metabolic disease (e.g. obesity or diabetes), a dysregulated immune system, cardiac disease (e.g. coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or aorta disease), heartburn, dermatological conditions (e.g. eczema and itch), GERD, platelet disorders (e.g. essential thrombocytosis), and pain disorders.

[0290] In some embodiments, the serotonin-related disease or disorder or its symptom(s) are caused by high serotonin levels. In some embodiments, the serotonin-related disease or disorder or its symptoms caused by high serotonin levels is selected from the group consisting of: diarrhea, IBS-D, inflammatory bowel disease, anxiety, social phobia, sleep disorders, schizophrenia, cancer, obesity, diabetes, coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or platelet disorders (e.g. essential thrombocytosis).

[0291] In some embodiments, the serotonin-related disease or disorder or its symptom(s) caused by high serotonin levels is not a gut disease or disorder. In some embodiments, the serotonin-related disease or disorder or its symptom(s) caused by high serotonin levels is selected from the group consisting of anxiety, social phobia, sleep disorders, schizophrenia, cancer, obesity, diabetes, coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or platelet disorders (e.g. essential thrombocytosis).

[0292] In some embodiments, the serotonin-related disease or disorder or its symptom(s) are caused by low serotonin levels. In some embodiments, the serotonin-related disease or disorder or its symptom(s) caused by low serotonin levels is selected from the group consisting of: constipation, IBS-C, depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, heartburn, dermatological conditions (e.g., eczema and itch), gastroesophageal reflux disease (GERD), or pain disorders.

[0293] In some embodiments, the serotonin-related disease or disorder or its symptom(s) caused by low serotonin levels is not a gut disease or disorder. In some embodiments, the serotonin-related disease or disorder or its symptom(s) caused by low serotonin levels is selected from the group consisting of depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, dermatological conditions (eczema and itch), and pain disorders.

[0294] It is noteworthy that both high and low serotonin levels have been connected to certain anxiety and sleep disorders. In some instances, it is clear that a serotonin level, whether higher or lower, can influence health, thereby emphasizing the importance of serotonin regulation. Where the gut microbiota is centrally involved in maintaining serotonin levels, a dysbiosis that causes a deviation from

normal levels can be treated by restoring a healthy gut microbiota or altering the dysbiosis.

[0295] In some embodiments, the method further comprises decreasing at least one symptom of a serotonin-related disease or disorder in the subject selected from the group consisting of: fatigue, insomnia, stress, persistent anxiety, persistent sadness, social withdrawal, substance withdrawal, irritability, thoughts of suicide, thoughts of self-harm, restlessness, low sex drive, lack of focus, loss of appetite, high blood pressure, low blood pressure, high heart rate, low heart rate, constipation, diarrhea, chronic pain, heartburn, fatigue, trouble breathing, stomach aches, nosebleeds, gum, or stomach bleeding, headaches, weight gain, and burning of the skin, altered inflammatory markers, neurodevelopment, or seizures.

[0296] In some embodiments, the process of identifying a subject with a serotonin-related disease or disorder can be carried out by a trained psychologist, psychiatrist, gastroenterologist, cardiologist, neurologist, or otherwise appropriate medical provider. For instance, a psychiatrist, psychologist, or neurologist can diagnose a subject with a serotonin-related disease or disorder of the central nervous system by evaluating the subject's behavior for symptoms of serotonin-related disease or disorder. One of skill in the art will understand that mental illness can also be identified in a subject with the aid of the Diagnostic and Statistical Manual of Mental Disorders (DSM-5) (American Psychiatric Association).

[0297] In one or more embodiments, the process of identifying a subject with a serotonin-related disease or disorder can comprise diagnosing the subject with a serotonin-related disease or disorder. In some embodiments, the serotonin-related disease or disorder is identified or diagnosed using functional magnetic resonance imaging (fMRI). In some embodiments, the serotonin-related disease or disorder can be identified with standard psychological and neurological surveys, or in other methods known to experts in the field. In some embodiments, a serotonin-related disease or disorder can be diagnosed using gastrointestinal related methods, such as a colonoscopy, fecal consistency test, or fecal swab.

[0298] In some embodiments, a subject in need of treatment with a therapeutic composition described herein can be identified by identifying low levels of serotonin in the subject's blood, serum, stool, or other bodily fluid. The amount of serotonin can be measured by LC/MS or another technique known in the art. In some embodiments, the amount of serotonin in the brain can be measured using proton magnetic resonance (PMR), or another similar technique.

[0299] In some embodiments, a subject in need of treatment with a therapeutic composition described herein can be identified by identifying low or high levels of serotonin-modulating bacteria in the subject's stool or cecum, using such methods as 16S rDNA next-generation sequencing (NGS; e.g., IlluminaTM) or quantitative PCR. In some embodiments, the percentage of serotonin-modulating bacteria in the subject's gut represents more than 9%, about 9%, about 8%, about 7%, about 6%, about 5%, about 4%, about 3%, about 2%, about 1%, or less than about 1% of the total 16S sequences measured in the subject's stool or cecal sample.

[0300] Accordingly, the present disclosure provides for the treatment of one or more serotonin-related disease or disorders by administering to the subject one or combina-

tions of one or more live serotonin-modulating bacteria, one or more dead-serotonin modulating bacteria, one or more conditioned medium(s) of one or more serotonin-modulating bacteria, one or more cell pellet(s) of serotonin-modulating bacteria, and/or one or more metabolites and/or proteins (derived from serotonin-modulating bacteria). The present disclosure provides for the treatment of one or more serotonin-related disease or disorder by treatment with a prebiotic.

Treatment Methods

[0301] The therapeutic compositions described herein can be administered to a patient in need thereof, for instance for the treatment of a serotonin-related disease or disorder. In some embodiments, the method of treatment can comprise first diagnosing a patient who can benefit from treatment by a therapeutic composition described herein. In some embodiments, the method further comprises administering to the patient a therapeutic composition described herein.

[0302] As used herein, the terms “treat,” “treatment,” “treating,” or “amelioration” refer to therapeutic treatments, wherein the object is to reverse, alleviate, ameliorate, inhibit, slow down or stop the progression or severity of a condition associated with a disease or disorder, e.g. a serotonin-related disease or disorder. The term “treating” includes reducing or alleviating at least one adverse effect or symptom of a condition, disease or disorder associated with a serotonin-related disease or disorder. Treatment is generally “effective” if one or more symptoms or clinical markers are reduced. Alternatively, treatment is “effective” if the progression of a disease is reduced or halted. That is, “treatment” includes not just the improvement of symptoms or markers, but also a cessation of, or at least slowing of, progress or worsening of symptoms compared to what would be expected in the absence of treatment. Beneficial or desired clinical results include, but are not limited to, alleviation of one or more symptom(s), diminishment of extent of disease, stabilized (i.e., not worsening) state of disease, delay or slowing of disease progression, amelioration or palliation of the disease state, remission (whether partial or total), and/or decreased mortality, whether detectable or undetectable. The term “treatment” of a disease also includes providing relief from the symptoms or side-effects of the disease (including palliative treatment).

[0303] As described herein, levels of serotonin can be increased or decreased in a serotonin-related disease or disorder and/or in subjects with a serotonin-related disease or disorder, that is, that level of serotonin can deviate from a normal level.

[0304] In some embodiments of any of the aspects, the level of serotonin can be decreased in a serotonin-related disease or disorder and/or in subjects with a serotonin-related disease or disorder. Accordingly, in one aspect of any of the embodiments, described herein is a method of treating a serotonin-related disease or disorder in a subject in need thereof, the method comprising administering a composition comprising at least one serotonin modulating bacteria (e.g., a serotonin-increasing bacteria) and/or product(s) thereof as described herein to a subject determined to have a level of serotonin that is decreased relative to a reference. In one aspect of any of the embodiments, described herein is a method of treating a serotonin-related disease or disorder in a subject in need thereof, the method comprising: a) determining the level of serotonin in a sample obtained from a

subject; and b) administering a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein to the subject if the level of serotonin is decreased relative to a reference.

[0305] In some embodiments of any of the aspects, the method comprises administering composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein to a subject previously determined to have a level of serotonin that is decreased relative to a reference. In some embodiments of any of the aspects, described herein is a method of treating a serotonin-related disease or disorder in a subject in need thereof, the method comprising: a) first determining the level of serotonin in a sample obtained from a subject; and b) then administering a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein to the subject if the level of serotonin is decreased relative to a reference.

[0306] In one aspect of any of the embodiments, described herein is a method of treating a serotonin-related disease or disorder in a subject in need thereof, the method comprising: a) determining if the subject has a decreased level of serotonin; and b) administering a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein to the subject if the level of serotonin is decreased relative to a reference. In some embodiments of any of the aspects, the step of determining if the subject has a decreased level of serotonin can comprise i) obtaining or having obtained a sample from the subject and ii) performing or having performed an assay on the sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has a decreased level of serotonin can comprise performing or having performed an assay on a sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has a decreased level of serotonin can comprise ordering or requesting an assay on a sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has a decreased level of serotonin can comprise receiving the results of an assay on a sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has a decreased level of serotonin can comprise receiving a report, results, or other means of identifying the subject as a subject with a decreased level of serotonin.

[0307] In one aspect of any of the embodiments, described herein is a method of treating a serotonin-related disease or disorder in a subject in need thereof, the method comprising: a) determining if the subject has a decreased level of serotonin; and b) instructing or directing that the subject be administered a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein if the level of serotonin is decreased relative to a reference. In some embodiments of any of the aspects, the step of determining if the subject has a decreased level of serotonin can comprise i) obtaining or having obtained a sample from the subject and ii) performing or having performed an assay on the sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has a decreased level of serotonin

can comprise performing or having performed an assay on a sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has a decreased level of serotonin can comprise ordering or requesting an assay on a sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of instructing or directing that the subject be administered a particular treatment can comprise providing a report of the assay results. In some embodiments of any of the aspects, the step of instructing or directing that the subject be administered a particular treatment can comprise providing a report of the assay results and/or treatment recommendations in view of the assay results.

[0308] In some embodiments of any of the aspects, the level of serotonin can be increased in a serotonin-related disease or disorder and/or in subjects with a serotonin-related disease or disorder. Accordingly, in one aspect of any of the embodiments, described herein is a method of treating a serotonin-related disease or disorder in a subject in need thereof, the method comprising administering a composition comprising at least one serotonin modulating bacteria (e.g., a serotonin-reducing bacteria) and/or product(s) thereof as described herein to a subject determined to have a level of serotonin that is increased relative to a reference. In one aspect of any of the embodiments, described herein is a method of treating a serotonin-related disease or disorder in a subject in need thereof, the method comprising: a) determining the level of serotonin in a sample obtained from a subject; and b) administering a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein to the subject if the level of serotonin is increased relative to a reference.

[0309] In some embodiments of any of the aspects, the method comprises administering composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein to a subject previously determined to have a level of serotonin that is increased relative to a reference. In some embodiments of any of the aspects, described herein is a method of treating a serotonin-related disease or disorder in a subject in need thereof, the method comprising: a) first determining the level of serotonin in a sample obtained from a subject; and b) then administering a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein to the subject if the level of serotonin is increased relative to a reference.

[0310] In one aspect of any of the embodiments, described herein is a method of treating a serotonin-related disease or disorder in a subject in need thereof, the method comprising: a) determining if the subject has an increased level of serotonin; and b) administering a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein to the subject if the level of serotonin is increased relative to a reference. In some embodiments of any of the aspects, the step of determining if the subject has an increased level of serotonin can comprise i) obtaining or having obtained a sample from the subject and ii) performing or having performed an assay on the sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has an increased level of serotonin can comprise performing or having performed an assay on a sample obtained from the subject to determine/

measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has an increased level of serotonin can comprise ordering or requesting an assay on a sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has an increased level of serotonin can comprise receiving the results of an assay on a sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has an increased level of serotonin can comprise receiving a report, results, or other means of identifying the subject as a subject with an increased level of serotonin.

[0311] In one aspect of any of the embodiments, described herein is a method of treating a serotonin-related disease or disorder in a subject in need thereof, the method comprising: a) determining if the subject has an increased level of serotonin; and b) instructing or directing that the subject be administered a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein if the level of serotonin is increased relative to a reference. In some embodiments of any of the aspects, the step of determining if the subject has an increased level of serotonin can comprise i) obtaining or having obtained a sample from the subject and ii) performing or having performed an assay on the sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has an increased level of serotonin can comprise performing or having performed an assay on a sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of determining if the subject has an increased level of serotonin can comprise ordering or requesting an assay on a sample obtained from the subject to determine/measure the level of serotonin in the subject. In some embodiments of any of the aspects, the step of instructing or directing that the subject be administered a particular treatment can comprise providing a report of the assay results. In some embodiments of any of the aspects, the step of instructing or directing that the subject be administered a particular treatment can comprise providing a report of the assay results and/or treatment recommendations in view of the assay results.

[0312] In some embodiments, individuals that would benefit from an alteration of levels of the serotonin-modulating gut microbiota, serotonin-modulating gut-microbiota-derived metabolome, and/or serotonin-modulating gut-microbiota-derived proteome of the subject are identified via next-generation DNA and/or RNA sequencing of microbial communities in that individual's stool or tissue samples; metabolomics of stool, urine, blood, or similar samples; or genome sequencing of that individual; or some combination thereof. In some embodiments, serotonin is measured in the stool, blood, or tissue of the subject. In some embodiments, levels of serotonin modulating bacteria are measured. In such embodiments, low levels of serotonin-modulating gut microbiota can indicate the need to introduce, promote, or select for increased serotonin-modulating bacteria. In some embodiments, levels of genes involved in the production of microbiota-derived serotonin modulating metabolites or proteins are measured. In some embodiments, levels of serotonin-modulating bacteria, serotonin-modulating

metabolites, or serotonin-modulating proteins are altered relative to their initial quantitated amounts, after administering a therapeutic composition as described herein.

Administration

[0313] Therapeutic compositions as described herein can be administered via any of a number of different routes or in different regimens. As used herein, the term “administering,” refers to the placement of a compound or bacteria as disclosed herein into a subject by a method or route which results in at least partial delivery of the agent at a desired site. Pharmaceutical compositions comprising the compounds or bacteria disclosed herein can be administered by any appropriate route which results in an effective treatment in the subject. In some embodiments, administration comprises physical human activity, e.g., an injection, act of ingestion, an act of application, and/or manipulation of a delivery device or machine. Such activity can be performed, e.g., by a medical professional and/or the subject being treated. The period of viability of the bacterial cells after administration to a subject can be as short as a few hours, e.g., twenty-four hours, to a few days, to as long as several years, i.e., long-term engraftment.

[0314] In other words, as used herein “administer” and “administration” encompasses embodiments in which one person directs another to consume, ingest, or otherwise take into the body a bacteria, bacterial composition, bacterial conditioned media, bacterial cell pellet, purified bacterial metabolites, purified bacterial proteins, or combinations thereof in a certain manner and/or for a certain purpose, and also situations in which a user uses any of these compositions in a certain manner and/or for a certain purpose independently of or in variance to any instructions received from a second person. Non-limiting examples of embodiments in which one person directs another to consume a composition described herein in a certain manner and/or for a certain purpose include when a physician prescribes a course of conduct and/or treatment to a patient, when a parent commands a minor user (such as a child) to consume a composition described herein, when a trainer advises a user (such as an athlete) to follow a particular course of conduct and/or treatment, and when a manufacturer, distributor, or marketer recommends conditions of use to an end user, for example through advertisements or labeling on packaging or on other materials provided in association with the sale or marketing of a product.

[0315] In some embodiments, the methods described herein relate to treating a subject having or diagnosed as having a serotonin-related disease or disorder with a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein. Subjects having a serotonin-related disease or disorder can be identified by a physician using current methods of diagnosing a serotonin-related disease or disorder. Symptoms and/or complications of a serotonin-related disease or disorder which characterize these conditions and aid in diagnosis are well known in the art, as described above. Tests that can aid in a diagnosis of, e.g. a serotonin-related disease or disorder are described above and can include, in addition to standard measurements of serotonin itself, detection or measurement of gut bacteria that modulate serotonin, detection or measurement of genetic sequences of such bacteria, including 16S sequences and/or genetic sequences encoding proteins that modulate serotonin, or detection or measurement of bacterial metabo-

lites or proteins that modulate serotonin. A family history of a serotonin-related disease or disorder, or exposure to risk factors for a serotonin-related disease or disorder can also aid in determining if a subject is likely to have a serotonin-related disease or disorder or in making a diagnosis of a serotonin-related disease or disorder.

[0316] In some embodiments, the methods described herein comprise administering an effective amount of a composition or compositions described herein, e.g. a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein to a subject in order to alleviate a symptom of a serotonin-related disease or disorder. As used herein, “alleviating a symptom of a serotonin-related disease or disorder” is ameliorating any condition or symptom associated with the a serotonin-related disease or disorder. As compared with an equivalent untreated control, such amelioration comprises a reduction by at least 5%, 10%, 20%, 40%, 50%, 60%, 80%, 90%, 95%, 99% or more as measured by any standard technique. A variety of means for administering the compositions described herein to subjects are known to those of skill in the art. Such methods can include, but are not limited to oral, parenteral, intravenous, intramuscular, subcutaneous, transdermal, airway (aerosol), pulmonary, cutaneous, topical, injection, or intratumoral administration. Administration can be local or systemic.

[0317] The term “effective amount” as used herein refers to the amount of a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein needed to alleviate at least one or more symptom of the disease or disorder, and relates to a sufficient amount of pharmacological composition to provide the desired effect. The term “therapeutically effective amount” therefore refers to an amount of a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein that is sufficient to provide a particular anti-serotonin-related-disorder effect when administered to atypical subject. An effective amount as used herein, in various contexts, would also include an amount sufficient to delay the development of a symptom of the disease, alter the course of a symptom disease (for example but not limited to, slowing the progression of a symptom of the disease), or reverse a symptom of the disease. Thus, it is not generally practicable to specify an exact “effective amount”. However, for any given case, an appropriate “effective amount” can be determined by one of ordinary skill in the art using only routine experimentation.

[0318] Effective amounts, toxicity, and therapeutic efficacy can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dosage can vary depending upon the dosage form employed and the route of administration utilized. The dose ratio between toxic and therapeutic effects is the therapeutic index and can be expressed as the ratio LD₅₀/ED₅₀. Compositions and methods that exhibit large therapeutic indices are preferred. A therapeutically effective dose can be estimated initially from cell culture assays. Also, where a therapeutic composition’s active agent or ingredient comprises, consists essentially of, or consists of a metabolite or protein produced by a bacteria or bacterial composition as described herein, a dose can be formulated in animal models to achieve a concentration range in vivo

that includes the IC₅₀ (i.e., the concentration of a composition comprising at least one product of at least one serotonin modulating bacteria as described herein, which achieves a half-maximal inhibition of symptoms) as determined in cell culture, or in an appropriate animal model. Levels in biological samples can be measured, for example, by high performance liquid chromatography. The effects of any particular dosage can be monitored by a suitable bioassay, e.g., assay for serotonin, among others. The dosage can be determined by a physician and adjusted, as necessary, to suit observed effects of the treatment.

[0319] In some embodiments, the technology described herein relates to a pharmaceutical composition comprising a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein, and optionally a pharmaceutically acceptable carrier. In some embodiments, the active ingredients of the pharmaceutical composition comprise at least one serotonin modulating bacteria and/or product(s) as described herein. In some embodiments, the active ingredients of the pharmaceutical composition consist essentially of at least one serotonin modulating bacteria and/or product(s) as described herein. In some embodiments, the active ingredients of the pharmaceutical composition consist of at least one serotonin modulating bacteria and/or product(s) as described herein. Pharmaceutically acceptable carriers and diluents include saline, aqueous buffer solutions, solvents and/or dispersion media. The use of such carriers and diluents is well known in the art. Some non-limiting examples of materials which can serve as pharmaceutically-acceptable carriers include: (1) sugars, such as lactose, glucose and sucrose; (2) starches, such as corn starch and potato starch; (3) cellulose, and its derivatives, such as sodium carboxymethyl cellulose, methylcellulose, ethyl cellulose, microcrystalline cellulose and cellulose acetate; (4) powdered tragacanth; (5) malt; (6) gelatin; (7) lubricating agents, such as magnesium stearate, sodium lauryl sulfate and talc; (8) excipients, such as cocoa butter and suppository waxes; (9) oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; (10) glycols, such as propylene glycol; (11) polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol (PEG); (12) esters, such as ethyl oleate and ethyl laurate; (13) agar; (14) buffering agents, such as magnesium hydroxide and aluminum hydroxide; (15) alginic acid; (16) pyrogen-free water; (17) isotonic saline; (18) Ringer's solution; (19) ethyl alcohol; (20) pH buffered solutions; (21) polyesters, polycarbonates and/or polyanhydrides; (22) bulking agents, such as polypeptides and amino acids (23) serum component, such as serum albumin, HDL and LDL; (24) C₂-C₁₂ alcohols, such as ethanol; and (25) other non-toxic compatible substances employed in pharmaceutical formulations. Wetting agents, coloring agents, release agents, coating agents, sweetening agents, flavoring agents, perfuming agents, preservative and antioxidants can also be present in the formulation. The terms such as "excipient", "carrier", "pharmaceutically acceptable carrier" or the like are used interchangeably herein. In some embodiments, the carrier inhibits the degradation of the active agent, e.g. at least one serotonin modulating bacteria and/or product(s) as described herein.

[0320] In some embodiments, the pharmaceutical composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein can be a parenteral dose form. Since administration of parenteral dosage forms

typically bypasses the patient's natural defenses against contaminants, parenteral dosage forms are preferably sterile or capable of being sterilized prior to administration to a patient. Examples of parenteral dosage forms include, but are not limited to, solutions ready for injection, dry products ready to be dissolved or suspended in a pharmaceutically acceptable vehicle for injection, suspensions ready for injection, and emulsions. In addition, controlled-release parenteral dosage forms can be prepared for administration of a patient, including, but not limited to, DUROS®-type dosage forms and dose-dumping.

[0321] Suitable vehicles that can be used to provide parenteral dosage forms of at least one serotonin modulating bacteria and/or product(s) as disclosed within are well known to those skilled in the art. Examples include, without limitation: sterile water; water for injection USP; saline solution; glucose solution; aqueous vehicles such as but not limited to, sodium chloride injection, Ringer's injection, dextrose Injection, dextrose and sodium chloride injection, and lactated Ringer's injection; water-miscible vehicles such as, but not limited to, ethyl alcohol, polyethylene glycol, and propylene glycol; and non-aqueous vehicles such as, but not limited to, corn oil, cottonseed oil, peanut oil, sesame oil, ethyl oleate, isopropyl myristate, and benzyl benzoate. Compounds that alter or modify the solubility of a pharmaceutically acceptable salt of a serotonin modulating bacterial product as disclosed herein can also be incorporated into the parenteral dosage forms of the disclosure, including conventional and controlled-release parenteral dosage forms.

[0322] Pharmaceutical compositions comprising at least one serotonin modulating bacteria and/or product(s) can also be formulated to be suitable for oral administration, for example as discrete dosage forms, such as, but not limited to, tablets (including without limitation scored or coated tablets), pills, caplets, capsules, chewable tablets, powder packets, cachets, troches, wafers, aerosol sprays, or liquids, such as but not limited to, syrups, elixirs, solutions or suspensions in an aqueous liquid, a non-aqueous liquid, an oil-in-water emulsion, or a water-in-oil emulsion. Such compositions contain a predetermined amount of the pharmaceutically acceptable salt of the disclosed compounds, and can be prepared by methods of pharmacy well known to those skilled in the art. See generally, Remington: The Science and Practice of Pharmacy, 21st Ed., Lippincott, Williams, and Wilkins, Philadelphia PA. (2005).

[0323] Conventional dosage forms generally provide rapid or immediate drug release from the formulation. Depending on the pharmacology and pharmacokinetics of the drug, use of conventional dosage forms can lead to wide fluctuations in the concentrations of the drug in a patient's blood and other tissues. These fluctuations can impact a number of parameters, such as dose frequency, onset of action, duration of efficacy, maintenance of therapeutic blood levels, toxicity, side effects, and the like. Advantageously, controlled-release formulations can be used to control a drug's onset of action, duration of action, plasma levels within the therapeutic window, and peak blood levels. In particular, controlled- or extended-release dosage forms or formulations can be used to ensure that the maximum effectiveness of a drug is achieved while minimizing potential adverse effects and safety concerns, which can occur both from under-dosing a drug (i.e., going below the minimum therapeutic levels) as well as exceeding the toxicity level for the drug. In some embodiments, the composition comprising at least one sero-

tonin modulating bacteria and/or product(s) as described herein can be administered in a sustained release formulation.

[0324] Controlled-release pharmaceutical products have a common goal of improving drug therapy over that achieved by their non-controlled release counterparts. Ideally, the use of an optimally designed controlled-release preparation in medical treatment is characterized by a minimum of drug substance being employed to cure or control the condition in a minimum amount of time. Advantages of controlled-release formulations include: 1) extended activity of the drug; 2) reduced dosage frequency; 3) increased patient compliance; 4) usage of less total drug; 5) reduction in local or systemic side effects; 6) minimization of drug accumulation; 7) reduction in blood level fluctuations; 8) improvement in efficacy of treatment; 9) reduction of potentiation or loss of drug activity; and 10) improvement in speed of control of diseases or conditions. Kim, Chemg-ju, Controlled Release Dosage Form Design, 2 (Technomic Publishing, Lancaster, Pa.: 2000).

[0325] Most controlled-release formulations are designed to initially release an amount of drug (active ingredient) that promptly produces the desired therapeutic effect, and gradually and continually release other amounts of drug to maintain this level of therapeutic or prophylactic effect over an extended period of time. In order to maintain this constant level of drug in the body, the drug must be released from the dosage form at a rate that will replace the amount of drug being metabolized and excreted from the body. Controlled-release of an active ingredient can be stimulated by various conditions including, but not limited to, pH, ionic strength, osmotic pressure, temperature, enzymes, water, and other physiological conditions or compounds.

[0326] A variety of known controlled- or extended-release dosage forms, formulations, and devices can be adapted for use with the salts and compositions of the disclosure. Examples include, but are not limited to, those described in U.S. Pat. Nos. 3,845,770; 3,916,899; 3,536,809; 3,598,123; 4,008,719; 5,674,533; 5,059,595; 5,591,767; 5,120,548; 5,073,543; 5,639,476; 5,354,556; 5,733,566; and 6,365,185 B1; each of which is incorporated herein by reference. These dosage forms can be used to provide slow or controlled-release of one or more active ingredients using, for example, hydroxypropylmethyl cellulose, other polymer matrices, gels, permeable membranes, osmotic systems (such as OROS® (Alza Corporation, Mountain View, Calif USA)), or a combination thereof to provide the desired release profile in varying proportions.

[0327] In some embodiments of any of the aspects, the composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein described herein is administered as a monotherapy, e.g., another treatment for the serotonin-related disease or disorder is not administered to the subject.

[0328] In some embodiments of any of the aspects, the methods described herein can further comprise administering a second agent and/or treatment to the subject, e.g. as part of a therapy. The combination therapy, where employed, can be tailored to the particular indication. For example, where a serotonin-modulating bacteria or product(s) as described herein is administered to treat anxiety or depression, it can be administered in combination with an anti-anxiety or anti-depression drug or therapy as known in the art or approved for clinical treatment of anxiety or depres-

sion. Other indications can be similarly treated with serotonin modulating bacteria or their products as described herein in combination with agents known in the art or approved for the clinical treatment of those indications. As non-limiting examples, where the disease or serotonin-related disease or disorder is a metabolic disease, such as diabetes, one or more anti-diabetes drugs can be administered in combination with the compositions described herein. Alternatively, where the serotonin-related disease or disorder is cancer, the composition(s) described herein can be administered with one or more anti-cancer agents, e.g., chemotherapy agents or other anti-cancer agents known the art.

[0329] As a further non-limiting example, if a subject is to be treated for pain or inflammation related to or associated with a serotonin-related disease or disorder as described herein, the subject can also be administered a second agent and/or treatment known to be beneficial for subjects suffering from pain or inflammation. Examples of such agents and/or treatments include, but are not limited to non-steroidal anti-inflammatory drugs (NSAIDs—such as aspirin, ibuprofen, or naproxen); corticosteroids, including glucocorticoids (e.g. cortisol, prednisone, prednisolone, methylprednisolone, dexamethasone, betamethasone, triamcinolone, and beclomethasone); methotrexate; sulfasalazine; leflunomide; anti-TNF medications; cyclophosphamide; pro-resolving drugs; mycophenolate; or opiates (e.g. endorphins, enkephalins, and dynorphin), steroids, analgesics, barbiturates, oxycodone, morphine, lidocaine, and the like.

[0330] In certain embodiments, an effective dose of a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein can be administered to a patient once. In certain embodiments, an effective dose of a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein can be administered to a patient repeatedly. For systemic administration, subjects can be administered a therapeutic amount of a composition comprising for example a metabolite or product of a serotonin-modulating bacteria as described herein, such as, e.g. 0.1 mg/kg, 0.5 mg/kg, 1.0 mg/kg, 2.0 mg/kg, 2.5 mg/kg, 5 mg/kg, 10 mg/kg, 15 mg/kg, 20 mg/kg, 25 mg/kg, 30 mg/kg, 40 mg/kg, 50 mg/kg, or more.

[0331] In some embodiments, after an initial treatment regimen, the treatments can be administered on a less frequent basis. For example, after treatment biweekly for three months, treatment can be repeated once per month, for six months or a year or longer. Depending upon the indication, treatment according to the methods described herein can increase levels of a marker (e.g., serotonin or other marker) or symptom of a condition, e.g. a serotonin-related disease or disorder by at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80% or at least 90% or more. Alternatively, treatment according to the methods described herein can reduce levels of a marker (e.g., serotonin or other marker) or symptom of a condition, e.g. a serotonin-related disease or disorder by at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80% or at least 90% or more.

[0332] The dosage of a composition as described herein can be determined by a physician and adjusted, as necessary, to suit observed effects of the treatment. With respect to

duration and frequency of treatment, it is typical for skilled clinicians to monitor subjects in order to determine when the treatment is providing therapeutic benefit, and to determine whether to increase or decrease dosage, increase or decrease administration frequency, discontinue treatment, resume treatment, or make other alterations to the treatment regimen. The dosing schedule can vary from once a week to daily depending on a number of clinical factors, such as the subject's sensitivity to a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein. The desired dose or amount of activation can be administered at one time or divided into subdoses, e.g., 2-4 subdoses and administered over a period of time, e.g., at appropriate intervals through the day or other appropriate schedule. In some embodiments, administration can be chronic, e.g., one or more doses and/or treatments daily over a period of weeks or months. Examples of dosing and/or treatment schedules are administration daily, twice daily, three times daily or four or more times daily over a period of 1 week, 2 weeks, 3 weeks, 4 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, or 6 months, or more. Alternative examples include dosing daily, every other day, twice weekly, every 10 days, every two weeks, once a month, every six weeks, every two months, or less frequently. A composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein can be administered over a period of time, such as over a 5 minute, 10 minute, 15 minute, 20 minute, or 25 minute period.

[0333] The dosage ranges for the administration of a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein, according to the methods described herein depend upon, for example, the form of the composition, its potency, and the extent to which symptoms, markers, or indicators of a condition described herein are desired to be reduced, for example the percentage reduction or increase desired for serotonin. The dosage should not be so large as to cause adverse side effects. Generally, the dosage will vary with the age, condition, and sex of the patient and can be determined by one of skill in the art. The dosage can also be adjusted by the individual physician in the event of any complication.

[0334] The efficacy of a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein, e.g. the treatment of a condition described herein, or to induce a response as described herein (e.g. modulation of serotonin levels) can be determined by the skilled clinician. However, a treatment is considered "effective treatment," as the term is used herein, if one or more of the signs or symptoms of a condition described herein are altered in a beneficial manner, other clinically accepted symptoms are improved, or even ameliorated, or a desired response is induced e.g., by at least 10% following treatment according to the methods described herein. Efficacy can be assessed, for example, by measuring a marker, indicator, symptom, and/or the incidence of a condition treated according to the methods described herein or any other measurable parameter appropriate. Efficacy can also be measured by a failure of an individual to worsen as assessed by hospitalization, or need for medical interventions (i.e., progression of the disease is halted). Methods of measuring these indicators are known to those of skill in the art and/or are described herein. Treatment includes any treatment of a disease in an individual or an animal (some non-limiting

examples include a human or an animal) and includes: (1) inhibiting the disease, e.g., preventing a worsening of symptoms (e.g. pain or inflammation); or (2) relieving the severity of the disease, e.g., causing regression of symptoms. An effective amount for the treatment of a disease means that amount which, when administered to a subject in need thereof, is sufficient to result in effective treatment as that term is defined herein, for that disease. Efficacy of an agent can be determined by assessing physical indicators of a condition or desired response. It is well within the ability of one skilled in the art to monitor efficacy of administration and/or treatment by measuring any one of such parameters, or any combination of parameters. Efficacy can be assessed in animal models of a condition described herein, for example treatment of serotonin-related disease or disorder. When using an experimental animal model, efficacy of treatment is evidenced when a statistically significant change in a marker is observed, e.g. serotonin.

[0335] In vitro and animal model assays are provided herein which allow the assessment of a given dose of a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein. By way of non-limiting example, the effects of a dose of a composition comprising at least one serotonin modulating bacteria and/or product(s) as described herein can be assessed by a RIN14B cell culture model. A non-limiting example of a protocol for such an assay is described in Example 1.

[0336] The efficacy of a given dosage combination can also be assessed in an animal model, e.g. germ-free animal models or alternatively, in a specific pathogen-free (SPF) animal model, or in an animal model of a serotonin-related disease or disorder.

Definitions

[0337] For convenience, the meaning of some terms and phrases used in the specification, examples, and appended claims, are provided below. Unless stated otherwise, or implicit from context, the following terms and phrases include the meanings provided below. The definitions are provided to aid in describing particular embodiments, and are not intended to limit the claimed invention, because the scope of the invention is limited only by the claims. Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. If there is an apparent discrepancy between the usage of a term in the art and its definition provided herein, the definition provided within the specification shall prevail.

[0338] For convenience, certain terms employed herein, in the specification, examples and appended claims are collected here.

[0339] The term 'isolated' encompasses a bacterium or other entity or substance that has been (1) separated from at least some of the components with which it was associated when initially produced (whether in nature, such as human stool, or in an experimental setting, such as a Petri plate consisting of artificial growth medium), and/or (2) produced, prepared, purified, and/or manufactured by the hand of man. Isolated bacteria can be separated from at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, or more of the other components with which they were initially associated. In some embodiments, isolated bacteria are more than about 80%, about 85%, about 90%, about 91%, about 92%, about

93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or more than about 99% pure. As used herein, a substance is “pure” if it is substantially free of other components (such as other bacterial species). Thus, a bacterial culture or preparation grown out of a single colony and lacking other species or strains is a pure culture.

[0340] The terms “purify,” “purifying” and “purified” refer to a bacterium or other material that has been separated from at least some of the components with which it was associated either when initially produced or generated (e.g., whether in nature or in an experimental setting), or during any time after its initial production, as recognized by those skilled in the art of bacterial cultivation. A bacterium or a bacterial population can be considered purified if it is isolated at or after production, such as from a material or environment containing the bacterium or bacterial population, and a purified bacterium or bacterial population can contain other materials up to about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, or above about 90% and still be considered “isolated.”

[0341] In some embodiments, purified bacteria and bacterial populations are more than about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or more than about 99% pure. In the instance of bacterial compositions provided herein, the one or more bacterial types present in the composition can be independently purified from one or more other bacteria produced and/or present in the material or environment containing the bacterial type. Bacterial compositions and the bacterial components thereof are generally purified from residual habitat products. In the instance of bacterial conditioned medium or cell pellets, these are considered pure if derived from an isolated bacteria, or combination of bacteria intentionally mixed (e.g. two serotonin modulating bacteria, which when mixed, result in the production of metabolites or proteins not produced or not produced efficiently in isolation). In the case of purified metabolites or proteins, these are considered to be “isolated” if they are free of about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, or above about 90% of other components of a bacterial conditioned medium or cell pellet, wherein the other components are not the target purified metabolite or protein.

[0342] As used herein, “probiotic” is understood to mean live microorganisms which when administered in adequate amounts confer a health benefit on the host.

[0343] As used herein, “prebiotic” is understood to mean an ingredient that allows or promotes specific changes, in the composition and/or activity of the gastrointestinal microbiota that may or may not confer benefits upon the host.

[0344] As used herein, “medical food” is understood to mean a food which is formulated to be consumed or administered enterally under the supervision of a physician and which is intended for the specific dietary management of a disease or condition for which distinctive nutritional requirements, based on recognized scientific principles, are established by medical evaluation.

[0345] As used herein, “supplement” (also referred to as a dietary supplement) is understood to mean a product taken orally that comprises one or more ingredients (e.g., vitamins, minerals, amino acids, an isolated microbe or product thereof as described herein) that are intended to supplement

one's diet and are not considered food. As non-limiting examples, a supplement can be in the form of a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powder, or a granule.

[0346] As used herein “initial amount” is understood to mean the amount of a substance, e.g., serotonin, in an aliquot or sample, prior to administration of a therapeutic composition as described herein. Initial amount can be measured in terms of concentration. For instance, an initial amount can be measured in terms of micrograms of substance per milliliter of sample, e.g., micrograms of serotonin per milliliter of blood or serum g serotonin/mL blood or serum). The initial amount of serotonin can also be measured, for instance, as the amount of serotonin in regions of the brain, such as the prefrontal cortex prior to administration of a described composition. The amount of serotonin can be represented in terms of millimoles of serotonin per kg tissue (mmol serotonin per kg of brain tissue). The initial amount can also be measured, for instance, as the amount of serotonin in a subject's stool sample prior to administration of a described composition to the subject. The amount of serotonin can be represented in terms of micrograms of serotonin per gram of stool (ug serotonin/g stool). The initial amount can also be the level of expression of microbiota-derived serotonin modulating enzymes in the stool (log change of reads), as measured by qPCR or other appropriate method. The initial amount can also be the level(s) of microbiota-derived serotonin-modulating metabolite(s) (ug serotonin-metabolites/g stool) and/or protein(s) (ug serotonin-modulating protein/g stool). Unless otherwise defined herein, stool is weighed when wet or dry, i.e., without active drying, and within one hour of production of the stool. For instance, the stool can be weighed within 45 minutes, 30 minutes, 5 minutes, 10 minutes, or within 5 minutes of production of the stool.

[0347] As used herein, a “serotonergic response” means the response of a given organ (e.g., the subjects' cells, the brain, or vagus nerve) to differences in the concentrations of serotonin, serotonin-modulating bacteria (or their constituents—e.g. conditioned medium, cell pellets, purified metabolites, or purified proteins), or prebiotics to which it is exposed. A serotonergic response can include a change in concentrations of serotonin as well as expression levels and/or activity of different serotonin related genes/proteins, such as, but not limited to, tryptophan hydroxylase (Tph), Tph1 and Tph2, SERT, 5-HT_{1A}, 5-HT_{1B}, 5-HT_{1D}, 5-HT_{1E}, 5-HT_{1F}, 5-HT_{2A}, 5-HT_{2B}, 5-HT_{2C}, 5-HT₃, 5-HT₄, 5-HT_{5A}, 5-HT_{5B}, 5-HT₆, 5-HT₇

[0348] “Serotonin-modulating bacteria” is understood to mean bacteria that, when introduced to cell culture models or a host, can alter serotonin signaling and/or biosynthesis in a measurable way (e.g. LC/MS, ELISA, or other appropriate analytical assays) and by a statistically significant amount. In some embodiments, serotonin-modulating bacteria produce specific metabolites or proteins that interact with host cells to increase or reduce serotonin biosynthesis or signaling.

[0349] In some embodiments, “serotonin-modulating bacteria” produce these serotonin-modulating metabolites or proteins at physiological conditions of the human gut. In some embodiments, “serotonin-modulating bacteria” are naturally occurring. In some embodiments “serotonin-modulating bacteria” are engineered to produce metabolites

or proteins, or combinations thereof, that interact with host cells to increase or reduce serotonin biosynthesis or signaling.

[0350] In some embodiments a “serotonin-modulating bacteria” is understood to mean a bacteria belonging to the genus *Acidaminococcus*, *Agathobacter*, *Adlercreutzia*, *Akkermansia*, *Alistipes*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Bilophila*, *Bittarella*, *Blautia*, *Blautia*, *Butyricimonas*, *Clostridium*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dialister*, *Dorea*, *Dysosmobaacter*, *Eisenbergiella*, *Enterococcus*, *Enterorhabdus*, *Erysipelatoclostridium*, *Escherichia*, *Eubacterium*, *Faecalitalea*, *Flavonifractor*, *Flintibacter*, *Gemmiger*, *Gordonibacter*, *Hungatella*, *Intestinimonas*, *Lachnoclostridium*, *Lactobacillus*, *Lawsonibacter*, *Longibaculum*, *Mediterraneibacter*, *Mycolicibacterium*, *Oscillibacter*, *Parabacteroides*, *Parasutterella*, *Peptostreptococcus*, *Prevotella*, *Romboutsia*, *Ruminococcus*, *Sellimonas*, *Slackia*, *Streptococcus*, *Sutterella*, *Turicibacter*, or *Veillonella* that modulates serotonin in a host

[0351] In some embodiments, a “serotonin-modulating bacteria” is understood to mean a bacteria belonging to the species *Acidaminococcus intestini*, *Agathobacter rectalis*, *Akkermansia muciniphila*, *Adlercreutzia equolifaciens*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellullosilyticus* HB-227, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris* HB-33, *Bacteroides thetaiotomicron* HB-34, *Bacteroides uniformis* HB-13, *Bacteroides vulgatus* HB-10, *Bacteroides xylanisolvans* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium breve* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium longum* HB-234, *Bifidobacterium longum* HB-71, *Bilophila wadsworthia* HB-693, *Bittarella massiliensis* HB-477, *Blautia coccoides* HB-23, *Blautia obeum* HB-14, *Blautia wexlerae* HB-16, *Butyricimonas paravirosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium butyricum* HB-88, *Clostridium clostradioforme* HB-642, *Clostridium hathewayi* HB-152, *Clostridium innoculum* HB-82, *Clostridium lavalense* HB-452c, *Clostridium paraputrificum* HB-27, *Clostridium saudience* HB-142, *Clostridium scindens* HB-444, *Clostridium* sp. HB-358, *Clostridium sphenoides* HB-470, *Clostridium sporogenes* JCM 7836, *Clostridium sporogenes* McClung 2004, *Clostridium symbiosum* HB-67, *Clostridium tyrobutyricum* HB-469, *Clostridium hylemonae* HB-73, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus comes* HB-80, *Coprococcus comes* ATCC 27758, *Coprococcus eutactus* HB-155, *Coprococcus eutactus* ATCC 27759, *Dialister invisus* HB-387, *Dorea longicatena* HB-17, *Dysosmobaacter welbionis* HB-45, *Eisenbergiella tayi* HB-437, *Eisenbergiella tayi* HB-612, *Enterococcus durans* HB-48, *Enterococcus faecium* HB-640, *Enterococcus faecium* HB-85, *Enterorhabdus caecimuris* B7, *Enterorhabdus muris* WCA-131-CoC-2, *Erysipelatoclostridium ramosum* HB-24, *Escherichia coli* HB-490, *Eubacterium callanderi* HB-59, *Eubacterium eligens* HB-252, *Eubacterium rectale* HB-22, *Faecalitalea cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter butyricus* HB-344, *Gemmiger formicilis* HB-325, *Gemmiger* sp. HB-567, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Intestinimonas massiliensis* HB-651, *Lachnoclostridium* sp. HB-698, *Lactobacillus brevis* HB-87, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum muris* HB-79, *Longibaculum* sp. HB-681, *Mediterraneibacter faecis* HB-364, *Mycolicibacterium smegmatis* ATCC 19420, *Oscillibacter* sp. HB-28, *Parabacteroides distasonis* HB-20, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella excrementihominis* HB-330, *Peptostreptococcus russelii* RT-10B, *Prevotella copri* HB-373, *Prevotella* sp. HB-649, *Prevotella* sp. HB-333, *Romboutsia lituseburensis* HB-102, *Ruminococcus bicirculans* HB-105, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Ruminococcus* sp. HB-626, *Sellimonas intestinalis*

wadsworthensis, *Turicibacter sanguinis*, or *Veillonella atypica* that modulates serotonin in a host.

[0352] In some embodiments, a serotonin-modulating bacteria is understood to mean the strains *Acidaminococcus intestini* HB-95, *Agathobacter rectalis* HB-257, *Akkermansia muciniphila* BA-A-835, *Adlercreutzia equolifaciens* FJC-B9, *Alistipes onderdonkii* HB-311, *Alistipes putredinis* HB-324, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellullosilyticus* HB-227, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris* HB-33, *Bacteroides thetaiotomicron* HB-34, *Bacteroides uniformis* HB-13, *Bacteroides vulgatus* HB-10, *Bacteroides xylanisolvans* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium breve* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium longum* HB-234, *Bifidobacterium longum* HB-71, *Bilophila wadsworthia* HB-693, *Bittarella massiliensis* HB-477, *Blautia coccoides* HB-23, *Blautia obeum* HB-14, *Blautia wexlerae* HB-16, *Butyricimonas paravirosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium butyricum* HB-88, *Clostridium clostradioforme* HB-642, *Clostridium hathewayi* HB-152, *Clostridium innoculum* HB-82, *Clostridium lavalense* HB-452c, *Clostridium paraputrificum* HB-27, *Clostridium saudience* HB-142, *Clostridium scindens* HB-444, *Clostridium* sp. HB-358, *Clostridium sphenoides* HB-470, *Clostridium sporogenes* JCM 7836, *Clostridium sporogenes* McClung 2004, *Clostridium symbiosum* HB-67, *Clostridium tyrobutyricum* HB-469, *Clostridium hylemonae* HB-73, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus comes* HB-80, *Coprococcus comes* ATCC 27758, *Coprococcus eutactus* HB-155, *Coprococcus eutactus* ATCC 27759, *Dialister invisus* HB-387, *Dorea longicatena* HB-17, *Dysosmobaacter welbionis* HB-45, *Eisenbergiella tayi* HB-437, *Eisenbergiella tayi* HB-612, *Enterococcus durans* HB-48, *Enterococcus faecium* HB-640, *Enterococcus faecium* HB-85, *Enterorhabdus caecimuris* B7, *Enterorhabdus muris* WCA-131-CoC-2, *Erysipelatoclostridium ramosum* HB-24, *Escherichia coli* HB-490, *Eubacterium callanderi* HB-59, *Eubacterium eligens* HB-252, *Eubacterium rectale* HB-22, *Faecalitalea cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter butyricus* HB-344, *Gemmiger formicilis* HB-325, *Gemmiger* sp. HB-567, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Intestinimonas massiliensis* HB-651, *Lachnoclostridium* sp. HB-698, *Lactobacillus brevis* HB-87, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum muris* HB-79, *Longibaculum* sp. HB-681, *Mediterraneibacter faecis* HB-364, *Mycolicibacterium smegmatis* ATCC 19420, *Oscillibacter* sp. HB-28, *Parabacteroides distasonis* HB-20, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella excrementihominis* HB-330, *Peptostreptococcus russelii* RT-10B, *Prevotella copri* HB-373, *Prevotella* sp. HB-649, *Prevotella* sp. HB-333, *Romboutsia lituseburensis* HB-102, *Ruminococcus bicirculans* HB-105, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Ruminococcus* sp. HB-626, *Sellimonas intestinalis*

HB-443, *Slackia isoflavoniconvertens* HB-326, *Streptococcus gordonii* HB-62, *Streptococcus gordonii* HB-98, *Suttermella wadsworthensis* HB-259, *Turicibacter sanguinis* HB-147, or *Veillonella atypica* HB-251.

[0353] In some embodiments, a serotonin-modulating bacteria is understood to mean a bacteria comprising a 16S rDNA sequence at least about 95% identical to a 16S rDNA sequence selected from one of SEQ ID NOS: 1-114. As a non-limiting example, a serotonin-modulating bacteria comprises a 16S rDNA sequence with at least 95% identity, at least 96% identity, at least 97% identity, at least 98% identity, at least 99% identity, or 100% identity to a 16S rDNA sequence described herein (e.g., SEQ ID NOS: 1-114). [0354] “Physiologically relevant condition” of the human intestinal tract is understood to mean conditions found in the human gastrointestinal tract or relevant portion thereof (e.g., small intestine, colon, etc.). For example, a pH range of about 4.5-7.5. It can also mean conditions such as levels of nutrients or other bacteria and/or their metabolites/proteins as found in the human gut.

[0355] The term “gut” is understood to refer to the human gastrointestinal tract, also known as the alimentary canal. The gut includes the mouth, pharynx, esophagus, stomach, small intestine (duodenum, jejunum, ileum), large intestines (cecum and colon) and rectum.

[0356] As used herein, “bacterium” is understood as a single bacterial cell of a given species.

[0357] The term “treating” with regard to a subject, refers to improving at least one symptom of the subject’s disorder. Treating includes curing, improving, or at least partially ameliorating the disorder, and can, but need not necessarily encompass curing the disorder.

[0358] The terms “decrease”, “reduced”, “reduction”, or “inhibit” are all used herein to mean a decrease by a statistically significant amount. In some embodiments, “reduce,” “reduction” or “decrease” or “inhibit” typically means a decrease by at least 10% as compared to a reference level (e.g. the absence of a given treatment or agent) and can include, for example, a decrease by at least about 10%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or more. As used herein, “reduction” or “inhibition” does not encompass a complete inhibition or reduction as compared to a reference level. “Complete inhibition” is a 100% inhibition as compared to a reference level. A decrease can be preferably down to a level accepted as within the range of normal for an individual without a given disorder.

[0359] The terms “increased”, “increase”, “enhance”, or “activate” are all used herein to mean an increase by a statistically significant amount. In some embodiments, the terms “increased”, “increase”, “enhance”, or “activate” can mean an increase of at least 10% as compared to a reference level, for example an increase of at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% or up to and including a 100% increase or any increase between 10-100% as compared to a reference level, or at least about a 2-fold, or at least about a 3-fold, or at least about a 4-fold, or at least about a 5-fold or at least about a 10-fold increase, or any increase between

2-fold and 10-fold or greater as compared to a reference level. In the context of a marker or symptom, a “increase” is a statistically significant increase in such level.

[0360] The term “alter” or “modulate” as used herein in reference to a value or parameter means an increase or decrease in the parameter as those terms are defined herein.

[0361] As used herein, a “subject” means a human or animal. Usually the animal is a vertebrate such as a primate, rodent, domestic animal or game animal. Primates include chimpanzees, cynomolgous monkeys, spider monkeys, and macaques, e.g., Rhesus. Rodents include mice, rats, woodchucks, ferrets, rabbits and hamsters. Domestic and game animals include cows, horses, pigs, deer, bison, buffalo, feline species, e.g., domestic cat, canine species, e.g., dog, fox, wolf, avian species, e.g., chicken, emu, ostrich, and fish, e.g., trout, catfish and salmon. In some embodiments, the subject is a mammal, e.g., a primate, e.g., a human. The terms, “individual,” “patient”, “host,” and “subject” are used interchangeably herein.

[0362] Preferably, the subject is a mammal. The mammal can be a human, non-human primate, mouse, rat, dog, cat, horse, or cow, but is not limited to these examples. Mammals other than humans can be advantageously used as subjects that represent animal models of a serotonin-related disease or disorder. A subject can be male or female.

[0363] A subject can be one who has been previously diagnosed with or identified as suffering from or having a condition in need of treatment (e.g. a serotonin-related disease or disorder) or one or more complications related to such a condition, and optionally, has already undergone treatment for a serotonin-related disease or disorder or the one or more complications related to a serotonin-related disease or disorder. Alternatively, a subject can also be one who has not been previously diagnosed as having a serotonin-related disease or disorder or one or more complications related to a serotonin-related disease or disorder. For example, a subject can be one who exhibits one or more risk factors for a serotonin-related disease or disorder or one or more complications related to a serotonin-related disease or disorder or a subject who does not exhibit risk factors.

[0364] A “subject in need” of treatment for a particular condition can be a subject having that condition, diagnosed as having that condition, or at risk of developing that condition.

[0365] As used herein, the terms “protein” and “polypeptide” are used interchangeably herein to designate a series of amino acid residues, connected to each other by peptide bonds between the alpha-amino and carboxy groups of adjacent residues. The terms “protein”, and “polypeptide” refer to a polymer of amino acids, including modified amino acids (e.g., phosphorylated, glycated, glycosylated, etc.) and amino acid analogs, regardless of its size or function. “Protein” and “polypeptide” are often used in reference to relatively large polypeptides, whereas the term “peptide” is often used in reference to small polypeptides, but usage of these terms in the art overlaps. The terms “protein” and “polypeptide” are used interchangeably herein when referring to a gene product and fragments thereof. Thus, exemplary polypeptides or proteins include gene products, naturally occurring proteins, homologs, orthologs, paralogs, fragments and other equivalents, variants, fragments, and analogs of the foregoing.

[0366] In the various embodiments described herein, it is further contemplated that variants (naturally occurring or

otherwise), alleles, homologs, conservatively modified variants, and/or conservative substitution variants of any of the particular polypeptides described are encompassed. As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid and retains the desired activity of the polypeptide. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles consistent with the disclosure.

[0367] A given amino acid can be replaced by a residue having similar physiochemical characteristics, e.g., substituting one aliphatic residue for another (such as Ile, Val, Leu, or Ala for one another), or substitution of one polar residue for another (such as between Lys and Arg; Glu and Asp; or Gln and Asn). Other such conservative substitutions, e.g., substitutions of entire regions having similar hydrophobicity characteristics, are well known. Polypeptides comprising conservative amino acid substitutions can be tested to confirm that a desired activity, e.g. activity and/or specificity of a native or reference polypeptide is retained.

[0368] Amino acids can be grouped according to similarities in the properties of their side chains (in A. L. Lehninger, in *Biochemistry*, second ed., pp. 73-75, Worth Publishers, New York (1975)): (1) non-polar: Ala (A), Val (V), Leu (L), Ile (I), Pro (P), Phe (F), Trp (W), Met (M); (2) uncharged polar: Gly (G), Ser (S), Thr (T), Cys (C), Tyr (Y), Asn (N), Gln (Q); (3) acidic: Asp (D), Glu (E); (4) basic: Lys (K), Arg (R), His (H). Alternatively, naturally occurring residues can be divided into groups based on common side-chain properties: (1) hydrophobic: Norleucine, Met, Ala, Val, Leu, Ile; (2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln; (3) acidic: Asp, Glu; (4) basic: His, Lys, Arg; (5) residues that influence chain orientation: Gly, Pro; (6) aromatic: Trp, Tyr, Phe. Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Particular conservative substitutions include, for example; Ala into Gly or into Ser; Arg into Lys; Asn into Gln or into His; Asp into Glu; Cys into Ser; Gln into Asn; Glu into Asp; Gly into Ala or into Pro; His into Asn or into Gln; Ile into Leu or into Val; Leu into Ile or into Val; Lys into Arg, into Gln or into Glu; Met into Leu, into Tyr or into Ile; Phe into Met, into Leu or into Tyr; Ser into Thr; Thr into Ser; Trp into Tyr; Tyr into Trp; and/or Phe into Val, into Ile or into Leu.

[0369] In some embodiments, the polypeptide described herein (or a nucleic acid encoding such a polypeptide) can be a functional fragment of one of the amino acid sequences described herein. As used herein, a "functional fragment" is a fragment or segment of a polypeptide which retains at least 50% of the wild-type reference polypeptide's activity. A functional fragment can comprise conservative substitutions of the sequences disclosed herein.

[0370] In some embodiments, the polypeptide described herein can be a variant of a sequence described herein. In some embodiments, the variant is a conservatively modified variant. Conservative substitution variants can be obtained by mutations of native nucleotide sequences, for example. A "variant," as referred to herein, is a polypeptide substantially homologous to a native or reference polypeptide, but which has an amino acid sequence different from that of the native

or reference polypeptide because of one or a plurality of deletions, insertions or substitutions. Variant polypeptide-encoding DNA sequences encompass sequences that comprise one or more additions, deletions, or substitutions of nucleotides when compared to a native or reference DNA sequence, but that encode a variant protein or fragment thereof that retains activity. A wide variety of PCR-based site-specific mutagenesis approaches are known in the art and can be applied by the ordinarily skilled artisan to generate and test artificial variants.

[0371] Alterations of the native amino acid sequence can be accomplished by any of a number of techniques known to one of skill in the art. Mutations can be introduced, for example, at particular loci by synthesizing oligonucleotides containing a mutant sequence, flanked by restriction sites enabling ligation to fragments of the native sequence. Following ligation, the resulting reconstructed sequence encodes an analog having the desired amino acid insertion, substitution, or deletion. Alternatively, oligonucleotide-directed site-specific mutagenesis procedures can be employed to provide an altered nucleotide sequence having particular codons altered according to the substitution, deletion, or insertion required. Techniques for making such alterations are very well established and include, for example, those disclosed by Walder et al. (*Gene* 42:133, 1986); Bauer et al. (*Gene* 37:73, 1985); Craik (*BioTechniques*, January 1985, 12-19); Smith et al. (*Genetic Engineering: Principles and Methods*, Plenum Press, 1981); and U.S. Pat. Nos. 4,518,584 and 4,737,462, which are herein incorporated by reference in their entirities. Any cysteine residue not involved in maintaining the proper conformation of the polypeptide also can be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) can be added to the polypeptide to improve its stability or facilitate oligomerization.

[0372] Variant polypeptide-encoding DNA sequences encompass sequences that comprise one or more additions, deletions, or substitutions of nucleotides when compared to a native or reference DNA sequence, but that encode a variant protein or fragment thereof that retains activity. A wide variety of PCR-based site-specific mutagenesis approaches are known in the art and can be applied by the ordinarily skilled artisan.

[0373] A variant amino acid or nucleic acid sequence can be at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or more, identical to a native or reference sequence. The degree of homology (percent identity) between a native and a mutant sequence can be determined, for example, by comparing the two sequences using freely available computer programs commonly employed for this purpose on the world wide web (e.g. BLASTp or BLASTn with default settings).

[0374] A variant amino acid sequence can be at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or more, similar to a native or reference sequence. As used herein, "similarity" refers to an identical amino acid or a conservatively substituted amino acid, as described herein. Accordingly, the percentage of "sequence similarity" is the percentage of amino acids which is either identical or

conservatively changed; e.g., “sequence similarity”=(% sequence identity)+(% conservative changes). It should be understood that a sequence that has a specified percent similarity to a reference sequence necessarily encompasses a sequence with the same specified percent identity to that reference sequence. The skilled person will be aware of several different computer programs, using different mathematical algorithms, that are available to determine the identity or similarity between two sequences. For instance, use can be made of a computer program employing the Needleman and Wunsch algorithm (Needleman et al. (1970)); the GAP program in the Accelrys GCG software package (Accelrys Inc., San Diego U.S.A.); the algorithm of E. Meyers and W. Miller (Meyers et al. (1989)) which has been incorporated into the ALIGN program (version 2.0); or more preferably the BLAST (Basic Local Alignment Tool using default parameters); see e.g., U.S. Pat. No. 10,023,890, the content of which is incorporated by reference herein in its entirety.

[0375] In some embodiments, sequencing comprises 16S rRNA gene sequencing, which can also be referred to as “16S ribosomal RNA sequencing”, “16S rDNA sequencing” or “16s rRNA sequencing”. Sequencing of the 16S rRNA gene can be used for genetic studies as it is highly conserved between different species of bacteria, but it is not present in eukaryotic species. In addition to highly conserved regions, the 16S rRNA gene also comprises nine hypervariable regions (V1-V9) that vary by species. 16S rRNA gene sequencing typically comprises using a plurality of universal primers that bind to conserved regions of the 16S rRNA gene, PCR amplifying the bacterial 16S rRNA gene regions (including hypervariable regions), and sequencing the amplified 16S rRNA genes with a next-generation sequencing technology as described herein (see also e.g., U.S. Pat. Nos. 5,654,418; 6,344,316; and 8,889,358; and US Patent Application Numbers US 2013/0157265 and US 2018/0195111, which are incorporated by reference in their entireties).

[0376] As used herein, the term “nucleic acid” or “nucleic acid sequence” refers to any molecule, preferably a polymeric molecule, incorporating units of ribonucleic acid, deoxyribonucleic acid or an analog thereof. The nucleic acid can be either single-stranded or double-stranded. A single-stranded nucleic acid can be one nucleic acid strand of a denatured double-stranded DNA. Alternatively, it can be a single-stranded nucleic acid not derived from any double-stranded DNA. In one aspect, the nucleic acid can be DNA. In another aspect, the nucleic acid can be RNA. Suitable DNA can include, e.g., genomic DNA or cDNA or bacterial DNA. Suitable RNA can include, e.g., mRNA or bacterial RNA.

[0377] The term “expression” refers to the cellular processes involved in producing RNA and proteins and as appropriate, secreting proteins, including where applicable, but not limited to, for example, transcription, transcript processing, translation and protein folding, modification and processing. Expression can refer to the transcription and stable accumulation of sense (mRNA) or antisense RNA derived from a nucleic acid fragment or fragments of the invention and/or to the translation of mRNA into a polypeptide.

[0378] In some embodiments, the expression of a biomarker(s), target(s), or gene/polypeptide described herein is/are tissue-specific. In some embodiments, the expression

of a biomarker(s), target(s), or gene/polypeptide described herein is/are global. In some embodiments, the expression of a biomarker(s), target(s), or gene/polypeptide described herein is systemic.

[0379] “Expression products” include RNA transcribed from a gene, and polypeptides obtained by translation of mRNA transcribed from a gene. The term “gene” means the nucleic acid sequence which is transcribed (DNA) to RNA in vitro or in vivo when operably linked to appropriate regulatory sequences. The gene may or may not include regions preceding and following the coding region, e.g. 5' untranslated (5'UTR) or “leader” sequences and 3' UTR or “trailer” sequences, as well as intervening sequences (introns) between individual coding segments (exons).

[0380] “Marker” in the context of the present disclosure refers to an expression product, e.g., nucleic acid, polypeptide, or metabolite which is differentially present or differentially abundant in a sample taken from subjects having a serotonin-related disease or disorder, as compared to a comparable sample taken from control subjects (e.g., a healthy subject). The term “biomarker” is used interchangeably with the term “marker.”

[0381] In some embodiments, the methods described herein relate to measuring, detecting, or determining the level of at least one marker. As used herein, the term “detecting” or “measuring” refers to observing a signal from, e.g. a probe, label, or target molecule to indicate the presence of an analyte in a sample. Any method known in the art for detecting a particular label moiety can be used for detection. Exemplary detection methods include, but are not limited to, spectroscopic, fluorescent, photochemical, biochemical, immunochemical, electrical, optical or chemical methods. In some embodiments of any of the aspects, measuring can be a quantitative observation.

[0382] As used herein, a “reference” level refers to a level of, e.g., a marker as measured in or established for a sample representative of a known status. For example, a marker from a sample from an individual known not to have, or alternatively known to have, a given disease or disorder can be a reference. In one embodiment, a reference is the level in an individual without a given condition. In another embodiment, a reference is the level in an individual with a given condition.

[0383] In some embodiments of any of the aspects, a polypeptide, nucleic acid, or cell (e.g., a bacterial cell or a bacteria) as described herein can be engineered. As used herein, “engineered” refers to the aspect of having been manipulated by the hand of man. For example, a polypeptide is considered to be “engineered” when at least one aspect of the polypeptide, e.g., its sequence, has been manipulated by the hand of man to differ from the aspect as it exists in nature. As is common practice and is understood by those in the art, progeny of an engineered cell are typically still referred to as “engineered” even though the actual manipulation was performed on a prior entity.

[0384] As used herein, “contacting” refers to any suitable means for delivering, or exposing, an agent to at least one cell. Exemplary delivery methods include, but are not limited to, direct delivery to cell culture medium, perfusion, injection, or other delivery method well known to one skilled in the art. In some embodiments, contacting comprises physical human activity, e.g., an injection; an act of dispensing, mixing, and/or decanting; and/or manipulation of a delivery device or machine.

[0385] The term “statistically significant” or “significantly” refers to statistical significance and generally means a two standard deviation (2SD) or greater difference.

[0386] Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term “about.” The term “about” when used in connection with percentages can mean $\pm 1\%$.

[0387] As used herein, the term “comprising” means that other elements can also be present in addition to the defined elements presented. The use of “comprising” indicates inclusion rather than limitation.

[0388] The term “consisting of” refers to compositions, methods, and respective components thereof as described herein, which are exclusive of any element not recited in that description of the embodiment.

[0389] As used herein the term “consisting essentially of” refers to those elements required for a given embodiment. The term permits the presence of additional elements that do not materially affect the basic and novel or functional characteristic(s) of that embodiment of the invention.

[0390] The singular terms “a,” “an,” and “the” include plural referents unless context clearly indicates otherwise. Similarly, the word “or” is intended to include “and” unless the context clearly indicates otherwise. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of this disclosure, suitable methods and materials are described below. The abbreviation, “e.g.” is derived from the Latin exempli gratia, and is used herein to indicate a non-limiting example. Thus, the abbreviation “e.g.” is synonymous with the term “for example.”

[0391] Groupings of alternative elements or embodiments of the invention disclosed herein are not to be construed as limitations. Each group member can be referred to and claimed individually or in any combination with other members of the group or other elements found herein. One or more members of a group can be included in, or deleted from, a group for reasons of convenience and/or patentability. When any such inclusion or deletion occurs, the specification is herein deemed to contain the group as modified thus fulfilling the written description of all Markush groups used in the appended claims.

[0392] Unless otherwise defined herein, scientific and technical terms used in connection with the present application shall have the meanings that are commonly understood by those of ordinary skill in the art to which this disclosure belongs. It should be understood that this invention is not limited to the particular methodology, protocols, and reagents, etc., described herein and as such can vary. The terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention, which is defined solely by the claims. Definitions of common terms in immunology and molecular biology can be found in The Merck Manual of Diagnosis and Therapy, 20th Edition, published by Merck Sharp & Dohme Corp., 2018 (ISBN 0911910190, 978-0911910421); Robert S. Porter et al. (eds.), The Encyclopedia of Molecular Cell Biology and Molecular Medicine, published by Blackwell Science Ltd., 1999-2012 (ISBN 9783527600908); and Robert A. Meyers (ed.), Molecular Biology and Biotechnology: a Comprehensive Desk Reference, published by VCH Publishers, Inc., 1995 (ISBN

1-56081-569-8); Immunology by Werner Luttmann, published by Elsevier, 2006; Janeway’s Immunobiology, Kenneth Murphy, Allan Mowat, Casey Weaver (eds.), W. W. Norton & Company, 2016 (ISBN 0815345054, 978-0815345053); Lewin’s Genes XI, published by Jones & Bartlett Publishers, 2014 (ISBN-1449659055); Michael Richard Green and Joseph Sambrook, Molecular Cloning: A Laboratory Manual, 4th ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., USA (2012) (ISBN 1936113414); Davis et al., Basic Methods in Molecular Biology, Elsevier Science Publishing, Inc., New York, USA (2012) (ISBN 044460149X); Laboratory Methods in Immunology: DNA, Jon Lorsch (ed.) Elsevier, 2013 (ISBN 0124199542); Current Protocols in Molecular Biology (CPMB), Frederick M. Ausubel (ed.), John Wiley and Sons, 2014 (ISBN 047150338X, 9780471503385), Current Protocols in Protein Science (CPPS), John E. Coligan (ed.), John Wiley and Sons, Inc., 2005; and Current Protocols in Immunology (CPI) (John E. Coligan, ADA M Kruisbeek, David H Margulies, Ethan M Shevach, Warren Strobe, (eds.) John Wiley and Sons, Inc., 2003 (ISBN 0471142735, 9780471142737), the contents of which are all incorporated by reference herein in their entireties.

[0393] Other terms are defined herein within the description of the various aspects of the invention.

[0394] All patents and other publications; including literature references, issued patents, published patent applications, and co-pending patent applications; cited throughout this application are expressly incorporated herein by reference for the purpose of describing and disclosing, for example, the methodologies described in such publications that might be used in connection with the technology described herein. These publications are provided solely for their disclosure prior to the filing date of the present application. Nothing in this regard should be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior invention or for any other reason. All statements as to the date or representation as to the contents of these documents is based on the information available to the applicants and does not constitute any admission as to the correctness of the dates or contents of these documents.

[0395] The description of embodiments of the disclosure is not intended to be exhaustive or to limit the disclosure to the precise form disclosed. While specific embodiments of, and examples for, the disclosure are described herein for illustrative purposes, various equivalent modifications are possible within the scope of the disclosure, as those skilled in the relevant art will recognize. For example, while method steps or functions are presented in a given order, alternative embodiments can perform functions in a different order, or functions can be performed substantially concurrently. The teachings of the disclosure provided herein can be applied to other procedures or methods as appropriate. The various embodiments described herein can be combined to provide further embodiments. Aspects of the disclosure can be modified, if necessary, to employ the compositions, functions and concepts of the above references and application to provide yet further embodiments of the disclosure. These and other changes can be made to the disclosure in light of the detailed description. All such modifications are intended to be included within the scope of the appended claims.

[0396] Specific elements of any of the foregoing embodiments can be combined or substituted for elements in other embodiments. Furthermore, while advantages associated with certain embodiments of the disclosure have been described in the context of these embodiments, other embodiments can also exhibit such advantages, and not all embodiments need necessarily exhibit such advantages to fall within the scope of the disclosure.

[0397] The technology described herein is further illustrated by the following examples which in no way should be construed as being further limiting.

[0398] Some embodiments of the technology described herein can be defined according to any of the following numbered paragraphs:

[0399] 1. A therapeutic composition for increasing serotonin level in a mammalian subject in need thereof, the composition comprising an amount of a live isolated serotonin-increasing bacterial species, dead isolated serotonin-increasing bacterial species, conditioned medium from an isolated, cultured serotonin-increasing bacterial species, cell pellet of an isolated serotonin-increasing bacterial species, a purified metabolite produced by an isolated serotonin-increasing bacterial species, a purified protein produced by an isolated serotonin-increasing bacterial species, or a combination thereof sufficient to increase serotonin level in the subject, and an excipient or carrier suitable for delivery to the gut.

[0400] 2. The therapeutic composition of paragraph 1, wherein the isolated serotonin-increasing bacterial species increases serotonin in at least one of the following ways: production of serotonin; production of secreted metabolites or secreted proteins that induce serotonin production; production of ligands that induce serotonin production; or production of an agonist of a serotonin receptor or the trace amine-associated receptor (TAAR).

[0401] 3. The therapeutic composition of paragraph 1 or 2, wherein the isolated serotonin-increasing bacterial species is a serotonin-producing bacterial species.

[0402] 4. The therapeutic composition of any one of paragraphs 1-3, wherein the serotonin-producing bacterial species comprises one or more species selected from *Enterococcus durans*, *Clostridium lavalense*, *Clostridium asparagiforme*, *Ruminococcus gnavus*.

[0403] 5. The therapeutic composition of any one of paragraphs 1-4, wherein the serotonin-producing bacterial species comprises one or more species selected from *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516.

[0404] 6. The therapeutic composition of any one of paragraphs 1-5, wherein the serotonin-producing bacterial species comprises a 16S sequence at least 95% identical to a 16S sequence selected from SEQ ID NOS: 1-4.

[0405] 7. The therapeutic composition of any one of paragraphs 1-6, wherein the serotonin-producing bacterial species produces serotonin under conditions found in the mammalian gut.

[0406] 8. The therapeutic composition of any one of paragraphs 1-7, wherein the mammalian subject is a human subject.

[0407] 9. The therapeutic composition of paragraph 1, wherein the isolated serotonin-producing bacterial species encodes and expresses a decarboxylase enzyme that catalyzes the production of tryptamine from tryptophan.

[0408] 10. The therapeutic composition of paragraph 9, wherein the decarboxylase enzyme is a tryptophan decarboxylase.

[0409] 11. The therapeutic composition of paragraph 9 or 10, wherein the decarboxylase enzyme belongs to the EC number 4.1.1.105.

[0410] 12. The therapeutic composition of any one of paragraphs 9-11, wherein the decarboxylase enzyme is at least 50% identical to an enzyme comprising an amino acid sequence selected from SEQ ID Nos: 115-119.

[0411] 13. The therapeutic composition of paragraph 1, wherein the isolated serotonin-producing bacterial species encodes and expresses an enzyme that hydroxylates tryptamine to produce serotonin.

[0412] 14. The therapeutic composition of paragraph 13, wherein the enzyme that hydroxylates tryptamine is a tryptamine 5-hydroxylase.

[0413] 15. The therapeutic composition of paragraph 13 or 14, wherein the enzyme that hydroxylates tryptamine is at least 50% identical to the enzyme of SEQ ID NO: 134.

[0414] 16. The therapeutic composition of any one of paragraphs 13-15, wherein the enzyme that hydroxylates tryptamine is an anaerobic hydroxylase.

[0415] 17. The therapeutic composition of any one of paragraphs 1-16, wherein the isolated serotonin-producing bacterial species encodes and expresses a decarboxylase enzyme that catalyzes the production of tryptamine from tryptophan and an enzyme that hydroxylates tryptamine to produce serotonin.

[0416] 18. The therapeutic composition of any one of paragraphs 1-17, wherein the live isolated serotonin-producing bacterial species, dead isolated serotonin producing bacterial species, conditioned medium from an isolated, cultured serotonin-producing bacterial species or cell pellet of an isolated serotonin-producing bacterial species comprises a first bacterial species that encodes and expresses a decarboxylase enzyme that catalyzes the production of tryptamine from tryptophan and a second bacterial species that encodes and expresses an enzyme that hydroxylates tryptamine to produce serotonin.

[0417] 19. The therapeutic composition of any one of paragraphs 1-18, wherein the decarboxylase is a lysine decarboxylase family enzyme.

[0418] 20. The therapeutic composition of paragraph 1, wherein the live isolated serotonin-producing bacterial species, dead isolated serotonin producing bacterial species, conditioned medium from an isolated, cultured serotonin-producing bacterial species or cell pellet of an isolated serotonin-producing bacterial species comprises one or more bacterial species that encode and express an enzyme that converts tryptophan to 5-hydroxy-L-tryptophan (5-HTP).

[0419] 21. The therapeutic composition of paragraph 20, wherein the enzyme that converts tryptophan to 5-hydroxy-L-tryptophan (5-HTP) has an amino acid

- sequence at least 50% identical to a sequence selected from SEQ ID Nos: 120-126.
- [0420] 22. The therapeutic composition of paragraph 20 or 21, wherein the enzyme that converts tryptophan to 5-hydroxy-L-tryptophan (5-HTP) belongs to the EC number 1.14.16.4.
- [0421] 23. The therapeutic composition of paragraph 1, wherein the live isolated serotonin-producing bacterial species, dead isolated serotonin producing bacterial species, conditioned medium from an isolated, cultured serotonin-producing bacterial species or cell pellet of an isolated serotonin-producing bacterial species comprises a bacterial species that encodes and expresses an enzyme that converts 5-hydroxy-L-tryptophan to serotonin.
- [0422] 24. The therapeutic composition of paragraphs 23, wherein the enzyme that converts 5-hydroxy-L-tryptophan to serotonin is an aromatic L-amino acid decarboxylase.
- [0423] 25. The therapeutic composition of paragraph 23 or 24, wherein the enzyme that catalyzes the conversion of 5-hydroxy-L-tryptophan to serotonin belongs to the EC number 4.1.1.28.
- [0424] 26. The therapeutic composition of any one of paragraphs 23-25, wherein the enzyme that converts 5-hydroxy-L-tryptophan to serotonin is at least 50% identical to a sequence selected from SEQ ID NOS: 127-133.
- [0425] 27. The therapeutic composition of any one of paragraphs 20-22, wherein the isolated serotonin-producing bacterial species further encodes and expresses an enzyme that converts 5-hydroxy-L-tryptophan to serotonin.
- [0426] 28. The therapeutic composition of paragraph 27, wherein the enzyme that converts 5-hydroxy-L-tryptophan to serotonin is an aromatic L-amino acid decarboxylase.
- [0427] 29. The therapeutic composition of either of paragraphs 27 or 28, wherein the enzyme that converts 5-hydroxy-L-tryptophan to serotonin is at least 50% identical to a sequence selected from SEQ ID NOS: 127-133.
- [0428] 30. The therapeutic composition of paragraph 1, wherein the live isolated serotonin-producing bacterial species, dead isolated serotonin producing bacterial species, conditioned medium from an isolated, cultured serotonin-producing bacterial species or cell pellet of an isolated serotonin-producing bacterial species comprises a first bacterial species that encodes and expresses an enzyme that catalyzes the conversion of tryptophan to 5-hydroxy-L-tryptophan and a second bacterial species that encodes and expresses an enzyme that converts 5-hydroxy-L-tryptophan to serotonin.
- [0429] 31. The therapeutic composition of paragraph 30, wherein the enzyme that catalyzes the conversion of tryptophan to 5-hydroxy-L-tryptophan is a tryptophan hydroxylase.
- [0430] 32. The therapeutic composition of paragraph 30 or 31, wherein the enzyme that catalyzes the conversion of tryptophan to 5-hydroxy-L-tryptophan has an amino acid sequence at least 50% identical to a sequence selected from SEQ ID Nos: 120-126, and the enzyme that converts 5-hydroxy-L-tryptophan to serotonin is at least 50% identical to a sequence selected from SEQ ID NOS: 127-133.
- [0431] 33. The therapeutic composition of any one of paragraphs 20-22 or 30-32, wherein the enzyme that catalyzes the conversion of tryptophan to 5-hydroxy-L-tryptophan is a phenylalanine hydroxylase.
- [0432] 34. The therapeutic composition of paragraph 33, wherein the phenylalanine hydroxylase comprises an amino acid sequence comprising one or more of phenylalanine at the position corresponding to W192, isoleucine or leucine at the position corresponding to F197, and cysteine at the position corresponding to E219 of the phenylalanine hydroxylase of *Cupriavidus taiwanensis* (SEQ ID NO: 227).
- [0433] 35. A pharmaceutical composition comprising the therapeutic composition of any one of paragraphs 1-34, and a pharmaceutically acceptable carrier.
- [0434] 36. A method of increasing serotonin level in a mammalian subject in need thereof, the method comprising administering a composition of any one of paragraphs 1-35 to the subject, whereby a serotonin level is increased.
- [0435] 37. The method of paragraph 36, wherein the administering is to the gut of the subject.
- [0436] 38. The method of paragraph 36 or 37, wherein the level of serotonin in the gut is increased.
- [0437] 39. The method of any one of paragraphs 36-38, wherein the level of serotonin in circulation is increased.
- [0438] 40. A method of treating a disease or disorder involving or characterized by low serotonin in a subject in need thereof, the method comprising administering a composition of any one of paragraphs 1-35 to the subject, whereby the disease or disorder is treated.
- [0439] 41. The method of paragraph 40, wherein the administering is to the gut of the subject.
- [0440] 42. The method of paragraph 40 or 41, wherein the level of serotonin in the gut is increased.
- [0441] 43. The method of any one of paragraphs 40-42, wherein the level of serotonin in circulation is increased.
- [0442] 44. The method of any one of paragraphs 40-43, wherein the disease or disorder is selected from the group consisting of constipation, IBS-C, depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, heartburn, dermatological conditions (eczema and itch), GERD, and pain disorders.
- [0443] 45. The method of any one of paragraphs 40-44, wherein the disease or disorder is not a gut disease or disorder.
- [0444] 46. The method of any one of paragraphs 40-45, wherein the disease or disorder is selected from the group consisting of depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, dermatological conditions (eczema and itch), and pain disorders.
- [0445] 47. The therapeutic composition of paragraph 1, wherein the composition comprising an amount of a live isolated serotonin-increasing bacterial species,

dead isolated serotonin increasing bacterial species, conditioned medium from an isolated, cultured serotonin-increasing bacterial species, cell pellet of an isolated serotonin-increasing bacterial species, a purified metabolite produced by an isolated serotonin-increasing bacterial species, a purified protein produced by an isolated serotonin-increasing bacterial species, or a combination thereof sufficient to increase serotonin level in the subject, and an excipient or carrier suitable for delivery to the gut promotes production of serotonin by cells of a subject in which the composition is delivered to their gut.

[0446] 48. The therapeutic composition of paragraph 47, wherein the composition promotes expression of tryptophan hydroxylase 1 in cells of the subject.

[0447] 49. The therapeutic composition of paragraph 47 or 48, wherein the isolated serotonin-increasing bacterial species increases serotonin in at least one of the following ways: production of secreted metabolites or secreted proteins that induce serotonin production; production of ligands that induce serotonin production; or production of an agonist of a serotonin receptor or the trace amine-associated receptor (TAAR).

[0448] 50. The therapeutic composition of any one of paragraphs 47-49, wherein the isolated serotonin-increasing bacterial species increases serotonin through production of secreted metabolites or secreted proteins that induce serotonin production.

[0449] 51. The therapeutic composition of any one of paragraphs 47-50, wherein the isolated serotonin-increasing bacterial species comprises one or more species selected from the group consisting of: *Acidaminooccus intestini*, *Agathobacter rectalis*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis*, *Bacillus cereus*, *Bacteroides caccae*, *Bacteroides cellulosilyticus*, *Bacteroides dorei*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides koreensis*, *Bacteroides ovatus*, *Bacteroides plebeius*, *Bacteroides salyersiae*, *Bacteroides stercoris*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium breve*, *Bifidobacterium faecale*, *Bifidobacterium longum*, *Bilophila wadsworthia*, *Butyrimonas paraviriosa*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium clostridioforme*, *Clostridium hathewayi*, *Clostridium innoculum*, *Clostridium paraputreficum*, *Clostridium saudiense*, *Clostridium scindens*, *Clostridium tyrobutyricum*, *Clostridium hylemonae* HB-73, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dysosmobaeter welbionis*, *Eisenbergiella tayi* HB-437, *Eisenbergiella tayi* HB-612, *Enterococcus faecium* HB-640, *Enterococcus faecium* HB-85, *Erysipelotoclostridium ramosum* HB-24, *Eubacterium eligens* HB-252, *Faecalitalea cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter butyricus* HB-344, *Gemmiger formicilis* HB-325, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Lactobacillus brevis* HB-87, *Mediterraneibacter faecis* HB-364, *Oscillibacter* sp. HB-28, *Parabacteroides distasonis* HB-20, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella exrementihominis* HB-330, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Streptococcus gordonii* HB-62, *Streptococcus gordonii* HB-98, and *Turicibacter sanguinis* HB-147.

[0451] 53. The therapeutic composition of any one of paragraphs 47-52, wherein the isolated serotonin-increasing bacterial species comprises a 16S sequence at least 95% identical to a sequence selected from SEQ ID Nos 1, 2, and 5-69.

[0452] 54. The therapeutic composition of paragraph 47, wherein the isolated serotonin-increasing bacterial species increases serotonin through production of an agonist of a serotonin receptor or the trace amine-associated receptor (TAAR).

[0453] 55. The therapeutic composition of paragraph 54, wherein the isolated serotonin-increasing bacterial species encodes and expresses enzymes sufficient for the production of an agonist of a serotonin receptor or the trace amine-associated receptor (TAAR).

[0454] 56. The therapeutic composition of paragraph 54 or 55, wherein the isolated bacterial species comprises one or more species selected from the group consisting of: *Akkermansia muciniphila*, *Adlercreutzia equolifaciens*, *Clostridium sporogenes*, *Clostridium lavalense*,

[0450] 52. The therapeutic composition of any one of paragraphs 47-51, wherein the isolated serotonin-in-

Clostridium asparagiforme, *Coprococcus eutactus*, *Coprococcus comes*, *Enterococcus durans*, *Enterorhabdus muris*, *Enterorhabdus caecimuris*, *Mycobacterium smegmatis*, *Peptostreptococcus russelii*, and *Ruminococcus gnavus*.

[0455] 57. The therapeutic composition of any one of paragraphs 54-56, wherein the isolated bacterial species comprises one or more species selected from the group consisting of: *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516. In some embodiments, the 5-HT agonist-producing bacteria are greater than 95% similar by 16S sequencing to *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Clostridium sporogenes* JCM 7836, *Akkermansia muciniphila* BAA-835, *Clostridium sporogenes* McClung 2004, *Peptostreptococcus russelii* RT-10B, *Mycobacterium smegmatis* ATCC 19420, *Enterorhabdus muris* WCA-131-CoC-2, *Adlercreutzia equolifaciens* FJC-B9, *Enterorhabdus caecimuris* B7, *Coprococcus eutactus* ATCC 27759, and *Coprococcus comes* ATCC 27758.

[0456] 58. The therapeutic composition of any one of paragraphs 54-57, wherein the isolated bacterial species comprises a 16S sequence at least 95% identical to a sequence selected from SEQ ID Nos 1-4 and 105-114.

[0457] 59. The therapeutic composition of any one of paragraphs 54-58, wherein the agonist of the serotonin receptor or TAAR is selected from the group consisting of N-methyltryptamine, N,N-dimethyltryptamine, N-methylyserotonin, and N,N-dimethylyserotonin.

[0458] 60. The therapeutic composition of either of any one of paragraphs 54-59, wherein the isolated serotonin-increasing bacterial species encodes and expresses one or more enzymes that catalyze the methylation of tryptamine by a mechanism corresponding to that of human indolethylamine N-methyltransferase, or one or more enzymes at least 50% identical to the radical S-adenosyl-L-methionine-dependent, ergothioneine biosynthetic enzyme egtD, or one or more phosphatidylethanolamine N-methyltransferase enzymes (e.g., SEQ ID NOs: 228 or 229).

[0459] 61. The therapeutic composition of paragraph 47, wherein culture supernatant of the isolated bacterial species increases expression of tryptophan hydroxylase 1 (TPH-1) in cells of the host.

[0460] 62. The therapeutic composition of paragraph 61, wherein the isolated bacterial species comprises one or more species selected from the group consisting of *Enterococcus durans*, *Clostridium lavalense*, *Lactobacillus brevis*, *Bifidobacterium faecale*, *Anaerotruncus colihominis*, and *Clostridium ramosum*.

[0461] 63. The therapeutic composition of paragraph 61 or 62, wherein the isolated bacterial species comprises one or more species selected from the group consisting of *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Lactobacillus brevis* HB-87, *Bifidobacterium faecale* HB-159, *Anaerotruncus colihominis* HB-83, and *Clostridium ramosum* HB-24 or a combination thereof.

[0462] 64. The therapeutic composition of any one of paragraphs 61-63, wherein the isolated bacterial species comprises a 16S sequence at least 95% identical to

a sequence selected from the group consisting of SEQ ID Nos: 3, 4, 11, 28, 30 and 39.

[0463] 65. The therapeutic composition of paragraph 50, wherein the isolated bacterial species comprises one or more species selected from the group consisting of *Clostridium scindens*, *Bifidobacterium faecale*, *Enterococcus durans*, *Clostridium lavalense*, *Anaerotruncus colihominis*, and *Erysipelatoclostridium ramosum*.

[0464] 66. The therapeutic composition of paragraph 65, wherein the isolated bacterial species comprises one or more species selected from the group consisting of *Clostridium scindens* HB-444, *Bifidobacterium faecale* HB-159, *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Anaerotruncus colihominis* HB-83, and *Erysipelatoclostridium ramosum* HB-24.

[0465] 67. The therapeutic composition of paragraph 65 or 66, wherein the isolated bacterial species comprises a 16S sequence that is at least 95% identical to one of SEQ ID NOs: 3, 4, 11, 23, 28 and 39.

[0466] 68. The therapeutic composition of paragraph 47, wherein the isolated serotonin-increasing bacterial species increases serotonin through production of ligands that induce serotonin production.

[0467] 69. The therapeutic composition of paragraph 68, wherein a cell pellet from the isolated serotonin increasing bacterial species modulates serotonin when administered to a subject.

[0468] 70. The therapeutic composition of paragraph 68 or 69, wherein the isolated bacterial species comprises one or more species selected from the group consisting of *Anaerotruncus colihominis*, *Bacteroides caccae*, *Bacteroides clarus*, *Bacteroides dorei*, *Bacteroides finegoldii*, *Bacteroides ovatus*, *Bacteroides salyersiae*, *Bacteroides thetaiotaomicron*, *Bacteroides xylanisolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium faecale*, *Bittarella massiliensis*, *Blautia wexlerae*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium hathewayi*, *Clostridium saudicense*, *Clostridium scindens*, *Clostridium tyrobutyricum*, *Dialister invisus*, *Eisenbergiella tayi*, *Enterococcus durans*, *Enterococcus faecium*, *Eubacterium eligens*, *Gemmiger formicilis*, *Gordonibacter pamelaeae*, *Hungatella effluvii*, *Lactobacillus brevis*, *Longibaculum muris*, *Mediterraneibacter faecis*, *Parabacteroides distasonis*, *Parabacteroides merdae*, *Parasutterella exrementihominis*, *Prevotella copri*, *Prevotella* sp., *Prevotella* sp., *Romboutsia lituseburensis*, *Ruminococcus* sp., *Ruminococcus gnavus*, *Sellimonas intestinalis*, and *Sutterella wadsworthensis*.

[0469] 71. The therapeutic composition of any one of paragraphs 68-70, wherein the isolated bacterial species comprises one or more species selected from the group consisting of *Anaerotruncus colihominis* HB-83, *Bacteroides caccae* HB-11, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides ovatus* HB-70, *Bacteroides salyersiae* HB-32, *Bacteroides thetaiotaomicron* HB-34, *Bacteroides xylanisolvens* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium faecale* HB-159, *Bittarella massiliensis* HB-477, *Blautia wexlerae* HB-16, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium hathewayi*

HB-152, *Clostridium saudiense* HB-142, *Clostridium scindens* HB-444, *Clostridium tyrobutyricum* HB-469, *Dialister invisus* HB-387, *Eisenbergiella tayi* HB-612, *Enterococcus durans* HB-48, *Enterococcus faecium* HB-85, *Eubacterium eligens* HB-252, *Gemmiger formicilis* HB-325, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Lactobacillus brevis* HB-87, *Longibaculum muris* HB-79, *Mediterraneibacter faecis* HB-364, *Parabacteroides distasonis* HB-20, *Parabacteroides merdae* HB-63, *Parasutterella excrementihominis* HB-330, *Prevotella copri* HB-373, *Prevotella* sp HB-649, *Prevotella* sp. HB-333, *Romboutsia lituseburensis* HB-102, *Ruminococcus* sp. HB-626, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Sellimonas intestinalis* HB-443, and *Suttermella wadsworthensis* HB-259.

[0470] 72. The therapeutic composition of any one of paragraphs 68-71, wherein the isolated bacterial species comprises a 16S sequence at least 95% identical to a sequence selected from the group consisting of SEQ ID Nos 1-3, 5-30 and 70-82.

[0471] 73. The therapeutic composition of any one of paragraphs 68-72, wherein the cell pellet increases expression of TPH-1 in cells of the subject.

[0472] 74. The therapeutic composition of paragraph 73, wherein the isolated bacterial species comprises one or more species selected from *Clostridium lavalense*, *Lactobacillus brevis*, *Bifidobacterium faecale*, *Anaerotruncus colihominis*, and *Clostridium ramosum*.

[0473] 75. The therapeutic composition of paragraph 73 or 74, wherein the isolated bacterial species comprises one or more species selected from *Clostridium lavalense* HB-452c, *Lactobacillus brevis* HB-87, *Bifidobacterium faecale* HB-159, *Anaerotruncus colihominis* HB-83, and *Clostridium ramosum* HB-24.

[0474] 76. The therapeutic composition of any one of paragraphs 73-75, wherein the isolated bacterial species comprises one or more species that comprise a 16S sequence at least 95% identical to a sequence selected from SEQ ID Nos 4, 11, 28, 30, and 39.

[0475] 77. The therapeutic composition of any one of paragraphs 73-76, wherein the isolated bacterial species comprises one or more species selected from *Clostridium scindens*, *Bifidobacterium faecale*, *Enterococcus durans*, *Clostridium lavalense*, *Anaerotruncus colihominis*, and *Erysipelatoclostridium ramosum*.

[0476] 78. The therapeutic composition of any one of paragraphs 73-77, wherein the isolated bacterial species comprises one or more species selected from *Clostridium scindens* HB-444, *Bifidobacterium faecale* HB-159, *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, *Anaerotruncus colihominis* HB-83, and *Erysipelatoclostridium ramosum* HB-24.

[0477] 79. The therapeutic composition of any one of paragraphs 73-78, wherein the isolated bacterial species comprises one or more species that comprise a 16S sequence at least 95% identical to a sequence selected from SEQ ID Nos 3, 4, 11, 23, 28 and 39.

[0478] 80. The therapeutic composition of any one of paragraphs 1-35 or 47-79, wherein the isolated bacterial species are grown in medium containing one or more nutrients selected from the group consisting of conditioned medium from other bacteria, N-Acetyl-D-Galactosamine, N-Acetyl-D-Glucosamine, N-Acetyl-

β -D-Mannosamine, Adonitol, Amygdalin, D-Arabinol, Arbutin, D-Cellobiose, α -Cyclodextrin, β -Cyclodextrin, Dextrin, Dulcitol, i-Erythritol, D-Fructose, L-Fucose, D-Galactose, D-Galacturonic Acid, Gentiobiose, D-Gluconic Acid, D-Glucosaminic Acid, α -D-Glucose, α -D-Glucose 1-Phosphate, D-Glucose6-Phosphate, Glycerol, D,L- α -Glycerol Phosphate, m-Inositol, α -D-Lactose, Lactulose, Maltose, Maltotriose, D-Mannitol, D-Mannose, D-Melezitose, D-Melibiose, β -Methyl-DGlucose, α -Methyl-DGalactoside, β -Methyl-D-Galactoside, α -Methyl-D-Glucoside, β -Methyl-D-Glucoside, Mucin, Palatinose, D-Raffinose, L-Rhamnose, Salicin, D-Sorbitol, Stachyose, Sucrose, D-Trehalose, Turanose, Acetic Acid, Formic Acid, Fumaric Acid, Glyoxylic Acid, α -Hydroxybutyric Acid, β -Hydroxybutyric Acid, Itaconic Acid, α -Ketobutyric Acid, α -Ketovaleric Acid, D,L-Lactic Acid, L-Lactic Acid, D-Lactic Acid Methyl Ester, D-Malic Acid, L-Malic Acid, Propionic Acid, Pyruvic Acid, Pyruvic Acid Methyl Ester, D-Saccharic Acid, Succinamic Acid, Succinic Acid, Succinic Acid Mono-Methyl Ester, m-Tartaric Acid, Urocanic Acid, Alaninamide, L-Alanine, L-Alanyl-LGlutamine, L-Alanyl-LHistidine, L-Alanyl-LThreonine, L-Asparagine, L-Glutamic Acid, L-Glutamine, Glycyl-LAspartic Acid, Glycyl-LGlutamine, Glycyl-LMethionine, Glycyl-LProline, L-Methionine, L-Phenylalanine, L-Serine, L-Threonine, L-Valine, L-Valine plus L-Aspartic Acid, 2'-Deoxy Adenosine, Inosine, Thymidine, Uridine, Thymidine-5'-Monophosphate, and Uridine-5'-Monophosphate.

[0479] 81. The therapeutic composition of paragraph 47, wherein an isolated serotonin-increasing bacterial species in the composition produces tryptophan.

[0480] 82. The therapeutic composition of paragraph 81, wherein an isolated serotonin-increasing bacterial species in the composition encodes or expresses at least one enzyme involved in tryptophan production.

[0481] 83. The therapeutic composition of paragraph 81 or 82, wherein the enzyme involved in tryptophan production is selected from the group consisting of: Tryptophan synthase; Indole-3-glycerol phosphate synthase; Anthranilate phosphoribosyltransferase; Anthranilate synthase; and N-(5'-phosphoribosyl)anthranilate isomerase; 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase.

[0482] 84. The therapeutic composition of any one of paragraphs 81-83, wherein the enzyme involved in tryptophan production belongs to an EC number selected from the group consisting of: EC 4.2.1.20, EC 4.1.1.48, EC 2.4.2.18, EC 4.1.3.27, EC 5.3.1.24, and EC 5.3.1.36.

[0483] 85. The therapeutic composition of any one of paragraphs 81-84, wherein the enzyme involved in tryptophan production has an amino acid sequence at least 50% identical to a sequence selected from SEQ ID Nos 135-163.

[0484] 86. The therapeutic composition of paragraph 47, wherein an isolated serotonin-increasing bacterial species in the composition produces a metabolite of phenylalanine selected from phenethylamine, tyramine or N-methylated derivatives thereof that activate the TAAR system.

- [0485] 87. The therapeutic composition of paragraph 47, wherein the isolated serotonin-increasing bacterial species in the composition produces one or more indole-3-carboxylic acid derivatives of tryptophan.
- [0486] 88. The therapeutic composition of paragraph 86 or 87, wherein the indole-3-carboxylic acid derivative of tryptophan is one or more of indole-3-propionic acid, indole-3-acrylic acid, indole-3-lactic acid, indole-3-pyruvic acid, or indole-3-acetic acid.
- [0487] 89. The therapeutic composition of paragraph 87 or 88, wherein the isolated bacterial species comprises and expresses genes of the fldAIBC gene cluster.
- [0488] 90. The therapeutic composition of any one of paragraphs 87-89, wherein the isolated bacterial species encodes and expresses acyl-CoA dehydrogenase.
- [0489] 91. The therapeutic composition of any one of paragraphs 87-90, wherein the acyl-CoA dehydrogenase belongs to EC 1.3.99.3; EC 1.3.8.7; EC 1.3.8.8; or EC 1.3.8.9.
- [0490] 92. The therapeutic composition of paragraph 91, wherein the acyl-CoA dehydrogenase has an amino acid sequence at least 50% identical to a sequence selected from SEQ ID Nos 164-171.
- [0491] 93. The therapeutic composition of paragraph 47, wherein the isolated bacterial species encodes and expresses an enzyme with a sequence at least 50% identical to an enzyme having an amino acid sequence of any one of SEQ ID Nos 172-184.
- [0492] 94. The therapeutic composition of paragraph 93, wherein the isolated bacterial species encodes and expresses an enzyme belonging to an EC group selected from: EC 4.1.99.1; EC 2.8.3.17; EC 4.2.1.175; EC 5.6.1.9; and EC 2.1.1.
- [0493] 95. A pharmaceutical composition comprising the therapeutic composition of any one of paragraphs 47-94, and a pharmaceutically acceptable carrier.
- [0494] 96. A method of increasing serotonin level in a mammalian subject in need thereof, the method comprising administering a composition of any one of paragraphs 47-95 to the subject, whereby a serotonin level is increased.
- [0495] 97. The method of paragraph 96, wherein the administering is to the gut of the subject.
- [0496] 98. The method of paragraph 96 or 97, wherein the level of serotonin in the gut is increased.
- [0497] 99. The method of any one of paragraphs 96-98, wherein the level of serotonin in circulation is increased.
- [0498] 100. A method of treating a disease or disorder involving or characterized by low serotonin in a subject in need thereof, the method comprising administering a composition of any one of paragraphs 47-95 to the subject, whereby the disease or disorder is treated.
- [0499] 101. The method of paragraph 100, wherein the administering is to the gut of the subject.
- [0500] 102. The method of paragraph 100 or 101, wherein the level of serotonin in the gut is increased.
- [0501] 103. The method of any one of paragraphs 100-102, wherein the level of serotonin in circulation is increased.
- [0502] 104. The method of any one of paragraphs 100-103, wherein the disease or disorder is selected from the group consisting of constipation, IBS-C, depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, heartburn, dermatological conditions (eczema and itch), GERD, and pain disorders.
- [0503] 105. The method of any one of paragraphs 108-104, wherein the disease or disorder is not a gut disease or disorder.
- [0504] 106. The method of any one of paragraphs 108-105, wherein the disease or disorder is selected from the group consisting of depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, dermatological conditions (eczema and itch), and pain disorders.
- [0505] 107. A therapeutic composition for decreasing serotonin level in a mammalian subject in need thereof, the composition comprising an amount of a live isolated bacterial species, dead isolated bacterial species, conditioned medium from an isolated, cultured bacterial species, cell pellet of an isolated bacterial species, a purified metabolite produced by an isolated bacterial species, a purified protein produced by an isolated bacterial species, or a combination thereof sufficient to decrease serotonin level in the subject, and an excipient or carrier suitable for delivery to the gut.
- [0506] 108. The therapeutic composition of paragraph 107, wherein bacterial species consumes serotonin and/or reduces host biosynthesis of serotonin.
- [0507] 109. The therapeutic composition of paragraph 107 or 108, wherein the bacterial species is selected from one or more of *Bifidobacterium longum*, *Blautia coccoides*, *Blautia obeum*, *Clostridium butyricum*, *Coprococcus comes*, *Dorea longicatena*, *Eubacterium rectale*, *Lachnoclostridium* sp., and *Slackia isoflavoniconvertens*.
- [0508] 110. The therapeutic composition of any one of paragraphs 107-109, wherein the bacterial species is selected from one or more of: *Bifidobacterium longum* HB-234, *Blautia coccoides* HB-23, *Blautia obeum* HB-14, *Clostridium butyricum* HB-88, *Coprococcus comes* HB-80, *Dorea longicatena* HB-17, *Eubacterium rectale* HB-22, *Lachnoclostridium* sp. HB-698, and *Slackia isoflavoniconvertens* HB-326.
- [0509] 111. The therapeutic composition of paragraph 107-110, wherein the isolated bacterial species comprises a 16S sequence at least 95% identical to a sequence selected from SEQ ID Nos 96-104.
- [0510] 112. A method of decreasing serotonin in a mammalian subject in need thereof, the method comprising administering a composition of any one of paragraphs 107-111 to the subject, whereby a serotonin level is decreased.
- [0511] 113. The method of paragraph 112, wherein the administering is to the gut of the subject.
- [0512] 114. The method of paragraph 112 or 113, wherein the level of serotonin in the gut is decreased.
- [0513] 115. The method of any one of paragraphs 112-114, wherein the level of serotonin in circulation is decreased.
- [0514] 116. A method of treating a disease or disorder involving or characterized by high or elevated serotonin in a subject in need thereof, the method compris-

- ing administering a composition of any one of paragraphs 107-111 to the subject, whereby the disease or disorder is treated.
- [0515] 117. The method of paragraph 116, wherein the administering is to the gut of the subject.
- [0516] 118. The method of paragraph 116 or 117, wherein the level of serotonin in the gut is decreased.
- [0517] 119. The method of any one of paragraphs 116-118, wherein the level of serotonin in circulation is decreased.
- [0518] 120. The method of any one of paragraphs 116-119, wherein the disease or disorder is selected from the group consisting of diarrhea, IBS-D, inflammatory bowel disease, anxiety, social phobia, sleep disorders, schizophrenia, cancer, obesity, diabetes, coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or platelet disorders (e.g. essential thrombocytosis).
- [0519] 121. The method of any one of paragraphs 116-120, wherein the disease or disorder is not a gut disease or disorder.
- [0520] 122. The method of any one of paragraphs 116-121, wherein the disease or disorder is selected from the group consisting of anxiety, social phobia, sleep disorders, schizophrenia, cancer, obesity, diabetes, coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or platelet disorders (e.g. essential thrombocytosis).
- [0521] 123. A therapeutic composition comprising one or more live isolated serotonin-modulating bacteria, dead isolated serotonin modulating bacteria, conditioned medium(s) from an isolated, cultured serotonin-modulating bacteria, cell pellet(s) of isolated serotonin-modulating bacteria, purified metabolite(s) produced by isolated serotonin-modulating bacteria, purified protein(s) produced by an isolated serotonin-modulating bacteria, or a combination thereof, which alter serotonin signaling or biosynthesis in a subject in need thereof.
- [0522] 124. The therapeutic composition of paragraph 123, wherein the at least one isolated serotonin-modulating bacteria belongs to a genus selected from the group consisting of: *Acidaminococcus*, *Agathobacter*, *Adlercreutzia*, *Akkermansia*, *Alistipes*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Bilophila*, *Bittarella*, *Blautia*, *Blautia*, *Butyricimonas*, *Clostridium*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dialister*, *Dorea*, *Dysosmabacter*, *Eisenbergiella*, *Enterococcus*, *Enterorhabdus*, *Erysipela**to**clostridium*, *Escherichia*, *Eubacterium*, *Faecalitalea*, *Flavonifractor*, *Flintibacter*, *Gemmiger*, *Gordonibacter*, *Hungatella*, *Intestinimonas*, *Lachnocostridium*, *Lactobacillus*, *Lawsonibacter*, *Longibaculum*, *Mediterraneibacter*, *Mycolicibacterium*, *Oscillibacter*, *Parabacteroides*, *Parasutterella*, *Peptostreptococcus*, *Prevotella*, *Romboutsia*, *Ruminococcus*, *Sellimonas*, *Slackia*, *Streptococcus*, *Sutterella*, *Turicibacter*, and *Veillonella*.
- [0523] 125. The therapeutic composition of paragraph 123, wherein the at least one isolated serotonin-modulating bacteria are species selected from the group consisting of: *Acidaminococcus intestini*, *Agathobacter rectalis*, *Akkermansia muciniphila*, *Adlercreutzia equolifaciens*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis*, *Bacillus cereus*, *Bacteroides caccae*, *Bacteroides cellulosilyticus*, *Bacteroides clarus*, *Bacteroides dorei*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides koreensis*, *Bacteroides ovatus*, *Bacteroides plebeius*, *Bacteroides salyersiae*, *Bacteroides stercoris*, *Bacteroides thetaiotomicron*, *Bacteroides uniformis*, *Bacteroides vulgatus*, *Bacteroides xylanisolvans*, *Bifidobacterium adolescentis*, *Bifidobacterium breve*, *Bifidobacteriumfaecale*, *Bifidobacterium longum*, *Bilophila wadsworthia*, *Bittarella massiliensis*, *Blautia coccoides*, *Blautia obeum*, *Blautia wexlerae*, *Butyricimonas paraviriosa*, *Clostridium asparagiforme*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium butyricum*, *Clostridium clostridioforme*, *Clostridium hathewayi*, *Clostridium innoculum*, *Clostridium lavalense*, *Clostridium paraputrificum*, *Clostridium saudicense*, *Clostridium scindens*, *Clostridium sp.*, *Clostridium sporogenes*, *Clostridium sphenoides*, *Clostridium symbiosum*, *Clostridium tyrobutyricum*, *Clostridium hylemonae*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dorea longicatena*, *Dysosmabacter welbionis*, *Eisenbergiella tayi*, *Enterococcus durans*, *Enterococcus faecium*, *Enterorhabdus caecimuris*, *Enterorhabdus muris*, *Erysipela**to**clostridium ramosum*, *Escherichia coli*, *Eubacterium callanderi*, *Eubacterium eligens*, *Eubacterium rectale*, *Faecalitalea cylindroides*, *Flavonifractor plautii*, *Flintibacter butyricus*, *Gemmiger formicilis*, *Gemmiger sp.*, *Gordonibacter pamelaeae*, *Hungatella effluvii*, *Hungatella hathewayi*, *Intestinimonas butyriciproducens*, *Intestinimonas massiliensis*, *Lachnocostridium sp.*, *Lactobacillus brevis*, *Lawsonibacter asaccharolyticus*, *Longibaculum muris*, *Longibaculum sp.*, *Mediterraneibacter faecis*, *Mycolicibacterium smegmatis*, *Oscillibacter sp.*, *Parabacteroides distasonis*, *Parabacteroides goldsteinii*, *Parabacteroides johnsonii*, *Parabacteroides merdae*, *Parasutterella excrementihominis*, *Peptostreptococcus russellii*, *Prevotella copri*, *Prevotella sp.*, *Prevotella sp.*, *Romboutsia lituseburensis*, *Ruminococcus bicirculans*, *Ruminococcus gnarus*, *Ruminococcus sp.*, *Sellimonas intestinalis*, *Slackia isoflavoniconvertens*, *Streptococcus gordonii*, *Sutterella wadsworthensis*, *Turicibacter sanguinis*, and *Veillonella atypica*.
- [0524] 126. The therapeutic composition of paragraph 123, wherein the one or more serotonin-modulating bacteria include a strain selected from the group consisting of: *Acidaminococcus intestini* HB-95, *Agathobacter rectalis* HB-257, *Akkermansia muciniphila* BAA-835, *Adlercreutzia equolifaciens* FJC-B9, *Alistipes onderdonkii* HB-311, *Alistipes putredinis* HB-324, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellulosilyticus* HB-227, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris* HB-33, *Bacteroides thetaiotomicron* HB-34, *Bacteroides uniformis* HB-13, *Bacteroides vulgatus* HB-10, *Bacteroides xylanisolvans* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium breve* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium*

longum HB-234, *Bifidobacterium longum* HB-71, *Bifidobacterium wadsworthia* HB-693, *Bittarella massiliensis* HB-477, *Blautia coccoides* HB-23, *Blautia obeum* HB-14, *Blautia wexlerae* HB-16, *Butyricimonas paraviriosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium butyricum* HB-88, *Clostridium clostridioforme* HB-642, *Clostridium hathewayi* HB-152, *Clostridium innoculum* HB-82, *Clostridium lavalense* HB-452c, *Clostridium paraputreficum* HB-27, *Clostridium saudense* HB-142, *Clostridium scindens* HB-444, *Clostridium* sp. HB-358, *Clostridium sphenoides* HB-470, *Clostridium sporogenes* JCM 7836, *Clostridium sporogenes* McClung 2004, *Clostridium symbiosum* HB-67, *Clostridium tyrobutyricum* HB-469, *Clostridium hylemoniae* HB-73, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus comes* HB-80, *Coprococcus comes* ATCC 27758, *Coprococcus eutactus* HB-155, *Coprococcus eutactus* ATCC 27759, *Dialister invisus* HB-387, *Dorea longicatena* HB-17, *Dysosmobaacter welbionis* HB-45, *Eisenbergiella tayi* HB-437, *Eisenbergiella tayi* HB-612, *Enterococcus durans* HB-48, *Enterococcus faecium* HB-640, *Enterococcus faecium* HB-85, *Enterorhabdus caecimuris* B7, *Enterorhabdus muris* WCA-131-CoC-2, *Erysipelatoclostridium ramosum* HB-24, *Escherichia coli* HB-490, *Eubacterium callanderi* HB-59, *Eubacterium eligens* HB-252, *Eubacterium rectale* HB-22, *Faecalitalea cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter butyricus* HB-344, *Gemmiger formicilis* HB-325, *Gemmiger* sp. HB-567, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Intestinimonas massiliensis* HB-651, *Lachnoclostridium* sp. HB-698, *Lactobacillus brevis* HB-87, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum muris* HB-79, *Longibaculum* sp. HB-681, *Mediterraneibacter faecis* HB-364, *Mycolicibacterium smegmatis* ATCC 19420, *Oscillibacter* sp. HB-28, *Parabacteroides distasonis* HB-20, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella excrementihominis* HB-330, *Peptostreptococcus russelii* RT-10B, *Prevotella copri* HB-373, *Prevotella* sp. HB-649, *Prevotella* sp. HB-333, *Romboutsia lituseburensis* HB-102, *Ruminococcus bicirculans* HB-105, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Ruminococcus* sp. HB-626, *Sellimonas intestinalis* HB-443, *Slackia isoflavoniconvertens* HB-326, *Streptococcus gordonii* HB-62, *Streptococcus gordonii* HB-98, *Sutterella wadsworthensis* HB-259, *Turicibacter sanguinis* HB-147, and *Veillonella atypica* HB-251.

[0525] 127. The therapeutic composition of paragraph 123, wherein the one or more serotonin-modulating bacteria consists of a bacteria comprising a 16S rDNA sequence at least about 95% identical to a 16S rDNA sequence selected from one of SEQ ID NOS: 1-114.

[0526] 128. The therapeutic composition of paragraph 123, wherein the serotonin-modulating bacteria encode genes in their genome, which when expressed, result in

the production of one or more metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0527] 129. The therapeutic composition of paragraph 128, wherein the encoded genes are expressed at physiologically relevant conditions of the human gastrointestinal tract, resulting in the production of metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0528] 130. The therapeutic composition of paragraph 123, wherein the composition is in the form of a probiotic, prebiotic, a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powder, a granule, a medical food, a supplement, or a combination thereof.

[0529] 131. The therapeutic composition of paragraph 123, wherein the composition is formulated to be administered orally, intravenously, intramuscularly, intrathecally, subcutaneously, sublingually, buccally, rectally, vaginally, by the ocular route, by the otic route, nasally, via inhalation, by nebulization, cutaneously, transdermally, or a combination thereof.

[0530] 132. A pharmaceutical composition comprising the therapeutic composition of any one of paragraphs 123-131, and a pharmaceutically acceptable carrier.

[0531] 133. A method of treating a disease or disorder in a subject in need thereof, the method comprising administering to the subject an effective amount of a therapeutic composition comprising one or more live isolated serotonin-modulating bacteria, dead isolated serotonin modulating bacteria, conditioned medium(s) derived from an isolated serotonin-modulating bacteria, cell pellet(s) of isolated serotonin-modulating bacteria, purified metabolite(s) produced by isolated serotonin-modulating bacteria, purified protein(s) produced by isolated serotonin-modulating bacteria, or a combination thereof, thereby altering serotonin signaling or biosynthesis in the subject to treat the disease or disorder.

[0532] 134. The method of paragraph 133, wherein the disease or disorder is a serotonin-related disease or disorder.

[0533] 135. The method of paragraph 133, wherein the serotonin-related disease or disorder is selected from the group consisting of intestinal motility disorders, irritable bowel syndrome, inflammatory bowel disease, depression (e.g. major depressive disorder, treatment resistant depression, post-partum depression), anxiety disorders, addiction, social phobia, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, sleep disorders, schizophrenia, bone disease (e.g. osteoporosis), cancer (e.g. polycythemia vera or myelosclerosis), metabolic disease (e.g. obesity or diabetes), a dysregulated immune system, cardiac disease (e.g. coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or aorta disease), heartburn, dermatological conditions (e.g. eczema and itch), GERD, platelet disorders (e.g. essential thrombocytosis), and pain disorders.

[0534] 136. The method of paragraph 133, wherein the disease or disorder is caused by high serotonin levels and is selected from the group: diarrhea, IBS-D, inflammatory bowel disease, anxiety, social phobia, sleep disorders, schizophrenia, cancer, obesity, diabe-

tes, coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or platelet disorders (e.g. essential thrombocytosis).

[0535] 137. The method of paragraph 133, wherein the disease or disorder is caused by low serotonin levels and is selected from the group: constipation, IBS-C, depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, heartburn, dermatological conditions (eczema and itch), GERD, or pain disorders.

[0536] 138. The method of paragraph 133, wherein treating a disease or disorder comprises decreasing at least one symptom of the disease or disorder, selected from: fatigue, insomnia, stress, persistent anxiety, persistent sadness, social withdrawal, substance withdrawal, irritability, thoughts of suicide, thoughts of self-harm, restlessness, low sex drive, lack of focus, loss of appetite, high blood pressure, low blood pressure, high heart rate, low heart rate, constipation, diarrhea, chronic pain, heartburn, fatigue, trouble breathing, stomach aches, nosebleeds, gum, stomach bleeding, headaches, weight gain, burning of the skin, altered inflammatory markers, neurodevelopmental deficits, and/or seizures.

[0537] 139. The method of paragraph 133, wherein the at least one isolated serotonin-modulating bacteria belongs to a genus selected from the group consisting of: *Acidaminococcus*, *Agathobacter*, *Adlercreutzia*, *Akkermansia*, *Alistipes*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Bilophila*, *Bittarella*, *Blautia*, *Blautia*, *Butyricimonas*, *Clostridium*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dialister*, *Dorea*, *Dysosmobaacter*, *Eisenbergiella*, *Enterococcus*, *Enterorhabdus*, *Erysipelatoclostridium*, *Escherichia*, *Eubacterium*, *Faecalitalea*, *Flavonifractor*, *Flintibacter*, *Gemmiger*, *Gordonibacter*, *Hungatella*, *Intestinimonas*, *Lachnoclostridium*, *Lactobacillus*, *Lawsonibacter*, *Longibaculum*, *Mediterraneibacter*, *Mycolibacterium*, *Oscillibacter*, *Parabacteroides*, *Parasutterella*, *Peptostreptococcus*, *Prevotella*, *Romboutsia*, *Ruminococcus*, *Sellimonas*, *Slackia*, *Streptococcus*, *Sutterella*, *Turicibacter*, and *Veillonella*.

[0538] 140. The method of paragraph 133, wherein the at least one isolated serotonin-modulating bacteria are species selected from the group consisting of: *Acidaminococcus intestini*, *Agathobacter rectalis*, *Akkermansia muciniphila*, *Adlercreutzia equolifaciens*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis*, *Bacillus cereus*, *Bacteroides caccae*, *Bacteroides cellulosilyticus*, *Bacteroides clarus*, *Bacteroides dorei*, *Bacteroides finegoldii*, *Bacteroides fragilis*, *Bacteroides koreensis*, *Bacteroides ovatus*, *Bacteroides plebeius*, *Bacteroides salyersiae*, *Bacteroides stercoris*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, *Bacteroides vulgaris*, *Bacteroides xylinisolvens*, *Bifidobacterium adolescentis*, *Bifidobacterium breve*, *Bifidobacterium faecale*, *Bifidobacterium longum*, *Bilophila wadsworthia*, *Bittarella massiliensis*, *Blautia coccoides*, *Blautia obeum*, *Blautia wexlerae*, *Butyricimonas paravirosa*, *Clostridium asparagiforme*, *Clostridium aldenense*, *Clostridium bolteae*, *Clostridium butyricum*, *Clostridium clostradioforme*,

Clostridium hathewayi, *Clostridium innoculum*, *Clostridium lavalense*, *Clostridium paraputreficum*, *Clostridium saudiene*, *Clostridium scindens*, *Clostridium sp.*, *Clostridium sporogenes*, *Clostridium sphenoides*, *Clostridium symbiosum*, *Clostridium tyrobutyricum*, *Clostridium hylemonae*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Dialister invisus*, *Dorea longicatena*, *Dysosmobaacter welbionis*, *Eisenbergiella tayi*, *Enterococcus durans*, *Enterococcus faecium*, *Enterorhabdus caecimuris*, *Enterorhabdus muris*, *Erysipelatoclostridium ramosum*, *Escherichia coli*, *Eubacterium callanderi*, *Eubacterium eligens*, *Eubacterium rectale*, *Faecalitalea cylindroides*, *Flavonifractor plautii*, *Flintibacter butyricus*, *Gemmiger formicilis*, *Gemmiger sp.*, *Gordonibacter pamelaeae*, *Hungatella effluvii*, *Hungatella hathewayi*, *Intestinimonas butyriciproducens*, *Intestinimonas massiliensis*, *Lachnoclostridium sp.*, *Lactobacillus brevis*, *Lawsonibacter asaccharolyticus*, *Longibaculum muris*, *Longibaculum sp.*, *Mediterraneibacter faecis*, *Mycolibacterium smegmatis*, *Oscillibacter sp.*, *Parabacteroides distasonis*, *Parabacteroides goldsteinii*, *Parabacteroides johnsonii*, *Parabacteroides merdae*, *Parasutterella excrementihominis*, *Peptostreptococcus russellii*, *Prevotella copri*, *Prevotella sp.*, *Prevotella sp.*, *Romboutsia lituseburensis*, *Ruminococcus bicirculans*, *Ruminococcus gnavus*, *Ruminococcus sp.*, *Sellimonas intestinalis*, *Slackia isoflavonicconvertens*, *Streptococcus gordonii*, *Sutterella wadsworthensis*, *Turicibacter sanguinis*, and *Veillonella atypica*.

[0539] 141. The method of paragraph 133, wherein the one or more serotonin-modulating bacteria include a strain selected from the group consisting of: *Acidaminococcus intestini* HB-95, *Agathobacter rectalis* HB-257, *Akkermansia muciniphila* BAA-835, *Adlercreutzia equolifaciens* FJC-B9, *Alistipes onderdonkii* HB-311, *Alistipes putredinis* HB-324, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellulosilyticus* HB-227, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris* HB-33, *Bacteroides thetaiotaomicron* HB-34, *Bacteroides uniformis* HB-13, *Bacteroides vulgatus* HB-10, *Bacteroides xylinisolvens* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium breve* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium longum* HB-234, *Bifidobacterium longum* HB-71, *Bilophila wadsworthia* HB-693, *Bittarella massiliensis* HB-477, *Blautia coccoides* HB-23, *Blautia obeum* HB-14, *Blautia wexlerae* HB-16, *Butyricimonas paravirosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium bolteae* HB-442, *Clostridium butyricum* HB-88, *Clostridium clostradioforme* HB-642, *Clostridium hathewayi* HB-152, *Clostridium innoculum* HB-82, *Clostridium lavalense* HB-452c, *Clostridium paraputreficum* HB-27, *Clostridium saudiene* HB-142, *Clostridium scindens* HB-444, *Clostridium sp.* HB-358, *Clostridium sphenoides* HB-470, *Clostridium sporogenes* McClung 2004, *Clostridium symbiosum* HB-67,

Clostridium tyrobutyricum HB-469, *Clostridium hylemonae* HB-73, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus comes* HB-80, *Coprococcus comes* ATCC 27758, *Coprococcus eutactus* HB-155, *Coprococcus eutactus* ATCC 27759, *Dialister invisus* HB-387, *Dorea longicatena* HB-17, *Dysosmobaacter welbionis* HB-45, *Eisenbergiella tayi* HB-437, *Eisenbergiella tayi* HB-612, *Enterococcus durans* HB-48, *Enterococcus faecium* HB-640, *Enterococcus faecium* HB-85, *Enterorhabdus caecimuris* B7, *Enterorhabdus muris* WCA-131-CoC-2, *Erysipelato-clostridium ramosum* HB-24, *Escherichia coli* HB-490, *Eubacterium callanderi* HB-59, *Eubacterium eligens* HB-252, *Eubacterium rectale* HB-22, *Faecalitalea cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter butyricus* HB-344, *Gemmiger formicilis* HB-325, *Gemmiger* sp. HB-567, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Intestinimonas massiliensis* HB-651, *Lachnoclostridium* sp. HB-698, *Lactobacillus brevis* HB-87, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum muris* HB-79, *Longibaculum* sp. HB-681, *Mediterraneibacter faecis* HB-364, *Mycolicibacterium smegmatis* ATCC 19420, *Oscillibacter* sp. HB-28, *Parabacteroides distasonis* HB-20, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella excrementihominis* HB-330, *Peptostreptococcus russellii* RT-10B, *Prevotella copri* HB-373, *Prevotella* sp. HB-649, *Prevotella* sp. HB-333, *Romboutsia lituseburensis* HB-102, *Ruminococcus bicirculans* HB-105, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Ruminococcus* sp. HB-626, *Sellimonas intestinalis* HB-443, *Slackia isoflavoniconvertens* HB-326, *Streptococcus gordonii* HB-62, *Streptococcus gordonii* HB-98, *Sutterella wadsworthensis* HB-259, *Turicibacter sanguinis* HB-147, and *Veillonella atypica* HB-251.

[0540] 142. The method of paragraph 133, wherein the one or more serotonin-modulating bacteria consists of a bacteria comprising a 16S rDNA sequence at least about 95% identical to a 16S rDNA sequence selected from one of SEQ ID NOS: 1-114.

[0541] 143. The method of paragraph 133, wherein the serotonin-modulating bacteria encode genes in their genome, which when expressed, result in the production of one or more metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0542] 144. The method of paragraph 143, wherein the encoded genes are expressed at physiologically relevant conditions of the human gastrointestinal tract, resulting in the production of metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0543] 145. The method of paragraph 133, wherein the composition is in the form of a probiotic, prebiotic, a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powders, a granule, a medical food, supplement or a combination thereof.

[0544] 146. The method of paragraph 133, wherein the composition is administered orally, intravenously, intramuscularly, intrathecally, subcutaneously, sublingually, buccally, rectally, vaginally, by the ocular route,

by the otic route, nasally, via inhalation, by nebulization, cutaneously, transdermally, or a combination thereof

[0545] 147. The method of paragraph 133, further comprising identifying a subject in need of treatment by measuring a serotonin level in a sample from the subject, and comparing the level to a reference level.

[0546] 148. The method of paragraph 147, wherein the serotonin level is measured in stool, blood, or tissue of the subject.

[0547] 149. The method of paragraph 147, wherein a serotonin level less than the reference level identifies a subject in need of treatment.

[0548] 150. The method of paragraph 148, wherein the levels of serotonin in the stool, blood, or tissue of the subject are altered relative to their initial quantitated amounts, after administering the therapeutic composition.

[0549] 151. The method of paragraph 133, further comprising identifying a subject in need of treatment by measuring levels of fecal serotonin modulating bacteria.

[0550] 152. The method of paragraph 151, wherein the level of fecal serotonin-modulating bacteria is measured by fecal 16S rDNA sequencing, fecal shotgun metagenomic sequencing, measurement of fecal genes involved in the production of microbiota-derived serotonin modulating metabolites, measurement of proteins by sequencing or proteomics or comparable methods, or levels of fecal, blood, or tissue serotonin-modulating metabolites via LC/MS or comparable methods.

[0551] 153. The method of paragraph 152, wherein the levels of serotonin modulating bacteria, genes involved in the production of microbiota-derived serotonin modulating metabolites or proteins, or levels of serotonin-modulating metabolites are altered relative to their initial quantitated amounts after administering the therapeutic composition.

[0552] Some embodiments of the technology described herein can be defined according to any of the following numbered paragraphs:

[0553] 1. A therapeutic composition comprising one or more live isolated serotonin-modulating bacteria, dead isolated serotonin modulating bacteria, conditioned medium(s) from a isolated, cultured serotonin-modulating bacteria, cell pellet(s) of isolated serotonin-modulating bacteria, purified metabolite(s) produced by isolated serotonin-modulating bacteria, purified protein(s) produced by a isolated serotonin-modulating bacteria, or a combination thereof, which alter serotonin signaling or biosynthesis in a subject in need thereof.

[0554] 2. The therapeutic composition of paragraph 1, wherein the at least one isolated serotonin-modulating bacteria belongs to the genera *Acidaminococcus*, *Agathobacter*, *Alistipes*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Bilophila*, *Blaustia*, *Butyricimonas*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dialister*, *Dorea*, *Eisenbergiella*, *Enterococcus*, *Escherichia*, *Eubacterium*, *Faecalcatenata*, *Flavonifractor*, *Flintibacter*, *Gemmiger*, *Gordonibacter*, *Hungatella*, *Intestinimonas*, *Lachnoclostridium*, *Lactobacillus*, *Lawsonibacter*, *Longibaculum*, *Mediterraneibacter*, *Oscillibacter*, *Parabacteroides*,

Parasutterella, *Prevotella*, *Romboutsia*, *Ruminococcaceae*, *Ruminococcus*, *Sellimonas*, *Slackia*, *Streptococcus*, *Sutterella*, *Turicibacter*, or *Veillonella*.

[0555] 3. The therapeutic composition of paragraph 1, wherein the at least one isolated serotonin-modulating bacteria belongs to the species *Acidaminococcus intestini*, *Agathobacter rectalis*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis*, *Bacillus cereus*, *Bacteroides vulgatus*, *Bacteroides plebeius*, *Bacteroides koreensis*, *Bacteroides cellulosilyticus*, *Bacteroides fragilis*, *Bacteroides xylanisolvens*, *Bacteroides uniformis*, *Bacteroides stercoris*, *Bacteroides dorei*, *Bacteroides caccae*, *Bacteroides thetaiotaomicron*, *Bacteroides salyersiae*, *Bacteroides ovatus*, *Bacteroides finegoldii*, *Bacteroides clarus*, *Bifidobacterium faecale*, *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium brevis*, *Bilophila wadsworthia*, *Blautia producta*, *Blautia wexlerae*, *Blautia obeum*, *Butyrimonas paravirosa*, *Clostridium aldenense* HB-440, *Clostridium amygdalium* HB-152, *Clostridium bolteae* HB-442, *Clostridium butyricum* HB-88, *Clostridium clostradioforme* HB-642, *Clostridium inoculum* HB-82, *Clostridium lavalense* HB-452c, *Clostridium leptum* HB-73, *Clostridium paraputrificum* HB-27, *Clostridium ramosum* HB-24, *Clostridium saudiense* HB-142, *Clostridium scindens* HB-444, *Clostridium* sp. HB-358, *Clostridium sphenoides* HB-470, *Clostridium symbiosum* HB-67, *Clostridium tyrobutyricum* HB-469, *Collinsella aerofaciens* HB-04, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus eutactus* HB-155, *Coprococcus* sp. HB-80, *Dialister invisus* HB-387, *Dorea longicatena* HB-17, *Eisenbergiella* sp. HB-612, *Eisenbergiella tayi* HB-437, *Enterococcus durans* HB-85, *Enterococcus hirae* HB-48, *Enterococcus lactis* HB-640, *Escherichia coli* HB-490, *Eubacterium callanderi* HB-59, *Eubacterium eligens* HB-252, *Eubacterium limosum* HB-98, *Eubacterium rectale* HB-22, *Faecalcatena cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter* sp. HB-344, *Gemmiger formicilis* HB-325, *Gemmiger* sp. HB-567, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Intestinimonas massiliensis* HB-651, *Lachnoclostridium* sp. HB-698, *Lactobacillus brevis* HB-87, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum muris* HB-79, *Longibaculum* sp. HB-681, *Mediterraneibacter faecis* HB-364, *Oscillibacter rumenantium* HB-28, *Oscillibacter valericigenes* HB-45, *Parabacteroides distasonis* HB-20, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella exrementihominis* HB-330, *Prevotella copri* HB-373, *Prevotella* sp. HB-333, *Prevotella* sp. HB-649, *Romboutsia lituseburensis* HB-102, *Ruminococcaceae* sp. HB-477, *Ruminococcus bicirculans* HB-105, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Ruminococcus torques* HB-626, *Sellimonas intestinalis* HB-443, *Slackia isoflavoniconvertens* HB-326, *Streptococcus gordonii* HB-62, *Sutterella wadsworthensis* HB-259, *Turicibacter sanguinis* HB-147, and *Veillonella atypica* HB-251.

[0556] 4. The therapeutic composition of paragraph 1, wherein the one or more serotonin-modulating bacteria is/are selected from the strains *Acidaminococcus intestini* HB-95, *Agathobacter rectalis* HB-257, *Alistipes onderdonkii* HB-311, *Alistipes putredinis* HB-324, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellulosilyticus* HB-227, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris*

HB-33, *Bacteroides thetaiotaomicron* HB-34, *Bacteroides uniformis* HB-13, *Bacteroides vulgatus* HB-10, *Bacteroides xylanisolvens* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium brevis* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium longum* HB-234, *Bifidobacterium longum* HB-71, *Bilophila wadsworthia* HB-693, *Blautia obeum* HB-14, *Blautia producta* HB-23, *Blautia wexlerae* HB-16, *Butyrimonas paravirosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium amygdalium* HB-152, *Clostridium bolteae* HB-442, *Clostridium butyricum* HB-88, *Clostridium clostradioforme* HB-642, *Clostridium inoculum* HB-82, *Clostridium lavalense* HB-452c, *Clostridium leptum* HB-73, *Clostridium paraputrificum* HB-27, *Clostridium ramosum* HB-24, *Clostridium saudiense* HB-142, *Clostridium scindens* HB-444, *Clostridium* sp. HB-358, *Clostridium sphenoides* HB-470, *Clostridium symbiosum* HB-67, *Clostridium tyrobutyricum* HB-469, *Collinsella aerofaciens* HB-04, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus eutactus* HB-155, *Coprococcus* sp. HB-80, *Dialister invisus* HB-387, *Dorea longicatena* HB-17, *Eisenbergiella* sp. HB-612, *Eisenbergiella tayi* HB-437, *Enterococcus durans* HB-85, *Enterococcus hirae* HB-48, *Enterococcus lactis* HB-640, *Escherichia coli* HB-490, *Eubacterium callanderi* HB-59, *Eubacterium eligens* HB-252, *Eubacterium limosum* HB-98, *Eubacterium rectale* HB-22, *Faecalcatena cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter* sp. HB-344, *Gemmiger formicilis* HB-325, *Gemmiger* sp. HB-567, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii* HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Intestinimonas massiliensis* HB-651, *Lachnoclostridium* sp. HB-698, *Lactobacillus brevis* HB-87, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum muris* HB-79, *Longibaculum* sp. HB-681, *Mediterraneibacter faecis* HB-364, *Oscillibacter rumenantium* HB-28, *Oscillibacter valericigenes* HB-45, *Parabacteroides distasonis* HB-20, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella exrementihominis* HB-330, *Prevotella copri* HB-373, *Prevotella* sp. HB-333, *Prevotella* sp. HB-649, *Romboutsia lituseburensis* HB-102, *Ruminococcaceae* sp. HB-477, *Ruminococcus bicirculans* HB-105, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Ruminococcus torques* HB-626, *Sellimonas intestinalis* HB-443, *Slackia isoflavoniconvertens* HB-326, *Streptococcus gordonii* HB-62, *Sutterella wadsworthensis* HB-259, *Turicibacter sanguinis* HB-147, and *Veillonella atypica* HB-251.

[0557] 5. The therapeutic composition of paragraph 1, wherein the one or more serotonin-modulating bacteria consists of a bacteria comprising a 16S rDNA sequence at least about 95% identical to a 16S rDNA sequence selected from one of SEQ ID NOs: 1-105.

[0558] 6. The therapeutic composition of paragraph 1, wherein the serotonin-modulating bacteria encode genes in their genome, which when expressed, result in the production of one or more metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0559] 7. The therapeutic composition of paragraph 6, wherein the encoded genes are expressed at physiologically relevant conditions of the human gastrointestinal tract, resulting in the production of metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0560] 8. The therapeutic composition of paragraph 1, wherein the composition is in the form of a probiotic, prebiotic, a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powder, a granule, a medical food, or a combination thereof.

[0561] 9. The therapeutic composition of paragraph 1, wherein the composition is formulated to be administered orally, intravenously, intramuscularly, intrathecally, subcutaneously, sublingually, buccally, rectally, vaginally, by the ocular route, by the otic route, nasally, via inhalation, by nebulization, cutaneously, transdermally, or a combination thereof.

[0562] 10. A method of treating a disease or disorder in a subject in need thereof, the method comprising administering to the subject an effective amount of a therapeutic composition comprising one or more live isolated serotonin-modulating bacteria, dead isolated serotonin modulating bacteria, conditioned medium(s) derived from a isolated serotonin-modulating bacteria, cell pellet(s) of isolated serotonin-modulating bacteria, purified metabolite(s) produced by isolated serotonin-modulating bacteria, purified protein(s) produced by isolated serotonin-modulating bacteria, or a combination thereof, thereby altering serotonin signaling or biosynthesis in the subject to treat the disease or disorder.

[0563] 11. The method of paragraph 10, wherein the disease or disorder is a serotonin-related disease or disorder.

[0564] 12. The method of paragraph 10, wherein the serotonin-related disease or disorder is selected from the group consisting of intestinal motility disorders, irritable bowel syndrome, inflammatory bowel disease, depression (e.g. major depressive disorder, treatment resistant depression, post-partum depression), anxiety disorders, addiction, social phobia, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, sleep disorders, schizophrenia, bone disease (e.g. osteoporosis), cancer (e.g. polycythemia vera or myelosclerosis), metabolic disease (e.g. obesity or diabetes), a dysregulated immune system, cardiac disease (e.g. coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or aorta disease), heartburn, dermatological conditions (e.g. eczema and itch), GERD, platelet disorders (e.g. essential thrombocytosis), and pain disorders.

[0565] 13. The method of paragraph 10, wherein the disease or disorder is caused by high serotonin levels and is selected from the group: diarrhea, IBS-D, inflammatory bowel disease, anxiety, social phobia, sleep disorders, schizophrenia, cancer, obesity, diabetes, coronary artery disease, heart valve disease, congenital heart disease, cardiomyopathies, pericarditis, or platelet disorders (e.g. essential thrombocytosis).

[0566] 14. The method of paragraph 10, wherein the disease or disorder is caused by low serotonin levels

and is selected from the group: constipation, IBS-C, depression, anxiety, addiction, neurodegenerative disorders, autism spectrum disorder, sleep disorders, attention deficit hyperactivity disorder (ADHD), memory loss (e.g. dementia), learning difficulties, osteoporosis, heartburn, dermatological conditions (eczema and itch), GERD, or pain disorders.

[0567] 15. The method of paragraph 10, wherein treating a disease or disorder comprises decreasing at least one symptom of the disease or disorder, selected from: fatigue, insomnia, stress, persistent anxiety, persistent sadness, social withdrawal, substance withdrawal, irritability, thoughts of suicide, thoughts of self-harm, restlessness, low sex drive, lack of focus, loss of appetite, high blood pressure, low blood pressure, high heart rate, low heart rate, constipation, diarrhea, chronic pain, heartburn, fatigue, trouble breathing, stomach aches, nosebleeds, gum, stomach bleeding, headaches, weight gain, burning of the skin, altered inflammatory markers, neurodevelopmental deficits, and/or seizures.

[0568] 16. The method of paragraph 10, wherein the at least one isolated serotonin-modulating bacteria belongs to the genera *Acidaminococcus*, *Agathobacter*, *Alistipes*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Bilophila*, *Blautia*, *Butyricimonas*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dialister*, *Dorea*, *Eisenbergiella*, *Enterococcus*, *Escherichia*, *Eubacterium*, *Faecalcatena*, *Flavonifractor*, *Flintibacter*, *Gemmiger*, *Gordonibacter*, *Hungatella*, *Intestinimonas*, *Lachnosporobacter*, *Lactobacillus*, *Lawsonibacter*, *Longibaculum*, *Mediterraneibacter*, *Oscillibacter*, *Parabacteroides*, *Parasutterella*, *Prevotella*, *Romboutsia*, *Ruminococcaceae*, *Ruminococcus*, *Sellimonas*, *Slackia*, *Streptococcus*, *Sutterella*, *Turicibacter*, or *Veillonella*.

[0569] 17. The method of paragraph 10, wherein the at least one isolated serotonin-modulating bacteria belongs to the species *Acidaminococcus intestini*, *Agathobacter rectalis*, *Alistipes onderdonkii*, *Alistipes putredinis*, *Anaerotruncus colihominis*, *Bacillus cereus*, *Bacteroides vulgatus*, *Bacteroides plebeius*, *Bacteroides koreensis*, *Bacteroides cellulosilyticus*, *Bacteroides fragilis*, *Bacteroides xylinisolvans*, *Bacteroides uniformis*, *Bacteroides stercoris*, *Bacteroides dorei*, *Bacteroides caccae*, *Bacteroides thetaiotaomicron*, *Bacteroides salyersiae*, *Bacteroides ovatus*, *Bacteroides finegoldii*, *Bacteroides clarus*, *Bifidobacterium faecale*, *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium brevis*, *Bilophila wadsworthia*, *Blautia producta*, *Blautia wexlerae*, *Blautia obeum*, *Butyricimonas paraviriosa*, *Clostridium scindens*, *Clostridium inoculum*, *Clostridium bolteae*, *Clostridium aldenense*, *Clostridium saudiense*, *Clostridium lavalense*, *Clostridium amygdalum*, *Clostridium clostridioforme*, *Clostridium leptum*, *Clostridium tyrobutyricum*, *Clostridium ramosum*, *Clostridium paraputrificum*, *Clostridium sphenoides*, *Clostridium symbiosum*, *Clostridium sp.*, *Clostridium butyricum*, *Collinsella aerofaciens*, *Coprococcus comes*, *Coprococcus eutactus*, *Coprococcus sp.*, *Dialister invisus*, *Dorea longicatena*, *Eisenbergiella tayi*, *Eisenbergiella sp.*, *Enterococcus lactis*, *Enterococcus hirae*, *Enterococcus durans*, *Escherichia coli*, *Eubacterium limosum*,

Eubacterium eligens, *Eubacterium callanderi*, *Eubacterium rectale*, *Faecalcatena cylindroides*, *Flavonifractor plautii*, *Flintibacter* sp., *Gemmiger formicilis*, *Gemmiger* sp., Genus Species, *Gordonibacter pamelaeae*, *Hungatella hathewayi*, *Hungatella effluvii*, *Intestinimonas butyriciproducens*, *Intestinimonas massiliensis*, *Lachnoclostridium* sp., *Lactobacillus brevis*, *Lawsonibacter asaccharolyticus*, *Longibaculum muris*, *Longibaculum* sp., *Mediterraneibacter faecis*, *Oscillibacter ruminantium*, *Oscillibacter valericigenes*, *Parabacteroides distasonis*, *Parabacteroides johnsonii*, *Parabacteroides merdae*, *Parabacteroides goldsteinii*, *Parasutterella excrementihominis*, *Prevotella copri*, *Prevotella* sp., *Romboutsia lituseburensis*, *Ruminococcaceae* sp., *Ruminococcus gnavus*, *Ruminococcus bicirculans*, *Ruminococcus torques*, *Sellimonas intestinalis*, *Slackia isoflavoniconvertens*, *Streptococcus gordonii*, *Sutterella wadsworthensis*, *Turicibacter sanguinis*, or *Veillonella atypica*.

[0570] 18. The method of paragraph 10, wherein the one or more serotonin-modulating bacteria is/are selected from the strains *Acidaminococcus intestini* HB-95, *Agathobacter rectalis* HB-257, *Alistipes onderdonkii* HB-311, *Alistipes putredinis* HB-324, *Anaerotruncus colihominis* HB-474, *Anaerotruncus colihominis* HB-83, *Bacillus cereus* HB-25, *Bacteroides caccae* HB-11, *Bacteroides cellulosilyticus* HB-227, *Bacteroides clarus* HB-30, *Bacteroides dorei* HB-12, *Bacteroides finegoldii* HB-31, *Bacteroides fragilis* HB-58, *Bacteroides koreensis* HB-385, *Bacteroides ovatus* HB-70, *Bacteroides plebeius* HB-237, *Bacteroides salyersiae* HB-32, *Bacteroides stercoris* HB-33, *Bacteroides thetaiotaomicron* HB-34, *Bacteroides uniformis* HB-13, *Bacteroides vulgatus* HB-10, *Bacteroides xylinisolvans* HB-35, *Bifidobacterium adolescentis* HB-179, *Bifidobacterium breve* HB-90, *Bifidobacterium faecale* HB-159, *Bifidobacterium longum* HB-234, *Bifidobacterium longum* HB-71, *Bilophila wadsworthia* HB-693, *Blautia obeum* HB-14, *Blautia producta* HB-23, *Blautia wexlerae* HB-16, *Butyrimonas paravirosa* HB-453, *Clostridium aldenense* HB-440, *Clostridium amygdalum* HB-152, *Clostridium bolteae* HB-442, *Clostridium butyricum* HB-88, *Clostridium clostridioforme* HB-642, *Clostridium inoculum* HB-82, *Clostridium lavalense* HB-452c, *Clostridium leptum* HB-73, *Clostridium paraputrificum* HB-27, *Clostridium ramosum* HB-24, *Clostridium saudense* HB-142, *Clostridium scindens* HB-444, *Clostridium* sp. HB-358, *Clostridium sphenooides* HB-470, *Clostridium symbiosum* HB-67, *Clostridium tyrobutyricum* HB-469, *Collinsella aerofaciens* HB-04, *Collinsella aerofaciens* HB-274, *Coprococcus comes* HB-376, *Coprococcus eutactus* HB-155, *Coprococcus* sp. HB-80, *Dialister invisus* HB-387, *Dorea longicatena* HB-17, *Eisenbergiella* sp. HB-612, *Eisenbergiella tayi* HB-437, *Enterococcus durans* HB-85, *Enterococcus hirae* HB-48, *Enterococcus lactis* HB-640, *Escherichia coli* HB-490, *Eubacterium eligens* HB-252, *Eubacterium limosum* HB-98, *Eubacterium rectale* HB-22, *Faecalcatena cylindroides* HB-664, *Flavonifractor plautii* HB-472, *Flintibacter* sp. HB-344, *Gemmiger formicilis* HB-325, *Gemmiger* sp. HB-567, *Gordonibacter pamelaeae* HB-15, *Hungatella effluvii*

HB-02, *Hungatella hathewayi* HB-01, *Intestinimonas butyriciproducens* HB-478, *Intestinimonas massiliensis* HB-651, *Lachnoclostridium* sp. HB-698, *Lactobacillus brevis* HB-87, *Lawsonibacter asaccharolyticus* HB-521, *Longibaculum muris* HB-79, *Longibaculum* sp. HB-681, *Mediterraneibacter faecis* HB-364, *Oscillibacter ruminantium* HB-28, *Oscillibacter valericigenes* HB-45, *Parabacteroides distasonis* HB-20, *Parabacteroides distasonis* HB-214, *Parabacteroides goldsteinii* HB-44, *Parabacteroides johnsonii* HB-03, *Parabacteroides merdae* HB-63, *Parasutterella exrementihominis* HB-330, *Prevotella copri* HB-373, *Prevotella* sp. HB-333, *Prevotella* sp. HB-649, *Romboutsia lituseburensis* HB-102, *Ruminococcaceae* sp. HB-477, *Ruminococcus bicirculans* HB-105, *Ruminococcus bicirculans* HB-268, *Ruminococcus gnavus* HB-40, *Ruminococcus gnavus* HB-516, *Ruminococcus torques* HB-626, *Sellimonas intestinalis* HB-443, *Slackia isoflavoniconvertens* HB-326, *Streptococcus gordonii* HB-62, *Sutterella wadsworthensis* HB-259, *Turicibacter sanguinis* HB-147, and *Veillonella atypica* HB-251.

[0571] 19. The method of paragraph 10, wherein the one or more serotonin-modulating bacteria consists of a bacteria comprising a 16S rDNA sequence at least about 95% identical to a 16S rDNA sequence selected from one of SEQ ID NOS: 1-105.

[0572] 20. The method of paragraph 10, wherein the serotonin-modulating bacteria encode genes in their genome, which when expressed, result in the production of one or more metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0573] 21. The method of paragraph 20, wherein the encoded genes are expressed at physiologically relevant conditions of the human gastrointestinal tract, resulting in the production of metabolites or proteins that influence subject serotonin signaling/biosynthesis.

[0574] 22. The method of paragraph 10, wherein the composition is in the form of a probiotic, prebiotic, a capsule, a tablet, a caplet, a pill, a troche, a lozenge, a powders, a granule, a medical food, or a combination thereof.

[0575] 23. The method of paragraph 10, wherein the composition is administered orally, intravenously, intramuscularly, intrathecally, subcutaneously, sublingually, buccally, rectally, vaginally, by the ocular route, by the otic route, nasally, via inhalation, by nebulization, cutaneously, transdermally, or a combination thereof

[0576] 24. The method of paragraph 10, further comprising identifying a subject in need of treatment by measuring a serotonin level in a sample from the subject, and comparing the level to a reference level.

[0577] 25. The method of paragraph 24, wherein the serotonin level is measured in stool, blood, or tissue of the subject.

[0578] 26. The method of paragraph 24, wherein a serotonin level less than the reference level identifies a subject in need of treatment.

[0579] 27. The method of paragraph 22, wherein the levels of serotonin in the stool, blood, or tissue of the subject are altered relative to their initial quantitated amounts, after administering the therapeutic composition.

[0580] 28. The method of paragraph 10, further comprising identifying a subject in need of treatment by measuring levels of fecal serotonin modulating bacteria.

[0581] 29. The method of paragraph 28, wherein the level of fecal serotonin-modulating bacteria is measured by fecal 16S rDNA sequencing, fecal shotgun metagenomic sequencing, measurement of fecal genes involved in the production of microbiota-derived serotonin modulating metabolites, measurement of proteins by sequencing or proteomics or comparable methods, or levels of fecal, blood, or tissue serotonin-modulating metabolites via LC/MS or comparable methods.

[0582] 30. The method of paragraph 22, wherein the levels of serotonin modulating bacteria, genes involved in the production of microbiota-derived serotonin modulating metabolites or proteins, or levels of serotonin-modulating metabolites are altered relative to their initial quantitated amounts after administering the therapeutic composition.

EXAMPLES

Example 1: Identification of Serotonin-Modulating Bacteria

Culturing Bacteria from Human Stool

[0583] Bacteria from human stool samples (leveraging microbiological methods to enrich and select for unique diversity—e.g. plating stool samples on multiple bacterial mediums with a variety of carbon and nitrogen sources, including those found in the human gastrointestinal tract and/or listed within this specification, at different concentrations; plating stool sample on bacterial mediums with antibiotics or bile acids, to selectively kill certain bacterial populations; treating stool samples prior to plating with oxygen, antibiotics, or chloroform), were tested for the ability to influence serotonin release in the RIN14B serotonin release assay.

RIN14B Serotonin Release Assay

[0584] To run the RIN14B serotonin release assay, RIN14B cells (ATCC® CRL-2059™) were first grown following manufacturer's protocols (ATCC). RIN14B cells were then seeded in 24-well plates at $10^5/\text{cm}^2$ in 500 μL RPMI complete culture medium (GIBCO), and incubated at 37° C. in the CO₂ incubator for 48 hours. At this point, the stimuli (e.g., bacterial supernatant or cell pellets) were then prepared under aseptic conditions.

[0585] To prepare the stimuli for the RIN14B serotonin release assay, isolated bacteria were grown in vegetable-based bacteriological mediums and/or bacteriological mediums with mammalian components. In some embodiments, the mediums included at least one of the following: conditioned medium from other bacteria, N-Acetyl-D-Galactosamine, N-Acetyl-D-Glucosamine, N-Acetyl-β-D-Manosamine, Adonitol, Amygdalin, D-Arabitol, Arbutin, D-Cellobiose, α-Cyclodextrin, β-Cyclodextrin, Dextrin, Dulcitol, i-Erythritol, D-Fructose, L-Fucose, D-Galactose, D-Galacturonic Acid, Gentiobiose, D-Gluconic Acid, D-Glucosaminic Acid, α-D-Glucose, α-D-Glucose 1-Phosphate, D-Glucose6-Phosphate, Glycerol, D,L-α-Glycerol Phosphate, m-Inositol, α-D-Lactose, Lactulose, Maltose, Maltotriose, D-Mannitol, D-Mannose, D-Mezelitose,

D-Melibiose, 3-Methyl-DGlucose, α-Methyl-DGalactoside, β-Methyl-D-Galactoside, α-Methyl-D-Glucoside, β-Methyl-D-Glucoside, Mucin, Palatinose, D-Raffinose, L-Rhamnose, Salicin, D-Sorbitol, Stachyose, Sucrose, D-Trehalose, Turanose, Acetic Acid, Formic Acid, Fumaric Acid, Glyoxylic Acid, α-Hydroxybutyric Acid, β-Hydroxybutyric Acid, Itaconic Acid, α-Ketobutyric Acid, α-Ketovaleric Acid, D,L-Lactic Acid, L-Lactic Acid, D-Lactic Acid Methyl Ester, D-Malic Acid, L-Malic Acid, Propionic Acid, Pyruvic Acid, Pyruvic Acid Methyl Ester, D-Saccharic Acid, Succinamic Acid, Succinic Acid, Succinic Acid Mono-Methyl Ester, m-Tartaric Acid, Urocanic Acid, Alaninamide, L-Alanine, L-Alanyl-LGlutamine, L-Alanyl-LHistidine, L-Alanyl-LThreonine, L-Asparagine, L-Glutamic Acid, L-Glutamine, Glycyl-LAspartic Acid, Glycyl-LGlutamine, Glycyl-LMethionine, Glycyl-LProline, L-Methionine, L-Phenylalanine, L-Serine, L-Threonine, L-Valine, L-Valine plus L-Aspartic Acid, 2'-Deoxy Adenosine, Inosine, Thymidine, Uridine, Thymidine-5'-Mono-phosphate, or Uridine-5'-Monophosphate. In some embodiments of any of the aspects, the isolated bacteria are grown in HM2 media. HM2 comprises: Vigitone infused Broth (Sigma™; e.g., 37 g/L); Yeast Extract (Fisher™; e.g., 5 g/L); MOPS 1M Buffer (Teknova™; e.g., 50 mL/L); Cysteine hydrochloride (10% stock) (Sigma™; e.g., 10 mL/L); and Hemin+Vitamin K (Remele™; e.g., 1 mL/L).

[0586] Samples of the bacterial cultures were collected at timepoints of 24 and 48 hours. In some embodiments, the strains were growth at atmospheric oxygen, microaerophilic conditions, or anaerobic conditions, at temperatures ranging from 20 to 50 degrees Celsius. At this point cultures underwent centrifugation to separate bacterial cell pellets and supernatant. Supernatant was then sterilized via passage through a 0.1 m or 0.22 m filter. Bacterial pellets were washed with Hanks' Balanced Salt Solution (HBSS) (GIBCO) buffer, and protein concentration using the Pierce™ Rapid Gold BCA Protein Assay Kit, per manufacturer's protocols (THERMO SCIENTIFIC).

[0587] Supernatant or washed bacterial cell pellet was then introduced into the RIN14B cell cultures. RIN14B culture supernatant was aspirated without disturbing the monolayer, and then washed with 250 μL of washing solution (HBSS supplemented with 0.1% Bovine Serum Albumin (SIGMA) and 2 uM Fluoxetine hydrochloride (SIGMA)). The washing solution was then aspirated, and 250 $\mu\text{L}/\text{well}$ of stimuli was added to the cell cultures (base diluent=HBSS). The stimulate included at least one of the following: (A) Cell pellets tested at 100 g/mL and 20 g/mL, (B) Supernatants tested at 50% and 10% dilutions, (C) Heat Inactivated stimuli that were incubated at 96° C. for 15 min in a heating block, (D) Negative controls (e.g., HBSS, 1% DMSO, fresh bacterial culture media), or (E) Positive control (e.g., 15 μM Ionomycin, prepared in DMSO). Stimuli were incubated for one hour at 37° C. in the CO₂ incubator, and RIN14B supernatants were collected by centrifuging assay plates at 6000×g for 5 min, and supernatants were stored at 4° C. until use. Serotonin concentration in the RIN14B supernatant was quantitated by ELISA (EAGLE BIOSCIENCES) according to manufacturer's instructions.

[0588] After testing over 100 strains, many organisms were identified that had significant impact on serotonin release compared to positive controls, as well as organisms that had no impact (see e.g., FIG. 1-FIG. 4, Tables 1A-1D). Notably, effects were found with both conditioned mediums

and cell pellets from these organisms, indicating multiple mechanisms (e.g., at least one metabolic in origin mechanism, and at least one protein-driven mechanism). In some embodiments, bacteria and/or bacterial metabolites modulate serotonin through a Toll-like receptor (TLR)-mediated mechanism. Non-limiting examples of TLRs related to bacterial sensing include TLR1, TLR2, TLR4, TLR5, TLR6, and/or TLR9.

[0589] Without wishing to be bound by theory, identification of the specific metabolites and/or proteins driving the alterations in serotonin in this model (e.g., by performing genome analysis, metagenomics, metabolomics and/or proteomics on strong inducers of serotonin vs. bacteria with no impact) can indicate the specific mechanisms. Alternatively, standard bio-assay purification techniques can be employed (e.g., fractionating active conditioned mediums using LC/MS or equivalent methods, eventually identifying a fraction with purified compounds that could be identified via NMR), or genetic screens of serotonin-modulating organisms can be employed (e.g. creating a transposon library of the active strains, and then screening for an inactive close, thus identifying genes eliciting the serotonin-modulating effects). These mechanisms can then be leveraged to identify additional bacteria with these characteristics (e.g. using genome analysis) to then deliver into therapeutic compositions. Furthermore, these data can be leveraged with human stool transcriptomic cohorts to identify not just bacteria which have the capability to perform these functions, but those bacteria that actively do so with a human under physiologically relevant conditions. These organisms will likely have superiority over others with the same genetic potential. Likewise, organisms can be engineered to perform these functions and then be delivered to the host.

Human Gut Simulator

[0590] The serotonin-modulating strains described herein can influence 5-HT signaling in the presence of a complex

human gut microbiome. In a non-limiting example, several 5-HT modulating strains were introduced into a human gut simulator, and the cell pellets and supernatants of the entire community were then introduced to RIN14B cells at multiple time points. Here, by testing the supernatant and cell pellet of the entire mock community (with and without the 5-HT modulating bacteria added), it was found that several of the 5-HT modulating strains positively impacted 5-HT signaling (see e.g., FIG. 3, FIG. 4). Briefly, this was done by inoculating a diluted human fecal sample into a gut simulator vessel loaded with pre-reduced Gifu Anaerobic Medium (GAM), diluted at 1:10 strength. After allowing the human-derived community to normalize for 48 hours, the 5-HT modulating bacteria were spiked into the gut simulator. Samples were collected from the gut simulator 48 hours later, and the impact of the collective cell pellet and supernatant of the community was tested in 5-HT release using the RIN14B cell culture assay.

[0591] The change in 5-HT signal of this mock community could be directly due to the ability of the introduced bacteria to produce metabolites and/or proteins that cause the effect. Alternatively, this could be due to a shift in the native microbiome, to a more 5-HT modulating state (e.g., increasing levels of native 5-HT modulating bacteria). This can also be a combination of these effects (e.g., activity of the introduced 5-HT modulating bacteria, as well as a shift to a more potent 5-HT modulating microbial community). Without being bound by theory, the signal of introduced 5-HT modulating bacteria can also be amplified by the presence of native 5-HT modulating bacteria, either through provision of nutrients essential for the introduced 5-HT modulating bacteria for growth or engraftment, or precursors of 5-HT modulating pathways (e.g., tryptophan).

Strains

TABLE 1A

| 5-HT Modulating Potential of 114 Human-Derived Strains—Pathways of 5-HT Modulation | | | | | | | |
|--|--|---------------|---------------------------|---------------------------|-----------------------|--------------|------------------|
| Pathway of 5-HT Modulation | | | | | | | |
| SEQ ID NO | Strain | 5-HT Producer | 5-HT Positive Supernatant | 5-HT Positive Cell Pellet | No or Low 5-HT Impact | 5-HT Reducer | Agonist Producer |
| 1 | <i>Ruminococcus gnavus</i> HB-40 | X | X | X | | | X |
| 2 | <i>Ruminococcus gnavus</i> HB-516 | X | X | X | | | X |
| 3 | <i>Enterococcus durans</i> HB-48 | X | | X | | | X |
| 4 | <i>Clostridium lavalense</i> HB-452c | X | | | | | X |
| 5 | <i>Hungatella effluvii</i> HB-02 | | | X | X | | |
| 6 | <i>Bacteroides caccae</i> HB-11 | | X | X | | | |
| 7 | <i>Bacteroides dorei</i> HB-12 | | X | X | | | |
| 8 | <i>Clostridium saudience</i> HB-142 | | X | X | | | |
| 9 | <i>Gordonibacter pamelaeae</i> HB-15 | | X | X | | | |
| 10 | <i>Clostridium hathewayi</i> HB-152 | | X | X | | | |
| 11 | <i>Bifidobacterium faecale</i> HB-159 | | X | X | | | |
| 12 | <i>Bifidobacterium adolescentis</i> HB-179 | | X | X | | | |
| 13 | <i>Parabacteroides distasonis</i> HB-20 | | X | X | | | |
| 14 | <i>Eubacterium eligens</i> HB-252 | | X | X | | | |
| 15 | <i>Bacteroides fiugoldii</i> HB-31 | | X | X | | | |
| 16 | <i>Bacteroides salyersiae</i> HB-32 | | X | X | | | |
| 17 | <i>Gemmiger formicilis</i> HB-325 | | X | X | | | |
| 18 | <i>Parasutterella excrementihominis</i> HB-330 | | X | X | | | |
| 19 | <i>Bacteroides xylinosolvens</i> HB-35 | | X | X | | | |
| 20 | <i>Mediterraneibacter faecis</i> HB-364 | | X | X | | | |
| 21 | <i>Clostridium aldenense</i> HB-440 | | X | X | | | |
| 22 | <i>Clostridium bolteae</i> HB-442 | | X | X | | | |

TABLE 1A-continued

| 5-HT Modulating Potential of 114 Human-Derived Strains—Pathways of 5-HT Modulation | | | | | | | |
|--|--|----------------------------|----------------------------|---------------------------|-----------------------|--------------|------------------|
| SEQ ID NO | Strain | Pathway of 5-HT Modulation | | | | | |
| | | 5-HT Producer | 5-HT Positive Supernantant | 5-HT Positive Cell Pellet | No or Low 5-HT Impact | 5-HT Reducer | Agonist Producer |
| 23 | <i>Clostridium scindens</i> HB-444 | | X | X | | | |
| 24 | <i>Clostridium tyrobutyricum</i> HB-469 | | X | X | | | |
| 25 | <i>Eisenbergiella tayi</i> HB-612 | | X | X | | | |
| 26 | <i>Parabacteroides merdae</i> HB-63 | | X | X | | | |
| 27 | <i>Bacteroides ovatus</i> HB-70 | | X | X | | | |
| 28 | <i>Anaerotruncus colihominis</i> HB-83 | | X | X | | | |
| 29 | <i>Enterococcus faecium</i> HB-85 | | X | X | | | |
| 30 | <i>Lactobacillus brevis</i> HB-87 | | X | X | | | |
| 31 | <i>Hungatella hathewayi</i> HB-01 | | X | | | | |
| 32 | <i>Parabacteroides johnsonii</i> HB-03 | | X | | | | |
| 33 | <i>Bacteroides vulgatus</i> HB-10 | | X | | | | |
| 34 | <i>Bacteroides uniformis</i> HB-13 | | X | | | | |
| 35 | <i>Turicibacter sanguinis</i> HB-147 | | X | | | | |
| 36 | <i>Coprococcus eutactus</i> HB-155 | | X | | | | |
| 37 | <i>Bacteroides cellulosilyticus</i> HB-227 | | X | | | | |
| 38 | <i>Bacteroides plebeius</i> HB-237 | | X | | | | |
| 39 | <i>Erysipelatoclostridium ramosum</i> HB-24 | | X | | | | |
| 40 | <i>Bacillus cereus</i> HB-25 | | X | | | | |
| 41 | <i>Agathobacter rectalis</i> HB-257 | | X | | | | |
| 42 | <i>Ruminococcus bicirculans</i> HB-268 | | X | | | | |
| 43 | <i>Clostridium paraputrificum</i> HB-27 | | X | | | | |
| 44 | <i>Collinsella aerofaciens</i> HB-274 | | X | | | | |
| 45 | <i>Oscillibacter</i> sp. HB-28 | | X | | | | |
| 46 | <i>Alistipes onderdonkii</i> HB-311 | | X | | | | |
| 47 | <i>Alistipes putredinis</i> HB-324 | | X | | | | |
| 48 | <i>Bacteroides stercoris</i> HB-33 | | X | | | | |
| 49 | <i>Flintibacter butyricus</i> HB-344 | | X | | | | |
| 50 | <i>Coprococcus comes</i> HB-376 | | X | | | | |
| 51 | <i>Bacteroides koreensis</i> HB-385 | | X | | | | |
| 52 | <i>Eisenbergiella tayi</i> HB-437 | | X | | | | |
| 53 | <i>Dysosmabacter wellbionis</i> HB-45 | | X | | | | |
| 54 | <i>Butyrimonas paravirescens</i> HB-453 | | X | | | | |
| 55 | <i>Flavonifractor plautii</i> HB-472 | | X | | | | |
| 56 | <i>Anaerotruncus colihominis</i> HB-474 | | X | | | | |
| 57 | <i>Intestinimonas butyriciproducens</i> HB-478 | | X | | | | |
| 58 | <i>Bacteroides fragilis</i> HB-58 | | X | | | | |
| 59 | <i>Streptococcus gordoni</i> HB-62 | | X | | | | |
| 60 | <i>Enterococcus faecium</i> HB-640 | | X | | | | |
| 61 | <i>Clostridium clostridiiforme</i> HB-642 | | X | | | | |
| 62 | <i>Faecalitalea cylindroides</i> HB-664 | | X | | | | |
| 63 | <i>Bilophila wadsworthia</i> HB-693 | | X | | | | |
| 64 | <i>Bifidobacterium longum</i> HB-71 | | X | | | | |
| 65 | <i>Clostridium hylemonae</i> HB-73 | | X | | | | |
| 66 | <i>Clostridium innoculum</i> HB-82 | | X | | | | |
| 67 | <i>Bifidobacterium breve</i> HB-90 | | X | | | | |
| 68 | <i>Acidaminococcus intestini</i> HB-95 | | X | | | | |
| 69 | <i>Streptococcus gordoni</i> HB-98 | | X | | | | |
| 70 | <i>Romboutsia lituseburensis</i> HB-102 | | | X | | | |
| 71 | <i>Blautia wexlerae</i> HB-16 | | | X | | | |
| 72 | <i>Sutterella wadsworthensis</i> HB-259 | | | X | | | |
| 73 | <i>Bacteroides clarus</i> HB-30 | | | X | | | |
| 74 | <i>Prevotella</i> sp. HB-333 | | | X | | | |
| 75 | <i>Bacteroides thetaiotaomicron</i> HB-34 | | | X | | | |
| 76 | <i>Prevotella copri</i> HB-373 | | | X | | | |
| 77 | <i>Dialister invisus</i> HB-387 | | | X | | | |
| 78 | <i>Sellimonas intestinalis</i> HB-443 | | | X | | | |
| 79 | <i>Bittarella massiliensis</i> HB-477 | | | X | | | |
| 80 | <i>Ruminococcus</i> sp. HB-626 | | | X | | | |
| 81 | <i>Prevotella</i> sp. HB-649 | | | X | | | |
| 82 | <i>Longibaculum muris</i> HB-79 | | | X | | | |
| 83 | <i>Ruminococcus bicirculans</i> HB-105 | | | | X | | |
| 84 | <i>Parabacteroides distasonis</i> HB-214 | | | | X | | |
| 85 | <i>Veillonella atypica</i> HB-251 | | | | X | | |
| 86 | <i>Clostridium</i> sp. HB-358 | | | | X | | |
| 87 | <i>Parabacteroides goldsteinii</i> HB-44 | | | | X | | |
| 88 | <i>Clostridium sphenoides</i> HB-470 | | | | X | | |
| 89 | <i>Escherichia coli</i> HB-490 | | | | X | | |
| 90 | <i>Lawsonibacter asaccharolyticus</i> HB-521 | | | | X | | |

TABLE 1A-continued

| 5-HT Modulating Potential of 114 Human-Derived Strains—Pathways of 5-HT Modulation | | | | | | | | |
|--|---|----------------------------|---------------------------|---------------------------|-----------------------|--------------|------------------|---|
| SEQ ID NO | Strain | Pathway of 5-HT Modulation | | | | | | |
| | | 5-HT Producer | 5-HT Positive Supernatant | 5-HT Positive Cell Pellet | No or Low 5-HT Impact | 5-HT Reducer | Agonist Producer | |
| 91 | <i>Gemmiger</i> sp. HB-567 | | | | X | | | |
| 92 | <i>Eubacterium callanderi</i> HB-59 | | | | X | | | |
| 93 | <i>Intestinimonas massiliensis</i> HB-651 | | | | X | | | |
| 94 | <i>Clostridium symbiosum</i> HB-67 | | | | X | | | |
| 95 | <i>Longibaculum</i> sp. HB-681 | | | | X | | | |
| 96 | <i>Blautia obeum</i> HB-14 | | | | | X | | |
| 97 | <i>Dorea longicatena</i> HB-17 | | | | | X | | |
| 98 | <i>Eubacterium rectale</i> HB-22 | | | | | X | | |
| 99 | <i>Blautia coccoides</i> HB-23 | | | | | X | | |
| 100 | <i>Bifidobacterium longum</i> HB-234 | | | | | X | | |
| 101 | <i>Slackia isofilavoniconvertens</i> HB-326 | | | | | X | | |
| 102 | <i>Lachnoclostridium</i> sp. HB-698 | | | | | X | | |
| 103 | <i>Coprococcus comes</i> HB-80 | | | | | X | | |
| 104 | <i>Clostridium butyricum</i> HB-88 | | | | | X | | |
| 105 | <i>Clostridium sporogenes</i> JCM 7836 | | | | | | X | |
| 106 | <i>Akkermansia muciniphila</i> BAA-835 | | | | | | X | |
| 107 | <i>Clostridium sporogenes</i> McClung 2004 | | | | | | X | |
| 108 | <i>Peptostreptococcus russellii</i> RT-10B | | | | | | | X |
| 109 | <i>Mycobacterium smegmatis</i> ATCC 19420 | | | | | | | X |
| 110 | <i>Enterorhabdus muris</i> WCA-131-CoC-2 | | | | | | | X |
| 111 | <i>Adlercreutzia equolifaciens</i> FJC-B9 | | | | | | | X |
| 112 | <i>Enterorhabdus caecimuris</i> B7 | | | | | | | X |
| 113 | <i>Coprococcus eutactus</i> ATCC 27759 | | | | | | | X |
| 114 | <i>Coprococcus comes</i> ATCC 27758 | | | | | | | X |

TABLE 1B

| 5-HT Modulating Potential of 104 Human-Derived Strains - Serotonin Release in ng/mL (HM2 media) Measured by ELISA (bolded number indicates a significant amount of serotonin release over pre-determined threshold; see e.g., final row) | | | | | |
|--|--|----------------------|----------------------|-------------|-------------|
| Serotonin Release in ng/mL (HM2) Measured by ELISA | | | | | |
| SEQ ID | | RIN14B - Supernatant | RIN14B - Cell Pellet | | |
| NO | Strain | 50% | 10% | 100 ug/mL | 20 ug/mL |
| 1 | <i>Ruminococcus gnavus</i> HB-40 | 523.2 | — | 53.7 | 23.6 |
| 2 | <i>Ruminococcus gnavus</i> HB-516 | 378.0 | 151.9 | 46.2 | 56.8 |
| 3 | <i>Enterococcus durans</i> HB-48 | 86.8 | 49.9 | 12.4 | 49.3 |
| 4 | <i>Clostridium lavalense</i> HB-452c | 88.5 | 37.2 | 29.5 | 29.0 |
| 5 | <i>Hungatella effluvii</i> HB-02 | 57.9 | 51.2 | 46.7 | 66.5 |
| 6 | <i>Bacteroides caccae</i> HB-11 | 59.0 | 20.7 | 44.1 | 13.2 |
| 7 | <i>Bacteroides dorei</i> HB-12 | 64.9 | 17.0 | 45.4 | 10.3 |
| 8 | <i>Clostridium saudiense</i> HB-142 | 71.2 | 55.0 | 63.3 | 47.5 |
| 9 | <i>Gordonibacter pamelaeae</i> HB-15 | 42.7 | 53.7 | 43.0 | 13.3 |
| 10 | <i>Clostridium hathewayi</i> HB-152 | 62.5 | 63.1 | 62.7 | 40.7 |
| 11 | <i>Bifidobacterium faecale</i> HB-159 | 92.7 | 68.7 | 54.4 | 37.1 |
| 12 | <i>Bifidobacterium adolescentis</i> HB-179 | 23.7 | 46.3 | 27.2 | 46.8 |
| 13 | <i>Parabacteroides distasonis</i> HB-20 | 39.9 | 48.1 | 61.8 | 30.6 |
| 14 | <i>Eubacterium eligens</i> HB-252 | 55.1 | 12.3 | 59.8 | 21.9 |
| 15 | <i>Bacteroides finegoldii</i> HB-31 | 54.8 | 11.8 | 51.9 | 7.3 |
| 16 | <i>Bacteroides salyersiae</i> HB-32 | 27.4 | 48.7 | 43.2 | 45.5 |
| 17 | <i>Gemmiger formicilis</i> HB-325 | 67.0 | 13.2 | 57.8 | 22.4 |
| 18 | <i>Parasutterella excrementihominis</i> HB-330 | 64.7 | 11.2 | 61.5 | 38.9 |
| 19 | <i>Bacteroides xylinosolvens</i> HB-35 | 72.3 | 19.7 | 44.6 | 8.2 |
| 20 | <i>Mediterraneibacter faecis</i> HB-364 | 76.7 | 8.1 | 61.0 | 38.4 |
| 21 | <i>Clostridium aldenense</i> HB-440 | 78.0 | 57.4 | 76.3 | 48.7 |
| 22 | <i>Clostridium bolteae</i> HB-442 | 90.7 | 59.2 | 66.8 | 57.9 |
| 23 | <i>Clostridium scindens</i> HB-444 | 84.8 | 71.2 | 71.8 | 50.4 |
| 24 | <i>Clostridium tyrobutyricum</i> HB-469 | 56.2 | 26.1 | 40.2 | 8.6 |
| 25 | <i>Eisenbergiella tayi</i> HB-612 | 36.0 | 42.2 | 45.7 | 28.4 |
| 26 | <i>Parabacteroides merdae</i> HB-63 | 16.8 | 42.9 | 50.4 | 1.4 |
| 27 | <i>Bacteroides ovatus</i> HB-70 | 66.6 | 7.8 | 46.5 | 12.0 |

TABLE 1B-continued

5-HT Modulating Potential of 104 Human-Derived Strains - Serotonin Release in ng/mL (HM2 media) Measured by ELISA (bolded number indicates a significant amount of serotonin release over pre-determined threshold; see e.g., final row)

| SEQ ID | NO | Strain | Serotonin Release in ng/mL (HM2) Measured by ELISA | | | |
|--------|----|--|---|--------------|-------------|-------------|
| | | | 50% | 10% | 100 ug/mL | 200 ug/mL |
| 28 | | <i>Anaerotruncus colihominis</i> HB-83 | 44.2 | 62.6 | 52.5 | 72.9 |
| 29 | | <i>Enterococcus faecium</i> HB-85 | 72.5 | 37.9 | 5.3 | 49.1 |
| 30 | | <i>Lactobacillus brevis</i> HB-87 | 95.5 | 39.0 | 50.7 | 16.1 |
| 31 | | <i>Hungatella hathewayi</i> HB-01 | 132.7 | 37.0 | 13.4 | 11.2 |
| 32 | | <i>Parabacteroides johnsonii</i> HB-03 | 25.6 | 43.4 | 22.4 | 13.2 |
| 33 | | <i>Bacteroides vulgaris</i> HB-10 | 33.3 | 152.9 | 23.1 | 24.5 |
| 34 | | <i>Bacteroides uniformis</i> HB-13 | 40.2 | 49.7 | 15.6 | 28.8 |
| 35 | | <i>Turicibacter sanguinis</i> HB-147 | 39.9 | 58.8 | 9.2 | 1.1 |
| 36 | | <i>Coprococcus eutactus</i> HB-155 | 59.4 | 8.9 | 32.7 | 11.7 |
| 37 | | <i>Bacteroides cellulosilyticus</i> HB-227 | 61.8 | 57.1 | 20.8 | 27.4 |
| 38 | | <i>Bacteroides plebeius</i> HB-237 | 79.4 | 51.6 | 35.5 | 39.4 |
| 39 | | <i>Erysipelotroctridium ramosum</i> HB-24 | 50.8 | 22.3 | 31.9 | 38.0 |
| 40 | | <i>Bacillus cereus</i> HB-25 | 24.4 | 100.3 | 0.7 | 1.0 |
| 41 | | <i>Agathobacter rectalis</i> HB-257 | 35.1 | 44.4 | 1.0 | 19.1 |
| 42 | | <i>Ruminococcus bicirculans</i> HB-268 | 124.1 | 26.6 | 9.7 | 11.7 |
| 43 | | <i>Clostridium paraputreficum</i> HB-27 | 22.5 | 42.9 | 4.2 | 23.7 |
| 44 | | <i>Collinsella aerofaciens</i> HB-274 | 68.6 | 13.7 | 22.0 | 4.7 |
| 45 | | <i>Oscillibacter</i> sp. HB-28 | 107.6 | 23.5 | 27.1 | 6.8 |
| 46 | | <i>Alistipes onderdonkii</i> HB-311 | 59.6 | 78.5 | 31.6 | 34.9 |
| 47 | | <i>Alistipes putredinis</i> HB-324 | 47.4 | 66.2 | 14.9 | 24.6 |
| 48 | | <i>Bacteroides stercoris</i> HB-33 | 32.4 | 53.3 | 27.3 | 39.3 |
| 49 | | <i>Flintibacter butyricus</i> HB-344 | 73.8 | 14.6 | 34.9 | 8.0 |
| 50 | | <i>Coprococcus comes</i> HB-376 | 70.8 | 21.6 | 31.7 | 10.9 |
| 51 | | <i>Bacteroides Koreensis</i> HB-385 | 70.3 | 52.6 | 29.5 | 30.5 |
| 52 | | <i>Eisenbergiella tayi</i> HB-437 | 41.1 | 54.1 | 2.4 | 14.7 |
| 53 | | <i>Dysosmobaacter wellbionis</i> HB-45 | 82.0 | 35.5 | 25.2 | 11.0 |
| 54 | | <i>Butyrimonas paraviriosa</i> HB-453 | 54.4 | 32.7 | 23.2 | 29.0 |
| 55 | | <i>Flavonifractor plautii</i> HB-472 | 53.6 | 34.4 | 17.4 | 27.5 |
| 56 | | <i>Anaerotruncus colihominis</i> HB-474 | 42.2 | 44.8 | 1.0 | 5.9 |
| 57 | | <i>Intestinimonas butyriciproducens</i> HB-478 | 22.0 | 42.7 | 8.4 | 38.7 |
| 58 | | <i>Bacteroides fragilis</i> HB-58 | 48.2 | 47.0 | 17.7 | 26.5 |
| 59 | | <i>Streptococcus gordonii</i> HB-62 | 284.4 | 23.3 | 22.1 | 4.2 |
| 60 | | <i>Enterococcus faecium</i> HB-640 | 106.2 | 44.0 | 37.7 | 17.7 |
| 61 | | <i>Clostridium clostridioforme</i> HB-642 | 52.8 | 56.8 | 5.7 | 9.3 |
| 62 | | <i>Faecalitalea cylindroides</i> HB-664 | 42.3 | 47.9 | 11.3 | 20.1 |
| 63 | | <i>Bilophila wadsworthia</i> HB-693 | 34.1 | 40.6 | 36.1 | 25.1 |
| 64 | | <i>Bifidobacterium longum</i> HB-71 | 3.5 | 51.9 | 8.5 | 4.9 |
| 65 | | <i>Clostridium hylemonae</i> HB-73 | 36.0 | 69.9 | 4.7 | 12.1 |
| 66 | | <i>Clostridium innoculum</i> HB-82 | 42.2 | 109.9 | 1.0 | 7.7 |
| 67 | | <i>Bifidobacterium breve</i> HB-90 | 3.9 | 44.1 | 1.0 | 1.0 |
| 68 | | <i>Acidaminococcus intestini</i> HB-95 | 15.7 | 154.4 | 1.0 | 10.4 |
| 69 | | <i>Streptococcus gordonii</i> HB-98 | 142.7 | 48.1 | 17.1 | 17.6 |
| 70 | | <i>Romboutsia lituseburensis</i> HB-102 | 6.7 | 14.7 | 20.0 | 47.7 |
| 71 | | <i>Blautia wexlerae</i> HB-16 | 19.9 | 9.2 | 20.2 | 45.2 |
| 72 | | <i>Sutterella wadsworthensis</i> HB-259 | 2.3 | 9.8 | 5.0 | 50.7 |
| 73 | | <i>Bacteroides clarus</i> HB-30 | 41.6 | 21.8 | 51.5 | 10.7 |
| 74 | | <i>Prevotella</i> sp. HB-333 | 13.6 | 21.8 | 22.4 | 46.3 |
| 75 | | <i>Bacteroides thetaiotaomicron</i> HB-34 | 45.8 | 33.6 | 30.8 | 48.0 |
| 76 | | <i>Prevotella copri</i> HB-3 73 | 41.5 | 34.1 | 21.3 | 79.1 |
| 77 | | <i>Dialister invisus</i> HB-387 | 39.2 | 37.5 | 56.1 | 49.9 |
| 78 | | <i>Sellimonas intestinalis</i> HB-443 | 22.5 | 13.6 | 15.1 | 41.7 |
| 79 | | <i>Bittarella massiliensis</i> HB-477 | 21.6 | 29.8 | 12.3 | 41.4 |
| 80 | | <i>Ruminococcus</i> sp. HB-626 | 18.9 | 38.1 | 22.8 | 59.5 |
| 81 | | <i>Prevotella</i> sp. HB-649 | 10.9 | 1.0 | 9.7 | 44.5 |
| 82 | | <i>Longibaculum muris</i> HB-79 | 49.3 | 37.6 | 45.7 | 16.4 |
| 83 | | <i>Ruminococcus bicirculans</i> HB-105 | 45.7 | 30.8 | 28.1 | 19.8 |
| 84 | | <i>Parabacteroides distasonis</i> HB-214 | 43.2 | 34.6 | 9.8 | 35.1 |
| 85 | | <i>Veillonella atypica</i> HB-251 | 25.0 | 28.5 | 3.4 | 24.3 |
| 86 | | <i>Clostridium</i> sp. HB-358 | 44.7 | 3.5 | 33.6 | 12.7 |
| 87 | | <i>Parabacteroides goldsteinii</i> HB-44 | 31.3 | 27.7 | 6.9 | 19.9 |
| 88 | | <i>Clostridium sphenoides</i> HB-470 | 36.5 | 25.8 | 39.9 | 33.0 |
| 89 | | <i>Escherichia coli</i> HB-490 | 35.8 | 23.4 | 28.3 | 10.9 |
| 90 | | <i>Lawsonibacter asaccharolyticus</i> HB-521 | 33.3 | 23.2 | 20.5 | 1.0 |
| 91 | | <i>Gemmiger</i> sp. HB-567 | 36.9 | 27.4 | 24.0 | 1.0 |
| 92 | | <i>Eubacterium callanderi</i> HB-59 | 36.1 | 27.4 | 25.7 | 27.4 |
| 93 | | <i>Intestinimonas massiliensis</i> HB-651 | 29.2 | 21.7 | 1.0 | 38.0 |

TABLE 1B-continued

| 5-HT Modulating Potential of 104 Human-Derived Strains - Serotonin Release in ng/mL (HM2 media) Measured by ELISA (bolded number indicates a significant amount of serotonin release over pre-determined threshold; see e.g., final row) | | | | | |
|--|--|---|-----------------|----------------------|-----------------|
| | | Serotonin Release in ng/mL (HM2) Measured by ELISA | | | |
| SEQ ID | Strain | RIN14B - Supernatant | | RIN14B - Cell Pellet | |
| | | 50% | 10% | 100 ug/mL | 200 ug/mL |
| 94 | <i>Clostridium symbiosum</i> HB-67 | 32.5 | 26.4 | 1.9 | 30.1 |
| 95 | <i>Longibaculum</i> sp. HB-681 | 36.1 | 30.1 | 6.7 | 20.1 |
| 96 | <i>Blautia obeum</i> HB-14 | 9.0 | 6.4 | 6.6 | 30.4 |
| 97 | <i>Dorea longicatena</i> HB-17 | 22.8 | 3.5 | 5.8 | 18.8 |
| 98 | <i>Eubacterium rectale</i> HB-22 | 22.7 | 14.6 | 6.4 | 22.3 |
| 99 | <i>Blautia coccoides</i> HB-23 | 16.2 | 31.7 | 1.0 | 9.1 |
| 100 | <i>Bifidobacterium longum</i> HB-234 | 23.1 | 36.3 | 1.0 | 13.2 |
| 101 | <i>Slackia isoflavoniconvertens</i> HB-326 | 12.5 | 6.4 | 6.3 | 36.8 |
| 102 | <i>Lachnoclostridium</i> sp. HB-698 | 16.8 | 25.3 | 2.3 | 27.2 |
| 103 | <i>Coprococcus comes</i> HB-80 | 15.7 | 5.3 | 4.9 | 11.4 |
| 104 | <i>Clostridium butyricum</i> HB-88 | 25.7 | 18.4 | 1.0 | 9.3 |
| Pre-determined threshold | | >50.0 | >40.0 | >40.0 | >40.0 |

TABLE 1C

| 5-HT Modulating Potential of 104 Human-Derived Strains - Serotonin Release in ng/mL (HM2) Measured by LC/MS (bolded number indicates a significant amount of serotonin release over pre-determined threshold; see e.g., final row). | | | | | |
|---|--|---|-------------|-----------------------|-------------|
| | | Serotonin Release in ng/mL (HM2) Measured by LC/MS | | | |
| SEQ ID | Strain | RIN14B - Supernatant | | Bacterial supernatant | |
| | | 50% | 10% | 50% | 10% |
| 1 | <i>Ruminococcus gnavus</i> HB-40 | 331.3 | — | 380.6 | 89.5 |
| 2 | <i>Ruminococcus gnavus</i> HB-516 | 225.6 | 48.8 | 123.2 | 66.6 |
| 3 | <i>Enterococcus durans</i> HB-48 | 15.6 | 8.5 | 11.0 | 4.5 |
| 4 | <i>Clostridium lavalense</i> HB-452c | 22.0 | 7.8 | 10.6 | 4.2 |
| 5 | <i>Hungatella effluvii</i> HB-02 | — | — | — | — |
| 6 | <i>Bacteroides caccae</i> HB-11 | 7.3 | 4.1 | 0.3 | 1.1 |
| 7 | <i>Bacteroides dorei</i> HB-12 | 13.6 | 5.0 | 0.5 | 0.5 |
| 8 | <i>Clostridium saudicense</i> HB-142 | 5.4 | 3.0 | 0.3 | 0.5 |
| 9 | <i>Gordonibacter pamelaeae</i> HB-15 | 5.7 | 8.8 | 0.9 | 0.0 |
| 10 | <i>Clostridium hathewayi</i> HB-152 | — | — | — | — |
| 11 | <i>Bifidobacterium faecale</i> HB-159 | 9.1 | 5.0 | 1.0 | 0.5 |
| 12 | <i>Bifidobacterium adolescentis</i> HB-179 | — | — | — | — |
| 13 | <i>Parabacteroides distasonis</i> HB-20 | — | — | — | — |
| 14 | <i>Eubacterium eligens</i> HB-252 | 9.6 | 3.8 | 0.4 | 0.7 |
| 15 | <i>Bacteroides finegoldii</i> HB-31 | 9.1 | 3.8 | 0.9 | 0.8 |
| 16 | <i>Bacteroides salyersiae</i> HB-32 | 7.9 | 11.0 | 1.4 | 0.2 |
| 17 | <i>Gemmiger formicilis</i> HB-325 | — | — | — | — |
| 18 | <i>Parasutterella excrementihominis</i> HB-330 | — | — | — | — |
| 19 | <i>Bacteroides xylosolvens</i> HB-35 | 9.1 | 4.6 | 0.5 | 0.0 |
| 20 | <i>Mediterraneibacter faecis</i> HB-364 | — | — | — | — |
| 21 | <i>Clostridium aldenense</i> HB-440 | — | — | — | — |
| 22 | <i>Clostridium bolteae</i> HB-442 | — | — | — | — |
| 23 | <i>Clostridium scindens</i> HB-444 | 9.9 | 9.9 | 0.5 | 0.7 |
| 24 | <i>Clostridium tyrobutyricum</i> HB-469 | 6.0 | 5.8 | 0.2 | 0.9 |
| 25 | <i>Eisenbergiella tayi</i> HB-612 | — | — | — | — |
| 26 | <i>Parabacteroides merdae</i> HB-63 | 13.8 | 7.7 | 1.1 | 0.1 |
| 27 | <i>Bacteroides ovatus</i> HB-70 | — | — | — | — |
| 28 | <i>Anaerotruncus colihominis</i> HB-83 | 8.4 | 11.1 | 0.6 | 0.0 |
| 29 | <i>Enterococcus faecium</i> HB-85 | — | — | — | — |
| 30 | <i>Lactobacillus brevis</i> HB-87 | 4.8 | 9.0 | 1.1 | 0.5 |
| 31 | <i>Hungatella hathewayi</i> HB-01 | — | — | — | — |
| 32 | <i>Parabacteroides johnsonii</i> HB-03 | — | — | — | — |
| 33 | <i>Bacteroides vulgatus</i> HB-10 | — | — | — | — |
| 34 | <i>Bacteroides uniformis</i> HB-13 | — | — | — | — |
| 35 | <i>Turicibacter sanguinis</i> HB-147 | 15.4 | 9.3 | 0.4 | 0.1 |
| 36 | <i>Coprococcus eutactus</i> HB-155 | 10.2 | 5.0 | 0.3 | 0.6 |
| 37 | <i>Bacteroides cellulosilyticus</i> HB-227 | — | — | — | — |

TABLE 1C-continued

| SEQ ID | | Serotonin Release in ng/mL (HM2) Measured by LC/MS | | | |
|--------|--|---|-----------------------|-----|-----|
| NO | Strain | RIN14B - Supernatant | Bacterial supernatant | 50% | 10% |
| 38 | <i>Bacteroides plebeius</i> HB-237 | — | — | — | — |
| 39 | <i>Erysipelotoclostridium ramosum</i> HB-24 | 27.8 | 5.5 | 0.4 | 0.0 |
| 40 | <i>Bacillus cereus</i> HB-25 | — | — | — | — |
| 41 | <i>Agathobacter rectalis</i> HB-257 | — | — | — | — |
| 42 | <i>Ruminococcus bicirculans</i> HB-268 | — | — | — | — |
| 43 | <i>Clostridium paraputrificum</i> HB-27 | — | — | — | — |
| 44 | <i>Collinsella aerofaciens</i> HB-274 | 8.4 | 6.3 | 0.5 | 0.7 |
| 45 | <i>Oscillibacter</i> sp. HB-28 | — | — | — | — |
| 46 | <i>Alistipes onderdonkii</i> HB-311 | 3.5 | 7.1 | 0.3 | 0.9 |
| 47 | <i>Alistipes putredinis</i> HB-324 | — | — | — | — |
| 48 | <i>Bacteroides stercoris</i> HB-33 | — | — | — | — |
| 49 | <i>Flintibacter butyricus</i> HB-344 | — | — | — | — |
| 50 | <i>Coprococcus comes</i> HB-376 | 7.0 | 9.1 | 0.6 | 0.8 |
| 51 | <i>Bacteroides koreensis</i> HB-385 | — | — | — | — |
| 52 | <i>Eisenbergiella tayi</i> HB-437 | — | — | — | — |
| 53 | <i>Dysosmabacter welltonis</i> HB-45 | — | — | — | — |
| 54 | <i>Butyrimonas paraviriosa</i> HB-453 | 21.3 | 11 | 0.5 | — |
| 55 | <i>Flavonifractor plautii</i> HB-472 | — | — | — | — |
| 56 | <i>Anaerotruncus colihominis</i> HB-474 | — | — | — | — |
| 57 | <i>Intestinimonas butyriciproducens</i> HB-478 | — | — | — | — |
| 58 | <i>Bacteroides fragilis</i> HB-58 | — | — | — | — |
| 59 | <i>Streptococcus gordonii</i> HB-62 | — | — | — | — |
| 60 | <i>Enterococcus faecium</i> HB-640 | — | — | — | — |
| 61 | <i>Clostridium clostridiiforme</i> HB-642 | — | — | — | — |
| 62 | <i>Faecalitalea cylindroides</i> HB-664 | 4.2 | 7.8 | 0.3 | 0.6 |
| 63 | <i>Bilophila wadsworthia</i> HB-693 | — | — | — | — |
| 64 | <i>Bifidobacterium longum</i> HB-71 | — | — | — | — |
| 65 | <i>Clostridium hylemonae</i> HB-73 | — | — | — | — |
| 66 | <i>Clostridium innoculum</i> HB-82 | — | — | — | — |
| 67 | <i>Bifidobacterium breve</i> HB-90 | — | — | — | — |
| 68 | <i>Acidaminococcus intestini</i> HB-95 | — | — | — | — |
| 69 | <i>Streptococcus gordonii</i> HB-98 | 5.7 | 10.8 | 0.6 | 0.7 |
| 70 | <i>Romboutsia lituseburensis</i> HB-102 | — | — | — | — |
| 71 | <i>Blautia wexlerae</i> HB-16 | — | — | — | — |
| 72 | <i>Sutterella wadsworthensis</i> HB-259 | — | — | — | — |
| 73 | <i>Bacteroides clarus</i> HB-30 | 6.6 | 4.1 | 0.2 | 0.8 |
| 74 | <i>Prevotella</i> sp. HB-333 | — | — | — | — |
| 75 | <i>Bacteroides thetaiotomicron</i> HB-34 | — | — | — | — |
| 76 | <i>Prevotella copri</i> HB-373 | 10.1 | 2.9 | 0.9 | 0.8 |
| 77 | <i>Dialister invisus</i> HB-387 | — | — | — | — |
| 78 | <i>Sellimonas intestinalis</i> HB-443 | — | — | — | — |
| 79 | <i>Bittarella massiliensis</i> HB-477 | — | — | — | — |
| 80 | <i>Ruminococcus</i> sp. HB-626 | 4.7 | 7.1 | 0.8 | 0.0 |
| 81 | <i>Prevotella</i> sp. HB-649 | — | — | — | — |
| 82 | <i>Longibaculum muris</i> HB-79 | — | — | — | — |
| 83 | <i>Ruminococcus bicirculans</i> HB-105 | — | — | — | — |
| 84 | <i>Parabacteroides distasonis</i> HB-214 | — | — | — | — |
| 85 | <i>Veillonella atypica</i> HB-251 | — | — | — | — |
| 86 | <i>Clostridium</i> sp. HB-358 | — | — | — | — |
| 87 | <i>Parabacteroides goldsteinii</i> HB-44 | — | — | — | — |
| 88 | <i>Clostridium sphenoides</i> HB-470 | — | — | — | — |
| 89 | <i>Escherichia coli</i> HB-490 | — | — | — | — |
| 90 | <i>Lawsonibacter asaccharolyticus</i> HB-521 | — | — | — | — |
| 91 | <i>Gemmiger</i> sp. HB-567 | — | — | — | — |
| 92 | <i>Eubacterium callanderi</i> HB-59 | — | — | — | — |
| 93 | <i>Intestinimonas massiliensis</i> HB-651 | — | — | — | — |
| 94 | <i>Clostridium symbiosum</i> HB-67 | — | — | — | — |
| 95 | <i>Longibaculum</i> sp. HB-681 | — | — | — | — |
| 96 | <i>Blautia obeum</i> HB-14 | — | — | — | — |
| 97 | <i>Dorea longicatena</i> HB-17 | — | — | — | — |
| 98 | <i>Eubacterium rectale</i> HB-22 | — | — | — | — |
| 99 | <i>Blautia coccoides</i> HB-23 | — | — | — | — |
| 100 | <i>Bifidobacterium longum</i> HB-234 | — | — | — | — |
| 101 | <i>Slackia isoflavitoniconvertens</i> HB-326 | — | — | — | — |
| 102 | <i>Lachnoclostridium</i> sp. HB-698 | — | — | — | — |
| 103 | <i>Coprococcus comes</i> HB-80 | — | — | — | — |

TABLE 1C-continued

5-HT Modulating Potential of 104 Human-Derived Strains - Serotonin Release in ng/mL (HM2) Measured by LC/MS (bolded number indicates a significant amount of serotonin release over pre-determined threshold; see e.g., final row).

| | | Serotonin Release in ng/mL (HM2) Measured by LC/MS | | | |
|--------|------------------------------------|---|----------------|-----------------------|----------------|
| SEQ ID | NO | RIN14B - Supernatant | | Bacterial supernatant | |
| | | Strain | 50% | 10% | 50% |
| 104 | <i>Clostridium butyricum</i> HB-88 | — | — | — | — |
| | Pre-determined threshold | | >9.1 | >7.0 | >2.0 |

TABLE 1D

5-HT Modulating Potential of 104 Human-Derived Strains - Serotonin Release in ng/mL (BHI medium) Measured by LC/MS; and Tryptamine in 50% Bacterial Supernatant (ng/mL) Measured by LC/MS (bolded number indicates a significant amount of serotonin or tryptamine release over pre-determined threshold; see e.g., final row).

| | | Serotonin Release in ng/mL (BHI medium) Measured by LC/MS | | Tryptamine in 50% Bacterial Supernatant (ng/mL) Measured by LC/MS | |
|--------|--|---|--------------|--|----------------|
| SEQ ID | NO | RIN-14B | | Bacterial Supernatant | |
| | | Strain | 50% | 50% | HM2 |
| 1 | <i>Ruminococcus gnavus</i> HB-40 | 136.6 | 131.6 | 36529.2 | 20667.9 |
| 2 | <i>Ruminococcus gnavus</i> HB-516 | — | — | 21308.7 | — |
| 3 | <i>Enterococcus durans</i> HB-48 | 17.6 | 9 | 756.2 | 733.8 |
| 4 | <i>Clostridium lavalense</i> HB-452c | 15.4 | 6.6 | 729 | 488.7 |
| 5 | <i>Hungatella effuvii</i> HB-02 | — | — | — | — |
| 6 | <i>Bacteroides caccae</i> HB-11 | — | — | 45.3 | — |
| 7 | <i>Bacteroides dorei</i> HB-12 | 6.7 | 4.1 | 48.1 | 22.6 |
| 8 | <i>Clostridium saudiense</i> HB-142 | — | — | 40.9 | — |
| 9 | <i>Gordonibacter pamelaeae</i> HB-15 | — | — | 58.5 | — |
| 10 | <i>Clostridium hathewayi</i> HB-152 | — | — | — | — |
| 11 | <i>Bifidobacterium faecale</i> HB-159 | 10.1 | 2.4 | 47.3 | 21.5 |
| 12 | <i>Bifidobacterium adolescentis</i> HB-179 | — | — | — | — |
| 13 | <i>Parabacteroides distasonis</i> HB-20 | — | — | — | — |
| 14 | <i>Eubacterium eligens</i> HB-252 | — | — | 52.7 | — |
| 15 | <i>Bacteroides finegoldii</i> HB-31 | — | — | 47.4 | — |
| 16 | <i>Bacteroides salyersiae</i> HB-32 | — | — | 40.2 | — |
| 17 | <i>Gemmiger formicilis</i> HB-325 | — | — | — | — |
| 18 | <i>Parasutterella excrementihominis</i> HB-330 | — | — | — | — |
| 19 | <i>Bacteroides xylosolyticus</i> HB-35 | — | — | 38.3 | — |
| 20 | <i>Mediterraneibacter faecis</i> HB-364 | — | — | — | — |
| 21 | <i>Clostridium aldenense</i> HB-440 | — | — | — | — |
| 22 | <i>Clostridium bolteae</i> HB-442 | — | — | — | — |
| 23 | <i>Clostridium scindens</i> HB-444 | 10.1 | 2.3 | 60.7 | 22.6 |
| 24 | <i>Clostridium tyrobutyricum</i> HB-469 | — | — | 51.9 | — |
| 25 | <i>Eisenbergiella tayi</i> HB-612 | — | — | — | — |
| 26 | <i>Parabacteroides merdae</i> HB-63 | — | — | 41.5 | — |
| 27 | <i>Bacteroides ovatus</i> HB-70 | — | — | — | — |
| 28 | <i>Anaerotruncus colihominis</i> HB-83 | — | — | 48.4 | — |
| 29 | <i>Enterococcus faecium</i> HB-85 | — | — | — | — |
| 30 | <i>Lactobacillus brevis</i> HB-87 | 11.5 | 3.3 | 60.1 | 23.4 |
| 31 | <i>Hungatella hathewayi</i> HB-01 | — | — | — | — |
| 32 | <i>Parabacteroides johnsonii</i> HB-03 | — | — | — | — |
| 33 | <i>Bacteroides vulgatus</i> HB-10 | — | — | — | — |
| 34 | <i>Bacteroides uniformis</i> HB-13 | — | — | — | — |
| 35 | <i>Turicibacter sanguinis</i> HB-147 | 5.6 | 3.2 | 45.2 | 24.2 |
| 36 | <i>Coprococcus eutactus</i> HB-155 | 8.3 | 2.1 | 46.5 | 22.9 |
| 37 | <i>Bacteroides cellulosilyticus</i> HB-227 | — | — | — | — |
| 38 | <i>Bacteroides plebeius</i> HB-237 | — | — | — | — |
| 39 | <i>Erysipelatoclostridium ramosum</i> HB-24 | 10.5 | 3.1 | 50.5 | 21.5 |
| 40 | <i>Bacillus cereus</i> HB-25 | — | — | — | — |
| 41 | <i>Agathobacter rectalis</i> HB-257 | — | — | — | — |
| 42 | <i>Ruminococcus bicirculans</i> HB-268 | — | — | — | — |
| 43 | <i>Clostridium paraputrificum</i> HB-27 | — | — | — | — |
| 44 | <i>Collinsella aerofaciens</i> HB-274 | — | — | 43.6 | — |

TABLE 1D-continued

5-HT Modulating Potential of 104 Human-Derived Strains - Serotonin Release in ng/mL (BHI medium) Measured by LC/MS; and Tryptamine in 50% Bacterial Supernatant (ng/mL)
Measured by LC/MS (bolded number indicates a significant amount of serotonin or tryptamine release over pre-determined threshold; see e.g., final row).

| SEQ ID | NO | Strain | Serotonin Release in ng/mL (BHI medium) Measured by LC/MS | | Tryptamine in 50% Bacterial Supernatant (ng/mL) Measured by LC/MS | |
|--------|-----|--|--|-----------------------|---|------------------|
| | | | RIN-14B | Bacterial Supernatant | HM2 | BHI |
| | 45 | <i>Oscillibacter</i> sp. HB-28 | — | — | — | — |
| | 46 | <i>Alistipes onderdonkii</i> HB-311 | — | — | 52.2 | — |
| | 47 | <i>Alistipes putredinis</i> HB-324 | — | — | — | — |
| | 48 | <i>Bacteroides stercoris</i> HB-33 | — | — | — | — |
| | 49 | <i>Flintibacter butyricus</i> HB-344 | — | — | — | — |
| | 50 | <i>Coprococcus comes</i> HB-376 | — | — | 50.6 | — |
| | 51 | <i>Bacteroides koreensis</i> HB-385 | — | — | — | — |
| | 52 | <i>Eisenbergiella tayi</i> HB-437 | — | — | — | — |
| | 53 | <i>Dysosmabacter welbionis</i> HB-45 | — | — | — | — |
| | 54 | <i>Butyrimonas paraviriosa</i> HB-453 | 14.8 | 3.2 | 51.7 | 22.3 |
| | 55 | <i>Flavonifractor plautii</i> HB-472 | — | — | — | — |
| | 56 | <i>Anaerotruncus colihominis</i> HB-474 | — | — | — | — |
| | 57 | <i>Intestinimonas butyriciproducens</i> HB-478 | — | — | — | — |
| | 58 | <i>Bacteroides fragilis</i> HB-58 | — | — | — | — |
| | 59 | <i>Streptococcus gordonii</i> HB-62 | — | — | — | — |
| | 60 | <i>Enterococcus faecium</i> HB-640 | — | — | — | — |
| | 61 | <i>Clostridium clostridiiforme</i> HB-642 | — | — | — | — |
| | 62 | <i>Faecalitalea cylindroides</i> HB-664 | 9.2 | 2.8 | 52.9 | 21.8 |
| | 63 | <i>Bilophila wadsworthia</i> HB-693 | — | — | — | — |
| | 64 | <i>Bifidobacterium longum</i> HB-71 | — | — | — | — |
| | 65 | <i>Clostridium hylemonae</i> HB-73 | — | — | — | — |
| | 66 | <i>Clostridium innoculum</i> HB-82 | — | — | — | — |
| | 67 | <i>Bifidobacterium breve</i> HB-90 | — | — | — | — |
| | 68 | <i>Acidaminococcus intestini</i> HB-95 | — | — | — | — |
| | 69 | <i>Streptococcus gordonii</i> HB-98 | — | — | 42.5 | — |
| | 70 | <i>Romboutsia lituseburensis</i> HB-102 | — | — | — | — |
| | 71 | <i>Blautia wexlerae</i> HB-16 | — | — | — | — |
| | 72 | <i>Sutterella wadsworthensis</i> HB-259 | — | — | — | — |
| | 73 | <i>Bacteroides clarus</i> HB-30 | — | — | 42 | — |
| | 74 | <i>Prevotella</i> sp. HB-333 | — | — | — | — |
| | 75 | <i>Bacteroides thetaiotaomicron</i> HB-34 | — | — | — | — |
| | 76 | <i>Prevotella copri</i> HB-373 | — | — | 49.7 | — |
| | 77 | <i>Dialister invisus</i> HB-387 | — | — | — | — |
| | 78 | <i>Sellimonas intestinalis</i> HB-443 | — | — | — | — |
| | 79 | <i>Bittarella massiliensis</i> HB-477 | — | — | — | — |
| | 80 | <i>Ruminococcus</i> sp. HB-626 | 9.9 | 2.7 | 42.5 | 20.3 |
| | 81 | <i>Prevotella</i> HB-HB-649 | — | — | — | — |
| | 82 | <i>Longibaculum muris</i> HB-79 | — | — | — | — |
| | 83 | <i>Ruminococcus bicirculans</i> HB-105 | — | — | — | — |
| | 84 | <i>Parabacteroides distasonis</i> HB-214 | — | — | — | — |
| | 85 | <i>Veillonella atypica</i> HB-251 | — | — | — | — |
| | 86 | <i>Clostridium</i> sp. HB-358 | — | — | — | — |
| | 87 | <i>Parabacteroides goldsteinii</i> HB-44 | — | — | — | — |
| | 88 | <i>Clostridium sphenoides</i> HB-470 | — | — | — | — |
| | 89 | <i>Escherichia coli</i> HB-490 | — | — | — | — |
| | 90 | <i>Lawsonibacter asaccharolyticus</i> HB-521 | — | — | — | — |
| | 91 | <i>Gemmiger</i> sp. HB-567 | — | — | — | — |
| | 92 | <i>Eubacterium callanderi</i> HB-59 | — | — | — | — |
| | 93 | <i>Intestinimonas massiliensis</i> HB-651 | — | — | — | — |
| | 94 | <i>Clostridium symbiosum</i> HB-67 | — | — | — | — |
| | 95 | <i>Longibaculum</i> sp. HB-681 | — | — | — | — |
| | 96 | <i>Blautia obeum</i> HB-14 | — | — | — | — |
| | 97 | <i>Dorea longicatena</i> HB-17 | — | — | — | — |
| | 98 | <i>Eubacterium rectale</i> HB-22 | — | — | — | — |
| | 99 | <i>Blautia coccoides</i> HB-23 | — | — | — | — |
| | 100 | <i>Bifidobacterium longum</i> HB-234 | — | — | — | — |
| | 101 | <i>Slackia isoflavoniconvertens</i> HB-326 | — | — | — | — |
| | 102 | <i>Lachnoclostridium</i> sp. HB-698 | — | — | — | — |
| | 103 | <i>Coprococcus comes</i> HB-80 | — | — | — | — |
| | 104 | <i>Clostridium butyricum</i> HB-88 | — | — | — | — |
| | | Pre-determined threshold | >10.0 | >3.2 | >103.0 | >103.0 |

TABLE 2

Summary of SEQ ID NOs

| Sequence Category | SEQ ID NOs |
|---|------------------|
| 5-HT Producer 16S rDNA sequence | 1-4 |
| 5-HT Modulating Supernatant Producers 16S rDNA sequence | 1-2; 5-69 |
| 5-HT Modulating Pellet Producers 16S rDNA sequence | 1-3, 5-30; 70-82 |
| 5-HT Non- or Low Modulators 16S rDNA sequence | 83-95 |
| 5-HT Negative Modulators 16S rDNA sequence | 96-104 |
| 5-HT Agonist Producers 16S rDNA sequence | 1-4; 105-114 |
| Example Tryptophan Decarboxylases (e.g., EC 4.1.1.105) | 115-119 |
| Example Tryptophan Hydroxylases (e.g., EC 1.14.16.4) | 120-126 |
| Example Aromatic L-amino acid decarboxylases (e.g., EC 4.1.1.28) | 127-133 |
| Example Anaerobic Hydroxylase | 134 |
| Example Tryptophan Production Enzymes (EC 4.2.1.20, EC 4.1.1.48, EC 2.4.2.18, EC 4.1.3.27, EC 5.3.1.24, EC 5.3.1.36) | 135-163 |
| Example Acyl-CoA dehydrogenases (e.g., EC 1.3.99.3, EC 1.3.8.7; EC 1.3.8.8; EC 1.3.8.9) | 164-171 |
| Other bacterial enzymes involved in 5-HT agonist or modifier production (e.g., EC 4.1.99.1; EC 2.8.3.17; EC 4.2.1.175; EC 5.6.1.9; EC 2.1.1.—) | 172-184 |
| Example Decarboxylases (see e.g., FIG. 1) (e.g., EC 1.1.1; EC 1.1.1.40; EC 4.1.1; EC 4.1.1.18; EC 4.1.1.17; EC 4.1.1.19; EC 4.1.1.20; EC 4.1.1.23; EC 4.1.1.3; EC 4.1.1.36; EC 4.1.1.41; EC 4.1.1.44; EC 4.1.1.65; EC 4.1.1.81; EC 4.1.1.96; EC 6.3.2.5; or EC 6.4.1.2) | 185-226 |
| Example Phenylalanine Hydroxylase (e.g., EC 1.14.16.1) | 227 |
| Example N-methylated tryptophan derivative-producing enzymes (e.g., EC 2.1.1.44; EC 2.1.1.— or EC 2.1.1.17) | 228-229 |

SEQUENCE LISTING

Sequence total quantity: 229

SEQ ID NO: 1 moltype = DNA length = 1301
 FEATURE Location/Qualifiers
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 source 1..1301 mol_type = unassigned DNA
 organism = Ruminococcus gnavus

SEQUENCE: 1

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geaatca

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organism = Enterococcus durans

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moltype = DNA length = 1268
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 source 1..627
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 organism = Hungatella effluvii
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 note = HB-11_Bacteroides_caccae
 source 1..1396
 mol_type = unassigned DNA
 organism = Bacteroides caccae
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 source 1..1400
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 organism = Bacteroides dorei
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source                 1..1386
mol_type = unassigned DNA
organism = Clostridium saudiense
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source 1..1380 mol_type = unassigned DNA
organism = Gordonibacter pamelaeae
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source 1..1341
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organism = Clostridium hathewayi
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organism = Bifidobacterium faecale
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| | note = n is a, c, g, or t | |
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| | organism = Parabacteroides distasonis | |

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| SEQUENCE: 13 | | | | | | |
| ggcgccgagcc | tgaccnccn | agtccggtga | gggatgaagg | ttctatggat | cgtaaaac | 60 |
| ttttataaagg | gaataaaatg | cgggacgtgt | cccggtttgt | atgtaccc | tgaataagg | 120 |
| tcggctaact | ccgtgcgc | agccgcggta | atacggagg | tccgagcg | atccggattt | 180 |
| atgggttta | aaagggtcg | aggccgcctt | ttaagtcc | gggtgaaa | gtgtggctaa | 240 |
| ccatagattt | ggccgtt | aaatgggggt | tgatgtatgt | tgaggcaggc | ggaatgcgt | 300 |
| gtgttagcggt | gaaatgttta | gatatcacgc | agaaacccca | ttgcgaaggc | agcgtcc | 360 |
| gcccattgt | acgctgtatgc | acgaaagcgt | ggggatcaaa | caggattaga | taccctgtt | 420 |
| gtccacgc | taaaatgt | tcatactgt | tttgcgat | agtgtaa | gcacacgc | 480 |
| agcggttaatg | gatccac | ggggatcgc | cggtcaac | gaaatc | gaaattgac | 540 |
| ggggccccc | caagcgagg | aatatgtgtt | ttaattcgt | gatacgc | gaaacctacc | 600 |
| cgggtttt | ccgatcc | ccgagggtt | aaacac | cttagcaat | ccgttgcga | 660 |
| gtgtcgat | gttgcgtc | agctcgtgt | gtgaggtgt | ggcttaa | gttgcgtc | 720 |
| cgcaccc | ccactatgtt | actaacatgt | gtatgttgg | actctgg | gactgc | 780 |
| gtaaatgtcg | aggaaggccg | ggatgac | tttttttttt | ggcccttata | tcggggccg | 840 |
| cacacgtt | acaatggcgt | ggacaatgg | aaatccat | ggcgcacagg | gcaatcccc | 900 |
| aaacccatgtc | tcgttgc | tcggatgt | caacccat | ccgtgtact | ggatccgt | 960 |
| gtaaatgcgc | atcagccat | ggccgggt | taatgttcc | ggccctgt | acacccccc | 1020 |
| tcagccat | ggagccgggg | gtaccc | tcgttgc | aaaggatc | cct | 1073 |

| | | |
|---------------|-----------------------------------|---------------|
| SEQ_ID_NO: 14 | moltype = DNA | length = 1411 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..1411 | |
| | note = HB-252_Eubacterium_eligens | |
| source | 1..1411 | |
| | mol_type = unassigned DNA | |
| | organism = Eubacterium eligens | |

| | | | | | | |
|--------------|------------|------------|------------|-----------|-----------|------|
| SEQUENCE: 14 | | | | | | |
| aagtccgaa | aaggcattt | cagacaggat | atcttcgggt | tatgtaa | gtcttat | 60 |
| tgatgtccgg | acgggtt | aacgcgtgg | taacctgc | tgtactgg | gatagc | 120 |
| ggaaaacggct | gttataat | ccatagc | caatgttgc | tgcata | gtgtttt | 180 |
| cgggtgtata | agatggacc | cgctgtt | atgtatgtt | tgagata | acccacca | 240 |
| gacgacgtca | gtagccgacc | tgaggggt | accggccaca | ttgggact | gacacggcc | 300 |
| agactccat | ggggccgc | agtggtt | atgcaca | ggggaaact | ctgtgc | 360 |
| gacgcccgc | gggttgc | gtatgtt | atgtt | atgtt | atgtt | 420 |
| gacggtaat | gactaa | ctccgg | atacgttgc | cgaccc | ggaaat | 480 |
| ggagcaacgc | ttatccgt | ttactgg | taaagg | gtatgtt | ggcc | 540 |
| gaagtgtaaa | tccgggctc | aacccgg | ctgtttt | actgt | atgtt | 600 |
| ggagggttgc | gttgcattt | tagtgc | gtgaaat | atgtt | ggaaac | 660 |
| agtggcgaag | ggggctt | tgatgtt | tgatgtt | tgatgtt | tgatgtt | 720 |
| aacaggat | ataccctt | tttgc | cgatgtt | gtatgtt | ggcc | 780 |
| cataagggt | tcgggtcc | agcaac | ataatgtt | cacccgg | gtacgtt | 840 |
| aagaatgaa | tccaaaggaa | ttgacggg | cccgcaca | cggtgg | gatgtt | 900 |
| ttcgaagcaa | cgcgaaga | cttacca | cttgacat | cactgac | acagtaat | 960 |
| gtcccttct | tcgggac | ggagac | gggtgc | atgtt | tcgtgt | 1020 |
| agatgttgc | ttaaatcc | caacgc | aaccctat | cttagt | agcgtt | 1080 |

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tgggcactct agggagactg ccaggataa cctggaggaa ggtggggatg acgtcaaatc 1140
atcatgcccc ttatgacttg ggctcacac 9tgcataaat ggcgttaaca aagtgaagcg 1200
aagtctgtag gccaagcaaa tcacaaaaat aacgtctcaq ttccgattgt achtgcac 1260
tcgactacat gaagctggaa tcgctagtaa tcgcagatca gaatgctgcg gtgaatacgt 1320
tcccgggtct tgtacacacc gcccgtcaca ccatgggatg cgaaaatgcc cgaagtccgt 1380
gacctaaca gagaaggagc cgccgaaggc a 1411
```

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SEQ ID NO: 15 moltype = DNA length = 1391
FEATURE Location/Qualifiers
misc_feature 1..1391
note = HB-31_Bacteroides_finegoldii
source 1..1391
mol_type = unassigned DNA
organism = Bacteroides finegoldii
```

```
SEQUENCE: 15
gcagtcgagg ggcagcattt tagttgtct qcaaactaaa gatggcgacc ggcgcacggg 60
ttagtaacac gtatccaacc tgccgataac tcagggatag ctttcgaaa gaaagattaa 120
tacctgtatgg cataggatta tcgcgtatca atccattaa aqaatttcg ttatcgatgg 180
ggatgcgttc cattaggcg ttggtgatgg aacggctcaaa caaaccttcg atggataggg 240
gttctgagag gaagggtcccc cacatggaa ctgagacacg gtccaaactc ctacggagg 300
cagcagttag gaatattggt caatggacgg gagtctgaac cagccaagta gcgtgaagga 360
tgactgcct atgggttgta aacttcttt atacgggaaat aaagtgtatcc acgtgtgggt 420
ttttgtatgt accgttatgaa taaggatcg ctaactccgt ggcgcggcc ggggttaac 480
ggaggatccg agcggtatcc ggatggatgg ggtttaaagg gacgcgtatgt ggattgtta 540
gtcagttgtg aaagtttgcg gctcaaccgt aaaattgcg ttgatactgg cagtctttag 600
tacagtagag gtggggcgaa ttctgttgtt agcggtaaaa tgcttagata tcacgaagaa 660
ctcgatgtc gaaaggcagct cactggactg caactgacac ttagtgcgtc aagtgtgggt 720
atcaaacagg attagatacc ctggtagtc acacagtaaa cgtatgtatcc tcgcgttgg 780
cgatataccg taagcgccca agcgaageg ttaagtattt caccctgggg gtaacggccgc 840
aacgggtaaa ctcggaaaggaa ttgacggggg cccgcacaaag cggaggaaata tgggtttaa 900
ttcgtatgtc cgcggaaac cttacccggg cttaaatttac atttgcgaaata tctggaaaca 960
ggtagccgt aaggcaaatg tgaagggtgt gcatgggtt cgtcgtcgtc tgccgtgagg 1020
tgccgttta aagtgcataa cgagcgaac ccttacccgtt agttactaac aggtcatgt 1080
gaggactctg gagagactgc cgtcgtaaga tggagggatg gtcgtcaatca 1140
gcacggccct taacgtccggg gctacacacgg tgggttacacg aaggcagcta 1200
cctgggtgaca ggtgtatcc cccaaaccatc tctctcgtt cggatcgaaatc tctgcacccc 1260
gacttcgtga agctgttgc gctgtatcc cgcgtatccg catggggccg tgaatacgtt 1320
cccgccctt gtacacaccg cccgtcaago catgaaagcc gggggatcgtt gaagtacgt 1380
acccgcgaggaa g 1391
```

```
SEQ ID NO: 16 moltype = DNA length = 1400
FEATURE Location/Qualifiers
misc_feature 1..1400
note = HB-32_Bacteroides_salyersiae
misc_feature 1387
note = n is a, c, g, or t
source 1..1400
mol_type = unassigned DNA
organism = Bacteroides salyersiae
```

```
SEQUENCE: 16
gcagtcgagg ggcatcgagg ttagcaata caccgtggc gaccggcgca cgggtgatg 60
acacgtatcc aacctgcctt ttactcgggg atgccttc gaaagaaaga ttaatacccg 120
atggcataac ataacctctt gggttggta ttaaagaat tcggtagagg atgggtatgc 180
gttccattag gcagttggcg gggtaacggc ccaccaaacc ttgcgtatggt aggggttctg 240
agaggaaatg ccccccacat ggaactgaga cacggccaa actccatccg gggcggcc 300
tgaggaatat tggtaatggc gcgagaccc gaaacccggc agtgcgtga aggtgcac 360
ccctatggt tggtaaactt ttttatggt gaaataaagt tggccacgtt ggcattttgt 420
atgtaccata tgaataaggta tggcttaact cgcgtccggc agccgggtt atacggagg 480
tccgagccgtt atccggattt atgggttta aagggtggatc aggtggatc gtaagtcaat 540
tggtaaagggt tggccgttca cctgtttaat gcaatgttca ctgcgtgtt tgtagtacat 600
agagggtggc ggaatccgtg tggtagccgt gaaatgttca gatatacga agaactccga 660
tttgcgtggc agctcaactgg actgcactgtt aactgtatcc tggaaatgtt ggggttcaaa 720
caggattaga taccctggta gtccacacag taaacgtatc atactcgctg tttgcgtat 780
acagtagccg gcaacccgaa agccatgtt atccacccgtt ggggtggatc cggcaacccgt 840
gaaactcaaa ggaatttgcg gggggccgtca caagcgagg aacatgttgcg ttaattccgt 900
gatacgcgac gacccattcc cgggtttaat tggccaaatc atatggccga aacggccatcg 960
ccgcacggca ttgtgtggta tggccgtatcc tggccgtatcc tggccgtatcc ggggtgtccg 1020
cttaagtggc ataaacggcc caacccctt tttccgttac taacaggatc tgctgaggac 1080
tctggagaga ctggccgtatcc aagatgttgcg gaaagggtggg atgcgttcaatc acggccatcc 1140
cccttacgtc cggggccgtaca cactgttcaatc aatggggggatc acaggccgtt gctacacacgc 1200
gatgtgtatcc caatccctaa agcccttcg acgttcgtatcc gaaatgttgcg acccggactt 1260
gtgaagctgg atccgtatcc aatcgccatc cggccacggc ggggtgttcaatc acggccatcc 1320
ccttgcgtac acggccgttcaatc aacccatggg agccggggatc acctgttcaatc acggccatcc 1380
aggagcntcc tagggtaaaa 1400
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SEQ ID NO: 17 moltype = DNA length = 1364
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atatccgata gtatattaaa accgcgttgg tttactatta aagaatttcg gttatcgatg 180
gggatcggtt ccattatgtt gttggggggg taacggccca ccaagactac gatggatagg 240
ggttctgaga ggaaggcccc ccacattggaa actgagacac ggtccaaact cctacgggg 300
gcagcgttga ggaatattgg tcaatggacg agagtctgaa ccagccaagt acgctgttggg 360
atgactgccc tatgggttgt aaacctttt tatatggaa taaagtattc cacgtgtggg 420
attttgtatg taccatatga ataaggatcg gctaactccg tgccagcagc cgccgttaata 480
cgaggatcc gacgttatac cggattttt gggtttaaaag ggagcgttgg tggattttta 540
agtcaattttgc gaaaggttgc ggctcaaccc taaaatttgc gttgaaaccc gcagtcttgc 600
gtacagtaga ggtggggcga attcgtgttgc tagcgtgttgc atgcttagat atcacgaaga 660
actccgattt cgaaggccacg tcataactgac gcaactgttgc ctgtatgttgc aaatgttggg 720
tatcaaacacg gatttagatc cttgttgcgac cacacgttgc acgttgcataa ctctgtttt 780
gcgatataca gtaagccggcc aagcgaaacg attaaggatattt ccacccgtttt agtacgcgg 840
caacccgttgc actcaaaggaa atttgcgggg gcccgcacaa gcccggaaac atgtggttta 900
atttcgtatg acgcgggggg ccttacccgg gctttaaattt caaatgttgc atctggaaac 960
aggttagccg caggccattt gtaatgggttgc tgcatgggttgc tgcgttgcgttgc ttgcgttgc 1020
gtgtcggtt aagtccata acgcgcaccc cccttattttt tagttttttt cagggttatgc 1080
tgaggactt agagagactt ccgttgcgttgc atgttgcggaa ggtggggatgt acgttcaatc 1140
acgcacggccccc ttatcgccgg ggcttacacat gttttttttttt ggggggttaca gaaggccgtt 1200
acctccggcc acggatgtttttt tcccaaaaaac ctcttcgttgc tggatgttgc gttttttttt 1260
cgacttcgtt aagctgttgc cttgttgcgttgc cttgttgcgttgc cttgttgcgttgc 1320
tcccgccgtt tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1380
aaccgcgttgc agtgcataaccc gttttttttt gttttttttt gttttttttt gttttttttt 1392

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SEQ ID NO: 20          moltype = DNA  length = 1358
FEATURE                Location/Qualifiers
misc_feature           1..1358
note = HB-364_Mediterraneibacter_faecis
source                 1..1358
mol_type = unassigned DNA
organism = Mediterraneibacter faecis

SEQUENCE: 20
tttgttgcgtt aagtggccggac ggggttggat tttttttttt tttttttttt tttttttttt 60
taaacgtttag aaatgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt 120
aaaaaaactccg gtgggtatgtt gttttttttt tttttttttt tttttttttt tttttttttt 180
cttacccaaaccc gacgttgcgttgc tttttttttt tttttttttt tttttttttt tttttttttt 240
cacggccccc aaactccatgtt gttttttttt tttttttttt tttttttttt tttttttttt 300
gtatgtttttttt gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 360
aagaaaaatgtt cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 420
atacgtatgtt gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 480
gcaagttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 540
agatgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 600
ggaacacccatgtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 660
ggggggcaaaa cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 720
tcggggccatgtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 780
cgatgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 840
ggttttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 900
gtatgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 960
tgcgttgcgttgc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1020
ggttttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1080
gttcaatcat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1140
ggggggccatgtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1200
tctgcgttgcgttgc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1260
gaatactgttgc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1320
aagtcaattttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1380

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SEQ ID NO: 21          moltype = DNA  length = 1403
FEATURE                Location/Qualifiers
misc_feature           1..1403
note = HB-440_Clostridium_aldenense
264
note = n is a, c, g, or t
source                 1..1403
mol_type = unassigned DNA
organism = Clostridium aldenense

SEQUENCE: 21
tgcgttgcgttgc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
cggtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 120
gctgtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 180
gtttttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 240
tcgtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 300
tacggggccatgtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 360
cgatgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 420
cctgtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 480
gggtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 540
aagcccccggccatgtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 600
taagtgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 660

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| | | | | | | |
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| aaggcggctt | actggactgt | aactgacgtt | gaggctcgaa | agcgtgggaa | gcaaacagga | 720 |
| ttagatacc | tgttagtcca | cgcgttaaac | gatgaatgtc | aggtgtcg | ggcaaaagcc | 780 |
| cctcgggtc | gcccgtaaac | gataaagcat | tccacctggg | gagtacg | tcgaaatga | 840 |
| aactcaaagg | aattgacggg | gacccgcaca | agcgggtgg | catgtgttt | aattcgaagc | 900 |
| aacgcgaaga | accttacca | gtcttgacat | ccccctgacc | ggacagtaac | gtgtcccttc | 960 |
| cttcgggaca | ggggagacag | gtggtgcatg | gttgtcg | tgagatgtt | 1020 | |
| ggttaagtcc | cgcaacgc | gcaaccctta | tccttagt | ccagcaccc | gggtgggac | 1080 |
| tctaggagga | ctggcaggga | taacctggag | gaaggtggg | atgacgtcaa | atcatcatgc | 1140 |
| cccttatgt | ttgggttaca | cacgtgtac | aatggcgtaa | acaaaggggag | gcggccctgc | 1200 |
| gaaggtgagc | aaatcccaa | aataacgtcc | cagttcgac | tgtgttgc | aacccgacta | 1260 |
| cacgaagtc | gaatcgtag | taatccgg | tcagaatgc | gcccgtt | 1320 | |
| tcttgcac | accgcggc | acaccatggg | agtgcgaac | gcccgaagtc | agtgcacca | 1380 |
| ccgataagg | gggagtgcc | gaa | | | | 1403 |

| | | | | | | |
|---------------|-----------------------------------|---------------|------------|------------|-------------|------|
| SEQ ID NO: 22 | moltype = DNA | length = 1406 | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1406 | | | | | |
| source | note = HB-442_Clostridium_bolteae | | | | | |
| SEQUENCE: 22 | 1..1406 | | | | | |
| tgcagtcgaa | cgaagcaatt | aaaatgaagt | tttcggatgg | atttttgatt | gactgagtg | 60 |
| cggacgggt | agtaacgcgt | ggataaac | cttcacact | ggggataaca | gttagaaatg | 120 |
| actgtcta | ccgcataa | gcacagtacc | gcatggtac | gtgtgaaaaa | ctccgggtgt | 180 |
| gtgagatg | tccgcgtct | attagccat | tggcggtt | acggccacc | aaagcgacga | 240 |
| tcagtagc | acctggagg | gtgacccgg | acattggac | tgagacacgg | cccaaaactcc | 300 |
| tacgggagg | gcagtg | aatattgc | aatgggc | agcctgtac | agcgacccg | 360 |
| cgtgatgt | gaagat | tttc | gttatgtaa | gtctatca | cagggaaat | 420 |
| cctgactaa | aagccccggc | taactac | ccagcagcc | cgttaata | tagggggca | 480 |
| gegttata | cgattact | gtgtaa | agcgttagac | gcgaagca | gtcgaatgt | 540 |
| aaacccagg | ctcaacc | gtactgtt | ggaaactgt | tttgatgt | gtcgaggagg | 600 |
| taagtggat | tcctatgt | gcgtgaaat | gcgttagat | targaggaa | accagtggc | 660 |
| aaggcgg | actggac | aactgac | gaggctcg | agcgtggg | gcaaacagga | 720 |
| ttakatacc | tgttagtcca | cgcgttaa | gatgtatgt | aggtgttgg | ggggcaaa | 780 |
| ccttcgg | cg | tcgaaac | gcagtaa | ttcacctgg | ggagtacgt | 840 |
| aaactca | gatgtac | ggaccgc | aaogggtg | gcatgtgtt | taattcga | 900 |
| caacgc | aac | tttacca | agtctgac | tccttgc | ccggcgtt | 960 |
| ccttcgg | aaag | gagaca | gggtgtc | gtgtcg | gtgagatgt | 1020 |
| gggttaat | gtc | caac | gtttagt | gtccac | ggagcagg | 1080 |
| actctatgg | gact | ccagg | gataacc | aggaa | ggatgtac | 1140 |
| gcccctt | at | tttggct | cacacgt | acaatgg | aaacaaagg | 1200 |
| gtgtatgt | gcaaa | tttccca | aaaatacgt | cccagt | tct | 1260 |
| tacacg | tggat | ctgt | agtaatc | gc | tcggttcc | 1320 |
| ggtcttgc | acacc | cccg | tcacat | ggatgtac | acgcgg | 1380 |
| aactcga | ag | gggg | agac | gtcgt | gaccc | 1406 |

| | | | | | | |
|---------------|------------------------------------|---------------|----------|------------|-----------|------|
| SEQ ID NO: 23 | moltype = DNA | length = 1057 | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1057 | | | | | |
| source | note = HB-444_Clostridium_scindens | | | | | |
| SEQUENCE: 23 | 1..1057 | | | | | |
| tgcagcgc | ccgcgt | gatgtat | ttcggtat | aaacttctat | cagcaggaa | 60 |
| gaagatg | acgt | actgt | aaga | ggccc | ggtaactac | 120 |
| acgtagg | ggc | tttat | ccggat | tgggt | gggagcgt | 180 |
| aaggccat | gt | ccggact | gggtca | at | tttggact | 240 |
| agtgtcg | gg | ggact | gttgc | gtatgt | gtcgatgt | 300 |
| aacaccat | gt | gttgc | gg | at | tttggat | 360 |
| ggagcaaa | aa | gttgc | gttgc | gttgc | ggaa | 420 |
| gggtgg | cc | gttgc | gttgc | gttgc | gttgc | 480 |
| ttcgcaaa | g | gttgc | gttgc | gttgc | gttgc | 540 |
| ttaattc | gt | gttgc | gttgc | gttgc | gttgc | 600 |
| taacgc | tc | gttgc | gttgc | gttgc | gttgc | 660 |
| tcgtgat | tt | gttgc | gttgc | gttgc | gttgc | 720 |
| ttyggat | gg | gttgc | gttgc | gttgc | gttgc | 780 |
| caaatcat | tc | gttgc | gttgc | gttgc | gttgc | 840 |
| gaggcga | cc | gttgc | gttgc | gttgc | gttgc | 900 |
| tgcaactc | gt | gttgc | gttgc | gttgc | gttgc | 960 |
| atacg | ttt | gttgc | gttgc | gttgc | gttgc | 1020 |
| ggcgg | ac | gttgc | gttgc | gttgc | gttgc | 1057 |

| | | |
|---------------|---------------------|---------------|
| SEQ ID NO: 24 | moltype = DNA | length = 1381 |
| FEATURE | Location/Qualifiers | |

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misc_feature          1..1381
                      note = HB-469_Clostridium_tyrobutyricum
source               1..1381
                      mol_type = unassigned DNA
                      organism = Clostridium tyrobutyricum
SEQUENCE: 24
tgcagtcgag cgtgaaccc cttegggggt ggatttagcgg cgacgggtt agtaaacacgt 60
gggttaacctg cctcaaaagtg gggatagcc ttccgaaaagg aagattaataa ccgcataaaag 120
ccaagttca catgaaattt ggatggaaagg agtaattcgc tttgagatgg acccgccg 180
cattagtttag ttgggtgggt aatggcctac caagacagcg atgcgttagcc gacctgagag 240
gttgatcgcc cacatggaa tgagataacg gtcacgactc atacggggagg cagcagtggg 300
gaatattcga caatggcgca aagcctgtatc cagcaacccgc ggcgtgatgt tgaagggttt 360
cggtttgtttaa agctctgtct ttggggacga taatgacggt accaaaggag gaagccacgg 420
ctaactacgt ggcacgacgg gccgttataatc gttaggtggcg agcgttgccc ggatttactg 480
ggcgtaaagg gtgcgttaggc ggtatgtttaa gtgagatgtt aaatccccg gcttaacttg 540
gttgctgtcat ttcaaactgg atatcttagat tgcaggaa gagaatggaa ttcttagtgt 600
agcggttggaa tgcgttagata tttagaaagaa caccagtggc gaaggcgatt ctctggactg 660
taactgaacgc tgaggcacca aagcgctgggtt agcaaacagg attagatacc ctggtagtcc 720
acgcggatcaaa cgtatgtatc taggtgttagg aggtatcgc accttctgtt ccgcgttataa 780
cacattaaatc atcccgcttcc ggaatgtacat tgcgttacatc aaaaactcaaa ggaatttacg 840
ggggcccgca caagcagccg agcattgtgtt ttaattcga gcaacccgcgaa gaaccttacc 900
tggactgttgc atccctgtaa taaccttagat ataggcgaag cccttccggg cagggagaca 960
gttgggtcat gtttgcgttgc agtgcgtgtt gttggatgtt aggttaatgc ctgcacacgg 1020
cgcaacccctt atttgttagt gttcaatccatc agtgcgttgc accttacggata ctggcccggt 1080
taacgcggag ggagggtgggg atgacgttca atcatcatgc cccttatgtc cagggcaaca 1140
cacgtgttac aatgggcaga acaaaggagaa gcaataccgcg gaggtggggc caaactcaaa 1200
aactgttccatc agtgcgttgc ggcgttgcgtt acgtgcgttgc atgaaggtgg agttgttgc 1260
aattcgcgaat cgcgtatgtc cgggttataatc gttcccgccgc ctgttacaca ccggcccgatc 1320
caccatgaga gctggcaaca cccgttac gttgttgcgtt gtaagaggac gcccggcaag 1380
g

SEQ ID NO: 25           moltype = DNA length = 1402
FEATURE                  Location/Qualifiers
misc_feature          1..1402
                      note = HB-612_Eisenbergiella_tayi
source               1..1402
                      mol_type = unassigned DNA
                      organism = Eisenbergiella tayi
SEQUENCE: 25
tgcagtcgaa cggagttatc cagaggaagt ttccggatgtt aatccggcgtt acttagtggc 60
ggacgggttgc gtaacccgtt gggaaacctgc cctgttccggg gggataaacat ttggaaatag 120
gtgtcaataac cgcataagcg cacagttca catgaagcaat tggggatgttccgggtt 180
caaggatgttgc cccgttgcgtt ttggggatgtt ggcgttccgggtaa cggccgttccggg 240
cgttgggttgc cctggggatgtt gggatgttccgggtaa cggccgttccgggtaa 300
acggggggca gcaatgtgggtt atttgttca atggggggaa ccctgttccgggtaa cggccgttccggg 360
gttggatgttgc aagtatttgc gtatgttgcgtt ctctatgttccgggtaa 420
ctgtactaaatc acggccgggtt aactacgttgc cggccgttccgggtaa 480
cggttccgggtt atttactggg tggggatgttccgggtaa cggccgttccgggtaa 540
aaccctggcc tcaacccgtt gactgttccgggtaa cggccgttccgggtaa 600
aaggccgttccgtt cttgttccgggtaa cggccgttccgggtaa 660
aggccgttccgtt cttgttccgggtaa cggccgttccgggtaa 720
tagatattccatc ggtatgttccatc ggggttccgggtaa cggccgttccgggtaa 780
catccgttccgggtaa cttgttccgggtaa cggccgttccgggtaa 840
aactcaaaatc aatttgcgttgc ggggttccgggtaa cggccgttccgggtaa 900
aacgcgttccgtt cttgttccgggtaa cggccgttccgggtaa 960
cttccgttccgggtaa cttgttccgggtaa cggccgttccgggtaa 1020
gggttaatgttccgtt cttgttccgggtaa cggccgttccgggtaa 1080
cttccgttccgggtaa cttgttccgggtaa cggccgttccgggtaa 1140
cccttccgttccgggtaa cttgttccgggtaa cggccgttccgggtaa 1200
tggatgttccgtt cttgttccgggtaa cggccgttccgggtaa 1260
acatgttccgtt cttgttccgggtaa cggccgttccgggtaa 1320
gttccgttccgggtaa cttgttccgggtaa cggccgttccgggtaa 1380
accgcgttccgtt cttgttccgggtaa cggccgttccgggtaa 1402

SEQ ID NO: 26           moltype = DNA length = 1400
FEATURE                  Location/Qualifiers
misc_feature          1..1400
                      note = HB-63_Parabacteroides_merdae
source               1..1400
                      mol_type = unassigned DNA
                      organism = Parabacteroides merdae
SEQUENCE: 26
tgcagtcgag gggcgttccgtt cttgttccgggtaa cggccgttccgggtaa 60
gatgttccgtt cttgttccgggtaa cggccgttccgggtaa 120
accccttccgtt cttgttccgggtaa cggccgttccgggtaa 180
gggttccgtt cttgttccgggtaa cggccgttccgggtaa 240

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| | | | | | | |
|------------|------------|-------------|-------------|-------------|-------------|------|
| ggttctgaga | ggaaggccc | ccacatttgtt | actgagacac | ggaccaaact | cctacggag | 300 |
| gcagcagtga | ggaatattgg | tcaatggccg | agaggctgaa | ccagccaagt | cgcgtgaagg | 360 |
| aagaaggata | tatggttgt | aaacttctt | tataggggaa | taaagtggag | gacgtgtcct | 420 |
| ttttgat | taccatatga | ataagcatcg | gctaactccg | tgccagcagc | cgcggtaata | 480 |
| cggaggatgc | gagcgttac | cggattttt | gggtttaaag | ggtcgttagg | tggtgattta | 540 |
| agtccagcgt | gaaagttgt | ggctcaacca | aaaatttgc | gtttaacttgc | gtttaacttgc | 600 |
| gtgtgttgta | ggtaggcga | atgcgtgtt | tagcgggtaa | atgcatagat | atcacgcaga | 660 |
| actccgattt | cgaaggcage | ttacttaacc | ataactgaca | ctgaagcacc | aaagcgtggg | 720 |
| gatcaaacag | gattagatac | cctggtagtc | cacgcgtaa | acgtatgtt | ctaggagttt | 780 |
| gegatataat | gtaagetcta | cagcggaaag | gtaaagtaat | ccacccgtgg | agtacgcgg | 840 |
| caacgggtaa | actcaaaagg | attgacgggg | gccccacaa | gcccggggaa | atgtggttt | 900 |
| attcgtat | acgcggggaa | ccttacccgg | gtttaacttgc | agtcttgcac | gagtggaaac | 960 |
| actcttctt | gcaatagcag | attacgggg | gctgtatgtt | tgctgtcagc | tcgtgtccgt | 1020 |
| aggtgtccgc | ttaagtgc | taacggggcc | aacccttata | actgttact | aacagggtgaa | 1080 |
| gctgaggact | tcgtgtggac | tgccgggtaa | agctgtgggg | tgacgtcaaa | 1140 | |
| tcagcacgg | ccttacatcc | ggggccacac | acgtgttaca | atggatgtt | caaaggccag | 1200 |
| ctacctgg | acaggatgt | aatctccaa | ccatgtctca | gttcggatcg | gagtctgaa | 1260 |
| ctcgactcc | tgaagctgg | tgcgttagt | atcgccatc | agccatgggg | cgggttata | 1320 |
| gttcccccgg | cttgatcac | ccggccgtca | agccatgggg | gccccgggtt | cctgttttt | 1380 |
| gttaaccgc | ggatcgccct | | | | | 1400 |

| | | |
|---------------|---------------------------------|---------------|
| SEQ ID NO: 27 | moltype = DNA | length = 1393 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..1393 | |
| | note = HB-70_Bacteroides_ovatus | |
| source | 1..1393 | |
| | mol_type = unassigned DNA | |
| | organism = Bacteroides ovatus | |

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|--------------|-------------|-------------|--------------|-------------|--------------|------|
| SEQUENCE: 27 | | | | | | |
| tgcaagtgcg | gggcggcatt | tttagttgt | tgcaaaactgaa | agatggcgac | cggcgacacgg | 60 |
| gtgagtaaca | cgtatccaa | ctggcgataa | ctccggataa | gcctttcgaa | agaaaaggatta | 120 |
| ataccggata | gcatacgtaa | atccatgtat | attttttata | aagaatttgc | gttattcgat | 180 |
| gggatgggtt | ccat tagttt | gttgggggg | taacggccca | ccaagacaac | gatggatagg | 240 |
| ggttctgaga | ggaaggccc | ccacattgg | actgagacac | ggtccaaact | cctacggag | 300 |
| gcagcagtga | ggaatattgg | tcaatgggg | agagccgtgaa | ccagccaaat | agcgtgtgg | 360 |
| atgaaggatc | tatgggtct | aaacttctt | tatatggggaa | taaagtatttc | cacgtgtgg | 420 |
| attttgtat | taccatata | ataaggatcg | gctaactccg | tgccagcagc | cgcggtaata | 480 |
| cggaggatcc | gagcgttac | cggattttt | gggtttaaag | ggagcgttagg | tggttgcgtt | 540 |
| agtccagttt | gaaagttgt | ggctcaaccc | aaaatttgc | gtttaacttgc | gcgttgcgtt | 600 |
| gtacatgt | gggtggggca | attcgtgtt | tagcgggtaa | atgcgttagat | atcacgaaga | 660 |
| actccgattt | cgaaggcage | tcactagact | gtcactgaca | ctgtatgtc | aaagcgtggg | 720 |
| tatcaaacag | gattagatac | cctggtagtc | cacacagtaa | acgtatgtt | ctcgctgttt | 780 |
| gegatataca | gtaaggggg | aaggcggaaag | attaagtatt | ccacccgtgg | agtacgcgg | 840 |
| caacgggtaa | actcaaaagg | attgacgggg | gccccacaa | gcccggggaa | atgtggttt | 900 |
| attcgtat | acgcggggaa | ccttacccgg | gtttaatttgc | caacaaataa | tatggggaaac | 960 |
| agtatagccg | taaggctgtt | gttgaagggt | tgcgtatgtt | tgctgtcagc | gttccgtgt | 1020 |
| gtgtcggtt | aagtgcata | acgacgcga | cccttatctt | tagttaactaa | caggctatgc | 1080 |
| tgaggactt | agagagactg | ccgtcgtaa | atgtggggaa | gttggggatg | acgttcaatc | 1140 |
| agacggcc | ttacgtccgg | ggctcacac | gtttaacaat | gggggggtaca | gaaggccgt | 1200 |
| acctgggtac | aggatgttac | tccaaaaaac | ctctctatgt | tcggatgtt | gtctgtcaacc | 1260 |
| cgacttcgt | aagctgggtt | cgctgtat | cgccatgtt | ccatggggcc | gttgaatacgt | 1320 |
| tccggggctt | tgtacacacc | ggccgtcaag | ccatggaaag | cggggggtacc | tgaagtatgt | 1380 |
| aaccgc | aaagg | agc | | | | 1393 |

| | | |
|---------------|--|--------------|
| SEQ ID NO: 28 | moltype = DNA | length = 865 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..865 | |
| | note = HB-83_Anaerotruncus_colihominis | |
| source | 1..865 | |
| | mol_type = unassigned DNA | |
| | organism = Anaerotruncus colihominis | |

| | | | | | | |
|--------------|-------------|-------------|-------------|------------|-------------|-----|
| SEQUENCE: 28 | | | | | | |
| cgaggatcc | gttttgaat | tttccggatgg | atgaatgtaa | gtttagtggc | ggacgggtgt | 60 |
| tttacacgtg | atgcaacctg | cttccatgtt | ggccatgggg | gggataacac | ccggaaaccc | 120 |
| cgcgtatgt | tgccggggca | catggccatgt | caacccaaagg | agcaatccgc | tgaaagatgg | 180 |
| gtcccggtcc | gattagccag | ttgggggggt | aacggccac | caaagccac | atcggttagcc | 240 |
| ggactgagag | gttgaacggc | cacattggga | ctgagacac | gcccggactc | ctacggggagg | 300 |
| cagcagttgg | ggatattgca | caatggggca | aaggctgtat | cagcgtacgc | cgctgtgggg | 360 |
| agacggctt | cggttgcata | acccctgtt | ttggggaaaga | aatgtacgtt | acccaaaggag | 420 |
| gaagctccgg | ctaactacgt | gccagcggcc | gcccgtatcc | gttggggatc | agcgtgttcc | 480 |
| ggaattactgt | ggtgttaaagg | gagcgtatgt | ggggatggca | tgtaatgtt | aatccatcg | 540 |
| gctcaacccg | ttggcggttt | ctaaactgtt | gttcttgcgtt | tgtaatgtt | aaatccatcg | 600 |
| tcctagtgt | tgccgtgaaat | tgccgtatgt | tgccgtatgt | tgccgtatgt | tgccgtatgt | 660 |
| gttgggtttt | aactgacgt | gaggctcgaa | agcgtggggaa | gcaacacgg | ttagatacc | 720 |
| tggtagtcca | cgccgtaaac | gttggat | atgtgtgggg | ggactgacc | cttccgtgt | 780 |
| gcagatccaaca | caataagtaa | tccacccgtgg | gagtcacggcc | gcaagggtt | aactcaaaagg | 840 |

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| | |
|--|--|
| aattgacggg ggcccgacaca agcag | 865 |
| SEQ ID NO: 29 | moltype = DNA length = 678 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..678 |
| | note = HB-85_Enterococcus_faecium |
| source | 1..678 |
| | mol_type = unassigned DNA |
| | organism = Enterococcus faecium |
| SEQUENCE: 29 | |
| gtcgtaacgt tcttttcca ccggagttt ctccacggaa aaaagaagag tggcgaacgg | 60 |
| gtgagtaaca cgtggtaac ctggccatca gaaggggata acacttggaa acagggtgcta | 120 |
| ataccgtata acaatcgaaa ccgcattgtt ttgatattgaa aggccgttcc ggggtgtcgct | 180 |
| gtatggatgga cccgcgtgc attatgttggt tggtgaggta acggctacc aaggccacga | 240 |
| tgcatacgcc accttgatgg gtatggcc acattgggac tgagacacgg cccaaactcc | 300 |
| tacgggaggg aqcaatgggg aatcttcggc aatggacgaa aqctctgaccc agcaacccg | 360 |
| cgtgagtggaa gaagggtttc ggatcgtaaa actctgttgt tagagaagaa caaggatgag | 420 |
| agtaactgtt catcccttga cggtatctaa ccagaaagcc acggctact acgtgcccac | 480 |
| agccgcgtta atacgttagt ggcaagcggtt gtccggattt attgggctta aagcgagcgc | 540 |
| aggccgtttt ttaatgtctga tggtaaagcc cccggctcaa cccgggaggg tcattggaaa | 600 |
| ctgggagact tgagtgacca agaggagagt ggaattccat gtgtagcggt gaaatgcgta | 660 |
| gatatatggaa ggaacacc | 678 |
| SEQ ID NO: 30 | moltype = DNA length = 771 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..771 |
| | note = HB-87_Lactobacillus_brevis |
| source | 1..771 |
| | mol_type = unassigned DNA |
| | organism = Lactobacillus brevis |
| SEQUENCE: 30 | |
| cgagcttcg ttgaatgacg tgcttgact gatttcaaca atgaagcgag tggcgaactg | 60 |
| gtgagtaaca cgtgggaaat ctggccagaa gcaggggata acacttggaa acagggtgcta | 120 |
| ataccgtata acaacaaaat ccgcattgtt ttgtttgaa aggccgttcc ggctatcact | 180 |
| tctggatgat cccgcgtgc attatgttggt tggtgaggta aaggccccacc aagcacatga | 240 |
| tacgttagccg accttgatgg gtaatggcc acattgggac tgagacacgg cccaaactcc | 300 |
| tacgggaggg aqcaatgggg aatcttcac aatggacgaa aqctctgatgg agcaatccg | 360 |
| cgtgagtggaa gaagggtttc ggatcgtaaa actctgttgt taaagaagaa cacctttgag | 420 |
| agtaactgtt caagggtttt cggatatttta ccagaaagcc acggctact acgtgcccac | 480 |
| agccgcgtta atacgttagt ggcaagcggtt gtccggattt attgggctta aagcgagcgc | 540 |
| aggccgtttt ttaatgtctga tggtaaagcc ttcggcttaa cccggagaagt gcatcgaaa | 600 |
| ctgggagact tgagtgacca agaggacagt ggaactccat gtgtagcggt ggaatgcgta | 660 |
| gatatatggaa gaaacacc | 720 |
| tcgaaagcat gggtagcgaa caggattttaa taccctggta gtccatgcgt | 771 |
| SEQ ID NO: 31 | moltype = DNA length = 671 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..671 |
| | note = HB-01_Hungatella_hathewayi |
| source | 1..671 |
| | mol_type = unassigned DNA |
| | organism = Hungatella hathewayi |
| SEQUENCE: 31 | |
| ttgacttagc ggcggacggg tgagtaacgc gtgggtaacc tgccttacac tgggggataa | 60 |
| cagttagaaa tgactgtctaa taccgcataa ggcgcacaggc cgcgcattgtc ttgtgtgaaa | 120 |
| aactccgggtg gtgtatggc gaccgcgtc tgatttaggtt gttgggggg taacggccca | 180 |
| ccaaaggccg gatcaatgcg cgcattgtt ggggtgacccg ccacattggg actgagacac | 240 |
| ggcccaaact cctacgggg gcaatgggg gcaatattgg acaatgggg aaagctgtat | 300 |
| ccacggccgc cgcgtgtgt aagaatgtt tccgtatgtt aagcttatac agcaggaaag | 360 |
| aaaatgtacgg taccgtatc ayaagccccg gctaactacg tgccgcacgc cgcgttaata | 420 |
| cgttagggggc aacgttatac cggatatttcc ggggtgttaaa ggatgttgcg cggatgttgc | 480 |
| agtctgtatc gaaaggccgg ggctcaaccc cggatgttgcg ttggaaactg ttgactgttgc | 540 |
| gtgcaggaga ggtaaatgttgc attcttagtgc tagcggttgc atgcgtatgttattggagga | 600 |
| acaccatgttgc gaaaggccgg ttaatgttgc gtaactgttgc ttggggctcg aaagctgtgg | 660 |
| gagcaacacag g | 671 |
| SEQ ID NO: 32 | moltype = DNA length = 788 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..788 |
| | note = HB-03_Parabacteroides_johnsonii |
| misc_feature | 730 |
| | note = n is a, c, g, or t |
| source | 1..788 |
| | mol_type = unassigned DNA |
| | organism = Parabacteroides johnsonii |
| SEQUENCE: 32 | |

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| | | | | | | |
|--------------|-------------|-------------|-------------|------------|------------|-----|
| tgcagtcgag | gggcagcggg | ggcagcaatg | cctgcccggcg | accggcgcac | gggtgagtaa | 60 |
| cgcgtatgca | acttgcatac | cagaggaa | tagcccgccg | aaagtccgt | taatgtccca | 120 |
| taaaacaggg | gtccccatg | ggaatatttg | ttaaagatttc | atcgctgata | gataggcatg | 180 |
| cgttccatta | ggcagttgc | ggggtaacgg | cccacccaaac | cgacgatgga | taggggtct | 240 |
| gagaggaagg | tccccacat | tggactgag | acacggtcca | aactccatc | ggaggcagca | 300 |
| gtgaggaata | tttgtcaatg | gccgggaggc | tgaaccacgac | aagtccgt | aaggatgaag | 360 |
| gatctatgg | ttgttaaactt | ctttatac | ggaataaaatg | gtgggacgt | tcccathtt | 420 |
| tatgttacccgt | atgataaagc | atcgctaa | tccgtccac | cagccgcgt | aatacggagg | 480 |
| atgcgcgcgt | tatccggatt | tattgggtt | aaagggtgc | taggtgt | tttaagtcag | 540 |
| cggtgaaatgt | tttgtggctca | accataaaaat | tgccgttgaa | actggatgac | ttgagtata | 600 |
| tttaggttgg | ccggatgcgt | gggttgcgg | tgaatgcat | agatatac | cagaactccg | 660 |
| atttgcgaaagg | cagcttacta | aactataact | gacactgaag | cacgaaacgg | tggggatcaa | 720 |
| acaggattan | ataccctgg | agtccacgca | gtaaacgatg | attactagga | gtttgcata | 780 |
| gacagtaa | | | | | | 788 |

SEQ_ID NO: 33 moltype = DNA length = 1396
 FEATURE Location/Qualifiers
 misc_feature 1..1396
 note = HB-10_Bacteroides_vulgatus
 source 1..1396
 mol_type = unassigned DNA
 organism = Bacteroides vulgatus

SEQUENCE: 33

| | | | | | | |
|-------------|--------------|-------------|-------------|------------|------------|------|
| tgcagtcgag | gggcagcatg | gtcttagctt | gctaaggccc | atggcgaccc | gcccacgggt | 60 |
| gagtaacacg | tatccaacct | gcccgtact | cttggacagc | cttctgaaag | gaagattaat | 120 |
| acaagatggc | atcatagatc | cgccatgtca | catgattaaa | ggtattccgg | tagacgatgg | 180 |
| ggtatgcgttc | cattagatag | taggggggt | aacggcccat | ctatgttccg | atggatagg | 240 |
| gttcttagag | gaaagggtcccc | ccatctggaa | ctgagacacg | gtccaaactc | ctacgggagg | 300 |
| cagcagtgag | aatatttgg | caatgggcga | gaggctgaac | cagccaaatg | gcgtgaagga | 360 |
| tgactgcct | atgggttgg | aacttcttt | ataaaggaa | aaagtccgtt | atgcatacc | 420 |
| gtttgcgtatg | ataggatgg | taaggatgg | ctaactccgt | gcccacggcc | gcggtaatac | 480 |
| ggaggatccg | agcgttatcc | ggatttttgc | gggtttaaagg | gaggctatg | ggatgtttaa | 540 |
| gtcagttgt | aaagtttgcg | gctcaaccgt | aaaaatttgc | ttgatactgg | atatcttgc | 600 |
| tgcagtttag | gcaggccgaa | ttcgtgggt | agcggtaaa | tgcttagata | tcacgaagaa | 660 |
| cttcgcgttgc | gaaggcagcc | tgcttaagtc | caactgcac | tgaggctcga | aagtgtgg | 720 |
| atcaaacagg | attagatacc | cttggtagcc | acacggtaaa | cgatgcatac | tcgctgttgc | 780 |
| cgatatactg | caagcggcca | agcggaaacgg | ttaagttttc | cacctgggg | gtacggccgc | 840 |
| aacggtaaa | ctcaaaggaa | ttgacggggg | cccgacaa | cgaggaaaca | tgtggttaa | 900 |
| tttcgcgtata | ccgcgggaa | ctttaatttgc | agatgaat | cggtgaagac | 960 | |
| cgtaaaggcgc | aaggcatctg | ttaaagggtgc | gcatgggttgc | cgtagctcg | tgccgtgagg | 1020 |
| tgtccgttta | agtgcataa | cgaggcgaac | ccttgggtgc | agttactaac | aggttctgc | 1080 |
| gaggactctg | acaagactgc | catgttata | tgtgaggaa | gtggggatga | cgtcaatca | 1140 |
| gcacggccct | tacgttccgg | gctacacacg | tgttacaatc | gggggtacag | aggccgcgt | 1200 |
| ccacgcgcgt | ggatgcatac | ccccaaatcc | tctctcgtt | cgactggag | tctgcacacc | 1260 |
| gactccacga | actgtggattc | gctgttata | cgccatcagc | cacggccgg | tgaatacgtt | 1320 |
| cccgccctt | gtacacaccg | cccgtaago | catgggagcc | gggggtacct | gaagtgcgt | 1380 |
| accgcgagg | gccc | | | | | 1396 |

SEQ_ID NO: 34 moltype = DNA length = 1398
 FEATURE Location/Qualifiers
 misc_feature 1..1398
 note = HB-13_Bacteroides_uniformis
 source 1..1398
 mol_type = unassigned DNA
 organism = Bacteroides uniformis

SEQUENCE: 34

| | | | | | | |
|--------------|--------------|-------------|--------------|-------------|------------|------|
| catgcagtcg | aggggcagca | tgaacttgc | ttgtctaagg | tgtatggcgac | cgccgcacgg | 60 |
| gtgagtaaca | cgtatccaa | ctggcgatg | ctcggggata | gcctttcgaa | agaaaatgat | 120 |
| ataccatcg | gtatgttct | tccgcgtt | ggaacttata | agaatttcg | gtcatcgatg | 180 |
| gggatgcgtt | ccattagggt | gttgggggg | taacggccca | ccaaacgcctc | gttggatagg | 240 |
| gtttcttaga | gaaagggtcccc | ccatctggaa | actgagacac | ggtccaaact | cctacgggag | 300 |
| gcagcagtga | ggaatatttg | tcaatggac | agagtctgaa | ccagccaaat | agcgtgaagg | 360 |
| atgactgcct | tatgggttgc | aaacttctt | tatacggaa | taaaatgtt | cacgtgtg | 420 |
| tttttgtatg | taccgtatg | ataaggatgc | gtcaactccg | tgccacgc | cgccgtataa | 480 |
| cgaggatcc | gaggcttac | cggttttttgc | gggttttaaag | ggaggctgtt | cggttgcgtt | 540 |
| agtcaatgttgc | gaaagggttgc | ggctcaacc | taaaatttgc | ttgtatctgc | gggtgtctgc | 600 |
| gtacagtaga | ggcaggccga | atttgcgttgc | taggggtgaa | atgtttagat | atcacgaaga | 660 |
| actccgttgc | cgaggcagc | tttgcgttgc | gtactgcac | ctgtatgc | aaagtgttgc | 720 |
| tatcaaacag | gattatgtac | cctggtagtgc | cacacgttac | acgtatgaa | ctcgctgtt | 780 |
| gcgtatata | gttagccgtt | aaaggcgtt | gtttagtatt | ccacccgttgc | agtagccgc | 840 |
| caacccgttgc | actcaaaggaa | atttgcgttgc | ggccgcacaa | cgccggaaac | atgtgttgc | 900 |
| atttgcgtat | acgcggaggaa | ccttacccgg | gcttgcatttgc | caactgcat | atgtggagac | 960 |
| atgtcagccg | caaggcagtt | gttgcgttgc | gtatgttgc | tcgtatgc | gttgcgttgc | 1020 |
| gtgtccgtt | aagtgcatac | acggcgttgc | cccttacatgc | tagttaccat | cagggtatgc | 1080 |
| tggggactct | gtcgagactg | ccgtcgtaag | atgtgaggaa | ggtggggatg | acgtcaatc | 1140 |
| agcacggccc | ttacgttccgg | gggtacacac | gtgttacaat | gggggttaca | gaaggcaggt | 1200 |

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```
acacgggtgac gtgatgctaa tcccgaaago ctctctcagt tcggatttgc gtcgtcaacc 1260
cgactccatg aagctggatt cgctgatata cgccatcatcg ccacggcgccg gtgaatacgt 1320
tcccggccct tgtacacacc gccccgtcaag ccatgaaagc cgggggtacc tgaagtgcgt 1380
aaccgcaagg agcgcctt 1398
```

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SEQ ID NO: 35 moltype = DNA length = 1388
FEATURE Location/Qualifiers
misc_feature 1..1388
note = HB-147_Turicibacter_sanguinis
source 1..1388
mol_type = unassigned DNA
organism = Turicibacter sanguinis
```

```
SEQUENCE: 35
tgcaagtggcg cgaaccactt cgggtggtag cggcgaacgg gtgagtaaca cgtaggat 60
ctgccccatca gacggggaca acgatggaa acgatcgcta ataccggata ggacgaaagt 120
ttaaagggtgc ttccggcacca ctgtatggatg agcctgcgcg cgtttagtcta gttggtaggg 180
taaaggcccta ccaaggcgac gatgtggtagc cgacctggata ggggtgaacgg ccacactggg 240
actcgagacac ggcggccact cctacgggag gcacgttgc ggaatcttcg gcaatgggg 300
aaaggcctgac cggacaaacgc cgcgtgtatg atgaaggccct tgggggttgc aaattctgtt 360
ataaaggaaag aatggctcta tgtaggaaatg cgttagtgcgt gacggtactt tatgagaaag 420
ccacggctaa ctacgtgcca gcacggcgcc taatacgtag gtggcgagcg ttatccggaa 480
ttattggggc taaaggacgcgc gcagggtgggtt gattaagtctt gatgtgaaag cccacggctt 540
aaccggtggag ggtcattggaa aactggtagc cttggagtgc gaagaggggaa gtggaaatcc 600
atgtgttagcg tgtagaatatg tagagatatg gaggaaacacc agtggcgaaatc ggggtttcc 660
ggtctgtac tgacacttag ggcggaaatgc gtggggagca aacaggatata gataccctgg 720
tagtccacgc cgttaaacatg gatgtgtttt cgttgggggtt cgttgggggtt tgcgtgaaat 780
aacgcattaa gcaacttgcgc tggggatgtt ggttgcgaatc cttggggatc aaggaaatgt 840
cggggggcccg cacaaggcggtt ggacgttgcgtt gtttattccg aagcaacccgcg aagaaccccta 900
ccagggtttt acataccgtt gacccgttca gatgttgcgtt tttcccttcg gggacaatgg 960
atacagggtgg tgcattgggt tcgttgcgtt gtgtcgttagt atgtgggggtt aagtcccgca 1020
acgaggcggaa cccctgtgtcgt tagtggccatc ctttgcgttgcgtt gggacttcaa cggactgtcc 1080
atgtgacaaac tggggggatgtt gtttggatgtt gtttgcgttgcgtt gtttgcgttgcgtt 1140
ctacacacgt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt 1200
tcataaaaggc aatctcgatc cggattgttag gctgtcaactc gcctacatgaa agttggaaatc 1260
gtctgtttttt ggtttttttt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt 1320
ccgttcacacc acggagatttt acaacaccggc aatgtttttt cttttttttt gtttgcgttgcgtt 1380
tgccctttttt 1388
```

```
SEQ ID NO: 36 moltype = DNA length = 1389
FEATURE Location/Qualifiers
misc_feature 1..1389
note = HB-155_Coprococcus_eutactus
source 1..1389
mol_type = unassigned DNA
organism = Coprococcus eutactus
```

```
SEQUENCE: 36
tgcaagtggcg cgttggatgc tccggccgtat ttatggccgg acgggttgcgtt 60
aacgcgtgggg taacctgcctt catabagggg gatagcgat gggaaacgcgtt ggtaaaacccg 120
cataaggccca cgggtgtcgat tgacacatgt tgaaaacactt ccgggtgttat gagatggacc 180
cgccgtctgtat tagtgcgtttt tgtaggttgc gggccaccaaa ggccgacgtc agtggccgc 240
ctggaggggtt gaaacggccaccc atttggggactt agacacggcccaaaacttca cggggaggcc 300
cagtggggatgtt tattttttttt ctttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt 360
atgtttttttt tattttttttt tattttttttt tattttttttt tattttttttt tattttttttt 420
gcacccggctt aatacggtttt acggccgtt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt 480
tttactgtgtt gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 540
caacccggatc acgttgggtt gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 600
ctatgtgtttt gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 660
ttggactgtttt ctgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 720
gtatgtttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 780
cgccaaacggca tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 840
tttgcgtttttt cccggccaccaat cgggtggatc gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt 900
cttaccaatgtt ttggactgtttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 960
agagacatgtt ggtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1020
caacggccgtt aacccctttt tccatgtttt tttttttttt tttttttttt tttttttttt tttttttttt 1080
ccggggatgtt cccggggatgtt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt 1140
gggtttttttt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt 1200
cctttttttt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt 1260
tcgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1320
ggccgtttttt cccatggggatgtt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt gtttgcgttgcgtt 1380
gtttttttttt 1389
```

```
SEQ ID NO: 37 moltype = DNA length = 1380
FEATURE Location/Qualifiers
misc_feature 1..1380
note = HB-227_Bacteroides_cellulosilyticus
source 1..1380
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mol_type = unassigned DNA
organism = Bacteroides cellulosilyticus

SEQUENCE: 37
atgcagtcga gggcagcat gacctagcaa taggtttagt gcgaccggcg cacgggttag 60
taaacatcgat ccaacatccc ggtttattccg ggatagccct tcgaaagaaa gattaatacc 120
ggatagtata acggaaaggc atctttttgtt tattaaagaa ttgcataac cgatggggat 180
gcgttccatt agtttggggc cggggtaacg gcccaccaacg acatcgatgg ataggggttc 240
ttagaggaaat gtccccccaca ttgaaactga gacacggtcc aaactcttcg gggaggcagc 300
agtggaaat attggtaat ggacgagagt ctgaaccgcg caagtagcgt gaaggatgac 360
tgcctatgg gttgttactt tcttttataa tggaaataaa gtgagccacg tgggtttttt 420
tgtatgtacc actcgatccaa ggatcggtca actccgtgcg cagcggccg ggtataacgg 480
aggatcccg cggttatccgg atttattttggg tttaaaggga gcgttagccg actattaagt 540
cagctgtgaa agtttgcggc tcaaccgtaa aattgcagg tatactggtc gtcttgagtg 600
cagtagggat aggccggatt ctgtgtgtgg cggtagaaat cttagatata acgaaagaact 660
ccgatggcg aggcagctt ctggatgtca actggacgtg atgctcgaaa gtgtgggtat 720
caaaacggat tagataccctt ggtagtccac agacataaagg atgataactc gctgttgcg 780
atatacagca acggccaaag cgaaaacgtt aagtattccca cctggggagt acggccggca 840
cggtttaact caaaggaaat gacggggggcc cgccacaaggc gggggacatg tgggttaatt 900
cgatgtatcg cgaggaaccc taccgggtttaaatttgcgt ctgaaataatt tggaaacacg 960
ttacgcgttaa ggcagatgtt aagggtctgc atgggtctgc ttagctgtg ccgtgaggtg 1020
tcggcttaag tgccataacg acgcoaaccctt ttatctttttttag ttactaacaag gtcgtgtca 1080
ggactctaga gagaactccggc tcgtaaaggat tgaggaaagggt gggggatgacg tcaaatcagc 1140
acggccggcc cttccggggcc tacacacgtg ttacaatgggg gggtagacgaa ggccgttaca 1200
cagcgtatgtt atgcttaatcc caaaaggctt tctcgttgc gattggatgc tgcaccccg 1260
ctccatgttccatggatttcg tagtaatcgcc gcatcageccca cggccgggtg aatacggtcc 1320
cgccgcctgtt acacaccggcc cgtaagccca tggaaaggccggc gggtagctgaa agtccgttaac 1380

SEQ ID NO: 38      moltype = DNA length = 1400
FEATURE          Location/Qualifiers
misc_feature    1..1400
note = HB-237_Bacteroides_plebeius
source          1..1400
mol_type = unassigned DNA
organism = Bacteroides plebeius

SEQUENCE: 38
tgcagtcgag gggcagcagt ggattgaagc ttgtttcaat tgctcgccga cccggccacg 60
ggtgagtaac gctgtatccaa ccttccgtac actcaggatgg agcctttcgaa aagaaagatt 120
aataacctgtat ggtatgtat gatttgcgtat tatcatcattt aaagattttt cgggttacga 180
tggggatgtcg tttccatttttgggtttagt tagtggccg ggttaacggcc caccttgcgt acgtggata 240
gggggttctgtt gggggatgttgg gggccatcgaa gggatgttgcg gggatggccaa ctccttccggg 300
aggcagcagt gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 360
ggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 420
ggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 480
tacggggatgttgg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 540
taaatttgcgtt gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 600
gagtgccgtt gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 660
gaactccgtat gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 720
ggtatcaac acggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 780
ttggcgatata cggccggcc ctttccgtt gggatgttgcg gggatgttgcg gggatgttgcg 840
ggcaacccgtt aactcaaaat gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 900
taatttgcgtat acggccggcc acggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 960
acatgttgcgtt gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 1020
aggatgttgcgtt gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 1080
gtccgttgcgtt gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 1140
tcggccggcc ctttccgtt gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 1200
ctacccgtt acggccggcc acggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 1260
ccggccggcc cggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 1320
gttccggccggcc ctttccgtt gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 1380
gtaaccggccaa ggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 1400

SEQ ID NO: 39      moltype = DNA length = 770
FEATURE          Location/Qualifiers
misc_feature    1..770
note = HB-24_Erysipelatoclostridium_ramosum
source          1..770
mol_type = unassigned DNA
organism = Erysipelatoclostridium ramosum

SEQUENCE: 39
gtcgaaacccggc acggatgttgcg ttcggatgttgcg gaaacgggttgcg gtaatatacata agttaacccgtc 60
ccttagacagg gggataactt ttggaaacgtt tagttaaaggat cgcatacgatggat cggacacgttc 120
atgggttacccgg tattaaatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 180
gtccgttgcgtt gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 240
ccggccacac tggggacttgcg acacggccca gacttccatcg gggatgttgcg gggatgttgcg gggatgttgcg 300
ttccgttgcgtt gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 360
tgttataatcc ttggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 420
acttttatttttggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg gggatgttgcg 480

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|-------------------|-------------|--|-------------|-------------|-------------|------|
| agcggttatcc | ggaattattt | ggcgtaaaga | gggggcaggc | ggcagcaagg | gtctgtggtg | 540 |
| aaaggcctgaa | gottaacttc | agtaaccat | agaaccagg | cagctagaat | gcaggagagg | 600 |
| atcggtggaat | tccatgtgt | gggtggaaa | gcttagat | atggagaaac | accagtggcg | 660 |
| aaggcgacga | tctggctgc | aactgacgt | cagtcggaa | acgtgtggga | gcaaatagga | 720 |
| ttagatacc | tagtagtcca | cgccgtaaac | gatgagtaat | aagtgttgg | | 770 |
| SEQ ID NO: 40 | | | | | | |
| FEATURE | | | | | | |
| misc_feature | 1..784 | note = HB-25_Bacillus_cereus | | | | |
| source | 1..784 | mol_type = unassigned DNA | | | | |
| | | organism = Bacillus cereus | | | | |
| SEQUENCE: 40 | | | | | | |
| tgcagtcgag | cgaatggatt | aagagcttc | tcttatgaat | ttagcggccc | acgggtgagt | 60 |
| aacacgtgg | taacctgccc | ataaactgg | qataactccg | ggaaacccgg | gctaataccg | 120 |
| gataacattt | tgaaccgcatt | ggttcgaat | tgaaggcgg | cttcggctgt | cacttatgg | 180 |
| tgaccccgcc | tccgcatagg | tagtgggt | ggtaacggct | caccaaggca | acgtgcgt | 240 |
| gcccacactg | gaggggatcg | gccacactgg | gactgagaca | cgccggcagac | tcctacggga | 300 |
| ggcagcagta | ggaaatcttc | cgcaatggac | gaaaatctgt | cgagacaa | ccgcgtgagt | 360 |
| gatgaaggct | ttcgggtcg | aaaactctgt | tgtagggaa | gacaatgtc | tagttgaata | 420 |
| agttggcacc | ttgacggta | ctaaccagaa | agccacggct | aactacgtc | cagcagccgc | 480 |
| gtgtataatcg | agggtggca | cggtatccgg | aattattggg | cgtaaaggcgc | gcgcagggtgg | 540 |
| tttcttaatcg | ctgtatggaa | agccccacgg | tcaaccgtgg | agggtatcg | gaaactggga | 600 |
| gacttgagt | cagaagagga | aagtggaaatt | ccatgtgt | cggtgaaat | cgttagagata | 660 |
| tggaggaaca | ccagtgccg | aggcgactt | ctggtctgt | actgacactg | aggcgccgaaa | 720 |
| ggctggggag | caaacaggat | tagataccct | ggtagtccac | gcccgtaaac | atgagtgtca | 780 |
| agtgt | | | | | | 784 |
| SEQ ID NO: 41 | | | | | | |
| FEATURE | | | | | | |
| misc_feature | 1..1397 | note = HB-257_Agathobacter_rectalis | | | | |
| source | 1..1397 | mol_type = unassigned DNA | | | | |
| | | organism = Agathobacter rectalis | | | | |
| SEQUENCE: 41 | | | | | | |
| tgcagtcgaa | cgaagcactt | tatttgattt | ctttcgggac | tgattatttt | tgactgagt | 60 |
| ggcgccgggg | tgatgttac | tggtggtaacc | tgcttgc | agggggat | aaatgtggaaa | 120 |
| cggctgtcaa | taccgcataa | gcccacgg | tcgcatgt | cgtgtgaaa | aactccgg | 180 |
| gtataaagat | gaccggcg | ggatgtca | gttgggtgg | taacggccca | ccaaggcgc | 240 |
| gatccatagc | cgacctgaga | gggtgaccgg | ccacattggg | actgagacac | ggcccaact | 300 |
| cctacgggg | cgacgtgg | ggaatattgg | acaatgggg | aaagctgt | gcacgcacgc | 360 |
| cgcgtgacgg | agaagatcg | tcgtgtatgc | aatgttctatc | agcggatgg | ataatgcgg | 420 |
| taacctgacta | agaagcaccg | gctaaatagg | tgccagcgc | cgccgtataa | cgtatgttgc | 480 |
| aagcgttatac | cggttactt | gggtgtaaag | ggacgcgcgg | cggtgcggca | agtcgtatgt | 540 |
| gaaaggccgg | ggctcaacc | cggtactcg | ttggaaact | tcgtactaga | gtgtcggggg | 600 |
| ggtaaaggcga | attcttgcgt | tcgggtgaa | atgcgtatgt | attaggaga | acaccatgt | 660 |
| cgaaggccgc | ttacttgcgt | ataacttgcgt | ctgggttgc | aaagctgtgg | gagcaaacag | 720 |
| gattagatac | ccttgcgt | cacggcgtaa | acgtgtata | ctagggtgt | ggaagcattt | 780 |
| cttctcggt | cggtcgcaaa | cgcgtatgt | attccacgtt | ggggatgt | tcgtcaagaa | 840 |
| gaaactcaaa | ggaatttgac | ggggacccgc | caagcgttgg | agcatgtgtt | ttatttgcga | 900 |
| gcaacgcgaa | gaaaccttacc | aaatgttgc | atcttgcgt | ccgggtactt | atcgtactt | 960 |
| cttctcggt | caggagtgc | agggttgtca | ttgttgtgt | cagctgtgt | cgtgtatgt | 1020 |
| ttgggtttaatcg | ccgcgtcaac | gcccgttac | tatctttat | agccacgggt | caagccgggc | 1080 |
| actcttagaga | gactgttgc | gataacatcg | aggaaaggcgg | ggatgtacgtc | aaatcatcat | 1140 |
| gccccctttagt | acttgggtca | cacacgtgt | acaatggcg | aaacaaagg | aaacaaagg | 1200 |
| gtgaaggcga | gcaaatctca | aaaataaacgt | tcgtgttgc | actgtgttgc | gcaacccgac | 1260 |
| tacacgttgc | ttgtatcg | agtaatcgca | gatcagaat | ctgggttgc | tacgttcccg | 1320 |
| ggtcttgcgt | acaccggccg | tcacaccat | ggagttgggg | atgcccgaag | ccgtgtac | 1380 |
| aaccgaaagg | aaggac | | | | | 1397 |
| SEQ ID NO: 42 | | | | | | |
| FEATURE | | | | | | |
| misc_feature | 1..1384 | note = HB-268_Ruminococcus_bicirculans | | | | |
| source | 1..1384 | mol_type = unassigned DNA | | | | |
| | | organism = Ruminococcus bicirculans | | | | |
| SEQUENCE: 42 | | | | | | |
| gcagtcgaac | gagagaagag | aagcttgcgtt | ttctgtatct | gtggcggac | ggtggtgtac | 60 |
| acgtgacaa | tctgccttgc | agggggat | accgattgg | aacgtatgtt | aataccgc | 120 |
| aacataattt | aaccgcatt | tttgattatc | aaagattat | cgctgttgc | tgagctcg | 180 |
| tctgatttgc | tagtggtaa | ggtaacggct | taccaaggcg | acgtatgt | gcccgtact | 240 |
| gagggttgc | ggccacattt | ggactgagac | acggcccg | ctcctacgg | aggcagcgt | 300 |
| ggggaaatatt | gcacaatgg | ggaaactctgt | atgcgtatgt | gcccgtgt | ggaagaagg | 360 |

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|-------------------------|-------------------------|-------------|--------------|------|
| ttttaggattg taaacacctgt | tcttcaggga cgaaaaaaaaga | cggtaacctgt | ggagggaaagct | 420 |
| cccgctact acgtgcacgc | agccggggta atacgttaggg | agcgagcgtt | gtccggaaat | 480 |
| actgggtgtaa aaggggacgt | aggccgggatc | gcaagtca | tgtgaaaact | 540 |
| ccccataaaact | gcatttgaaa | ctgtgttct | tgagtgaatg | 600 |
| gtgtagegggt | gaaatgcgt | gatatttagga | ggaacatca | 660 |
| gtttaactg acgctggggc | tcgaaagcgt | ggggagcaaa | caggattaga | 720 |
| gtccacgcgc | taaacgtga | ttacttaggt | tggggggact | 780 |
| aaacgcataa | agtaatccac | ctggggaggta | cgaccgcac | 840 |
| acggggggccc | gcacaaggcag | tggagatgt | ggattaattc | 900 |
| accaggatctt | gacatgtat | gcatgtca | gagatgtat | 960 |
| agacagggtgg | tgcatgttgc | tgctcgtc | gtgtcgatgt | 1020 |
| acgagcgcac | cccttactgt | tagttgtac | gcaagagcac | 1080 |
| caaaacgggg | gaaggtgggg | atgacgtcaa | atcatcatgc | 1140 |
| cacgtactac | aatggctgtc | aacaggaggaa | tgcaaaagcgg | 1200 |
| aaaggcgtt | tagttcggt | tgttaggtgc | aaccgcctca | 1260 |
| taatcgaga | tcagatgt | cggtgtgata | cggtccggg | 1320 |
| acgccccatggg | agtcggtaac | accgcgaagcc | tgtgtctaa | 1380 |
| aagg | | | ccgcaaggag | 1384 |

| | |
|---------------|---|
| SEQ ID NO: 43 | moltype = DNA length = 909 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..909 |
| | note = HB-27_Clostridium_paraputrificum |
| source | 1..909 |
| | mol_type = unassigned DNA |
| | organism = Clostridium paraputrificum |

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|--------------|--------------|---------------|--------------|--------------|--------------|-----|
| SEQUENCE: 43 | | | | | | |
| tgcaatcgat | cgtatgggtt | ccttcggggaa | cggattagcg | cgccgggggt | gagtaacac | 60 |
| tgggcaacct | gccttata | ggggatagc | cttccgaaag | gaagattaa | atccgcataa | 120 |
| atttgtat | cgcatgtat | agcaattaaa | ggagcaatcc | gtctataat | gggcccgcgg | 180 |
| cgcattatgt | atgtgggtat | gtacgggtc | accaaggcgc | cgatgtat | ccgacatcgat | 240 |
| agggtgtatcg | gccatgtat | gactgtat | cgccatgtat | ccctacggga | ggcagcgtat | 300 |
| ggaaatattt | cacaatgggg | gaaaccctgt | tgcaatcgat | ccgcgtat | gatgacggcc | 360 |
| ttcgggttgt | aaagctctgt | ctttggggac | gataatgacg | gtacccaagg | aggaagccac | 420 |
| ggctaactac | gtgcggcgc | ccgcgtat | acgtatgttgc | caagcgttgc | ccggatttac | 480 |
| tgggcgtaaa | ggggatgtat | ggggatgtat | tgtatgtat | tgtatgtat | gggctcaacc | 540 |
| tgggtgtatgc | atccaaact | ggaaatctat | atgtatgtat | atgtatgtat | gggaaatgtat | 600 |
| gtagcgtat | aatcgatgtat | gattatggaa | aacaccatgt | gcgaaaggcga | ctttctggac | 660 |
| tgtactatgc | gtatgtatgtat | gaaacgtat | ggagcaaaac | ggattatgtat | ccctgtatgtat | 720 |
| ccacgcgcata | aaatgtatgtat | actatgtatgtat | gtatgtatgtat | tgatgtatgtat | ccgcgcgtat | 780 |
| acgcattatgt | tattccgcct | ggggatgtat | gtatgtatgtat | ggggatgtat | aaatgtatgtat | 840 |
| cgggggcccg | cacaatgtat | ggagatgtat | gtatgtatgtat | aaatgtatgtat | aggatgtat | 900 |
| ccttagactt | | | | | | 909 |

| | |
|---------------|---------------------------------------|
| SEQ ID NO: 44 | moltype = DNA length = 1360 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..1360 |
| | note = HB-274_Collinsella_aerofaciens |
| misc_feature | 1249 |
| | note = n is a, c, g, or t |
| misc_feature | 1349 |
| | note = n is a, c, g, or t |
| misc_feature | 1360 |
| | note = n is a, c, g, or t |
| source | 1..1360 |
| | mol_type = unassigned DNA |
| | organism = Collinsella aerofaciens |

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|--------------------|------------------|------------------|----------------|----------------|----------------|------|
| SEQUENCE: 44 | | | | | | |
| tgcaatcgat | ccgcacccct | ctccgggggg | aagcgatgttgc | cgaaacggctg | atgtatgtat | 60 |
| ggagaacatcg | cccccccccc | cgggatagcc | ccccggaaagg | acgggtatata | ccggatacc | 120 |
| ccggccgcgc | catggcgccc | gggtatata | ccgcacggg | ggggatgtat | ccgcggccca | 180 |
| tcaggtatgtat | ggcggtgtat | cgccccaccc | tgccgacaa | gggtatgtat | gtttagagac | 240 |
| cgaccggccat | gatggggact | gagacacggc | ccagactctt | acggggaggc | gcagtgggg | 300 |
| atcttgcgcata | atggggggat | ccctgcgcata | gcgacgcgcgc | gtgcggggac | gaggccctcg | 360 |
| gtgtatgtatgtat | cgctttatgtat | agggatgtat | caagactgtat | cctgcgcata | agggccggcc | 420 |
| taactatgtatgtat | ccagcgcgcgc | cggtatata | tagggggcgc | gcgttatcc | gattatgtat | 480 |
| gcgtatgtatgtat | cgcgatgtatgtat | gccccggcgg | ccgggggtcg | aagcggtatgtat | ctcaatccccc | 540 |
| cgaagcccccc | ggaaatctccat | cggttgggt | ccggatgtatgtat | ggggatgtatgtat | acccgggtat | 600 |
| gcggatgtatgtat | ggtatgtatgtat | cggtatgtatgtat | ccggatgtatgtat | ggggatgtatgtat | acccgggtat | 660 |
| gaccgcgcgc | ggggatgtatgtat | cggtatgtatgtat | ccggatgtatgtat | ggggatgtatgtat | acccgggtat | 720 |
| agccgtatgtatgtat | gtatgtatgtatgtat | cggtatgtatgtat | ccggatgtatgtat | ggggatgtatgtat | acccgggtat | 780 |
| attaatgtatgtatgtat | ccgcctgggg | atgtatgtatgtat | cggtatgtatgtat | ccggatgtatgtat | ggggatgtatgtat | 840 |
| gccccgcacaa | gcagcgcgc | atgtatgtatgtat | atgtatgtatgtat | atgtatgtatgtat | ccgttaccagg | 900 |
| gtttatgtatgtatgtat | ttgggtatgtatgtat | atgtatgtatgtat | atgtatgtatgtat | atgtatgtatgtat | ccgttaccagg | 960 |
| gcgtatgtatgtatgtat | cgatgtatgtatgtat | ttgggtatgtatgtat | atgtatgtatgtat | atgtatgtatgtat | ccgttaccagg | 1020 |
| ccccggccgc | tgttgcctat | gggtatgtatgtat | ggggatgtatgtat | ggggatgtatgtat | ccgttaccagg | 1080 |

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|-------------------------------------|-------------|------------|-------------|-------------|-------------|------|
| gccccggagg | gcggggacga | cgtcaagtca | tcatgcccct | tatgccctgg | gctgcacacg | 1140 |
| tgttacaatgc | gcgggtacag | aggatgcga | cccccgcagg | gggagcgat | cccgaaagc | 1200 |
| cggccccagg | cgggattggg | ggctgcaacc | cgccccatg | aagtccgg | tgcgtat | 1260 |
| cgcggatcg | catgcgggg | tgaatgcgtt | cccgccctt | gtacacaccc | cccgtcacac | 1320 |
| caccggatc | gtctgcaccc | gaagtgcng | gccccaccgn | | | 1360 |
| SEQ ID NO: 45 | | | | | | |
| FEATURE | | | | | | |
| misc_feature | | | | | | |
| 1..967 | | | | | | |
| note = HB-28_Oscillibacter_sp. | | | | | | |
| misc_feature | | | | | | |
| 8 | | | | | | |
| note = n is a, c, g, or t | | | | | | |
| source | | | | | | |
| 1..967 | | | | | | |
| mol_type = unassigned DNA | | | | | | |
| organism = Oscillibacter sp. | | | | | | |
| SEQUENCE: 45 | | | | | | |
| ctgaccncngc | aacgcgcgt | gaaggaga | ggtttccggg | ttgttaaactt | cttttgtcag | 60 |
| ggaagagtag | aagggttac | ctgacgata | agccacggct | aactacgtgc | cagcagccgc | 120 |
| gttataatcg | agggtggca | cgttgcgg | atttactggg | tgttaaggc | gtgcagccgg | 180 |
| gccccggatc | caggatgtaa | atctgggg | ttaacctcca | aactgttatt | gaaactgttag | 240 |
| gtcttgatg | ccggagagg | tatcggatt | ccttgcgttag | cggtgaaatg | cgttagatata | 300 |
| aggaagaaaca | ccagggtgcg | aggcgatata | ctggacggca | actgtacgg | aggcgcgaaa | 360 |
| gctgtgggg | caaaccaggat | tagatacc | ggtagtccac | gctgttaaac | atggatacta | 420 |
| ggtgtgcggg | gactgacccc | ctgcgtccg | cgttacac | aataagtata | ccacctgggg | 480 |
| agtagatcg | caaggtgaa | actcaaaagg | attgacgggg | gcccgcacaa | gccccgtgatt | 540 |
| atgtgggta | attcgaag | acgcgaagaa | ccttaccagg | gcttgcacatc | ctactaacga | 600 |
| agtagagata | catcagg | ccttgggg | aagttagagac | agggtgtca | ttgttgtcgt | 660 |
| cagtcgtgt | cgttagatgt | ttggtaa | cccgcaaccc | gcttgcacaa | tattgttagt | 720 |
| tgttacgc | gagactcta | gcttgcacaa | cgtaggaaag | gtggggacga | 780 | |
| cgtcaaatca | tatgc | tatgtcctgg | ggctacacac | gtataacaat | ggcggtcaac | 840 |
| agggggggc | aaaggccgcg | ggcagagac | acccccaaac | ggcgteccag | ttcggtatgc | 900 |
| aggctgcac | cggctgcgt | gaagtgcgg | tcgcttagta | tcggttatca | gcatgcgcg | 960 |
| gtgtata | | | | | | 967 |
| SEQ ID NO: 46 | | | | | | |
| FEATURE | | | | | | |
| misc_feature | | | | | | |
| 1..1394 | | | | | | |
| note = HB-311_Alistipes_onderdonkii | | | | | | |
| source | | | | | | |
| 1..1394 | | | | | | |
| mol_type = unassigned DNA | | | | | | |
| organism = Alistipes onderdonkii | | | | | | |
| SEQUENCE: 46 | | | | | | |
| tgcgtgcgag | gggcgcacgg | atttgcgtt | gtttcaattt | ccggcgcaccc | gcccgcacgg | 60 |
| gcgttaacgcg | tatgttaccc | acctataaca | ggggcataac | actgtgaaat | tgttactaat | 120 |
| tccccatata | atccggagag | gcatcttcc | gggttggaaa | ctccgggtt | tatagatgg | 180 |
| catgcgtgt | attatgtat | tggtgaggta | acggcttacc | aaggcaacga | tacatagggg | 240 |
| gactgtgggg | ttaacc | acatgtgtt | ttagacacgg | accaggactcc | tacggggaggc | 300 |
| agcaatgggg | aatatgggtc | atggcgcga | atgttgcacc | agccatgcgc | cgttggggaa | 360 |
| gacggcttca | ttaggtttaa | actgttttgc | tacggggtaa | aacttaccta | cgttgcgtgt | 420 |
| actgttacgt | tcgttacgaa | aaggatcg | taactccgt | ccagcgcgc | cggttataac | 480 |
| gaggatccaa | gggttaccc | gatttttg | gtttaaagg | tgcgttgcgc | gtttgtataag | 540 |
| ttaggtgtt | aatccgggg | cttaactcc | gaaatgcctc | taataactgtt | agacttagaga | 600 |
| gtatgttgc | taggcggat | gtatgttgc | gctgttat | gttttagat | catacagaac | 660 |
| accgttgc | aaggcagctt | accaaactat | atctgacgtt | gaggcgcga | agcgtgggg | 720 |
| gcaaaacgg | ttagatcc | ttaggttca | cgcgat | actgtataact | cggtgtccgc | 780 |
| gatacacat | cgtgtactaa | cgatgtact | taatgttaccc | acctggggag | tacgttgc | 840 |
| agaatgttac | tcaaaaggat | tgacgggg | ccgcacaaac | ggaggaaat | gtgggtttaat | 900 |
| tcgtatgtac | gcgaggaa | ttaccgg | ttgaaatgtt | ctgacgtt | tggaaacagg | 960 |
| atttccctt | ggggcgggg | actatgtt | gtatgttgc | cggtgttgc | tgccgttgc | 1020 |
| tgtcggtt | atgtccat | cgatgttgc | cccttacccgt | agttgtccat | agggtcaat | 1080 |
| gggcacttgc | ggggactgc | cgttgcgt | cgatgttgc | gtggggat | cggttataat | 1140 |
| gcacggccct | tacgttgc | gcttacac | tggttataat | gttaggtac | agggttgc | 1200 |
| cycctgtgg | ggatgttac | tcgttacgtt | cggttgcgtt | gctgttat | 1260 | |
| gcctccatgt | atgttgc | gcttacat | ggggcgggg | tgaatgtt | 1320 | |
| cccgccctt | gtacacaccc | cccgat | catgttgc | gggggtgc | gaatgttgc | 1380 |
| accgcacca | gcca | | | | | 1394 |
| SEQ ID NO: 47 | | | | | | |
| FEATURE | | | | | | |
| misc_feature | | | | | | |
| 1..1395 | | | | | | |
| note = HB-324_Alistipes_putredinis | | | | | | |
| source | | | | | | |
| 1..1395 | | | | | | |
| mol_type = unassigned DNA | | | | | | |
| organism = Alistipes putredinis | | | | | | |
| SEQUENCE: 47 | | | | | | |
| tgcgtgcgag | gggcgcata | atggatagca | atatctatgg | ttggcgcaccc | cgacgcgg | 60 |

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|-------------|-------------|--------------|--------------|-------------|-------------|------|
| cgttaacgcgt | atgcaaccta | ccttaaacag | gggataaca | ctgagaatt | ggtaactaata | 120 |
| ccccataata | tcatagaagg | catctttat | ggttggaaat | tccgatggg | agagatggc | 180 |
| atgcgttgta | tttagctgtt | gggtgggtta | cggctcacca | aggcgacgt | acataggggg | 240 |
| actgagaggt | taaccccca | cactggact | gagacacgga | ccagactcct | acgggaggca | 300 |
| gcagtggaga | atattggtca | atggacgca | gtctgaacca | gcccgtccgc | gtgcaggatg | 360 |
| acggcttat | gagttgtaaa | ctgttttgt | acgagggtta | acgcagatac | gtgtatctgt | 420 |
| ctgaaaatgt | cgtacgaata | aggatcggt | aactccgtgc | cagecggcgc | ggtaatacgg | 480 |
| aggattcaag | cgttattccg | attttatggg | ttttaagggtt | gcgttagccg | tttgataagt | 540 |
| tagaggtgaa | atttcggggc | tcaaccctga | acgtgcctc | aatactgtg | agcttagagag | 600 |
| tagttgcgg | aggcggaaatg | tatgtgttag | cggtaaaatg | tttagagatc | atacagaaaca | 660 |
| ccgattggca | aggcggatg | tatgtgttag | cggtaaaatg | tttagagatc | atacagaaaca | 660 |
| caaaccaggat | aggcggatg | tatgtgttag | cggtaaaatg | tttagagatc | atacagaaaca | 660 |
| atacacacgt | ggtactaag | cgaaaagcgat | aagtattcca | cctggggagt | acgttcgca | 840 |
| gaatgaaact | caaaggaaat | gacggggggcc | cgcacaacgg | gaggaacatg | ttgtttaat | 900 |
| cgatgatacg | cggggggcc | tacccgggt | tgaaaggtag | cgacgattt | tgaaaggagga | 960 |
| tttcccttcg | gggcgcgaaa | ctagggtctg | catgggttc | gtcagctcgt | gccgtgagg | 1020 |
| gtcgggtta | gtccccataac | gagcgcaacc | cctaccgtt | gttgcacatca | ggtaagctg | 1080 |
| ggcaactctgg | ggggactggc | gggtttaagcc | gagagggagg | ttggggatgac | gtcaaatcag | 1140 |
| cacggccctt | acgtccgggg | ctacacacgt | gttacaatgg | tagtacaga | gggcagctac | 1200 |
| cacgcgtatgg | gatgcgaatc | tcgaaaggct | atctcgttcc | ggatttgggg | ctgaaacccg | 1260 |
| cctccatgaa | gttggattcg | cttagataatcg | cgcacatcagcc | atggcgoggt | gaatacgttc | 1320 |
| ccgggccttg | tacacaccgc | ccgtcaagcc | atgggagccg | gggggtgcctg | aagttcgtga | 1380 |
| ccgcaaggag | cgacc | | | | | 1395 |

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|---------------|------------------------------------|---------------|
| SEQ ID NO: 48 | moltype = DNA | length = 1371 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..1371 | |
| | note = HB-33_Bacteroides_stercoris | |
| misc_feature | 1192..1194 | |
| | note = n is a, c, g, or t | |
| misc_feature | 1310 | |
| | note = n is a, c, g, or t | |
| misc_feature | 1334..1335 | |
| | note = n is a, c, g, or t | |
| misc_feature | 1365 | |
| | note = n is a, c, g, or t | |
| source | 1..1371 | |
| | mol_type = unassigned DNA | |
| | organism = Bacteroides stercoris | |

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|--------------|--------------|--------------|--------------|-------------|--------------|------|
| SEQUENCE: 48 | | | | | | |
| tgcaagtgcgg | gggcgcgcattc | atcaaaggctt | gcttgtatgg | atggcgacccg | gcccgcacgggt | 60 |
| gagtaacacg | tatccaacct | gccgacaaca | ctgggatagc | ctttcgaaag | aaagattaat | 120 |
| acccggatgtt | atagtttcc | cgcgcgtgggt | gactattaaat | aaattttcggt | tttgcgtatggg | 180 |
| gatgcgttcc | attaggcgt | ttgggggtta | acggccccacc | aaaccaacaga | ttggatagggg | 240 |
| ttctgagagg | aaaggcccc | acatttggaa | tgagacacgg | tccaaactcc | tacggggaggc | 300 |
| agcagtgggg | aatattggtc | aatggacgag | agtctgaacc | agccaaatgt | cgtgaaggat | 360 |
| gactgcctt | ttgggttta | actttttta | taacgggaaata | aatgtgacca | cgtgtggctt | 420 |
| tttgcgtatgt | ccgtatgtat | aaggatcgcc | taactccgtt | ccagcagccg | cggttataacg | 480 |
| gaggatccg | gggttataccg | gattttatgg | gtttaaaagg | agcgttagccg | ggttgtttaag | 540 |
| tcagttgtga | aaagtttgcgg | ctcaaccgt | aaattgcagt | tgataactggc | gacctgtttagt | 600 |
| gcaacacagg | taggcggaaat | tcgtgtgtt | ggcggttaat | gtttagatata | cacgaagaac | 660 |
| tccgatttgcg | aggcgcgtt | actggattgt | aactgcgtt | gtatgtcgaa | agtgtgggtt | 720 |
| tcaaacacgaa | ttagatacc | tggtagtcca | ccacatcata | gtatgtact | cgtgtttggc | 780 |
| gatatacagt | cagggccaa | gcttgcataac | gagcgcaacc | cttacgtata | gttacttagca | 840 |
| acgggttacac | tcaaaaggat | tgacggggcc | ccgcacaaacg | ggaggaaat | gtgggtttaat | 900 |
| tcgatgtatc | cgcgaggaa | ttacccgggg | ttaaatttgc | actgcggaa | tcggaaacgg | 960 |
| tttttttcg | ggacagttgt | ggagggtt | catgggttc | gtcagctcgt | gccgtgagg | 1020 |
| gtcggctta | gtgcataac | gagcgcaacc | cttacgtata | gttacttagca | gttacttagca | 1080 |
| aggactctat | cgagactggc | gtcgtatgt | gttggggatgg | ttggggatgac | gtcaaatcag | 1140 |
| cacggccctt | acgtccgggg | ctacacacgt | gttacaatgg | gggggtacaga | annnagctac | 1200 |
| acggcgacgt | gggtgtatac | ccggaaaggct | ctctcgttcc | ggatttgggt | ctgaaacccg | 1260 |
| actccatgaa | gttggattcg | cttagataatcg | cgcacatcagcc | acggcgoggn | gaatacgttc | 1320 |
| ccgggccttg | tacnnnacccgc | ccgtcaagcc | atggaaaggccg | gggggnacccg | a | 1371 |

| | | |
|---------------|------------------------------------|---------------|
| SEQ ID NO: 49 | moltype = DNA | length = 1372 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..1372 | |
| | note = HB-344_Flribacter_butyricus | |
| source | 1..1372 | |
| | mol_type = unassigned DNA | |
| | organism = Flintibacter butyricus | |

| | | | | | | |
|--------------|--------------|-------------|------------|------------|-------------|-----|
| SEQUENCE: 49 | | | | | | |
| gagggttcgg | ccaaaggtagaa | taggtatgttt | agtggcgac | gggtgagtaa | cgcgtgagta | 60 |
| acctgcctt | gagttggggaa | taacacagt | aaaatttgc | taataccgc | taatgcattt | 120 |
| gggtcgtat | tttgcgtat | ccaaaggat | atcgcttgc | gttggactcg | cgtctgat | 180 |
| gctgggttgc | ggggcaacccg | cccaaccaagg | cgacgtatcg | tagccggact | gagagggttgg | 240 |

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| | | | | | | |
|-------------|-------------|-------------|--------------|--------------|--------------|------|
| ccggccacat | tgggactgag | acacggccca | gactcctacg | ggaggcagca | gtggggata | 300 |
| ttggccaatg | ggcgcgaaggc | tgcccgacca | acgocgcgtg | aaggaaagaag | gttttcgggt | 360 |
| tgtaaacttc | ttttgtcagg | gacgaaggcaa | gtgacggtaac | ctgacgaata | agccacggct | 420 |
| aactacgtgc | cagcagccgc | ggttaatcgt | agggtggcaag | cgttatccgg | atttactggg | 480 |
| tgtaaaggcg | gtgttagggcg | gaaagcaagt | cagatgtgaa | aactgtggc | tcaaccacaca | 540 |
| gcctgcattt | gaaactgttt | ttcttgagta | ctggagaggc | agatggatt | cctagtgtag | 600 |
| cggtgaaatg | cgtagatatt | aggaggaaca | ccagtggcga | aggcgatctg | ctggacagca | 660 |
| actgacgtgc | aggcgcgaaa | gcgtggggag | caaacadggat | tagataccct | ggtagtcac | 720 |
| gctgtaaacg | atggatacta | ggtgtggggg | gtctgacccc | ctccgtgcgc | cagttAACAC | 780 |
| aataaagtatc | ccacccgtggg | agtgatcg | caagggttggaa | actcaaaaggaa | attgacgggg | 840 |
| gccccacaaa | ggcgttgagg | atgtggattt | attcgaagca | acgcgaaggaa | ccttaccagg | 900 |
| gcttgacatc | ccgggtggcgg | gcttagagat | aaggccttct | cttcggagac | gccgggtgaca | 960 |
| ggtgtgtcat | ggttgtcgtc | agctcggtgc | gtgagatgtt | gggttaagtgc | ccgcaacaggag | 1020 |
| cgcacccctt | atgtttagtt | gctacgcga | agcaactgtgc | cgagactggc | gttgacaaaa | 1080 |
| cggaggaagg | tggggatgac | gtcaacatcat | catggccctt | atgtcctggg | ccacacacgt | 1140 |
| actacaatgg | tggtaaacag | agggaaaggaa | gactgtgaag | tggagcaaac | cccttaaaagc | 1200 |
| catcccattt | cggtatcgag | gctcaacccc | gcctgcgtga | agttggaaatc | gtctgttttt | 1260 |
| gcggatcgcg | atgcggcggt | gaatacgttc | ccgggccttg | tacacacccgc | ccgtcacacc | 1320 |
| atgagagtcg | ggaacaccccg | aagtccgtag | cctaaccgc | aggaggccgc | gg | 1372 |

| | | |
|---------------------------------|---------------------|---------------|
| SEQ_ID_NO: 50 | moltype = DNA | length = 1357 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..1357 | |
| note = HB-376_Coprococcus_comes | | |
| source | 1..1357 | |
| mol_type = unassigned DNA | | |
| organism = Coprococcus comes | | |

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|--------------|-------------|-------------|--------------|-------------|-------------|------|
| SEQUENCE: 50 | | | | | | |
| ttgtgactga | gtggcgacg | ggtgagtaac | gcgtgggtaa | cctgcctcat | acagggggat | 60 |
| aacagttaga | aatgactgtc | aatccgcatt | aaggaccacag | agccgcattgg | ctcgggtggg | 120 |
| aaaactccgg | ttgttatgaga | tggaccggcg | tctgatttag | tagttgggg | gttaacggcc | 180 |
| taccaacgca | acatcgatg | gcccacccgt | gagggtgacc | ggccacatcg | ggacttgagac | 240 |
| acggccaaa | ccctcactggg | aggcagcagt | ggggatattt | gcacaatggg | ggaaacctcg | 300 |
| atgcagcgc | ggccgcgtgc | cgaagaagta | tttcggtatg | taaagctcta | tcagcaggga | 360 |
| agaaaatgtac | gttacccgtac | taaagacgc | cggtctaaata | cgtgcggaca | gccggggtaa | 420 |
| taacgtatgtt | gcaagcggtt | tccggattta | ctgggtgtaa | aggggagcgtt | gacggctgt | 480 |
| taaagtctgaa | gtgaaaggccc | ggggctcaac | ccggggacttg | ctttggaaac | tatcgactgt | 540 |
| gagtgtcgaa | gaggtaagt | gaattcccg | tgtagcggtt | aatatgcgt | atattgggg | 600 |
| gaacaccagt | ggcgcaggcg | gcttactgg | cgatgactga | cggtggactt | cgaaaacgcgt | 660 |
| ggggagcaac | aggatggat | accctggtag | tccacccgt | aaacgtatgc | tacttaggtt | 720 |
| cgggggggca | agctttccgg | tgcggcagca | aacgcataaa | gtagtccacc | tggggagttac | 780 |
| gttcgcaga | atgaaaactca | aaggaaattt | cgggggacccg | cacaaggcgtt | ggagcatgt | 840 |
| gtttaatttcg | aagcaacgcg | aaggaaacctt | cctgtctttt | acatcccggt | gaccggcggt | 900 |
| taatgacgccc | tttttttcgg | aacaccgggt | acaggtgggt | catgggttgc | gtcagtcgt | 960 |
| gtctgttagat | gttgggttta | gtcccccaac | cttataatca | gtatccgtca | gtatccgtca | 1020 |
| attcggtatgg | gcactcttgc | gagactgcca | gggataaacc | ggagggaaagg | ggggatgacg | 1080 |
| tcaatcatc | atgcggccat | tgccgggg | tacacacgtt | ctacaatggc | gtaaaacaag | 1140 |
| ggaaggcgac | ctgcgggggt | aaggcaaaat | gtctcaatgc | ggattgttagt | | 1200 |
| ctgcaactcg | actatcatgg | gctggaaatc | cttagataatcg | cgaaatcaca | tgtcgccgt | 1260 |
| aataacgttcc | cggggtttgt | acacacccgc | cgtcacacca | tggggatgg | taacgcccga | 1320 |
| agtcaatgt | ccaaaccgtaa | ggaggggagct | gccgaag | | | 1357 |

| | | |
|-------------------------------------|---------------------|---------------|
| SEQ_ID_NO: 51 | moltype = DNA | length = 1396 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..1396 | |
| note = HB-385_Bacteroides_koreensis | | |
| source | 1..1396 | |
| mol_type = unassigned DNA | | |
| organism = Bacteroides koreensis | | |

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|--------------|--------------|-------------|------------|-------------|--------------|-----|
| SEQUENCE: 51 | | | | | | |
| catgcaatgc | gagggggcgc | attttagttt | gcttgcacaa | tgaagatggc | gaccggcgca | 60 |
| cgggtgagta | acacgtatcc | aacctggcga | taactccgg | atagccttc | gaaagaaaga | 120 |
| ttaataccgg | atagcatacg | aatatcgat | gatattttta | ttaaagaattt | tcgggtatcg | 180 |
| atggggatgc | gttcattatgt | tttgggtgg | gggtaacggc | ccaccaaggac | tacgtatgg | 240 |
| agggggatcg | agggggatcg | ccccccattt | ggaaacttgg | cgacggccaa | acttcacgg | 300 |
| gaggcagcag | tgaggaaat | tggccatgtt | cgccggggcc | gaaccaggcca | agtagcggt | 360 |
| aggatgttgc | ctctatgggt | cgttaacttc | ttttatatgg | gaataaaagg | ttccacgtgt | 420 |
| ggaattttgt | atgttaccata | tgaataagg | tgcgtactt | ccgtgcgcgc | agccgcggta | 480 |
| atacggagg | tccgaggcggt | atccggattt | atggggttt | aggggagcgt | agggtggattt | 540 |
| ttaagtcaatgt | gttggaaatgt | tgcggcttca | cggttttttt | cgatgtt | cgatgtt | 600 |
| ttagtacatgt | agagggtggc | ggaatttcgt | gttgggggtt | gaaatgttca | gatatccacgt | 660 |
| agaactccgt | tttgcggaggc | agtcactat | actgttactt | acactgtatc | tgcggatgt | 720 |
| gggttatcaaa | caggattttaga | taccctggta | gtccacacag | taaaccgtat | ataactcgct | 780 |
| tttgcgtat | acagtaatgc | gccaaggcgaa | agcattaaat | attccacccgt | ggggatgtacgc | 840 |
| cgccaaacgtt | gaaactcaaa | ggaatttgac | ggggcccgca | caaggcgagg | aacatgttgg | 900 |
| ttaatttcgt | gatacgcgag | gaacccattt | cgggcttaaa | tttgcacaca | atataatttg | 960 |

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| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aacagtata | ccgttaaggct | gttgtgaagg | tgctgcattgg | ttgtcgtag | ctcggtccgt | 1020 |
| gaggttcgg | cttaagtgc | ataaccgacg | caacccttac | ctttagtac | taacaggctca | 1080 |
| tgctgaggac | ttagagaga | ctgcgcgtcgt | aagatgttag | gaagggtgggg | atgacgtcaa | 1140 |
| atcacgcacgg | cccttacgtc | cgggctaca | cacgttac | aatgggggtt | acagaaggcg | 1200 |
| gctacctgtt | gacaggatgc | taatccccaa | aacctctctc | agttcggtac | gaagtctgca | 1260 |
| acccgacttc | gtgaagctgg | atccgttagt | aatcgccat | cagccatggc | gcccgtgaata | 1320 |
| cgttcccggg | ccttgcac | accggccgtc | aagccatgaa | agccgggggt | acctgaagta | 1380 |
| cgttaaccgc | aggagc | | | | | 1396 |

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|---------------|-----------------------------------|---------------|-------------|-------------|-------------|------|
| SEQ ID NO: 52 | moltype = DNA | length = 1383 | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1383 | | | | | |
| | note = HB-437_Eisenbergiella_tayi | | | | | |
| source | 1..1383 | | | | | |
| | mol_type = unassigned DNA | | | | | |
| | organism = Eisenbergiella tayi | | | | | |
| SEQUENCE: 52 | | | | | | |
| cgagggaaagg | ttcggatgg | atcaggata | acttagtggc | ggacgggtga | gtaacgcgtg | 60 |
| ggaaaacctgc | cctgtaccgg | gggataaacac | tttagaaatag | gtgctaatac | cgcataaagcg | 120 |
| cacggaaactg | catggttctg | tgtaaaaaac | tccgggttga | caggatggc | ccgcgtctga | 180 |
| ttagccagg | ggcagggtaa | cggcctacca | aagcgcacgt | cagtagccgg | cctgagaggg | 240 |
| tgaacggcoca | cattggact | gagacacggc | ccaaactcct | acgggaggca | gcagtggga | 300 |
| atattgcaca | atggggaaa | ccctgtatc | gacgcgcgc | gtgagtgaag | aagtatttcg | 360 |
| gtatgtaaag | ctctatcgc | agggaaagaa | atgcgcgtac | ctgactaaga | agccccggct | 420 |
| aactacgtgc | cagcagccgc | ggtataacgt | agggggcaag | cggttatccgg | atttactggg | 480 |
| tgtaaaggaa | gggttagacgg | catggcaagd | cagatgtgaa | aacccaggc | tcaacccctgg | 540 |
| gattgcattt | ggaactgc | gggttaggt | caggagatg | aagcggattt | ctttagtgtg | 600 |
| cgggttataatg | cgtatgatt | aggaggaaaca | ccagtggcga | aggccgttta | ctggactgtta | 660 |
| actgacgttg | aggctcgaaa | gcgtggggag | caaacaggat | tagataccct | ggtagtccac | 720 |
| gccccgtaaacg | atgatgtca | ggtgttaggt | ggtatggacc | catcggtgcc | gcagctaaacg | 780 |
| caataaaggaa | tccacatggg | gagtcgttgc | gcaagaatgaa | aactcaagg | aatttgcacgg | 840 |
| gacccgcaca | agcgttggag | catgtgtt | aattcgaagc | aacgcgaaga | acccatccaa | 900 |
| gtcttgacat | ccaaatgacg | tgctgtaaa | gaggcattcc | ttcggggca | ttggagacag | 960 |
| gtgtgtcatg | gttgcgtca | gctcggtcg | tgagatgtt | gtttaagtcc | cgcaacgcag | 1020 |
| gcaaccctta | ttcttagt | ccagcaggta | gagctgggg | ctctaaggag | actgcgggg | 1080 |
| ataaccctgg | ggaaggcggg | gtatgc | aatcatcatg | ccccctatga | tttggctac | 1140 |
| acacgtgtca | caatgcgt | aacaaaggga | aggcagacag | tgtatgtgg | caaatccacg | 1200 |
| aaataaacgtc | tcagttcg | ttttagtctg | caactcgact | acatgaagct | ggaatcgta | 1260 |
| gtatatcgca | atcgcatgt | cgccgtgaat | acgttccgg | gtcttgcata | caccggccgt | 1320 |
| cacaccatgg | gagttggaaa | tgcccgaa | gtgtgaccta | accgaaagg | aggagcagcc | 1380 |
| gaa | | | | | | 1383 |

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|---------------|--------------------------------------|---------------|--------------|--------------|--------------|------|
| SEQ ID NO: 53 | moltype = DNA | length = 1403 | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1403 | | | | | |
| | note = HB-45_Dysosmobacter_welbionis | | | | | |
| source | 1..1403 | | | | | |
| | mol_type = unassigned DNA | | | | | |
| | organism = Dysosmobacter welbionis | | | | | |
| SEQUENCE: 53 | | | | | | |
| tgcaatcgaa | cgaggacaccc | ttgactgagg | tttcggccaa | atgataggaa | tgcttagtgg | 60 |
| cggactgttg | agtaacgcgt | gaggaaacca | ccttccagag | ggggacaaca | gttggaaacg | 120 |
| actgtctaata | ccgcacgtac | catgacccgg | qcatcccggt | catgtcaaaag | attttacgc | 180 |
| tggaaatgtt | cctcgctct | gattagctag | atgggtgggt | aacggccac | catggcgacg | 240 |
| atcaatgc | ggactgtggag | gttgcaccgc | cacattggga | ctgagatacg | gcccgactc | 300 |
| ctacgggg | cagcgttgc | gaatattgg | caatggcgc | aagtctgacc | cagcaacgc | 360 |
| gccccgtaaagg | agaaggctt | ccgggtgtaa | acttctttt | tcagggaaa | gtagaagacg | 420 |
| gtacctgtac | aataagccac | ggctaaactac | gtgccagca | ccgcgttaat | acgttagtgg | 480 |
| caaggcgtt | ccgggtttac | tggtgttaaa | gggcgtcag | ccggccggc | aagtccatg | 540 |
| tgaatattcg | aggcttaacc | tccaaatgc | atttgaaact | gttagtcttgc | agtaccggag | 600 |
| agggttacgtt | atcccttgc | gttaggttgc | aatgcgttgc | tataaggaa | aacccatgt | 660 |
| gccaaggcgg | ataactggac | ggcaactgtac | ggtgaggcgc | gaaagegtgg | ggagcaaaaca | 720 |
| ggatttagata | ccctgtgt | ccacgctgt | aacgatgtat | acttaggtgt | cggggactga | 780 |
| ccccctcgct | gcgcgttta | acacataaa | tatcccaccc | ttggggat | gatcgcaagg | 840 |
| ttgaaactca | aaaggaaattt | cgggggccca | cacaaggcgtt | ggatattgttgc | gtttaattcg | 900 |
| aaccaacgcg | aaagacctt | ccaggcgttgc | acatccat | aacgaatgt | agatacatca | 960 |
| ggtgccc | ggggaaagta | gagacagggt | gtgcgttgc | gtcgtagtgc | cgtgtcgta | 1020 |
| gatgttgggt | taagtccgc | aacgacgtca | acccttatttgc | ttagttgc | cgcaagagca | 1080 |
| ccttaggg | actgcgttgc | acaaaacgg | ggaagggtgg | gacgcgtca | aatcatcat | 1140 |
| ccccctatgt | cctgggttac | acacgtata | caatggcggt | caacagagg | aggcaaaaggcc | 1200 |
| gccccggc | gaaaaccccc | aaaaggcgtc | ccagttcg | tcgcaggcgt | caacccgcct | 1260 |
| gccccgttac | caccggccgt | cacaccatg | gagtcgggaa | caccgc | ccgtacgtca | 1320 |
| accgcacgga | gggcggggcc | gaa | | | | 1380 |

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|---------------|---------------|---------------|
| SEQ ID NO: 54 | moltype = DNA | length = 1400 |
|---------------|---------------|---------------|

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|--|--|
| FEATURE | Location/Qualifiers |
| misc_feature | 1..1400 |
| misc_feature | note = HB-453_Butyricimonas_paravirosa |
| misc_feature | 18 |
| misc_feature | note = n is a, c, g, or t |
| misc_feature | 45 |
| misc_feature | note = n is a, c, g, or t |
| misc_feature | 1078 |
| misc_feature | note = n is a, c, g, or t |
| source | 1..1400 |
| | mol_type = unassigned DNA |
| | organism = Butyricimonas paravirosa |
| SEQUENCE: 54 | |
| tgcaagtgcgg gggcagcngc gggtagtgc aatacatctt cggcnccggc accggcgac 60 | |
| gggtgatcaa cacgtgtca accaaccccg taccggaga taacccggg aaacgtggac 120 | |
| taaacatccca taacactgtt tagtcgtatq qtgtctgat taaaattccg qtggatccgg 180 | |
| acgggcacgc ggcacattag gtatgtggcg gggtaacggc ccaccaagcc gacgtgtct 240 | |
| agggggttcg agaggaaatgg ccccccacat ggaacttgaga cacgggtccag actcttacgg 300 | |
| gaggcagcag tgaggatataat tggtaatgg gcgagagcct gaaccaggcca agtgcgtgt 360 | |
| gggaaagaatgt gtctatggcc tggtaaacctc ttttgcggc gaagaataaa aggtacgtgt 420 | |
| accttcttgc cagtagtgc cgaataagca tcggctaact cctgtccagc agccgcggta 480 | |
| atacggggga tgcgagcgtt atccggattt atgggttta aaggccggcgtt aggccggacg 540 | |
| ccaaagtgcgg ggttaaaagac tgcactaaat ctgttagcact cctgtgaaac tggcgactg 600 | |
| gagacgacgac gaggaggagcg gaacaatgtt agtagccgtt aatgttctt atatcactt 660 | |
| gaaccccgat agcgaaggca gcttccagg ctgcgtatgtt cgctgtatgtc cgagagcgtg 720 | |
| ggtagcgtac aggttagatgtt accttgcgtt tccacgcgtt aaacgtatgtc cactgtatgt 780 | |
| tggcgatatac cccgcgggtt tcaagcgaaat ttatgttgcgtt agccacccgg ggaggtacgtc 840 | |
| ggcacaacgtt aaacttcaag gatattggcgcc gggccgcac aagccggaga acatgtgtt 900 | |
| taatttcgtat atacgcgagg aaccttaccc ggggttaaat gtggatgtca tgagggtggaa 960 | |
| acagtttctt ccctcgggac tatttcacaatg gtgtctgtt gttgtctca gctctgtccg 1020 | |
| tgagggttcg ggttaatgtt cataacgacgc gcaaccccttcc tggccatgtt ccageggntg 1080 | |
| aaggccgggg ccctgtcgatc acgtccacccg taaaggcgca ggaaggccgg gatgacgtca 1140 | |
| aatcagcacg gcccttacac ccggggcgac acacgtgttta caatggccgg tacagaggc 1200 | |
| agccacccggg tgacccggag cgaatcttca aagccgggtcg tagttccggac tggagtctgc 1260 | |
| aaccccgactt cacaatgtt gatttcgtatc taatcgcgttca tggccatgtt ccgggttgaat 1320 | |
| acgttcccccgg gccttgcatac caccggccgtt caagccatgtt aagccggag tacctgtt 1380 | |
| tccgtgaccgc gagaacgggtt 1400 | |
| SEQ ID NO: 55 | |
| FEATURE | moltype = DNA length = 1402 |
| misc_feature | Location/Qualifiers |
| 1..1402 | |
| note = HB-472_Flavonifractor_plautii | |
| source | 1..1402 |
| | mol_type = unassigned DNA |
| | organism = Flavonifractor plautii |
| SEQUENCE: 55 | |
| gcagtcgac ggggtgtca tgacggaggat ttctgtccaaat ggattggatgtt accttagtgc 60 | |
| ggacgggtga gtaacgcgtt agggaaacctgc ctggagagg ggaataaacat tccgaaaggaa 120 | |
| gtgtctaatac cgcgtatgtc agtgggtgtt catggctctg actgcacaaat attttatgtt 180 | |
| cttgagatggc ctgcgtctg attagctatgtt agggccgggtt acggccaccat taggcacgtt 240 | |
| tcaatgtgcg gactgtgggg ttgacccggc acatggggatgtt tgagacacccg cccagactcc 300 | |
| tacggggggc agcgtggggg aatattgggc aatggggcgca agcgttgcacc agcaacggccg 360 | |
| cgtgtaaaggaa gaagggttcc ggggtgtaaa ctcttttgtt cggggacgaa acaaatagtt 420 | |
| gtaccggacg aataaggccac ggctaaatctt acgtccacgttcc cccgggttataat acgttaggtgg 480 | |
| caaggcgttat ccggatttac tgggtgtaaa gggcgtgttgc gggggatgttgc aagtccatgt 540 | |
| tgtaaaacttgg gggctcaacc tccagctgttcc atttggaaatctt gtatgttcttgc atgtgtgttgc 600 | |
| aggccatcttgc aatccgtgtt gtagccgttgc atgcgtatgttataatggggg aacaccatgtt 660 | |
| gcgaaggccg attgtgttgc acgtactgttgc gctgaggccgc gaaaggctgttgg ggagccaaaca 720 | |
| ggatttagata ccctgtgttgc acatgggttgc acatgggtgttgc ggggggtcttgc 780 | |
| ccccctccgtt cccggcgtt acacaataatg tattttccatgtt gggggatgttgc atcgcaagggt 840 | |
| tgtaaaacttgg aagaatgttgc gggggccgtt acaaaggccgtt gatgtgttgc tttatgttgc 900 | |
| agcaacccgttca agaacccttac cagggttgcata cttccacttca acgaaggccgtt gatgttccatgtt 960 | |
| gtgtcccttcg gggaaaatgttgc agacagggttgc tgcgtatgttgc tgcgtatgttgc tgcgtatgttgc 1020 | |
| atgttgggtt aagtcccgatc acgtccgttgc cccttattgtt tagtgcgttgc gcaaggccgtt 1080 | |
| tctagcgttgc ctggccgttca caaaatgttgc gaaagggtgggg acgtccgttgc atcatgttgc 1140 | |
| cccttattgttgc ctggccgttca cacaatgttgc aatgggtgttgc aacccgttgc gcaatccgtt 1200 | |
| cgagggttgc gaaatccgttca aacccgttgc cagggttgc tgcgtatgttgc aacccgttgc 1260 | |
| tatgttgcgttgc gaaatgttgc tgcgtatgttgc tgcgtatgttgc gcaatccgtt 1320 | |
| ccttgcgttgc acccgttgc acaccatgttgc agtccgttgc aacccgttgc cgttgcgttgc 1380 | |
| ccgcaaggag ggcgcgcgttgc ag 1402 | |
| SEQ ID NO: 56 | |
| FEATURE | moltype = DNA length = 1382 |
| misc_feature | Location/Qualifiers |
| 1..1382 | |
| note = HB-474_Anaerotruncus_colihominis | |
| source | 1..1382 |

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mol_type = unassigned DNA
organism = Anaerotruncus colihominis

SEQUENCE: 56
tgcaagtgcgaa cggagcttac gtttgaagt tttcggatgg atgaatgtaa gcttagtgcc 60
ggacgggtga gtaaacatgtc agcacacctgc ctttcagagg gggataacag ccggaaacgg 120
ctgcataatac cccatgtatgt tgccggggca catgcccctg caaccaaagg agcaatcgc 180
tgaaaagatgg gtcgcgtcc gattagccag ttggcggggtt aacggccac caaagcgacg 240
atcggtagcc ggactgagag gttaacccgc cacatttggta ctgagacacg gcccagactc 300
ctacgggagg cagcgtggg ggatattgca caatggcgca aaggctgtg cagcgacgcc 360
gcgtgaggga agacggctt cggattgtaa acctctgtct ttggggaaaga aaatqacgg 420
accggaaatgg gaaatccgg ctaactacgt gccagcagcc gggataatac gttagggagca 480
agcggtgtcc ggaattactg ggtttaaagg gagcgtgagc gggatggcaaa gtagaatgtt 540
aaatccatcg gtcacccgg tggctgcgtt ctaaaactgcg gttcttgatg gaatgtagagg 600
caggcgaaat ttcttagtga gcggtaatggat gcttagat tagggagaa accagtggcg 660
aaggcggectt aactgacgt gaggctcgaa aecgtgggga gcaaaacggaa 720
tttagatacc cttgttgtcc cggcgtaaaaatgattactt aggtgttggg ggactgaccc 780
cttcgggtcc gcaatggca caataaggta tccacctggg gtagtacggcc gcaagggttga 840
aactcaaaagg aatttgcggg ggccggcaca agcagtggag tatgtgttt aattcgaagc 900
aacgcgaaga accttacccg gtcttcacatggatccatgc gggatgcata gcttagatg aggtgaagcc 960
cttcggggca tccagggcagg tgggtcatgg ttgtcgctcg ctcgtgtcgat gatgttgg 1020
gttaagtcccc gcaacgagcg caacccttat tattatgttc tacgcaagag cactctaatt 1080
agactggcggt tgacaaaaacg gaggaaagggtt gggatgacgt caaatcatca tgcccctt 1140
gacactgggtt acacacatcg tacaatggca ctaaaacaga ggccggcgac acccgcgagg 1200
gaagcgaatc cccggaaaatg tcttcgttc agatgcagc ctgcaacccg cctgcataa 1260
gtcggatgtt ctatgtatcg cggatcggca tggccgggtt aatacgttcc cgggctt 1320
acacaccggc cgtcacacca tgggatgtcg taacaccggaa agccagtatc ctaaccggaa 1380
gg 1382

SEQ ID NO: 57      moltype = DNA length = 1403
FEATURE           Location/Qualifiers
misc_feature     1..1403
note = HB-478_Intestinimonas_butyriciproducens
source            1..1403
mol_type = unassigned DNA
organism = Intestinimonas butyriciproducens

SEQUENCE: 57
tgcaagtgcgaa cggagcaccc ctgacggagt tttcggacaa cgaaaggaa tgcttagtgg 60
cgacgggttg agtaacgcgt gagaatccgc ctttggatgg gggataaca gcccggaaacg 120
gtctgtacttta cccgcgttgc tatccgtgcgatgttggatccaa gattttatcgc 180
tctggatgttgc acttcgcgtct gattagatgt tggtggatgat gatgttggatccac 240
atcggtagcc ggactgagag gttggccggc cacatttggta ctgagacacg gcccagactc 300
ctacgggagg cagcgtggg gaatattggg caatggcgca aaggctgtg cagcaacgcc 360
gcgtgaggaa agaaggccc cgggttggaa acctcttttgc tcaaggacgca agcaagtgc 420
gttacccgtac gaaataatca cggctacta cgtgccccgca gccgcggtaa tacgttaggt 480
gcacgcgttac tccggattt cttgggtttt agggcggtgtt gggcgggatgg caagtcgtat 540
gtgaaactta tgggtcaac ccatacgctg catttggaaatc tttacttttggatgttgg 600
gaggcggccg gaattccctg tggtagcggtt aataggcgat atatagggg gaacaccatg 660
ggcgaaaggcg cccgtgttgc cattaaatgcg cgtgtggccg cggaaaggcgat gggggcaac 720
aggattatag accctggtag tccacggcgtaa aacatggca tacttaggtgtt ggggggtct 780
acccctccg tgcccgatgtt aacacaataa gatatcccacc tgggggtatgac gatcgcaagg 840
ttgaaactca aaggaaatgg cggggcccg cacaaggcggtt ggagatgtgtt gtttaatcg 900
aagcaacgcg aagaacatca ccaggacttgc acatccatctt aacgaaggcg agatgcataa 960
gttgccttgc gggggaaatggt gggggatggt gttgtatgtt gttgtgttgcgtgt 1020
gtatgttgggtt taatggccgc aacggcgca acccttattt ttagttgtca cgcaaggaca 1080
cttcgtcgatg actcgccgtt acaaaacggg ggaagggtttt gacgcgtca aatcatcatg 1140
cccttatgtt cttggccac acacgtacta caatggcggtt aacaggagg aacggaaacgg 1200
gcggagggttgca gcaatccctt aaaaaggcgcc cccatggca ttggccgggtt aacatcccg 1260
gtatgtatcg ggaatgtatcg gtaatggccg atcagcatgc cggatgttggaaatcg 1320
gccttgatca cccggccgtt cacaccatgtt gggatgtttggaa ccccgaaatcg 1380
acagcaatgg gggcgccggcc gaa 1403

SEQ ID NO: 58      moltype = DNA length = 906
FEATURE           Location/Qualifiers
misc_feature     1..906
note = HB-58_Bacteroides_fragilis
source            1..906
mol_type = unassigned DNA
organism = Bacteroides fragilis

SEQUENCE: 58
gtttgttttcc tttgtggcg accggcgac ggggtgatggaa cacgtatcca acctggccctt 60
tactcggttgc aaagaaaatg taatacccgta tagcataatg attccgtatg 120
gtttcattat taaaggattt cggtaatggta tggggatgtcg ttccatttagg ttgttggatg 180
ggtaacggctt caccaaggcc tcgtatggata ggggttgcgtt gggggatggcc ccccaatgg 240
gaactgagac acggtccaaa ctcttacccggg aggccggatgtt gggatattt ggtcaatgg 300
cgcttgcgtt aaccaggccaa gtatgtgtt gggatggc gcttcatgggtc gtaaactct 360
tttatataatg aataaaggatgtatcg atgtatgtatgtatgtatgtatgaaataggat 420

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cggctaactc cgtgccagca gccgcggtaa tacggaggat ccgagcgta tccggattta 480
ttgggtttaa aaggagcgta ggtggactgg taagtcatgtt gtggaaagggtt gcggctcaac 540
cgtaaaatttgc cagttgatac tgcgttcatgg gatgtacgatgta gaggtggggcg gaattcggtt 600
tgttagcggtaa aatgttttagt atatcacaa gaaactccgtat tgcaaggca gctcaactgg 660
ctgcaactgta cactgtatgtc cgaaaatgtgtt ggtatcaaac aggatttagat accctggtag 720
tccacacagt aaacgatgaa tactcgctgtt tgccatata catgtacggg ccaagcgaaa 780
gcatthaagta ttccacactgg ggagtgacggc ggcaacgggtt aaactcaaa gaatttgacgg 840
ggggccgcac aagcggagga acatgtggtt taattcgatg atacgcgagg aaccttaccc 900
gggctt 906

SEQ ID NO: 59 moltype = DNA length = 775
FEATURE Location/Qualifiers
misc_feature 1..775
note = HB-62_Streptococcus_gordonii
source 1..775
mol_type = unassigned DNA
organism = Streptococcus gordonii

SEQUENCE: 59
tagaacgcac agtttataacc gtagttgtc acaccataga ctgtgagttt cgaacgggtt 60
agtaacgcgt aggttaacctg cctggtagcg gggataactt attggaaacgg atagctataa 120
ccgcataata ttaatttatttgc catgataattt gattgaaagg tgcaatttgc ccaactaccag 180
atggacccgtc gttgtttagt ctgttgcgtt aggttaacggc tcacccgtt gacgatacat 240
agccgacccgtc aggggttgcgtt cggccacactt gggacttgaga cacggccacg actccatacg 300
gaggcagcag tagggcaatctt cggccatggt acggaaatgtt gaccgagccaa cggccgtgtt 360
gttgaagaagg ttttcggatc gttaaaatgtt gttgttaaggg aagaacgggtt gttagatgtt 420
aaatgttccaa ctgttgcgtt atcttaccatgg aaagggttgcgtt ctaactatgtt gccagcagcc 480
ggcgtaatacc gtaggttgcgtt cggccatggt ggttttgcgtt ggccgtaaaggc gacgcggc 540
gggttagataa ttctgttgcgtt aagggttgcgtt gctttaaccatggt atgtacgtt ggaaatgtt 600
taacttgcgtt gcaaaatgggg agatgttgcgtt tccatgttgcgtt gcccgttgcgtt 660
atggagggaaac accgggttgcgtt aagggttgcgtt aactgttgcgtt gagggttgcgtt 720
agcggtggggaa gcaacacggat ttatgttgcgtt cggccgttgcgtt 775

SEQ ID NO: 60 moltype = DNA length = 1409
FEATURE Location/Qualifiers
misc_feature 1..1409
note = HB-640_Enterococcus_faecium
source 1..1409
mol_type = unassigned DNA
organism = Enterococcus faecium

SEQUENCE: 60
tgcgttgcgtt acgtttttttt ttccaccggaa gcttgcgttca cccggaaaaaag aagagtggcg 60
aacgggttgcgtt taacacgttgcgtt gtaacctgtccatc catcagaagg ggataaactt tggaaacagg 120
tgcgttgcgtt gtataacaatcg cggaaaccgcgtt cgggtttgtt gttggaaaggcgctt ctttccgggtt 180
tcgtgtatggt atggggccgcgtt ggttgcgtt cttgttgcgtt aggttaacggc tcaccaaggc 240
caacatgtatggt acggccgttgcgtt aggggttgcgtt cggccacatggt gggacttgaga cacggcccaa 300
actccatcggtt gaggcagcagtaggttgcgtt cggccatggt acggaaatgtt gaccgagccaa 360
cgccgcgtgtt gttggaaagggttgcgtt ctttccgggttgcgtt gttggatgtt gagaacaagg 420
atggaggttgcgtt cttgttgcgtt cttgttgcgtt cttgttgcgtt aactatgtt gacgcggc 480
ccacgttgcgtt cttgttgcgtt cttgttgcgtt cttgttgcgtt aactatgtt gacgcggc 540
agcgccggcgtt gtttccatggt tctgtatgttgcgtt aaggccccgggttgcgtt ggggttgcgtt 600
ggaaatgttgcgtt agacttgcgtt gcaaaatgggg agatgttgcgtt tccatgttgcgtt gcccgttgcgtt 660
gcgttagatgttgcgtt atggggaaatcgccgttgcgtt aaccgttgcgtt cttgttgcgtt aactgttgcgtt 720
gagggttgcgtt aaccgttgcgtt gcaaaatgggg atgggttgcgttgcgtt aaccgttgcgtt cttgttgcgtt 780
gttgcgttgcgtt aaccgttgcgtt gcaaaatgggg atgggttgcgttgcgtt aaccgttgcgtt cttgttgcgtt 840
ctccgcgttgcgtt ggggttgcgttgcgtt cttgttgcgttgcgtt aaccgttgcgtt cttgttgcgtt 900
aaggccggcgtt gtttccatggt tctgtatgttgcgtt aaccgttgcgtt cttgttgcgtt 960
tccttgcgttgcgtt aaccgttgcgtt cttgttgcgttgcgtt aaccgttgcgtt cttgttgcgtt 1020
gggttgcgttgcgtt aaccgttgcgtt cttgttgcgttgcgtt aaccgttgcgtt cttgttgcgtt 1080
atgttgcgttgcgtt ggggttgcgttgcgtt aaccgttgcgtt cttgttgcgttgcgtt aaccgttgcgtt 1140
gaagggttgcgttgcgtt aaccgttgcgtt cttgttgcgttgcgtt aaccgttgcgtt cttgttgcgtt 1200
aatggggaaatcgccgttgcgtt aaccgttgcgtt cttgttgcgttgcgtt aaccgttgcgtt cttgttgcgtt 1260
cagggttgcgttgcgtt aaccgttgcgtt cttgttgcgttgcgtt aaccgttgcgtt cttgttgcgtt 1320
tcacgttgcgttgcgtt aaccgttgcgtt cttgttgcgttgcgtt aaccgttgcgtt cttgttgcgtt 1380
atgttgcgttgcgtt aaccgttgcgtt cttgttgcgttgcgtt aaccgttgcgtt cttgttgcgtt 1409

SEQ ID NO: 61 moltype = DNA length = 1397
FEATURE Location/Qualifiers
misc_feature 1..1397
note = HB-642_Clostridium_clostridioforme
misc_feature 1327
note = n is a, c, g, or t
source 1..1397
mol_type = unassigned DNA
organism = Clostridium clostridioforme

SEQUENCE: 61
caggatgaac gctggccggcg tgcctaaacatc atgttgcgtt aaccgttgcgtt cttgttgcgtt 60

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| | | | | | | |
|-------------|------------|-------------|------------|-------------|-------------|------|
| gttttcggat | ggaatcttga | ttgactgagt | ggcgacggg | ttagtaacgc | gtggataacc | 120 |
| tcgcctcacac | tggggataaa | cagttagaaa | tgactgctaa | taccgcataa | gcgcacagt | 180 |
| ccgcatggca | gtgtgtgaaa | aactccggtg | tggtgagatg | gatecgctc | tgattagcca | 240 |
| gttggcgggg | taacggccca | ccaaagcgcac | gatcagtacg | cgacctgaga | gggtgacccg | 300 |
| ccacattggg | actgagacac | ggcccaaact | cctacgggg | gcagcgtgg | ggaatattgc | 360 |
| acaatggcg | aaagcctgat | gcagcgcacgc | cgegtgagtg | aagaagtatt | tcggatgtga | 420 |
| aagctctata | agcaggaaag | aaaatgcgg | tacctgacta | agaagccccg | gctaactacg | 480 |
| tgccagcgc | cgcggtaata | cgtaggggg | aagcggtatc | eggattact | gggtgttaag | 540 |
| ggagcgtaga | oggcgaagca | agtcgtaa | gaaaaccccg | ggctcaaccc | tggactgtct | 600 |
| ttggaaaactg | ttttgtgt | gtgtggaga | ggtaaatgtt | ttactctatg | tagecggtgaa | 660 |
| atgcgtatgt | attagggaa | acaccgtgg | cgaaggccgg | ttactggacg | ataactgacg | 720 |
| ttgaggctcg | aaagcgtggg | gagcaaacag | gattagatac | cctggtagtc | cacgcgtaa | 780 |
| acgatgaatg | ctagggttt | gggggcaag | cccttcgg | ccgcgcgaaa | cgcagtaagc | 840 |
| atcccacctg | ggggatgtac | tcgcaagaat | gaaactcaaa | ggaatttgacg | gggacccgca | 900 |
| caagcgtgg | agcatgtgt | ttaatcgaa | gcaacgcgaa | gaaccttacc | aagtcttgac | 960 |
| atccccctcg | cgggccgt | acgcggcctt | tccctcggtt | caggggagac | aggtgtqca | 1020 |
| tggtgtcg | cagtcgtgt | cgtgagatgt | tgggttaagt | cccgcaacga | gcgcacccct | 1080 |
| tatcccttagt | agcccagcag | tgaagggtgg | cactctagg | agactgcacg | ggataaacctg | 1140 |
| gaggaagggt | gggatgacgt | caaatcatca | tggcccttat | gatttgggt | acacacgtgc | 1200 |
| tacaatggc | taaacaagg | gaagcggac | agtgtatgtt | agcaaatccc | aaaaataacg | 1260 |
| tcccagttcg | gactgtatgc | tgcaacccga | ctacacga | ctggaaatcgc | tagtaatcgc | 1320 |
| gaatcanaat | gtcgccgt | atacgcccc | gggtcttgc | cacacccccc | gtcacaccat | 1380 |
| gggagtcgc | aaccccc | | | | | 1397 |

| | |
|---------------|---|
| SEQ ID NO: 62 | moltype = DNA length = 1384 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..1384 |
| | note = HB-664_Faecalitalea_cylindroides |
| misc_feature | 1227 |
| | note = n is a, c, g, or t |
| misc_feature | 1338 |
| | note = n is a, c, g, or t |
| source | 1..1384 |
| | mol_type = unassigned DNA |
| | organism = Faecalitalea cylindroides |

| | | | | | | |
|--------------|-------------|------------|-------------|-------------|------------|------|
| SEQUENCE: 62 | | | | | | |
| gtccaggatg | aacgctggcg | gcatgcctaa | tacatgcga | tgcgaacggac | cgaaggaaaa | 60 |
| gcttgcttt | cctgaagtca | gtggcgaacg | ggtgagat | acgttagtta | cctgcccatt | 120 |
| tgcggggggc | aacgcctgg | aacgggttac | aaaacccggat | aggttagagag | atcgcatgaa | 180 |
| cttcttata | aaagggttac | ggcccttac | atggatggc | ctggcgttca | ttagctatgt | 240 |
| ggtgaggtaa | cgccccacca | aggcgacat | gcatagccg | cctgagaggg | cgaacggcca | 300 |
| cattgggact | gagacacggc | ccaaactctt | acgggaggca | gcagtaggg | atttcgta | 360 |
| atggggggaa | ccctgttac | gcaatgcgc | gttgagatgt | acgggttccg | gttgtaaag | 420 |
| ctctgttgc | agagaaaaac | gacacggata | ggaaatgtat | cgtgggtat | gttatctcgc | 480 |
| cagaaagtca | ccgcttaacta | cgtgcagca | ggccgggtaa | tacgtatgt | gcaagcgat | 540 |
| tccggatga | ttgggggtaa | agggtgcgt | ggccggccgt | taagtcttgc | gtcaagccg | 600 |
| gcagctcaac | tgtgtatgc | tttgaaaact | ggccggcttgc | agtgcaagag | aggccgatgg | 660 |
| aactccatgt | gtacggtaa | aatgtatgt | tatatggaa | aacaccatgt | gcgaaggccg | 720 |
| tcgcctggc | tgcaactgt | gcttaagcac | gaaacgtgg | ggagcaataa | ggattagata | 780 |
| cccttagtagt | ccacgcgt | aacgtatg | actaagtgtt | gggggataaa | ctcagtctg | 840 |
| cagttaaatgc | aataagtct | ccgcctgggg | agttatgtac | caagtgttgc | actcaaagg | 900 |
| attgacgggg | gccccgacaa | ggggatgtat | atgtgggtt | atccgttgc | acgcgaagaa | 960 |
| ccttaccagg | cattgttac | ccggccaa | gctgtatgt | acgcggagg | ctatcccggt | 1020 |
| gacaggtgt | gcatgttgt | cgttgcgt | tgtcgttgc | tgttgggtt | agtccgcac | 1080 |
| cgagcgaac | ccttgcgt | tgttactacc | agtaatgtt | ggactatcat | cagactgcgc | 1140 |
| gtgacacacc | ggggaaatgt | ggggatgtac | tcaaatcat | atgccttca | tggcctggc | 1200 |
| tacacacgt | ctacaatggc | gcatacnaa | agcagcgtac | ccgtgagg | aggcgtatct | 1260 |
| cgcacaaatgtc | gtctgttac | ggattgtat | ctgcaacccg | acttcatgaa | gttggatcg | 1320 |
| ctagtaatcg | cgaaatcana | tgtcgcgt | ataacgttct | ggggcccttgc | acacacccgc | 1380 |
| cgtc | | | | | | 1384 |

| | |
|---------------|-------------------------------------|
| SEQ ID NO: 63 | moltype = DNA length = 1290 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..1290 |
| | note = HB-693_Bilophila_wadsworthia |
| misc_feature | 944 |
| | note = n is a, c, g, or t |
| misc_feature | 1117 |
| | note = n is a, c, g, or t |
| misc_feature | 1122 |
| | note = n is a, c, g, or t |
| misc_feature | 1165 |
| | note = n is a, c, g, or t |
| misc_feature | 1246 |
| | note = n is a, c, g, or t |
| misc_feature | 1260 |

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misc_feature          note = n is a, c, g, or t
                     1264
misc_feature          note = n is a, c, g, or t
                     1276
source                note = n is a, c, g, or t
                     1..1290
                     mol_type = unassigned DNA
                     organism = Bilophila wadsworthia

SEQUENCE: 63
tcagattgaa cgctggcgcc gtgttaaca catgcaagtgc gaacgtgaaa gtccttcggg 60
acgagtaaag tggcgacacgg gtgagaacgc cggtggataat ctacccttaa gatggggata 120
acggctggaa acggctgcata ataccgaata cggtccccat tttatcatg gggggaaaga 180
tggcctctgc ttgcaagcta tcgtttaagg atgagtcgcg gtcccattag ctatgtggcg 240
gggtaacggc ccaccaaaaggc gacgtatgggt agccggctcg agaggatgac cggccacact 300
ggaacttggaa cacgggtcccg actctacgg gaggcagcag tgccaaatat tgccaaatgg 360
gcgaaaggct gacgcacgcg cggccgtga gggatggaaat ttctcgatc gtaaacctct 420
gtcaggggggg aagaaaacccc ctcgtgtgaa taatgcgagg gtttgacggt acccccaaag 480
gaagcggccg ctaactccgt gcccacggc gggtaatac ggagggtgca aegcttaatc 540
ggaatcaactg ggcgtaaaggc gcacgttaggc ggcttggtaa gtcagggggtg aaatcccaca 600
gccccactgt ggaacttggct ttgtatgcg caggcttggg taccggagag ggtggcgaa 660
ttccagggtt aggagtggaa tccgttagata tctggaggaa caccgggtggc gaaggcgcc 720
acotggacgg taactgacgc tgagggtgca aagcgtgggtt agcaaacagg attagatacc 780
cttgttagtcc acgtcgatc cgtgggtgtc tgggtgtcgat gatgtatgtc tcgggtgcgt 840
agcttaacgcg ataaacccccc cgcctggggaa gtacggctgcg aaggctgaaa ctcaaaagaaa 900
ttgacggggg cccgcacaag cgggtggatc tgggtttaa ttcnatgca cgcgaagaac 960
cttacccagg cttgacatct agggaaacctt tccgttggaa aggggtgccc ttccggggagc 1020
cctaagcacag gtgtcgatc gtgtcgatc gtcgtgtgtc tgagggtgtg ggttaagtgc 1080
cgcaacgcg ccaaccccta tcttcgttgc ccacgttgcg angtgggca ctctggagag 1140
acccggccccc tcaacggggg ggaangtggg gacgacgtca agtcatcatg gcccattacgc 1200
ctggggctac acacgtacta caatggcgccg cacaagggtt agcgtanacccg cgagggtggan 1260
ccantcccaaa aaacgnntcc cagtcggat 1290

SEQ ID NO: 64      moltype = DNA length = 731
FEATURE           Location/Qualifiers
misc_feature      1..731
                     note = HB-71_Bifidobacterium_longum
source             1..731
                     mol_type = unassigned DNA
                     organism = Bifidobacterium longum

SEQUENCE: 64
tttgcttggt ggtggagatgc gcgacgggtt gagtaatgcg tgaccgaccc gccccatata 60
ccggaaatagc tcctggaaac ggggtgttaat gccggatgtc ccagttgtc gcatggcttt 120
ctggggaaacgc ttctcggtta tggatgggg tccgtctcata tcagctgtac ggcggggtaa 180
cgcccccaacgg tggcttcgtac gggtagccgg cggatggggggc cattggggact 240
gagataccgcg ccacgtccct acggggggca gcagttggggaa atatgcaca atggggccaa 300
gcctgtatgcg cgcacgcgcg gtgagggtatc gaggccttcg ggtttaaac ctctttatc 360
ggggggcaacgg cggagatgtatc ttatccgggtt gaataacgcgatc cggctaaacta cgtgccagca 420
ggccgggttac tacgtggatgc gcaacgttgc tccggatggaa aggggtcgta 480
gggggttgcgtt cgcgtccgtt gtggaaatgc atcgcttaac ggtggatccg cgccgggtac 540
gggggggtttt ggtgtggatgc gggggactgtt gatgttgcgaaatgtgttag 600
atatcgggaa gaacaccaat ggcgaaggca ggtctctggg ccgttactgc cgttgaggag 660
cgaaagcgatc gggagcgac accgttggatgc tccacggccgtt aaacgggtgg 720
tgtgtgtatgc 731

SEQ ID NO: 65      moltype = DNA length = 853
FEATURE           Location/Qualifiers
misc_feature      1..853
                     note = HB-73_Clostridium_hylemonae
misc_feature      787..789
                     note = n is a, c, g, or t
source             1..853
                     mol_type = unassigned DNA
                     organism = Clostridium hylemonae

SEQUENCE: 65
ctgtgtgaag agattatgtt gctaagatca gaactttgtt ttgactgtt ggcggacggg 60
tgagtaacgc gtggggcaacc tgcccttacac agggggataa cagctgaaa tggctgtctaa 120
taccgcataa gacctcagta ccgcattgtt gggggtaaa aactccgggtt gtgttgcgtt 180
ggcccgccgtc tgattaggta gttggtaggg taacggcata ccaagccgac gatcgtatc 240
cgacccgttgc ggggtgaccgg ccacattggg actgtggacac ggcccaactt cctacgggg 300
gcacgttgc gggatattgc acaatggggg aaacccctgtatc gcacgttgcgcg cgcgtgaagg 360
atgttgcgtt tccgtatgtt aacttctatc agcaggaaatgc aatgttgcgtt tacgttacta 420
agaagcccccg gctaactacg tgccagcgcg cggcgttata cgttggggc aagcgatc 480
cggtttactt ggggtgtaaag ggacgttgcgatc cggcatgttgc aatgttgcgtt gaaagccgg 540
ggctcaaccc cggggactgtt ttggaaactgt tcaggcttgc gttgtcgatc ggcgttgg 600
attccatgtt tccgttgcgtt aatgttgcgtt attaggatgc acaccgttgc cgaaggccgc 660
ttgtgtggatgc atgttgcgtt ttggggatgc aaacgttgcgtt gggcaaaatgc gatttgcgtt 720

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| | |
|---|-----|
| cctggtagtc cacggcgtaa acgatgatta ctaggtagtc ggaagcaaag ctttcgtg | 780 |
| ccgcagnnna cgcaataagt aatccacgt gggagtagt tcgcaagaat gaaactcaa | 840 |
| ggaattgacg ggg | 853 |
| SEQ ID NO: 66 moltype = DNA length = 752 | |
| FEATURE Location/Qualifiers | |
| misc_feature 1..752 | |
| note = HB-82_Clostridium_innoculum | |
| source 1..752 | |
| mol_type = unassigned DNA | |
| organism = Clostridium innoculum | |
| SEQUENCE: 66 | |
| ggaagcttgc ttccaaagag acttagtggc gaacgggtga gtaacacgta ggttaacctgc | 60 |
| ccatgtgccg gggataactg ctggaaaaccc tagctaaaatc cggatagtgta tacagagcgc | 120 |
| atgcctctgt tattaaacgc cccatcaagg cgtgaacatc gatggacctg cggcgattaa | 180 |
| gcttagttgg gaggtaacgg cccacaagg cgtatgtcg tagccggctt qagagggtaa | 240 |
| acggccacat tgggactgag acacggccca aactcttacg ggaggcagca gttaggaaatt | 300 |
| ttctgtcaatc gggggaaaccc tgaacggca atggcgccgt agtgaagaag gtcttcggat | 360 |
| cgtaaacgtc ttgttgaatg gaagaacggc tcatagagga aatgtatgg ggtgtacgg | 420 |
| agcttaccac aaagccacgg ctaactacgt gccagcagcc cgccgtataac gttagtggca | 480 |
| agcggttatcc ggaatcattt ggcgtaaagg gtgcgttagt ggctgtactaa gtctgttagt | 540 |
| aaaggcaatc gtcacccat tgtaactat gggaaactggt atgtctggat gcagaagagg | 600 |
| gcgtatggaaat tccatgtgt gcggtaaaat gcgtagatatt atggaggaa accagtggcg | 660 |
| aaggccgtcg ctgggtctgt aactgacact gaggcagca agcgtgggg gcaaatagga | 720 |
| ttagataccc tagtagtcca cgccgtaaac ga | 752 |
| SEQ ID NO: 67 moltype = DNA length = 761 | |
| FEATURE Location/Qualifiers | |
| misc_feature 1..761 | |
| note = HB-90_Bifidobacterium_breve | |
| source 1..761 | |
| mol_type = unassigned DNA | |
| organism = Bifidobacterium breve | |
| SEQUENCE: 67 | |
| tgcagtcgaa cgggatccat cagggttgc ttgggtggta gagtggcgaa cgggtgagta | 60 |
| atgcgtgacc gacctgcccc atgcacccga atagctctt gaaacgggtg gtaatgcgg | 120 |
| atgcctccat acatcgcatg gtgttgtgg aaacgcctt cggcatggta tgggtcgcg | 180 |
| tcctatcagc ttgatggcg ggtaaacggcc caccatggc tgcacgggta gcccggctga | 240 |
| gaggggcacc ggcacccatgg ggactggat acggcccaaga ctccctacgg aggccacgt | 300 |
| ggggatattt gcaacatggg cgcaagccgtt atgcagcgc gccgcgtgag ggtatggggc | 360 |
| cttcgggttg taaacctt ttgttaggg gcaaggact ttgttgttag tgcgtttttc | 420 |
| gaataagcac cggctaacta cgtgcagca gcccggtaa tacgttaggt gcaagcgta | 480 |
| tccggatattt tggggatggaa agggtcgta ggccgttccgt cgcgtccgt gtggaaatgc | 540 |
| atcgcttaac ggtggatccg cgccgggtt gggccgggtt gagtgcggta gggggactg | 600 |
| gaattccccc tgcatacggtt gaaatgttagt atatcgggaa gaacaccaat ggcgaaggca | 660 |
| ggctctctggg ccgttactgt cgctgaggag cgaaaggctg gggagccaa aggattagat | 720 |
| accctggtag tccacccgtt aaacgggttga tgctggatgt g | 761 |
| SEQ ID NO: 68 moltype = DNA length = 862 | |
| FEATURE Location/Qualifiers | |
| misc_feature 1..862 | |
| note = HB-95_Acidaminococcus_intestini | |
| source 1..862 | |
| mol_type = unassigned DNA | |
| organism = Acidaminococcus intestini | |
| SEQUENCE: 68 | |
| gttcttagt gcgaaacgggt gagaacacg tggggcaactt gcccctcaat tggggacaac | 60 |
| attccgaaag ggtatgtttaat accgaatgtg ctcccttc cgcattgggg agggaggaaa | 120 |
| gtatggccctt gtttgcggc tatecgcttca agatggggcc ggcgttgcatt agttagtgg | 180 |
| tggggtaacg gtcacccatgg gcgcatgtca tgagccggcc tgagaggatg aacggccaca | 240 |
| tttggactgt gacacggccc aaactcttac gggaggccgtt agtggggat cttccgcatt | 300 |
| ggacgaaatg ctgacggatc aacggccgtt gagtgcgtt ggttccgtt ttgtaaagct | 360 |
| ctgttgttag ggacgaaatc accgtgttccg aacaggctat ggttccgttgcgt gtacctaag | 420 |
| aggaaaggccac ggctaaatct gtcgcggcggc ccgcggtaat acgttaggtgg caagcggtgt | 480 |
| ccggatattt tggggatggaa ggcgttgc gccgggtttt aagtctgcg tgaaaatgcg | 540 |
| gggtttttttt ccgtatggcg ttggatactg gaaatgttgc gtgcaggaga ggaaagggg | 600 |
| attcccgatg tgcgtgttca atgcgttagat attggggatg acaccaggat cgaaggcc | 660 |
| tttctggact gtgtctgtacg ctggatgtttt gaaaggccggg tagcaaaacgg gattagata | 720 |
| ccggatgttcc tggggatggaa acgtatggata ctggatgttag gaggatgtca ccccttcgt | 780 |
| ggccggatgttcc acgcaataag tatcccgctt gggactacgt atgcgtatggat tgaaaactcaa | 840 |
| aggaaatttgc gggggccccc ac | 862 |
| SEQ ID NO: 69 moltype = DNA length = 673 | |
| FEATURE Location/Qualifiers | |
| misc_feature 1..673 | |
| note = HB-98_Streptococcus_gordonii | |

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| | | | | | | |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| acttgagtgc | cgagggggta | agcggaaattc | ctagtgttagc | ggtggaaatgc | gtagatatta | 600 |
| ggaggagaac | cagtggcgaa | ggccggcttc | tggacggtta | ctgaaccttg | ggctccaaag | 660 |
| cgtgggggac | aaacaggagg | atacacttc | gtgtccacg | ccgtaaacgc | tgaatactact | 720 |
| tgtcggggg | gcatggccct | tcggcgcc | cgcaaacgc | gtaaatattc | cacctggggg | 780 |
| gtacgtcg | aagaatgaaa | ctcaaaaggaa | ttgacggggg | ccccgcacaag | cgggtggagca | 840 |
| tgtggttaa | ttcgaagcaa | cgcgaagaa | cttaccaaant | cttgacatcc | ctctgaccgg | 900 |
| tctttaatcg | gacccttcct | tcggagcaga | nngacaaagg | ttgtgtatgg | tgtgtcgatcc | 960 |
| tctgttcgtg | agatgttggg | ttaagtcccg | caacgcgc | aaccctata | ctcgtatggcc | 1020 |
| agcatttaag | tgggggcac | tggggagact | gccaggggata | acctggggata | aggccgggat | 1080 |
| gacgtcaat | catcatgccc | tttatgattt | gggcatacaca | cgtgtacaaa | tggcgttaaac | 1140 |
| aaagggaagc | gagatcgtg | gatggagcaa | atccaaaaaa | taacgtccca | gttccggactg | 1200 |
| tagtctgcga | cccgactaca | cgaagctgg | atcgcttagt | atcgoggatc | agaatgcgc | 1260 |
| ggtaatacag | ttccggggtc | ttgtacnac | ccccgttcac | accatgggg | gtcagtaacg | 1320 |
| cccgaaatcg | gtgacccaaat | t | | | | 1341 |

```
SEQ ID NO: 72          moltype = DNA    length = 1327
FEATURE                  Location/Qualifiers
misc_feature             1..1327
note = HB-259_Sutterella_wadsworthensis
source                   1..1327
mol_type = unassigned DNA
organism = Sutterella wadsworthensis
```

SEQUENCE: 72

| | | | | | | |
|-------------|--------------|-------------|--------------|--------------|-------------|------|
| tgcgtcgaa | cggcagcgcg | gggagcttc | tccctggcgg | cgagtggcgc | acgggttgcgt | 60 |
| aatacatcg | aacgtgttt | ctagtgggg | ataactgccc | gaaaggccag | ctaataccgc | 120 |
| atggacact | agggtgtaa | ggggggatcg | caagactcg | cgtgtggaa | gcccgcgtat | 180 |
| tccgattac | tagtgtgtt | ggtaaaatgc | cacaaggcg | acgtatggta | gtctggctgt | 240 |
| gaggacgacc | agccacactc | ggactggagac | acggcccca | ctccatccggd | aggccaggct | 300 |
| ggggaaat | ggacaatggg | ggcaaccctg | atccagccat | gccgcgtgc | ggatgaagg | 360 |
| cttcggat | taaaactgtt | ttgtccggg | cgaaaaggga | tgccataaca | ccgcattccg | 420 |
| ctgcaggat | ctgaagaata | ggcacccgt | aactatgtc | cagcgcgc | ggtataatcg | 480 |
| agggtgttca | cgttaatcc | aattactgg | cgtaaaggct | gcgcggcg | ttctgttggaa | 540 |
| tagatgtgaa | atccccgggc | tcaaccctgg | aattgcata | atgactgcag | gacttggagg | 600 |
| tgtcagggaa | gggtggaaat | ccacgtgtag | cagtggaaat | cgttagat | tggaaagaaca | 660 |
| ccgcgtggcc | aggcagccct | ctggggacat | actgcgcctc | atgcacggaa | gcgtggggag | 720 |
| caaacaggat | tagataccct | ggtagtcac | gcccctaaac | atgtctacta | gttgggggg | 780 |
| acgatgtcc | ttggtaacgc | agctaaacgc | tgaagtagac | gcgcgggg | gtacggcg | 840 |
| aagattaaaa | ctcaaaaggaa | ttgacgggga | cccgacaca | cgggtggat | tgtggattaa | 900 |
| ttcgtatcgaa | cgcgaaaaac | cttacccatgc | cttgacatgc | caggaaaggcc | tgagatgtca | 960 |
| ggccgtggcc | gcaaggggaaat | ctggacacag | gtgtgtcgat | gctgtgtcg | gtctgtgtcg | 1020 |
| tgatgttgc | gggttaatgc | cgcaacacgc | gcaacccttgc | tcattatgttgc | ctacgaaagg | 1140 |
| gcaactat | gagactgcgc | gtgacaaac | ggagggaaagg | ggggatgtac | tcaagtcc | 1200 |
| atggccat | tggcttagggc | ctcacacatgc | atacaatgttgc | cggacacag | ggaagcga | 1260 |
| ccgcgtgg | aaggccatcc | cagaaaaccc | atcgtagtcc | ggattggcgt | ctgcgactcg | 1320 |
| actgcgtat | gtcggtatcg | ctgtatcg | cggatcgc | tgccgcgtgt | atacggttcc | 1380 |
| qqqctq | | | | | | 1327 |

```
SEQ ID NO: 73          moltype = DNA  length = 1391
FEATURE                Location/Qualifiers
misc_feature           1..1391
note = HB-30_Bacteroides_clarus
source                 1..1391
mol_type = unassigned DNA
organism = Bacteroides clarus
```

SEQUENCE: 73 Organism = *Bacteroides claus*

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| | |
|---|------|
| actccatcaa gctggattcg cttagaatcg cgcacgaccc acggcgccgt gaatacgttc | 1320 |
| ccgggccttg tacacaccgc cccgtcaagcc atgaaagccg ggggtacctg aagtacgtaa | 1380 |
| ccgcaaggag c | 1391 |
| SEQ ID NO: 74 moltype = DNA length = 1407 | |
| FEATURE Location/Qualifiers | |
| misc_feature 1..1407 | |
| note = HB-333_Prevotella_sp. | |
| source 1..1407 | |
| mol_type = unassigned DNA | |
| organism = Prevotella sp. | |
| SEQUENCE: 74 | |
| catgcagtgc tggggcagca tgggagatgc ttgcatttc cgatggcgac cggcgacgg 60 | |
| gttggatcaa cgttatcca ctgccttca ctccggcaca cccgtcgaa agacggatta 120 | |
| atgcgggatc cgtcattat aatttgcgaa aaggctttat ccgggtgagg 180 | |
| gtatgggatc cgtccgatc gcttgcggc qgggttaacgg cccaccgtgg cgacgatcg 240 | |
| taggggttct gaaaggaaagg tccccccat tggaaactgaa acacggtcca aactcctacg 300 | |
| ggaggcgacca gtggagaata ttggtcaatg ggcgaaagcc tgaaccaggc aagtagcgtg 360 | |
| caggaaagacg cccctatggg ttgttaactcg cttttgtcg ggaataaagg gggtcacgtg 420 | |
| tggcccttgc catgtaccgt acgaaatagg acggcataat cccgtccag cagcccggt 480 | |
| aatacggaaag gtccggcggt tatcoggatt tattgggtt aaaggggagcg tagggcgct 540 | |
| caaaaaggctg ttgttaatc tccgggctca accggggccg tgcagccgcg actgtgagac 600 | |
| tttggatgtgc ggaaggatcg cggaaatctg ggtgttagcg tggaaatgcgat agatatcag 660 | |
| aagaactctcg attgcgaaatc cggatccatc cggatgtatc ctcgaagggt 720 | |
| cgggtatcga acaggattag atacccctgtt agtccgcaca gtaaacatcgat gatgeccgc 780 | |
| gttggatctgt ttaatgtttt gcccggcaacg gaaaggcttta acgatccccac ctggggaggt 840 | |
| cggccggcaac ggtgaaactc aaaggatcg acggggggccg gcacaacggg aggaaacatgt 900 | |
| gggtttaattc gatgtatccgc gggaaacctt accccgggtt gaatttgcggg tgcatgggg 960 | |
| ggagacatcc ctttcttcg ggactctctgtt gaagggtctg catgggttc gtcagctctg 1020 | |
| gcccgtggatc gtccggcttaa acgtccatc gggccataac gggccaaacc cctctccgtt gttgccatcg 1080 | |
| ggttaaaggcc ggcacttgc ggacactgtc tccggcaagg gttggggatgac 1140 | |
| gttggatccgc acggccctt acgtccggggg ctacacactg gttaaatggg ggcatacaga 1200 | |
| gagcagggtt ttcggcaatgt cggccaaatc aaaaaatgtc ctctcgttc ggactgggg 1260 | |
| ctgcaacccg accccacgaa gctggattcg cttagaatcg cgcacatcgcc atggcgccgt 1320 | |
| gaatacgttc cccggcctt tacacaccgc cccgtcaagcc atgaaagccg gggggcgctg 1380 | |
| aagtccgtca cccgcgagggtt cggcccta 1407 | |
| SEQ ID NO: 75 moltype = DNA length = 1406 | |
| FEATURE Location/Qualifiers | |
| misc_feature 1..1406 | |
| note = HB-34_Bacteroides_thetaiotomicron | |
| misc_feature 954 | |
| note = n is a, c, g, or t | |
| source 1..1406 | |
| mol_type = unassigned DNA | |
| organism = Bacteroides thetaiotomicron | |
| SEQUENCE: 75 | |
| catgcagtgc agggggcagca ttccatgttgc ttgcacaaact ggagatggcg accggcgac 60 | |
| gggttggatcaa cacatcca acctgcgttgc aactcgccgttgc tagccttcg aaagaaatgg 120 | |
| taatacccgta tgggtataatc agaccgcgttgc gtcttgcgttgc taaagaattt cggttatcg 180 | |
| tggggatcgcc ttccatgttgc cgttgcgttgc ggttacggcgttgc caccacaaact tcgtggata 240 | |
| gggggttctcg gggggatcgcc ttccatgttgc ccccaatcg gtaacggatc acgggtccaaat ctcctacggg 300 | |
| aggcagcgttgc gggggatcgcc ttccatgttgc cggatgtatcgatc cggatgtatcgatc aaccagccaaatc gtagcgtgttgc 360 | |
| ggatgtactgc cttatgggtt gttttatggg aataaaatggg tccacatgtgttgc 420 | |
| gaattttgttgc tttttatggg gttttatggg aataaaatggg tccacatgtgttgc 480 | |
| tacggatgttgc cggatgtatcgatc cggatgtatcgatc cggatgtatcgatc aaccagccaaatc gtagcgtgttgc 540 | |
| taagtcaatgttgc tttttatggg gttttatggg aataaaatggg tccacatgtgttgc 600 | |
| gagttatcgatc gggggatcgcc ttccatgttgc cggatgtatcgatc cggatgtatcgatc aaccagccaaatc gtagcgtgttgc 660 | |
| gaactccgttgc gggggatcgcc ttccatgttgc cggatgtatcgatc cggatgtatcgatc aaccagccaaatc gtagcgtgttgc 720 | |
| ggttatcaacatgttgc tttttatggg gttttatggg aataaaatggg tccacatgtgttgc 780 | |
| tttggatcgcc ttccatgttgc cggatgtatcgatc cggatgtatcgatc aaccagccaaatc gtagcgtgttgc 840 | |
| ggcaacccgttgc aactcaaaatggg gttttatggg gttttatggg aataaaatggg tccacatgtgttgc 900 | |
| taatttcgttgc tttttatggg gttttatggg aataaaatggg tccacatgtgttgc 960 | |
| acatgtatcgatc gggggatcgcc ttccatgttgc cggatgtatcgatc cggatgtatcgatc aaccagccaaatc gtagcgtgttgc 1020 | |
| agggttgcgttgc tttttatggg gttttatggg aataaaatggg tccacatgtgttgc 1080 | |
| gttggatcgcc ttccatgttgc cggatgtatcgatc cggatgtatcgatc aaccagccaaatc gtagcgtgttgc 1140 | |
| tcggatgtatcgatc cggatgtatcgatc cggatgtatcgatc aaccagccaaatc gtagcgtgttgc 1200 | |
| cttccatgttgc tttttatggg gttttatggg aataaaatggg tccacatgtgttgc 1260 | |
| ccggacttgc tttttatggg gttttatggg aataaaatggg tccacatgtgttgc 1320 | |
| gttccatgttgc tttttatggg gttttatggg aataaaatggg tccacatgtgttgc 1380 | |
| gttccatgttgc tttttatggg gttttatggg aataaaatggg tccacatgtgttgc 1406 | |
| SEQ ID NO: 76 moltype = DNA length = 1373 | |
| FEATURE Location/Qualifiers | |
| misc_feature 1..1373 | |
| note = HB-373_Prevotella_copri | |

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source          1..1373
               mol_type = unassigned DNA
               organism = Prevotella copri

SEQUENCE: 76
cgtgcttcg ataggcgtcg accggcgac gggtagtaa cgctatcca acctgcccac 60
caacttggga taaccttgcg aaagtaagac taataccca tgatatctct agaagacatc 120
tgaagagat taaagattt tccgtatgg atggggatgc gtctgattag ctgttgccg 180
gggttaacggc ccaccaaggc aacgatca ggggttctg agagggaaatg cccccacatt 240
ggaactgaga cacggtccaa actctacgg gaggcagca tgaggaatat tggtaatgg 300
acgagactct gaaccggca agtgcgtgc aggaagacgg ccctatgggt tgtaaactgc 360
tttataaggg aataaaatgtg agtctcgta gacttttgc atgtaccta tgaataagg 420
ccggctaaatt ccgtgcgcg aecggcgta atacggaaagg tccgggggtt atccggattt 480
attgggtta aaggggcggt aggeccggaga ttaagcgtgt tggtaaatgt agatgctaa 540
catctgmact gcagcgcgca ctgggttctt tgagtacggca caaagtggc ggaattcggt 600
gtgtageggta gaaatcgatc gatatcacg agaactccga ttgcgaaggc agctcaactgg 660
agcccaactg acgctgaaac tcgaaatgtc gggtatcgaa caggattaga taccttggt 720
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agcattaaacg atcccacctg gggagtaegc cggcaacggta gaaactcaaa ggaattgacg 840
ggggcccgca caagcggagg aacatgtgtt ttaattcgat gatacggag gaaccttacc 900
cgggcttgaa ttgcagagga aggatttgc gacaatgacg ccctcggtt cctcttgaa 960
ggtgctcat ggttgcgtc agctcggtgc gtggatgtc ggcttaatgt ccataacgag 1020
cgcaaccctt ctcccttgtt gccatcaggta gaaagctggc actctggga caactgcccac 1080
gtaaagggtgtt aggaagggtgg ggatgcgtc aaatcagcagc ggcccttacg tccggggcta 1140
cacacgtgtt acaatggcag tcagacggag acggttccctt gcaaaaatggta tcaaattctt 1200
aaagcctgtc tcagttcgga ctgggtctg caacccgaccc acacgaaatgtt ggattcgta 1260
gtaatcgccg atcagccatg ggcgggtgaa tacgttcccg ggccttgcac acaccgccc 1320
tcaagccatg aaagccgggg ggccttgcataa gtcgtgaccg taaggagcgg oct 1373

SEQ ID NO: 77      moltype = DNA length = 1439
FEATURE           Location/Qualifiers
misc_feature     1..1439
note = HB-387_Dialister_invisus
misc_feature     928
note = n is a, c, g, or t
source            1..1439
               mol_type = unassigned DNA
               organism = Dialister invisus

SEQUENCE: 77
tgcaatcgaa caaaaagacgg aaagagcttg ctcttttcaag aatttgcgtgg caaaacgggtg 60
agtaacacgtt aacaaacactt ctttcaggat ggggacaaca gacggaaacg actgtataata 120
ccgaataatgtt tccaaagagcc gcatggccca tggaaagaaaa ggtggccctt acctgttaacg 180
tatcgccctga agaggggtttt gctgtgtattt agctgggtgg aggggttaacg gcccaccaag 240
ggcacgtatca gtagccgggtc tgaggatggat aacggccaca ctggaaactga gacacgggtcc 300
agacttcatac gggaggcagc agtggggatattt ctcccgcaat gggccaaacg ctgacggagc 360
aacggcccggtt ggtgtatgc ggccttcggg ttgtaaaact ctgtgtatccg ggacgaaag 420
gcagagtgcg aagaacaaac tgcatttgacg gtaccggaa agcaagccac ggctaaactac 480
gtgccagcagc ccggctgtat acgttaggtgg caagcgttgc cggatattat tgggggttaaaa 540
ggccgcgcagc ggggttccctt aaggcccttca ggggtttaacc cctgtatggg 600
aaggaaactt ggaagcttggat gtagccggata gggaaatgttgc attccctatgt tagccgttgc 660
atgcgttagat attagaaga acaccgggtt cgaaggcgcac ttctgtggacg aaaactgacg 720
ctggggccggc aaagcgtggg gggccaaacg gattagatc cctggtagtc cacggccgtaa 780
acgatggata tcaggatgtt gaggatcgtca ccctcttgcgtt gccggatgtt acgcaataaag 840
tatccgcctt gggaaatgtc atcgaatattt aaaaactcaaa aggaatttgc gggggccccc 900
acaacgggtt ggttatgtgg ttaattnga cgcacgcga agaaccttac caggcttgc 960
cattgtatgc gatctcgcaaa aatcggtttt ttttcttcggg aagacggaaa aacagggtgg 1020
gcacgggtttt cgtcgatcg tggatgttgc tggatgttgc tttctgtggacg 1080
ccctatatt tggccggccgc acgttaatgtt ggggactcaaa atgagacccgc cggccacac 1140
ggggaggaaag gggggacgcg cgtcaagtca tcatggccct tatgacctgg gctacacacg 1200
taactacaatgtt ggtgtcaaca aagagaagcg aaaccggcgaa gaagagcaaa cctcaaaaac 1260
acaccccccacg ttcagatgcg aggtgtcaac cccctgtcgat gggccggatggaa tggatgttgc 1320
tcggggccgcg gatatccatgtt tccggggccctt tggatcacacc gcccgtcaca 1380
ctatgagatgtt cagaaacacc cgaagccgtt gaggttacccg caaggagccca gccgtcgaa 1439

SEQ ID NO: 78      moltype = DNA length = 1396
FEATURE           Location/Qualifiers
misc_feature     1..1396
note = HB-443_Sellimonas_intestinalis
source            1..1396
               mol_type = unassigned DNA
               organism = Sellimonas intestinalis

SEQUENCE: 78
tgcaatcgatc gaaagcgctg ttttcagaat ctccggaggaa agaggacgc gactgaggccg 60
cgacgggggtt ggtgtcaac gggcaaccttgc cctcatacag ggggataaca gtttagaaatg 120
actgtataatgtt ccgcataaagc gcacaggacc gcatgggtgtt ggtgtaaaatc ctccgggtgtt 180
atgagatggatcccgccgttccgttgcgtt gggccgttgcgtt gggccgttgcgtt gggccgttgcgtt 240
tcagtagccgcg acctgtggagg gttggccgc acatggggac tggatgttgc cccaaactcc 300

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|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tacggggaggc | agcagtgggg | aatattgcac | aatgggggaa | accctgatgc | agcgacgccc | 360 |
| cgtgaaggaa | gaagtatttc | ggatgtaaa | cttcttatcag | caggaaaggaa | gatgacggtta | 420 |
| cctgagtaag | aagcacccgc | taataactgt | ccagcagccg | cgttaatacg | tatggtgcaa | 480 |
| gcgttatccg | gatttactgg | gtgtaaagggg | agegttagatc | gataggcaag | tctggagtga | 540 |
| aaacctcaggg | ctcaaccctg | ggactgttt | ggaaactgc | gatctggagt | gccggagagg | 600 |
| taaaggcggat | tcctagtgt | gccccgtaaa | gcgttagatc | taggaggaa | accagtggcg | 660 |
| aaggcggcgtt | actggacgg | gactgacgtt | gaggctcgaa | agcgtgggg | gcaaacaggaa | 720 |
| tttagatacc | ttgttagtcca | cgccgttaaa | gatgactact | aggtgtcggt | gtcaaaagca | 780 |
| catcgggtcc | gcagcaaa | caataagt | tcacacctggg | gagtagtgc | gcaagaatga | 840 |
| aactcaaaagg | aatttacggc | gaccggaca | agcgggtggg | catgtggtt | aattcgaagc | 900 |
| aacgcgaaga | accttacgt | gtcttgacat | ceggatgacg | ggcgatgtaa | gtgcgcgtcc | 960 |
| cttcggggca | tccgagacag | gttggatcgat | gtctcgatc | gctcgatcg | tgatgttt | 1020 |
| ggttaagtcc | cgcaacgagc | gcaaccctta | tcttcagtag | ccagcatata | agggtgggcac | 1080 |
| tctggagaga | ctggcagggg | gaaacctggg | gaagggtggg | atgacgtcaa | atcatcatgc | 1140 |
| cccttatggc | cagggtatca | cacgtgtac | aatggcgtaa | acaaggggaa | gcgagagggt | 1200 |
| gaccttgggg | gatccccaaa | aataacgt | cagttcgat | tgtatcttc | aactcgacta | 1260 |
| catgaagctg | gaatcgctag | taatcgccg | tcagcatgc | gcccgtata | cgttcccccgg | 1320 |
| tcttgtacac | accgcggcgtc | acaccatggg | agtcagtaac | gcccgaagcc | agtgacccaa | 1380 |
| ccttagagga | gggagc | | | | | 1396 |

| | | | | | | |
|---------------------------------------|---------------------|---------------|------------|-------------|-------------|------|
| SEQ ID NO: 79 | moltype = DNA | length = 1399 | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1399 | | | | | |
| note = HB-477_Bittarella_massiliensis | | | | | | |
| source | 1..1399 | | | | | |
| mol_type = unassigned DNA | | | | | | |
| organism = Bittarella massiliensis | | | | | | |
| SEQUENCE: 79 | | | | | | |
| cttcggcagc | gtcccccttg | cggttagact | actgacttcg | ggtgttaccc | gctctcatgg | 60 |
| tgtgacgggc | gggtgttaca | aggccccggg | acgttattcc | ccggccatgc | tgatccgcga | 120 |
| ttactagccaa | tcccgactt | atcggggcgt | gttgcagcc | gcaatccggaa | ctgagacccgc | 180 |
| ttttatagat | tcgtccacc | tcgggtttt | gctgtcat | gttagcggcc | attgttagtac | 240 |
| gtgtgtatcc | caggcataaa | aggcatgt | gatgttgcgt | catccccacc | ttccctccgtt | 300 |
| tttgtcaacgg | cagttcccg | agagtgtct | tgcgtatca | ctaacagtaa | gggttgcgt | 360 |
| cgttgcgggaa | cttaaccccaa | catttcacca | cacggatgt | cgacaacccat | gcaccacccgt | 420 |
| tcttaccgtc | ccccggggaa | actcccaatc | tcttggata | gcatatgt | tcaagactg | 480 |
| gttaagggttt | tcgcgttgc | tcgaataaa | ccacatactc | cactgttgt | gccccccccc | 540 |
| gtcaatttct | ttgagtttca | accttgcgg | cgtactcccc | agggtggatta | cttattgtgt | 600 |
| taactccggc | acgggggggg | tttacccccc | acaccta | atcattcg | acggcatgg | 660 |
| cttaccagggt | atctaaatct | gtttcatccc | catgttgcgt | agcctcagcg | tcaataaaag | 720 |
| cccaagcggc | cccttcgc | actgtgttc | ctcccgat | ctacgtatc | caccgctaca | 780 |
| ccggggattc | ccgcgtcc | tacttactc | aagaaccaca | gttttgcgcg | cagttcagg | 840 |
| gttgagccccc | tcgtatccac | acgcacta | tgatccgc | tacactccct | ttacaccag | 900 |
| taatttccgg | caacgcgtc | catctacgt | ttacccgcgc | tgtggc | acag | 960 |
| ttggcttc | ctgtgttacc | gtcattatc | tcccaaca | cagagggtt | caatccggaa | 1020 |
| accttcttcc | ctcagcggc | gtcgtgc | cagggttccc | cccattgtc | aatattccccc | 1080 |
| actgtgtcc | cccgatggag | tctggccgt | gtctcgttcc | caatgtggc | gttcaacctc | 1140 |
| tcagtccggc | tactgtatcgt | tcgttgg | ggccgttacc | ccgccaacta | gttaatcaga | 1200 |
| cgcgagccca | tctcagagcg | gtataatcc | tttttggcc | aggggtgtc | ccccgaccac | 1260 |
| cgtatgcgtt | attagcgtc | gtttcaact | gttgtcccc | actccgaggg | aggttgc | 1320 |
| cgttgttactc | accgcgtcc | cactaaca | atccatctc | ctagcaag | attccgtc | 1380 |
| atgtgtccgt | tcgactca | | | | | 1399 |

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|--------------------------------|---------------------|---------------|
| SEQ ID NO: 80 | moltype = DNA | length = 1346 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..1346 | |
| note = HB-626_Ruminococcus_sp. | | |
| source | 1..1346 | |
| mol_type = unassigned DNA | | |
| organism = Ruminococcus sp. | | |
| SEQUENCE: 80 | | |

| | | | | | | |
|------------|-------------|------------|------------|------------|-----------|-----|
| gctcaggatg | aacgcgtggcg | gcgtgcctaa | cacatgc | cgagcgtt | 60 | |
| tgaatcttc | gggaggaa | gcgaaatgt | ttagcggcg | acgggtg | 120 | |
| taacctgc | catacagggg | gataacgtt | agaaatgt | gctaataccg | cataaggc | 180 |
| caggacgc | ttgtcaatgt | tgaaaaact | aggtgtt | atggaccc | cggtctgt | 240 |
| agctatgtgg | tgaggat | gtcattatc | gcaacgtatc | gtagccgacc | tgagagggt | 300 |
| accggccaca | ttgggact | gacacggcc | aaacttctac | gggaggc | agtggggaa | 360 |
| attgcacaat | ggggaaacc | ctgtatgc | gacgcgcgt | gagcga | gtatccgt | 420 |
| atgtaaatgt | ctatcag | ggaaaaaat | gacgttact | gacta | caccgc | 480 |
| atacgtgc | gcagccgc | taatacgt | gtgtcaag | ttatccgt | ttactgggt | 540 |
| taaaggggac | gtagacgtt | aagcaatgt | ggagt | aaaa | cccgcc | 600 |
| ctgttttgc | aactgtt | atgtatgt | ggagagg | gttgc | atgtgt | 660 |
| gtgaaatgc | tagatatt | gaggaacacc | agtgcc | gcccgtact | ggacatgt | 720 |
| tgacgttgc | gtcgttgc | aacaggat | gatacc | ttactcc | ttactgggt | 780 |
| cgttaacat | gactactagg | tgtcggtt | caaaggcc | cggtcc | gccaac | 840 |
| taagtatgt | acctgggg | tacgttgc | agaat | ggat | tgacggg | 900 |

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|------------|------------|-------------|------------|-------------|------------|------|
| ccgcacaagg | ggtgagcat | gtggtaat | tcgaagca | gcagaaggacc | ttacctgccc | 960 |
| ttgacatccg | aatgcggc | gagataatgtc | gttttccctt | cgggacattc | gagacagggt | 1020 |
| gtgcgttgtt | gtcgtagct | cgtgtcgta | gatgttggtt | taagtccccgc | aacgagcgc | 1080 |
| acccttatct | ttagtagcca | gcaggtaaag | ctggggactc | tagagact | gccaggata | 1140 |
| acctggagga | aggtgtggat | gacgtcaa | atcatgccc | cttatggca | gggctacaca | 1200 |
| cgtgctacaa | ttgcgtaaac | aaagggaago | gagactgtga | agtggagcaa | atcccaaaaa | 1260 |
| taacgtctca | gttcggattt | tagtctgca | ctcgactaca | tgaactgtga | atcgctagta | 1320 |
| atcgcaatc | agaatgtcgc | gggtga | | | | 1346 |

| | | | | | | |
|---------------|---------------------|------------------------------|-------------|-------------|-------------|------|
| SEQ ID NO: 81 | moltype = DNA | length = 1439 | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1439 | note = HB-649_Prevotella_sp. | | | | |
| source | 1..1439 | mol_type = unassigned DNA | | | | |
| | | organism = Prevotella sp. | | | | |
| SEQUENCE: 81 | | | | | | |
| ctcaggatgt | acgctagta | caggtaaac | acatgcaagt | cgtggggcag | catggagat | 60 |
| gtttgcattt | ccccatggcg | acggcgac | gggtgatgtaa | tcgcgtatcca | acctgcccctt | 120 |
| cactccggca | cagcccgctg | aaagacggat | taatcgccga | tgcgtcaga | aagatgcata | 180 |
| ttaatttgc | gaaaggctt | atgcgggtga | gggatgggg | tgcgtccgt | tagctgtac | 240 |
| gcggggtaac | ggccacccgt | ggcacgtac | ggttaggggt | ctgaragggaa | gttcccccac | 300 |
| atttggaaactg | aracacggtc | caaactcta | cggggggcag | cagtggagaa | tatttgc当地 | 360 |
| tgggcgagag | cttgcggcc | ccaaatgc | tgcaggaga | cggccctatg | gggtgttaaac | 420 |
| tgttttgc | cgggataaa | gssgggtcag | tgtggccctt | tgcgtatacc | gtacgataaa | 480 |
| ggaccggcgt | atccgtgca | agcagccgcg | gtataacgga | aggtccggc | gttattccgga | 540 |
| tttatttgc | ttaaaggag | cgtggccgt | ctaaaaggcg | tgttgc当地 | tgttgc当地 | 600 |
| caacccggcgc | cgtgcagcgc | gaactgttag | acttgcgtgt | gcggaggata | tgcggattc | 660 |
| gtgtgttagc | ggtgaaatgc | atagatata | cgaagaactc | cgattgc当地 | ggcagcatgc | 720 |
| cgcagcatta | ctgacgctga | tgctcgaa | tgcgggtat | gaacaggatt | agataccctg | 780 |
| gtatgcggc | cagtaaacgc | tggactggcc | cgttgagcc | gtttaatgtt | ttgcggccaa | 840 |
| gcgaaaggcg | taatgcattcc | acctggggag | tacggccgc | acggtaa | tcaaaaggaa | 900 |
| tgcggggcgc | ccgcacaagg | ggggaaacat | gtggtaat | tgcgtat | gcggaggacc | 960 |
| ttacccggcgc | ttgaatttgc | ggtgcattgg | gtggagacat | cccttccctt | cgggactcct | 1020 |
| gttgcgggtgc | tcgtatgtt | tcgtcagtc | gtggggctt | gtgtcgcc | aagtgc当地 | 1080 |
| acgagcgc当地 | ccccctctcc | tagtgc当地 | cggtttaacg | cggggactct | gcggactcg | 1140 |
| cctccgc当地 | gagtgc当地 | gggtggggatg | acgtcaaatc | agcacggccc | ttacgtccgg | 1200 |
| ggctacacac | gtgttacaat | ggggatata | gagagcagg | tgc当地 | ggccggccaa | 1260 |
| tcaagaaatg | gtctctcgat | tcggactgg | gtctgc当地 | cgacccccc | aagtgc当地 | 1320 |
| cgtatgtat | cgcgcatcg | ccatggcc | gtgaaatacg | ttccgggctt | tgc当地 | 1380 |
| ggccgtcaag | ccatgaaaggc | cgggggcc | tgaatgc当地 | gaccgc当地 | gtcggccata | 1439 |

| | | | | | | |
|---------------|---------------------|---------------------------------|--------------|-------------|--------------|------|
| SEQ ID NO: 82 | moltype = DNA | length = 1396 | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1396 | note = HB-79_Longibaculum_muris | | | | |
| source | 1..1396 | mol_type = unassigned DNA | | | | |
| | | organism = Longibaculum muris | | | | |
| SEQUENCE: 82 | | | | | | |
| tgcgaagtgc | acgcaccgt | tcgggtgt | gtggcgaacg | ggtgatgtaat | acataagtaa | 60 |
| cctggcctt | cgaggggat | aactatgtt | aaacgatgtt | aaggccat | aggcataatt | 120 |
| ctcgcatgt | agttatgtt | aatatccaa | gggatagcga | gaggatggac | ttatggccga | 180 |
| ttagtgc当地 | ggtgagggtt | acggccacc | aaggcgac | tgcgtacgc | acctgagagg | 240 |
| gtggacggcc | acactggcc | tgagacacgg | cccgactcc | tacggggagc | agcactgagg | 300 |
| aattttcgc当地 | aatggcgaa | agcctgtt | agcaacgc当地 | cgtggggag | gaagtattt | 360 |
| gtgtatgtaa | cctctgttat | aaaggaa | cgggcgtat | agggatgac | atgcgtatgc | 420 |
| cggtacttta | tgagaaagcc | acggctaact | acgtgc当地 | agccgc当地 | atacgtatgt | 480 |
| ggcgagcg | atccggaaatc | attggggcgt | aaaggggagc | aggcggcaac | taggtctgc | 540 |
| gtgtaaa | cgaaatgc当地 | cttcggta | ccgtggaaac | cgaggagct | gatgtgc当地 | 600 |
| gaggatcg | gatgttccat | tgtacgg | aaatgc当地 | atatggag | gaacaccat | 660 |
| ggcgaaggcg | acgatctggg | ctgcaact | cgctcagtc | cgaaagcgt | ggggacaaat | 720 |
| aggattatgt | accctgtat | tccacggcc | aaacgatgt | tactaagt | ttggggctc当地 | 780 |
| acctcgtgc | tgcgtat | gcaatgtt | ctccgc当地 | gtgtatgtt | cgcaagaat | 840 |
| aaactcaatg | gaaatgtccgg | ggggccgc当地 | aaggcggat | ggatgtgg | taattcgaag | 900 |
| caacgc当地 | acccttacc | ggcttgc当地 | tacccctaa | ggctctagat | atagagat | 960 |
| agctatgtt | gatacagggt | gtgc当地 | gtgtcagct | cgtgtcgta | gatgtgg | 1020 |
| taagtccgc当地 | aacgagcgc当地 | accctgtt | ccaggtgc当地 | gcatgtt | ggggactct | 1080 |
| ggcgagactgc | ctctgc当地 | aggaggaa | cggggatgac | gtcaat | atcgccc当地 | 1140 |
| atgacccctggg | ctcacacatgt | gttacaatgtt | acggatc当地 | gggaagcgc当地 | ggcgaggg | 1200 |
| ggagcgaacac | ccagaaaccc | gttccatgtt | cgggactc | tctgc当地 | gactgc当地 | 1260 |
| agttgaaatc | gtctgtat | gcaatgc当地 | atgtc当地 | gtatacgtt | tcggccctt | 1320 |
| tacacaccgc当地 | ccgtc当地 | atgagatgtt | gtacacccgc当地 | ggccgggtt | cctaaaccgc当地 | 1380 |
| aggaaggagc当地 | tgtct | | | | | 1396 |

| | | |
|---------------|---------------|---------------|
| SEQ ID NO: 83 | moltype = DNA | length = 1381 |
|---------------|---------------|---------------|

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| | |
|---|--|
| FEATURE | Location/Qualifiers |
| misc_feature | 1..1381 |
| | note = HB-105_Ruminococcus_bicirculans |
| source | 1..1381 |
| | mol_type = unassigned DNA |
| | organism = Ruminococcus bicirculans |
| SEQUENCE: 83 | |
| catgtcgaaac agagaagaga agcttgcgtt tctgatctag tggcggacgg gtgagtaaca | 60 |
| cgtgagcaat ctgccttca gagggggata ccgattggaa acgatcgta ataccgata | 120 |
| acataatttg aaccatcgat ttgattata aqatttatc gctgaaaatg gagctccgct | 180 |
| ctgatttagt agttggtaag taaacggctt accaaggcga cgatcgtag ccggactgag | 240 |
| aggttgtcgc gocacattgg gactgagaca cggcccgacat tcctacggga ggcagcagt | 300 |
| ggaaatattg cacaatggag gaaactctga tgcagcgtat ccgctgtgagg gaagaagggt | 360 |
| ttaggatgtt aaacctctg ctcaggagc gaaaaaaatc ggtacctggag gaggaaatgc | 420 |
| cggctaacta cgtgccagca gccgcggta tacgtggagc gcgagcgtt tcggaaatta | 480 |
| ctgggtgtaa aggaaatcgta ggcggatcg caagtcaqat gtgaaaacta tggcttaac | 540 |
| ccataaaactg catttgcac tttgtgttctt gagtgaatg gaggtaagcg gaattcttag | 600 |
| tgttagcgtt aaatgcgtat atatttaggg gAACATCAGT ggcgaaggcg gcttactgg | 660 |
| ctttaactgtc cgctcgaggc cgaaacgcgtt gggaggaaatc aggatttagt accctggtag | 720 |
| tccacgcgtt aaacgtatgtat taatgtgtt gggggactgtt acccccttcg tgccgcac | 780 |
| aacgcataaa gtaatccacc tggggagtagt gaccgcagg ttgaaactca aaggaatgt | 840 |
| cggggggcccg cacaaggatgtt gattaattcg aagcaaccgc aagaacctta | 900 |
| ccagggttgc acatcgatcg catatcgatcg agatgatgtt gaaatcttcg gagacatata | 960 |
| gacagggtgtt gcatgttgcgtatcg tttgtgttgcgtt gttttgttgcgtt gttttgttgcgtt | 1020 |
| cgagcgttgc acatcgatgtt agttgtcgtt caagagcact ctatcgaggac tgccgttgc | 1080 |
| aaaacggagg aagggtgggg ttagctcaaa tcatatcgcc cttatgacc tgggccttcac | 1140 |
| acgtactaca atggctgtca acagaggatgtt gcaaggccgc gagggtggac gaaccctaa | 1200 |
| aaggcgttcc atgttgggtt gtaggtgtca accccgcctac aatgtcggtt aattgtcgat | 1260 |
| aatcgcatatc cagcatgtt cggtaatac gttcccgccc cttgtacaca ccgcgggtca | 1320 |
| cgccatggaa gtcggtaaca cccgaaggct gtatgtcaac cgcaaggagg acgcgtcga | 1380 |
| a | 1381 |
| SEQ ID NO: 84 | moltype = DNA length = 1357 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..1357 |
| | note = HB-214_Parabacteroides_distasonis |
| source | 1..1357 |
| | mol_type = unassigned DNA |
| | organism = Parabacteroides distasonis |
| SEQUENCE: 84 | |
| gcgaccggcg cacgggttag taacgcgtat gcaacttgc tatcagagg ggataaccc | 60 |
| gcgaaagtgc gactaatacc gcatgaagca gggccccgc atggggatat ttgctaaaga | 120 |
| ttcatcgctt atagataggc atgcgttca ttggcaatgtt ggcggggtaa cggccacca | 180 |
| aaccgcgtt ggtatgggtt tctgagggat aggtccccca cattggtaat gggacacgg | 240 |
| ccaaactctt acggggggca gcgtgtggat atattggtaa atggccgaga ggctgaacca | 300 |
| gccaagtcgc gtgaggatgtt aagttctat ggatcgtaaa ccttttat aagggataa | 360 |
| atgtcgggac gtgtcccggtt ttgtgttgcgtt cttatgtatc aggtcggtt aactccgtc | 420 |
| cagcagccgc gtaataatcg aggtatccgg aggtatccggg atttattggg tttaaagggt | 480 |
| gcgttagccgc cttttaatgtt cttatgtatc aggtatccggg tttaaagggtt aatgtcgat | 540 |
| gaaactgggg ggtttttttt gttttttttt gttttttttt gttttttttt gttttttttt | 600 |
| catagatatac acgcagaaacc cccgttgcgtt aggcaggatgtt ccaagccatt actgcacgt | 660 |
| atgcacgaaa ggtttttttt gttttttttt gttttttttt gttttttttt gttttttttt | 720 |
| atgtatcaatc gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt | 780 |
| cctggggatgtt acgcggccaa cgggtttttttt gttttttttt gttttttttt gttttttttt | 840 |
| gaggaaatcgatc gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt | 900 |
| tcgcacgttc tggaaacaga gttttttttt gttttttttt gttttttttt gttttttttt | 960 |
| cgttcgttgc tggccgttgc gttttttttt gttttttttt gttttttttt gttttttttt | 1020 |
| agttactaac aggtgtatgtt gttttttttt gttttttttt gttttttttt gttttttttt | 1080 |
| gcggggatgtt cgtttttttt gttttttttt gttttttttt gttttttttt gttttttttt | 1140 |
| gcgttgacaa gggggggccca cttttttttt gttttttttt gttttttttt gttttttttt | 1200 |
| cggatcggtt tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt | 1260 |
| catggcgccg tgaataatcgatc gttttttttt gttttttttt gttttttttt gttttttttt | 1320 |
| gggggttactt gaaatgtttttt gttttttttt gttttttttt gttttttttt gttttttttt | 1380 |
| gggggttactt gaaatgtttttt gttttttttt gttttttttt gttttttttt gttttttttt | 1387 |
| SEQ ID NO: 85 | moltype = DNA length = 1425 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..1425 |
| | note = HB-251_Veillonella_atypica |
| source | 1..1425 |
| | mol_type = unassigned DNA |
| | organism = Veillonella atypica |
| SEQUENCE: 85 | |
| tgcgttcgtt cggaaatcgatc tggaaatcgatc tttttttttt gttttttttt gttttttttt | 60 |
| gttaacgcgtt atcaacccgtt cttttttttt gttttttttt gttttttttt gttttttttt | 120 |
| cgcataatcgatc ccaatctcgat cttttttttt gttttttttt gttttttttt gttttttttt | 180 |
| tcactgtttttt gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt | 240 |

-continued

| | | | | | | |
|-------------|-------------|-------------|--------------|-------------|--------------|------|
| gatgatca | gtggcgtctg | agaggatgaa | cggccacatt | gggactgaga | cacggccag | 300 |
| actccctacgg | ggaggcagcag | tggggaaatct | tccgcataatgg | acgaaaagtct | gacggagcaa | 360 |
| cgcgcgcgtga | gtgtacgg | ccttcgggtt | gttaaagctct | gttatacggtt | acgaatggtt | 420 |
| cttgcggaa | tagtgcgagg | atttgcgg | accggaaatag | aaagccacgg | ctaactacgt | 480 |
| gccagcagcc | cggttaatac | gttagtgcc | agcgttgc | ggaattattt | ggcgtaaagc | 540 |
| gcccgcggc | ggatgggtca | gtctgttta | aaagttcggtt | gtttaacccc | gtgtatggat | 600 |
| ggaaactgcc | aatctagat | atcggagagg | aaagtggaaat | tectatgtta | gcggtaaatt | 660 |
| gegtatagat | taggaagaac | accatggcg | aggcgaactt | tctggacggaa | aactgacgct | 720 |
| gaggcggaa | agccagggg | gccaacggg | ttagatacc | cggtatgtct | ggccgttaaac | 780 |
| atgggtact | aggtaggtgg | gttgcgacc | ccttctgtgc | cgaggtaac | gcaataagta | 840 |
| ccccgcctgg | ggatgtcgac | cgcacgggtt | aaatctaaat | gaattgtacgg | gggcggcac | 900 |
| aagcgggtga | gtatgtggtt | taatttcgcg | caacgcga | aacccatcca | ggtcgttgcaca | 960 |
| tttgcgttgc | gaactagaga | tagttctct | tcttcggaa | ccagaaaaca | ggtgggtgcac | 1020 |
| gggttgcgtc | actctgtgc | gttagatgtt | gggttaaagt | ccgcacacgg | cgcaacccct | 1080 |
| atcttatgtt | ggccacactt | cgggtggggaa | ctcatgagat | actgcggcag | acaataccgga | 1140 |
| ggaaggcggg | gtatgtcgca | aatcatcatg | ccccatgtat | cctgggttac | acacgttacta | 1200 |
| caatgggagt | taatagacgg | aagcggaaacc | gcccgggttga | gccaacccga | gaaacactct | 1260 |
| ctcagttcgg | atcgttaggt | gcaactcgcc | tacgtgaatg | cggaatcgct | agtaatcgca | 1320 |
| ggtcagcata | ctgcgggtga | taacgttcc | ggccttgcac | acaccggcccg | tcacaccacg | 1380 |
| aaagtccggaa | gtgcggccaa | ccgggtgggt | aacccatcc | cggtgggttgc | agccaa | 1425 |

| | | |
|---------------|-------------------------------|---------------|
| SEQ ID NO: 86 | moltype = DNA | length = 1388 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..1388 | |
| | note = HB-358_Clostridium_sp. | |
| source | 1..1388 | |
| | mol_type = unassigned DNA | |
| | organism = Clostridium sp. | |

| | | | | | | |
|--------------|-------------|-------------|------------|-------------|------------|------|
| SEQUENCE: 86 | | | | | | |
| tgca | gggacggaaa | gggtgttgc | ccttcaagt | agtggcggtt | gggtgagtt | 60 |
| cgcgtgagca | acctgcctca | aaggggggaa | taacgttgc | aaacggacgc | taataccgca | 120 |
| tgcgttattc | gtatggatc | tatggatc | caaaaggcga | atccgc | tgcgttgc | 180 |
| gcccgttatt | agctatgttgc | tgggtttaa | ggcttacaa | gcgcacgtca | gtatgttgc | 240 |
| tgaggggttgc | aacggccaca | ttgggtact | gacacggccc | agactcctac | gggaggcagc | 300 |
| agtgggggat | attgttccat | ggggggat | ctgtatgc | aaacgcggcgt | gaaggaaag | 360 |
| gggtttcggaa | ttgttaaactt | ctgttcttgc | tgacgataat | gacggtagt | aaggaaag | 420 |
| ctccggctaa | ctacgtgc | gcacgcgcgg | taatacgt | ggagcgcgcg | ttgtccggaa | 480 |
| ttactgggttgc | taaaggggac | gttgcgggaa | gtatgtca | gtatgtaaaa | ctatgggtc | 540 |
| aaccgcata | ctgcgttgc | aactgttctt | cttgcgttgc | gttgcggcag | gccaat | 600 |
| gagtgtatgc | gtggaaatgc | tgatgtatgc | gaggaaac | atgtgcgttgc | gcccgttgc | 660 |
| gggttttgc | tgacgttgc | gtctgttgc | atggggatca | aaacaggata | gataccatgc | 720 |
| tagtccatgc | cgtaaaatgc | gattactagg | tgtgggttgc | ctgaccatt | ccgtgcgg | 780 |
| gttacacacaa | taatgtatcc | acccgtgggg | taacgcgcgc | agggttgc | aaatgc | 840 |
| tgacgggggc | ccgcacaa | atgttgc | gttgcgttgc | atgcgttgc | gccaat | 900 |
| ttaccaggc | ttgcacatgc | actaaacaa | tgatgtatca | ttatgtgc | ttcgccggaa | 960 |
| gtcgagac | gtgggtgc | gttgcgtc | gtcgatgt | gttgcgttgc | 1020 | |
| cgcaacacgc | gcaacccatgc | tcattatgc | ctacgc | gactctat | gagactgc | 1080 |
| ttgacacacaa | ggggaaatgc | ggggacgc | tcacatc | atgccttgc | tgacgttgc | 1140 |
| tacacacgt | tcataatgc | cgtaaaatgc | ggggaaat | actgtatgc | ggaggaaat | 1200 |
| cctaaaaacgc | gtcccgttgc | agattgc | ctgcaaccc | cctgtat | gtcgaaat | 1260 |
| cttagtacgc | cggtatgc | tgccgcgttgc | aatacgttgc | cggttgc | ttgttgc | 1320 |
| cgtcacacca | ttggagccgg | taataccgc | agtcgttgc | ataccgc | ggaggacgc | 1380 |
| ggccaa | ggccaa | | | | | 1388 |

| | | |
|---------------|--|--------------|
| SEQ ID NO: 87 | moltype = DNA | length = 800 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..800 | |
| | note = HB-44_Parabacteroides_goldsteinii | |
| source | 1..800 | |
| | mol_type = unassigned DNA | |
| | organism = Parabacteroides goldsteinii | |

| | | | | | | |
|--------------|-------------|--------------|-------------|-------------|------------|-----|
| SEQUENCE: 87 | | | | | | |
| gcagtcgagg | ggcagcacgg | tgttagcaata | cattgggtgc | gaccggcgca | cggttgcgtt | 60 |
| acccgtatgc | acccgtatgc | tcacgggg | ataacccggc | gaaatgcgtt | ctaataccgc | 120 |
| ataaaaacagg | gggtccat | ggaaatattt | gttgcgtat | tatgcgtat | atgtgggttc | 180 |
| gcgttccatt | agatgttgc | tgatgttgc | gttcacaa | tccacgttgc | atgggggttc | 240 |
| tgagggat | gtcccccaca | ctgttact | gacacggac | agactcctac | gggaggcagc | 300 |
| agtggat | atgttgc | ggggcgttgc | ctgacaccgc | caatgcgttgc | gaaggat | 360 |
| ggatctatgc | ttgttataact | gggttataat | tgaggaaatgc | gttgcgttgc | ttgttgc | 420 |
| gtatgtatgc | tatgtatgc | catgcgttgc | tcgcgttgc | gacgcgcgc | taatacgg | 480 |
| gtgcgtatgc | ttatccgtat | taatgggttgc | tgatgttgc | ttgttgc | ataatgtca | 540 |
| gggggttgc | aaccataaa | tttgcgttgc | aactgttgc | tttgcgttgc | ttgttgc | 600 |
| tttgaggat | tgccgtatgc | tggttgcgttgc | gttgcgttgc | gttgcgttgc | ttgttgc | 660 |
| gattgcgtatgc | gcaatataac | tgacact | gacgttgc | gttgcgttgc | ttgttgc | 720 |
| aacaggat | gataccatgc | tgatccacgc | agtaaacat | gattact | tgatgttgc | 780 |
| acacatgc | cgccacacgc | ttgttgc | ttgttgc | ttgttgc | ttgttgc | 800 |

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SEQ ID NO: 88      moltype = DNA  length = 1251
FEATURE           Location/Qualifiers
misc_feature      1..1251
note = HB-470_Clostridium_sphenoides
source            1..1251
mol_type = unassigned DNA
organism = Clostridium sphenoides

SEQUENCE: 88
tcaggatcaa cgctggcgcc gtgttaaca catgcaagtgc gaacgaagca atgaaggcga 60
atgttccgaa cagaagcttg attgacttag tggccggacgg gtgagtaacg cgtggaaac 120
ctgcctata caggggata acagtttagaa atgactgtca ataccgcata agcctgcac 180
atcgcgtatgc gcggaggaa aagggaatc ccggtataag atggtcccgc gtctgattag 240
ctagttgtta aggttaacggc ctaccaaggc gacgtacgt agccgacgtc agaggggtgac 300
cggccacatt gggactgaga cacggccca actcctacgg gaggcagcag tggggatata 360
tgacaatgg gggaaacctt gatgcagcga cgccgcgtga gtgaagaatg cattcgtat 420
gttaaagtct atcagcaggg aagaaagtga cagtacgtga gtaagaagcc ccggctaact 480
acgtgcgcgc acggcgggtt atacgttaggg ggcaagegtt atccggattt actgggtgtt 540
aaggggacgtt aggttgttact gcaagtca gatgaaaaggcc cctgtttttt cgtggggact 600
gtctttggaa ctgtggactt agatgtcagg agaggttaatg ggaatcttca gtgttagcgtt 660
gaaatgcgtt gatatttagga ggaacaccgg tggcgaaggc ggcttactgg actgttaactg 720
acactgaggc tcgaaaaggcgt ggggagcaaa caggattaga taccctgtta gtccacgcgt 780
taaacgtatgc atactgtttt ttggggatggc aagctcttcg gtgcgcgtc aaacgcataa 840
agtatttccac ctggggatgtt cgttgcacgg aatggaaacttcc aaggaaatgg acggggaccc 900
gcacaagcgg tggagcatgt ggtttatcc gaagcaacgc gaagaacctt accaagtctt 960
gacatctgga tgaccgggtt agagatagcc ctctcttcg gacgtatccaa gacagggtt 1020
gcatgggtt cgtcagctcg tttgtgttgc tttttttttt aatggggccaa cggcgcac 1080
ccttatctt agtagccaggc aggtttttttt gggaaacttca gagagacttc cgtggataac 1140
ggggaggaaatgg tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1200
tgctacaatgg cgttataacggc agggaaaggcga acccgcgaggc ggagcgaatc 1251

SEQ ID NO: 89      moltype = DNA  length = 927
FEATURE           Location/Qualifiers
misc_feature      1..927
note = HB-490_Escherichia_coli
source            1..927
mol_type = unassigned DNA
organism = Escherichia coli

SEQUENCE: 89
gcagcctgtatgc gcagccatgc cgcgtgtatgc aagaaggcct tcgggttgc aagtactttc 60
agcggggagg aagggtttttt agttatacc tttgtctattt gacgttaccc gcagaaggaa 120
caccggctaa ctccgttccca gcagccgcgg taatacggggat ggttgcacggc ttaatcgaa 180
ttactggggtaa taaatggcgcgc gcggccgggtt ttgttgcgttgc aatgttgcgttgc 240
aacctggggaa ctgcgtatgc tttttttttt tttttttttt tttttttttt tttttttttt 300
aggtgtacggc gtggaaatgtttt tttttttttt tttttttttt tttttttttt tttttttttt 360
ggacgaagac tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 420
tagtccacgcgc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 480
gtaacggcgtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 540
tgacggggggcc cccgcacaaatggcgtt tttttttttt tttttttttt tttttttttt 600
ttacctgggtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 660
gagacagggtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 720
aacggcgcacccctt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 780
ccagtatggaaatgg tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 840
ggctacacacatgg tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 900
acctcataaaatgg tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 927

SEQ ID NO: 90      moltype = DNA  length = 1237
FEATURE           Location/Qualifiers
misc_feature      1..1237
note = HB-521_Lawsonibacter_asaccharolyticus
source            1..1237
mol_type = unassigned DNA
organism = Lawsonibacter asaccharolyticus

SEQUENCE: 90
ctcaggatgaa acgtggcgcc cgtgtttttt acatgtttttt acatgtttttt acatgtttttt 60
gaggattttttt ccaattttttt tttttttttt tttttttttt tttttttttt tttttttttt 120
cctgcctttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 180
gaccggatggc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 240
cttgggtttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 300
cggccacattt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 360
tggggcaatgg tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 420
gtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 480
cttacgtttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 540
taaaggggcgtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 600
cttgcattttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 660
gtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 720
gtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 780
gtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 840
gtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 900
gtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 927

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| | | | | | | |
|-------------|-------------|------------|------------|------------|------------|------|
| tgacgcttag | gcccggaa | gtggggagca | aacaggatta | gataccctgg | tagtccacgc | 780 |
| tgtttaaacat | ggataactagg | tgtgggggg | ctgacc | ccgtgcggca | gttaacaca | 840 |
| taagtatccc | acctgggg | tacgtcgca | agggtt | aaaac | tgacggggc | 900 |
| ccgcacaa | gggtgg | gtggttaa | tccaa | ggaa | ttaccagg | 960 |
| tttgcacat | actaac | cagagat | tttaggt | ttcgggg | gtagagac | 1020 |
| gttgtgc | gttgcgt | gtctcg | tgagat | ttgtt | cgcaac | 1080 |
| geaacc | ttgttag | ctacgc | gactc | tgcc | tgacaa | 1140 |
| ggagga | ggggac | tcaatc | atgc | ttgtt | tacac | 1200 |
| ctacaat | gtt | aaa | ttgtt | ttgtt | cgta | 1237 |

SEQ ID NO: 91 moltype = DNA length = 1390

FEATURE
misc_feature
source
SEQUENCE:

| | | | | | | |
|----------------------------|---------------|--------|--------|---------|----------|------|
| moltype = DNA | length = 1390 | | | | | |
| Location/Qualifiers | | | | | | |
| 1..1390 | | | | | | |
| note = HB-567_Gemmiger_sp. | | | | | | |
| 1..1390 | | | | | | |
| mol_type = unassigned DNA | | | | | | |
| organism = Gemmiger sp. | | | | | | |
| SEQUENCE: 91 | | | | | | |
| tgca | ggat | ttttaa | aggctt | ttttaa | gggtgg | 60 |
| cgcgtg | actt | gggg | caac | gtt | ggat | 120 |
| taagccc | gtacc | gggg | aaac | gact | ttttaa | 180 |
| gcgttc | acta | gggg | aaa | aggattt | tttgcgtt | 240 |
| tgagagg | tttgc | gggg | ggcc | gacac | gggtgg | 300 |
| atgggg | tttgc | gggg | aaacc | actc | gggg | 360 |
| gtttt | tttgc | gggg | ttgtt | ggac | gtt | 420 |
| caccgg | tttgc | gggg | aaaa | gtt | gggtt | 480 |
| ttact | tttgc | gggg | tttt | gggtt | gggtt | 540 |
| aacc | tttgc | gggg | tttt | gggtt | gggtt | 600 |
| cgg | tttgc | gggg | tttt | gggtt | gggtt | 660 |
| gggc | tttgc | gggg | tttt | gggtt | gggtt | 720 |
| tagt | tttgc | gggg | tttt | gggtt | gggtt | 780 |
| gttta | tttgc | gggg | tttt | gggtt | gggtt | 840 |
| tgac | tttgc | gggg | tttt | gggtt | gggtt | 900 |
| ttacc | tttgc | gggg | tttt | gggtt | gggtt | 960 |
| agac | tttgc | gggg | tttt | gggtt | gggtt | 1020 |
| acg | tttgc | gggg | tttt | gggtt | gggtt | 1080 |
| acaaa | tttgc | gggg | tttt | gggtt | gggtt | 1140 |
| acac | tttgc | gggg | tttt | gggtt | gggtt | 1200 |
| aaa | tttgc | gggg | tttt | gggtt | gggtt | 1260 |
| agta | tttgc | gggg | tttt | gggtt | gggtt | 1320 |
| tcac | tttgc | gggg | tttt | gggtt | gggtt | 1380 |
| cga | tttgc | gggg | tttt | gggtt | gggtt | 1390 |

SEQ ID NO: 92 moltype = DNA length = 688

FEATURE
misc_feature
source
SEQUENCE:

| | | | | | | |
|-------------------------------------|--------------|-------|-------|-------|------|-----|
| moltype = DNA | length = 688 | | | | | |
| Location/Qualifiers | | | | | | |
| 1..688 | | | | | | |
| note = HB-59_Eubacterium_callanderi | | | | | | |
| 1..688 | | | | | | |
| mol_type = unassigned DNA | | | | | | |
| organism = Eubacterium callanderi | | | | | | |
| SEQUENCE: 92 | | | | | | |
| gtcg | aaat | tttgc | gggt | tttgc | gggt | 60 |
| gggt | tttgc | gggt | tttgc | gggt | gggt | 120 |
| taa | tttgc | gggt | tttgc | gggt | gggt | 180 |
| atgg | tttgc | gggt | tttgc | gggt | gggt | 240 |
| aacc | tttgc | gggt | tttgc | gggt | gggt | 300 |
| gagg | tttgc | gggt | tttgc | gggt | gggt | 360 |
| gtga | tttgc | gggt | tttgc | gggt | gggt | 420 |
| aat | tttgc | gggt | tttgc | gggt | gggt | 480 |
| ttgt | tttgc | gggt | tttgc | gggt | gggt | 540 |
| gttac | tttgc | gggt | tttgc | gggt | gggt | 600 |
| gttgg | tttgc | gggt | tttgc | gggt | gggt | 660 |
| gttgg | tttgc | gggt | tttgc | gggt | gggt | 688 |

SEQ ID NO: 93 moltype = DNA length = 1403

FEATURE
misc_feature
source
SEQUENCE:

| | | | | | | |
|---|---------------|-------|-------|-------|-------|-----|
| moltype = DNA | length = 1403 | | | | | |
| Location/Qualifiers | | | | | | |
| 1..1403 | | | | | | |
| note = HB-651_Intestinimonas_massiliensis | | | | | | |
| 1..1403 | | | | | | |
| mol_type = unassigned DNA | | | | | | |
| organism = Intestinimonas massiliensis | | | | | | |
| SEQUENCE: 93 | | | | | | |
| tcaggat | gaa | tttgc | gggtt | tttgc | gggtt | 60 |
| atgtt | tttgc | gggtt | tttgc | gggtt | gggtt | 120 |
| ctgc | tttgc | gggtt | tttgc | gggtt | gggtt | 180 |
| gtcgc | tttgc | gggtt | tttgc | gggtt | gggtt | 240 |

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| | | | | | | |
|------------|--------------|-------------|--------------|-------------|------------|------|
| agttggggg | gtaacggccc | accaagtgcga | cgatcagtag | ccggactgag | aggttggccg | 300 |
| gccacatgg | gactgagaca | cggccccagac | tcttacggga | ggcagcagtg | ggaaatattg | 360 |
| ggcaatggc | gcaagctga | cccagcaacg | ccgcgtgaag | gaagaaggct | ttcgggttgt | 420 |
| aaacttcctt | taacaggac | gaagcaagtgc | acggtagcttgc | ttaataaagc | cacggctaac | 480 |
| tacgtgcac | cagccgcgtt | aatacgtagg | tggcaagcgt | tatccggatt | tactgggtgt | 540 |
| aaaggcgtg | taggcggac | tgcgaatgt | atgtgaaaatc | tatgggtotca | accatagcc | 600 |
| tgcatttgaa | actgtatgttgc | ttgatgtcg | gagaggcaat | cgaaattccg | tgtgtacgg | 660 |
| tgaatcgct | agatatacg | aggaacacca | gtggcgaagg | eggattgtcg | gacgatacc | 720 |
| gacgctgagg | cgccaaagcg | tggggagca | acaggattag | ataccctgtt | agtccacgcc | 780 |
| gtaaacgat | gatactatgg | gtgggggttc | tgaccccttc | cggtccggcag | ctaacgcaat | 840 |
| aagtatccca | ctggggatgt | acgatcgc | ggttgaaact | caaaggaaatt | gacgggggcc | 900 |
| cgcacaacgc | gtgggatgt | tgggttaatt | cgaagcaacg | cgaagaaacct | taccagggt | 960 |
| tgacatctca | ctaacaacc | agagatggat | taggtgcctt | tcggggaaag | tagagacagg | 1020 |
| tggtgcatgg | ttgtcgatgt | ctcgatgtcg | gagatgttgt | gttaagtccc | gcaacgagcg | 1080 |
| caacccttat | tgttagttgc | tacgcaagag | cactctagcg | agactgcgt | tgacaaaacg | 1140 |
| gaggaaatgt | gggacgacgt | caaatacata | tgcccttat | gtccctggcc | acacacgtac | 1200 |
| tacaatggcg | gttaacagag | ggaggcaag | ccgcgaggca | gagcaaaccc | ctaaaagccg | 1260 |
| tcccagttgc | gattgcaggc | tgaaaaccgc | ctgtatgaag | tcggaaatcgc | tagaatcgc | 1320 |
| ggatcagcat | gcccgggt | atacgttccc | gggccttgt | cacacccccc | gtcacaccat | 1380 |
| gagagtccgg | aacacccgaa | gtc | | | | 1403 |

SEQ ID NO: 94 moltype = DNA length = 809
 FEATURE Location/Qualifiers
 misc_feature 1..809
 note = HB-67_Clostridium_symbiosum
 misc_feature 763
 note = n is a, c, g, or t
 source 1..809
 mol_type = unassigned DNA
 organism = Clostridium symbiosum

SEQUENCE: 94
 tgcaatcgaa cgaaggcgtt taacggaaatg tttcggatgg aagttgagat tgactgagtg 60
 gccgacgggtt gagaatcgcg tgggttaacct gccttgcactt gggggacaaat agttgaaat 120
 gactgtcaat acccgataag cgccacatgtat cgcacatgtac agtgcgtaaaa actccgggtt 180
 tacaatggcg acccgctgtt gatgtatgtt gttgttgcgtt aacggcttac caaggcgacg 240
 atcagtagcc gacgtcgagag ggttgcggcc cacattggga ctgagacacg gcccaaactc 300
 ctacgggaggc cagcaatgggggaaatattgc caatggggca aagcctgtatc cagcgacgcc 360
 gctgtgatgtt gagaatgtttt cggtatgtaa agtctatcata gcagggaaat aaatgacgg 420
 acctgtacttgc aaagccccgg ctaatcgatc gccagcagcc gccgttaatc gtatggggca 480
 agcggtatcc gatgttacttgc ggtgttgcgtt gacgtgtacg ggttgcgtt gtcgttgcgt 540
 aaaggccccggc gtcataactgc gggactgtt gttttttttt ttaacttgcgtt gtcgttgcgt 600
 gtaatgtggaa ttccatgttgcgtt gtcgttgcgtt gtcgttgcgtt ttagggggaa caccatgttgc 660
 gaaggccgact tactggacgta taatcgatcgt tgaggctcgaa aagcgttgcgtt gacaaacagg 720
 attagatacc ctggatgttgc acggccataaa cgatgtatc tanggtgtt gggggacaaa 780
 gtccttcgttgc gtcgttgcgtt gtcgttgcgtt 809

SEQ ID NO: 95 moltype = DNA length = 1287
 FEATURE Location/Qualifiers
 misc_feature 1..1287
 note = HB-681_Longibaculum_sp.
 misc_feature 182
 note = n is a, c, g, or t
 misc_feature 976
 note = n is a, c, g, or t
 misc_feature 1091
 note = n is a, c, g, or t
 misc_feature 1101
 note = n is a, c, g, or t
 misc_feature 1140
 note = n is a, c, g, or t
 misc_feature 1212
 note = n is a, c, g, or t
 source 1..1287
 mol_type = unassigned DNA
 organism = Longibaculum sp.

SEQUENCE: 95
 gtcaggatg aacgctggcg gctgtccaa tacatgcga tcggacgca tgcttcggca 60
 ttgatgtggcg aacgggttgcgtt gataatataa gcaacctgc cctgttgcgtt ggataactgc 120
 tggaaacccggc agtcaatggcc gcataggatc acatgcgttgc tgcgttgcgtt gttttttttt 180
 cnacggggata gcacaggatg ggggtttatgc cgcattgtatc agtgcgttgcgtt gtagagggtc 240
 accaggccggca cgatgcgttgc cccgttgcgttgc ggggtttgcgttgc gtcgttgcgttgc 300
 cggcccccggc ttctacggggaa ggcacgttgc gggatattttc ggcacatgggc gaaaggcttgc 360
 ccgagcaacgc cccgttgcgttgc gaaaggatgc ttcgttgcgtt gttttttttt tataaaggaa 420
 gaacggccgc gttttttttt gacaggccgttgc gtcgttgcgttgc gttttttttt gtcgttgcgttgc 480
 actacgttgcg acggccgcgttgc gtaatcgatc ggttgcgttgc gttttttttt atcattgggc 540
 gtaaaaggagg gtcgttgcgttgc gtcgttgcgttgc gtcgttgcgttgc gtcgttgcgttgc 600

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|-------------|------------|------------|-------------|-------------|-------------|------|
| aaccgcgtgga | aaccgcacag | ctagagagca | tcagaggatc | gcggaaattcc | atgtgttagcg | 660 |
| gtgaaaatcg | cgtagatata | tgaggaaacc | agtggcga | gcggcggtct | ggggtagcgc | 720 |
| tgacgc | tccgaa | aataggatta | gataccctag | tagtccacgc | | 780 |
| cgttaaacat | gagtgcta | tgttgggggt | cagacctcg | tgctgcagg | aacgcataa | 840 |
| gcactccgc | tgagtagtac | gttcgcaaga | atgaaactca | aaggattga | cgggggcccg | 900 |
| cacaaggcg | ggagcatgt | gtttaattcg | aagcaacccg | aagaacctta | ccaggcttgc | 960 |
| acatggagat | aaaggntctg | gagacagaga | gatagtta | tctcacacag | gtggtagcgt | 1020 |
| gttgtcg | tcgtgtcg | tgatgttg | gtttaagtcc | cgcaacccg | gcaacccctg | 1080 |
| ttgcgc | atgttgc | ntggggactc | tggcgagact | gcctctgca | gaggaggaan | 1140 |
| gcggggat | cgtaaataat | tcatgc | tatgacccctg | gtcacacacg | tgctacaatg | 1200 |
| gacggat | cgaggcg | agccgcgagg | ttggagcgaa | cccagaaacc | cgttcacagt | 1260 |
| tcggact | gcaact | cgactgc | | | | 1287 |

| | | |
|---------------|----------------------------|---------------|
| SEQ_ID NO: 96 | moltype = DNA | length = 1392 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..1392 | |
| misc_feature | note = HB-14_Blautia_obeum | |
| misc_feature | 944 | |
| misc_feature | note = n is a, c, g, or t | |
| misc_feature | 1295 | |
| misc_feature | note = n is a, c, g, or t | |
| misc_feature | 1355 | |
| misc_feature | note = n is a, c, g, or t | |
| source | 1..1392 | |
| source | mol_type = unassigned DNA | |
| source | organism = Blautia obeum | |

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|--------------|-------------|-------------|-------------|-------------|-------------|------|
| SEQUENCE: 96 | | | | | | |
| catgcagtgc | aacgggaaac | cttttattga | agcttcggca | gatttagctg | gtttcttagtg | 60 |
| geggacgggt | gagtaacgcg | tggtaacct | gccttataca | gggggataac | aaccagaaat | 120 |
| gggtgcta | ataccgcataa | cgcacaggac | cgcacatggcc | gggtgtaaaa | actccgggt | 180 |
| tataatagat | ggccgcgttgc | gatttagctg | ttggcgagggt | aacggccatc | caaggcgacg | 240 |
| atccatagcc | ggcctgagag | ggtaaacggc | cacattggga | ctgagacacg | gccccagactc | 300 |
| ctacgggagg | cagcaatggg | gaatattca | caatggggga | aaccctgtat | cagcqacgccc | 360 |
| gcgtgaagga | agaagtatct | cggtatgtaa | acttctatca | gcagggaga | tagtgcacgt | 420 |
| acctgactaa | aaagccccgg | ctaaactacgt | gccagcagcc | ggggtaatac | gttagggggca | 480 |
| agcgttatacc | ggatataact | gggtgtaaaa | gagcgtacac | ggactggcaa | gtctgtatgt | 540 |
| aaaggcgggg | gctcaatccc | tggactgc | tggaaactgt | tagtcttag | tgcccgagag | 600 |
| gtaagcggaa | ttcctagtgt | agcggtaaa | tgcgtagata | tttagggagaa | caccagtggc | 660 |
| gaaggcggct | tactgggac | taactgcgt | tgaggctggc | aagcgttggg | agcaaacagg | 720 |
| attagatacc | ctggtagtcc | acggcataa | cgatgataac | taggtgttgg | ggagcaaaagc | 780 |
| tcttcgggtc | cgccgc | gcatcaatgt | tccacctgg | ggagtagctt | cgcaaaatg | 840 |
| aaactcaaaag | gaattgacgg | ggaccggc | aacgggtgg | gcatgtgg | taattcaag | 900 |
| caacgcgaa | aacccttacca | agcttgc | tccctctgac | cgantctaa | ccgaatctt | 960 |
| ccttcgggg | gggggac | ggtgggtc | gggtgtcg | agetcgtgtc | gtgagatgtt | 1020 |
| gggtttaatgc | ccgcaacgg | cgcaacccct | atccccatgt | gccagcgtc | cggtgggca | 1080 |
| ctctgaggag | actggcaggg | ataacctgg | ggaaggcggg | gtgacgtca | aatcatcatg | 1140 |
| cccccattatg | tttgggttac | acacgtgtca | caatggcg | aacaaaggga | agcaagctg | 1200 |
| cgaaggtaa | caatattccaa | aaataaacgtc | ccagttcgga | ctgcagtc | caactcgact | 1260 |
| gcacgaact | ggaatcg | gtaatcgcg | atcanaatgc | cgccgtgaa | acgtcccccg | 1320 |
| ggtctgtac | acaccgcccc | tcacaccatg | gggantcagt | aacgccccaa | gtcagtgacc | 1380 |
| taactgc | aaa | ga | | | | 1392 |

| | | |
|---------------|--------------------------------|---------------|
| SEQ_ID NO: 97 | moltype = DNA | length = 1361 |
| FEATURE | Location/Qualifiers | |
| misc_feature | 1..1361 | |
| source | note = HB-17_Dorea_longicatena | |
| source | 1..1361 | |
| source | mol_type = unassigned DNA | |
| source | organism = Dorea longicatena | |

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|--------------|-------------|------------|-------------|-------------|------------|-----|
| SEQUENCE: 97 | | | | | | |
| acctttgt | ctgagcggcg | gacgggtgag | taacgcgttgc | gtaacatgc | tcatacagg | 60 |
| ggataacagt | tagaaatgac | tgctaatacc | gcataagacc | acggtagcc | atggtagact | 120 |
| ggtaaaaact | ccgggtgtat | gagatggacc | cgcgtctgt | taggtgtatg | gtggggtaac | 180 |
| ggccttacca | gocgcgatc | agtgccgc | ctgagagggt | gaccggccac | attgggact | 240 |
| agacacggcc | cagactcta | cgggggcc | cgtggggcc | tattgcacaa | tggaggaaac | 300 |
| tctgtatgc | cgacccgc | tgaaggatgt | agatattccg | tatgttaatct | tctatcagca | 360 |
| ggaaagaaaa | tgacggtacc | tgactaa | gccccggct | actacgtgc | agcagccg | 420 |
| gtaatacgt | ggggc | gttatccg | tttactgggt | gtaaaggag | cgtagacgg | 480 |
| acggcaaccc | agatgtaaa | gccccgggt | caaccccccgg | actgcatttgc | gaactgcgt | 540 |
| gctagatgt | cgaggaggca | agtgaaattc | ctatgttgc | gggtgaaatgc | gtagatatta | 600 |
| ggaggaacac | cagtggcg | ggccgcttc | tggacgtat | ctgacgttgc | ggctcgaa | 660 |
| cgtggggagc | aaacaggatt | agataccctg | gtatgtccac | cgtaaaacga | tgactgcgt | 720 |
| gtgtcggtgt | gcaaaagccat | tcgggtccgc | agctaacc | ataagcgtc | cacctggg | 780 |
| gtacgttcgc | aagaatgaaa | ctcaaggaa | ttgacgggg | cccgacaca | cggtggag | 840 |
| tgtggttaa | ttcgaagcaa | cgcgaaga | cttacctgt | cttgacatcc | cgatgacc | 900 |
| ttcgtatgg | aagctttct | tcggaacatc | ggtgacagg | ggtgc | atgtcg | 960 |

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|-------------|------------|-------------|-------------|------------|------------|------|
| tcgtgtcg | agatgtggg | ttaagtcccg | caacgagcgc | aaccctatac | ttcagtagcc | 1020 |
| aggcaggtaa | gttgttact | ctggagagac | tgccaggat | aacctggagg | aagggtggga | 1080 |
| tgacgtcaa | tcatcatgcc | ccttatgacc | agggtacac | acgtgtaca | atggcgtaaa | 1140 |
| caaaagaag | cgaactcgcg | aggtaagca | aatctcaaaa | ataacgtctc | agttcggatt | 1200 |
| gtagtctgc | actcgactac | atgaagctgg | aatcgctagt | aatcgagat | cagaatgtcg | 1260 |
| cggtgaatac | gttccgggt | cttgcacaca | ccgccccgtca | caccatggga | gtcagtaacg | 1320 |
| cccgaaagtca | gtgacccaac | cgtaaaggagg | gagctgcccga | a | | 1361 |

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|---------------|--|-------------|-------------|-------------|--------------|------|
| SEQ ID NO: 98 | moltype = DNA length = 1396 | | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1396 | | | | | |
| source | note = HB-22_Eubacterium_rectale 1..1396 mol_type = unassigned DNA organism = Eubacterium rectale | | | | | |
| SEQUENCE: 98 | | | | | | |
| gcaagtcgaa | cgaagcactt | tatttgcattt | ccttcgggac | tgatttatttt | gtgactgagt | 60 |
| ggccggacggg | tgagtaacgc | gtgggttaacc | tgccctgtac | agggggat | cagtggaaa | 120 |
| cggctgtcaa | taccgcataa | gcccgcggaa | tcgcgtatgc | cagtgtgaaa | aactccgggt | 180 |
| gtataagatg | gaccgcgtt | ggatagcta | gttggatgg | taacggccca | ccaaggcgac | 240 |
| gatccatagc | cgacctgaga | gggtgaccgg | ccacattgggg | actgagacac | ggcccaaact | 300 |
| cctacgggg | ggagcgtgg | ggaaatattgc | acaatggggc | aaagctgtat | gcagcgcacgc | 360 |
| cgcgtgacgc | agaagatgtt | tcggatgtat | aactctatc | agcaggaa | ataatgacgg | 420 |
| tacctgacta | agaagcaccg | gctaatacgc | tgccagcgc | cgccgtataa | cgtatggtgc | 480 |
| aagcgttatac | gggatattact | gggtgtaaag | ggagcgcagg | cggtgcggca | agtcgtatgt | 540 |
| gaaagccccc | ggctcaaccc | cggtactgc | ttggaaaact | tcgtactaga | gtgtcggagg | 600 |
| gtgtaa | cggtatgt | tagcgtgtat | atgcgtatgt | attaggagga | acaccagtgg | 660 |
| cgaaggcgc | ttactggac | ataactgc | tcgaggctgc | aaagctgtgg | gagcaaacag | 720 |
| gattagatac | cttgcgtatc | cacgcgtaa | acqatgtata | ctagggtgt | ggaagcatttgc | 780 |
| cttctcggt | cgcgtcggaa | cgcgtatgt | atttgcctgt | gggagtagct | tcgcaagaaat | 840 |
| gaaactcaaa | ggaaatggac | ggggatggca | caagcgtgg | agcatgtgtt | ttaattcgaa | 900 |
| gcaacgcgaa | gaaaccttacc | aaatgttgc | atcttcgtca | ccggacttta | accgtactt | 960 |
| cttctcggt | caggactgac | agggtgtca | ttgttgcgt | cagctcggt | cgtgagatgt | 1020 |
| tgggttaagt | ccgcacacga | gcccacccct | tatctttat | agccagcggt | ccggccgggc | 1080 |
| actcttagaga | gactgcgcgg | gataacccgt | ggatgcgtc | aaatcatcat | | 1140 |
| gcccccttata | acttgggtca | acaacgtgt | aaatggcg | aaacaaagg | aagcaaaat | 1200 |
| gtgaagccga | gaaaaatctca | aaaataacgt | ctcagttcg | actgtatgt | gcaacccgcac | 1260 |
| tacacgaagc | ttgaatcgct | agtaatcgca | gatcagaatg | ctgcgtggaa | tacgtcccc | 1320 |
| ggttttgtac | acacccccc | tcacaccatg | ggagttggaa | atgcccgaag | ccagtgcac | 1380 |
| aaccgaaagg | aaggag | | | | | 1396 |

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|---------------|---|-------------|-------------|-------------|-------------|-----|
| SEQ ID NO: 99 | moltype = DNA length = 758 | | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..758 | | | | | |
| source | note = HB-23_Blautia_coccoides 1..758 mol_type = unassigned DNA organism = Blautia coccoides | | | | | |
| SEQUENCE: 99 | | | | | | |
| tgcagtcgag | cgaagcagct | aagacaggat | ttcttcggat | tgaagtctt | gtgactgagc | 60 |
| ggccggacggg | tgagtaacgc | gtgggttaacc | tgccctat | agggggat | cagttagaaa | 120 |
| tgactgtat | taccgcataa | gcccgcggaa | ccgcgtatgc | tgttgtgaaa | aactccgggt | 180 |
| gtatgatgt | gaccgcgtt | tgatagcta | gttggaggggg | taacggccca | ccaaggcgac | 240 |
| gatcgtatgc | ccgcgtatgc | gggtgaaacgg | ccacattgggg | actgagacac | ggcccaact | 300 |
| cctacgggg | ggagcgtgg | ggaaatattgc | acaatggggg | aaaccctgtat | gcagcgcacgc | 360 |
| cgcgtgacgc | agaagatgtt | tcggatgtat | aacttctatc | agcaggaa | aaaatgacgg | 420 |
| tacctgacta | agaagccccg | gctaactacgc | tgccagcgc | cgccgtataa | cgtagggggc | 480 |
| aagcgttatac | gggatattact | gggtgtaaag | ggagcgtaga | cggaagagca | agtcgtatgt | 540 |
| gaaaaggctgg | ggctcaaccc | caggactgca | ttggaaaact | ttgttctaga | gtgcggagg | 600 |
| gtgtaa | cggtatgt | tagcgtgtaa | atgcgtatgt | attaggagga | acaccagtgg | 660 |
| cgaaggcgc | ttactggac | gtactgc | ttgaggctcg | aaagctgtgg | gagcaaacag | 720 |
| gattagatac | cttgcgtatc | cacgcgtaa | acgtatgt | | | 758 |

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|----------------|---|-------------|-------------|--------------|-----------|-----|
| SEQ ID NO: 100 | moltype = DNA length = 1064 | | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1064 | | | | | |
| source | note = HB-234_Bifidobacterium_longum 1..1064 mol_type = unassigned DNA organism = Bifidobacterium longum | | | | | |
| SEQUENCE: 100 | | | | | | |
| gcccgcgtatgc | atgcagcgcac | gccgcgttag | ggatggaggc | cttcgggttg | taaaccttt | 60 |
| ttatcggttgc | gcaagcgcac | gtgagtttac | ccgttgcataa | agcacccgt | aactacgtc | 120 |
| cacgcgtatgc | ggtataatcg | agggtgcac | cgttatccgg | aattattggg | cgtaaagg | 180 |
| tcgttagggc | ttcgtcgatgc | ccgttgcataa | agtcgcgt | ttaacgggttgc | atccgcggc | 240 |
| ggtaacggat | ggcttgcgtatgc | cggttagggc | gactggaaat | cccggtgtaa | cggtggat | 300 |

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|--------------|-------------|-------------|-------------|-------------|-------------|------|
| tgttagatatac | gggaagaaca | ccaatggcgaa | aggcagggtct | ctggggccgtt | actgacgctg | 360 |
| aggagacgaaa | gogtgggggag | cgaacaggat | tagataccct | ggtagtccac | gccgttaaacg | 420 |
| gtggatgtgc | gatgtggggc | ccgttccacg | ggttccgtgt | cggagctaa | gggttaagca | 480 |
| tcccgcctgg | ggagatacggc | cgcaaggcta | aaactcaaa | aaattgacgg | gggcccccac | 540 |
| aagcggcggaa | gcatgcggat | taattcgatg | caacgcgaag | aaccttacct | gggcttgaca | 600 |
| tgttccggac | ggtcgtagag | atacggctc | ctttcggggc | gggttccacag | gtggtgcatg | 660 |
| gtcgtcgatca | gctcggtcg | tgagatgtt | ggttaaagtct | cgcaacgcgc | gcaaccctcg | 720 |
| ccccgtgtg | ccatcggtt | atgcggggaa | ctcacggggg | accgcgggg | ttaactcgga | 780 |
| ggaaggtggg | gatgacgtca | gateatcatg | cccttacgt | ccagggtctc | acgcatgcta | 840 |
| caatggccgg | tacaacggg | tgccacgcgg | cgacgcggag | cgatccctg | aaaacggtc | 900 |
| tcagttcgga | tcgcgtcg | caactcgat | ggtgtcgcta | gtaatcgca | 960 | |
| atcagcaacg | tcgcgggtaa | tgctgttccg | ggccctgtac | acaccgcgg | tcaagtcatg | 1020 |
| aaagtggcga | gcacccgaag | ccgggtggct | aacccttgt | gggaa | | 1064 |

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|----------------|--|---------------|--------------|-------------|-------------|------|
| SEQ ID NO: 101 | moltype = DNA | length = 1382 | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1382 | | | | | |
| source | note = HB-326_Slackia_isoflavoniconvertens | | | | | |
| SEQUENCE: 101 | 1..1382 | | | | | |
| gcagtgcgaac | gagtaagacg | ccttcggggc | tggatagagt | ggcgaacggg | tgagtaacac | 60 |
| gtgaccaccc | tgccccctcc | tccgggacaa | cctcgggaa | ccgaggctaa | taccggatac | 120 |
| tcgggcccc | ccgcattgggg | ggccggggaa | ageccctggc | ggagggggatg | gggtcgccgc | 180 |
| ccatcaggaa | gacgggggggg | taacggggca | ccgtgcctgc | aacgggtacg | cgggctgaaa | 240 |
| ggcgcgttgc | ccacatgggg | actgcggac | ggcccgacact | catacgggag | gcagcgttg | 300 |
| ggaattttgc | gcaatggggg | caacccctgc | gcacgcacgc | cgcgtgcggg | acgaagtcat | 360 |
| tctgtacgtca | aaccgcgttc | agcgagggaa | aaccatgcac | gtactcgacg | aagaagcccc | 420 |
| ggctaactac | gtgcgcggc | ccgcggtaat | acgttaggggg | cgagcgttat | ccggaatcat | 480 |
| tggggctaaa | ggcgcgcggc | ggccgggttc | aacggggccgc | gtcgaagccg | gggggtcaac | 540 |
| ccccggaa | gcccccaact | ggaaaggctcg | gatgcggcag | gggggggggg | aattcccggt | 600 |
| gtacgcgtga | aatgcgcaga | tatcggggaa | aaacccgcac | gcgaaggcag | cctctgggc | 660 |
| cggcgcgc | gctgaggcgc | gaaagctggg | ggagcgaaca | ggattagata | cccttgttagt | 720 |
| cccaagccgt | aacgcgttgc | gctactgttg | ggggggaaacgc | tccctccgt | ccgaagccaa | 780 |
| cgcattaa | gcgcgcgttgc | ggggatcgg | ccgcgcggatc | aaaactcaaa | ggaattgcac | 840 |
| ggggccgc | caagcgcgg | agcatgttgc | ttaattcgc | gcaacgcgaa | gaaccttacc | 900 |
| agggcttgc | atacagggtg | agccggagag | atccgggtgc | cgagaggagc | ctatacagg | 960 |
| gtgtgcgtgc | tgtcgatcg | tcgtgcgtgc | agggtgttgg | ttaagtcccg | caacgcgcgc | 1020 |
| aaccccccgc | gcgtgttgc | agcatttcgt | tgggcactca | cgccggactg | ccggcgctca | 1080 |
| ggccggggaa | ggccggggacgc | acgtcaatgc | atcatgcggc | tcatgcctgc | ggccgcacac | 1140 |
| gtgtcataat | ggccggcaca | acgggttgc | accccgcgag | ggggagcgga | tccctaaagc | 1200 |
| cgcccccagt | tcggatcgca | ggctgcacc | cgccctgcgt | aagccggagt | tgcttagtat | 1260 |
| cgcgatcgt | cacgcgcggc | tgaatacg | cccgccctt | gtacacacgc | cccgctcacac | 1320 |
| caccgcgtc | gtctgcaccc | gaagccgcgc | ggcgaaaccc | gcaagggggc | ggaggcgctc | 1380 |
| aa | | | | | | 1382 |

| | | | | | | |
|-------------------------------------|---------------------|---------------|--------------|-------------|--------------|------|
| SEQ ID NO: 102 | moltype = DNA | length = 1403 | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1403 | | | | | |
| note = HB-698_Lachnoclostridium_sp. | | | | | | |
| misc_feature | 23 | | | | | |
| note = n is a, c, g, or t | | | | | | |
| source | 1..1403 | | | | | |
| mol_type = unassigned DNA | | | | | | |
| organism = Lachnoclostridium sp. | | | | | | |
| SEQUENCE: 102 | | | | | | |
| tgcagtcgaa | cgaagcaatc | tancggaaat | tttcggatgg | aagctgttgc | gactgagtgg | 60 |
| cggacgggtt | agtaacgcgt | ggtaacccgt | cctcacactg | ggggacaaca | gttagaaatg | 120 |
| actgtcataa | ccgcataa | gcacaggac | gcatgggtcc | gtgtggaaaa | ctccgggtgt | 180 |
| gtggatgtga | cccgccgttgc | attatgtgt | ttgtggggta | acggccatacc | aaggcgacgc | 240 |
| tcaatagccg | acctgagagg | gtgacggcc | acatggggac | tgagacacgg | cccaaactcc | 300 |
| tacggggaggc | agcagtgggg | aatattgcac | aatggggaa | accctgtatgc | agcgacggcg | 360 |
| cgtgagtgaa | gaagtatttc | gtgtatgtaa | gtcttacatcg | cagggaaggaa | aatgcgcgtt | 420 |
| cctgactaa | aagcccccgc | taactacgttgc | ccagcaggccg | cggtatatacg | tagggggca | 480 |
| gcgttataccg | gatttactgg | gtgtaaagggg | agcgttagacg | gtaaaggcaag | tctgttagtgc | 540 |
| aagcccccgg | ctcaaccccg | ggactgttttgc | ggaaactgttgc | taacttagagt | gtctggaggagg | 600 |
| taagcggaat | tccttagtgc | gcgggtaaat | gcgttagat | tagggggaaac | accagtggcg | 660 |
| aaggcggctt | actggacgtt | gaggctcgaa | agcgtggggg | gcaaaacagg | 720 | |
| tttagataccc | ttgttagtcc | cgccgttacac | gtatgttgc | ggacaaatgtc | 780 | |
| cttcgggtcc | gtcgcaacgc | caataatgt | tccacctgg | gagtagtc | gcaagaatgt | 840 |
| aactcaaaagg | aattgcggg | gacccgcaca | agcggtggag | catgtgggtt | aattcgaage | 900 |
| aacgcgcaga | accttacca | atcttgcac | ccctctgacc | ggcgagtaat | gtcgctttc | 960 |
| cttcgggaca | gaggagacag | gttgcgtat | gttgcgtgc | tgagatgttgc | 1020 | |
| gtttaagtcc | cgcaacgcgc | gcaaccctta | tcctaaatgt | ccagcgttc | ggctggccac | 1080 |
| tcttgggaga | ctgcgcgggaa | taaccttgc | gaaggtgggg | atgacgtcaa | atcatcatgc | 1140 |

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| | |
|--|--|
| cccttatgat ttggctaca cacgtgtac aatggcgtaa acaaagagaa gcgagaccgc | 1200 |
| gagggtggac aaatctcaa aataacgtct cagttcgac tgcaggctgc aactcgctg | 1260 |
| cacgaagctg gaatcgtag taatcgcaa tcagaatgtc gcggtgaata cggtccggg | 1320 |
| tcttgtacac accgcgcgtc acaccatggg agtcagtaat gcccgaagtc agtgacccaa | 1380 |
| ccgaaaggag ggagctgccg aag | 1403 |
| SEQ ID NO: 103 | moltype = DNA length = 1255 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..1255 |
| | note = HB-80_Coprococcus_comes |
| misc_feature | 1150 |
| | note = n is a, c, g, or t |
| source | 1..1255 |
| | mol_type = unassigned DNA |
| | organism = Coprococcus comes |
| SEQUENCE: 103 | |
| tttgtgactg agtggggac gggtagtaa cgctgtggta acctgcctca tacaggggga | 60 |
| taacagttag aaatgactgc taataccgca taagaccacg gagcccatg gctcagtggg | 120 |
| aaaactccg gtggtagatg atggacccgc gtcgtttagt gtatgtggg ggtaacggc | 180 |
| ctaccaccc aacgatcgt agccgacatcg agagggtgac cggccacatt gggactgaga | 240 |
| cacggccca actcctacgg gaggoagcg tggggatata tgcacaatgg gggaaacct | 300 |
| gatgcagcga ccggcgtgtc ggcgaagaatg atttcgttata gtaaagctt atcagcagg | 360 |
| aagaaaatgtc cggtagtata ctaagaagca cccggctaat acgtgcacg agccgcgtt | 420 |
| atacgtatgg tgcaagcggtt atccggattt actgggtgtt aaggaggtgt agacggctgt | 480 |
| gtaaatgttca agtggaaagcc cggggctaa cccgggact gctttggaaa ctatgcagct | 540 |
| agagtgttgg agaggatgtt ggaatttcca gtgttagcggtt gaaatgcgtt gatattggg | 600 |
| ggacacccaccc tggcgaaaggc ggcttactgg acgtgtactt acgttgaggc tcgaaaggcgt | 660 |
| ggggagccaa caggattaga taccctgttgc tccacgcggc taaacgtata ctactaggt | 720 |
| tcggggagca aagctttcg gtgcggcgcgaaacgcataa agtagtccac ctggggaggt | 780 |
| cgttcgcgaaatggaaactc aaaggaaatgg acggggaccgc gcacaagccg tggagcatgt | 840 |
| ggtttaatcc gaaacacccgtt acctgtctt gatcatccccg tgacccggcgt | 900 |
| gtaaatgcgc cttttttcgc gacacccgtt gacagggtgtt gcatgttgcgtc | 960 |
| tgtcgttggaa tggtgggtt agtccgcac cgttacccctc agtagccac | 1020 |
| attttggatg ggcactctgg agagactgcg aggataacc tggagggaa tggggatgac | 1080 |
| gtcaaaatcat catgccttgcgaaatggcgtt gatcacacgtt gctacaatgg cgtaaacaaa | 1140 |
| gggaagcaan cctgcgatggg taagcaatac tcaaaaatac cgtctcgtt cggattgttag | 1200 |
| tctgcgaaactc gactacatgcgactgtaatc gctgtgttgc atgtc | 1255 |
| SEQ ID NO: 104 | moltype = DNA length = 740 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..740 |
| | note = 104_HB-88_Clostridium_butyricum |
| source | 1..740 |
| | mol_type = unassigned DNA |
| | organism = Clostridium butyricum |
| SEQUENCE: 104 | |
| tgcagtgcg cgtatggact ccttcgggg tggattagcg gggacgggt gaggtaacacg | 60 |
| tgggttaaccttgcgttcataga gggaaatagc ctttcgaaatggaaatattt accgcataa | 120 |
| atttgtatgtc cggcatgttac agcaattaaa ggagataatcc gctatgtatgg gggccgcgt | 180 |
| cgcattatgtc agttgttgcgtt gtaacggctc accaaggcgca cgtatgcgtt ccgcacatgt | 240 |
| agggtgtatcg gccatgttgcgtt gactgttgcgtt cggcccaatggc tccatccggc ggcagcgt | 300 |
| ggaaatatttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 360 |
| ttccggatgtt aaagcttgcgtt ctttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 420 |
| ggctaaatccatgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 480 |
| tgggtgttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 540 |
| tgggtgttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 600 |
| gtacgggttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 660 |
| tgtaactgtc actgggttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 720 |
| ccacggccgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 780 |
| SEQ ID NO: 105 | moltype = DNA length = 1473 |
| FEATURE | Location/Qualifiers |
| misc_feature | 1..1473 |
| | note = LC037213.1 Clostridium sporogenes gene for 16S ribosomal RNA, partial sequence, strain: JCM 7836 |
| source | 1..1473 |
| | mol_type = unassigned DNA |
| | organism = Clostridium sporogenes |
| SEQUENCE: 105 | |
| agagtttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 60 |
| gatgttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 120 |
| tgcgttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 180 |
| tcgttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 240 |
| gttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 300 |
| ccacatttgcgttcatatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 360 |
| gaaatgggg gaaacccgttgc tgcagcaacg ccgcgtgtt gatgcgttgc | 420 |

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|--------------|-------------|-------------|-------------|-------------|------------|------|
| aaggccctgtt | ttctgggacg | ataatgacgg | taccagagga | ggaagccacg | gctaactacg | 480 |
| tgcgcagcgc | cgccgtaata | cgttaggtgg | gagcgttgcc | cggttact | gggcgttaag | 540 |
| gggtgcgttag | cggtgttta | agtggatgt | gaaatcccc | ggcttaact | gggggtctca | 600 |
| ttccaaactg | gatatctta | gtcaggaga | gaaagccga | attcttagt | tagcgtgaa | 660 |
| atgcgttag | attagaaga | acaccagtgg | cgaaggccgc | tttcgttact | gtaactgacg | 720 |
| ctgaggcaccg | aaagcgtggg | tagcaaacag | gattagatac | cctggtagtc | cacgecgtaa | 780 |
| acgatggata | ctagggttag | ggggtatca | ctccccctgt | gcccagtt | acacaataag | 840 |
| tatccgcct | ggggagtagc | gtcgaatgt | taaaactca | agaaatttac | gggggcccgc | 900 |
| acaaggcgcg | gagcatgtgg | ttaattcga | agoaacgcga | agaacctac | ctggacttga | 960 |
| catcccttc | atagcttaga | gatagtgtaa | gcccattcgg | gcaaggagac | agggtgtgca | 1020 |
| ttgttgtgt | cagtcgtgt | cgtgatgt | tagtttaatg | cctgcaacaga | gcgcacccct | 1080 |
| ttgttattatgt | tgcttaccatt | aagtggca | ctctaatgag | actgcctgg | taaccaggag | 1140 |
| gaagggtgggg | atgacgtcaa | atcatcatgc | cccttatgtc | cagggttaca | cacgtgtac | 1200 |
| aatggtaggt | acaataaagac | gcaagaccgt | gagggtggac | aaaacttata | aaacctatct | 1260 |
| cagttcgggt | tgttaggttc | aactcgceta | catgaagctg | gagttgtctg | taatcgcgaa | 1320 |
| tcagaatgtc | gcccgttata | cgttcccccgg | ccttgcacac | accgcggcc | acaccatgag | 1380 |
| agctggtaac | accgcgaagtc | cgtgaggtaa | ccgtaaaggag | ccagcggccg | aagggtggat | 1440 |
| taagtgtatgg | ggtgaagtcg | taacaaggta | acc | | | 1473 |

SEQ ID NO: 106 moltype = DNA length = 1433
 FEATURE Location/Qualifiers
 misc_feature 1..1433
 note = NR_042817.1 Akkermansia muciniphila ATCC BAA-835
 strain Muc 16S ribosomal RNA, partial sequence
 source 1..1433
 mol_type = unassigned DNA
 organism = Akkermansia muciniphila

SEQUENCE: 106
 aacgaacgcg ggcggcgtgg ataagacatg caagtgcac gagagaattt ctagttgtct 60
 aataatttc tagtggcgca cgggtgagta acacgtgatg aacctgcccc cgagagccgg 120
 atagccctgg gaaactggga ttaatccgc agatgtatcg aagattaaag cagaatgcg 180
 ctggggatg ggctcgcggc ctataggta gttgggtagg taacggctca ccaaggcgat 240
 gacgggttagc cggctctgaga ggtatgtccgg ccacacttga actgagacac ggtccagaca 300
 cctacgggtg gcagcagtcg agaattttt acaatggggg aaaccctgtat ggtgcacgc 360
 cggcgtgggg aatgaaggctt tcggattgtt aaaccctgtat catgtggggg caaattaaaa 420
 agatagttttt acaagggaa gagacggctt actctgttgc agcggccgc gtaatacaga 480
 ggttcaaaacg gttgttccgg atcaatgggg gtaaaggctgt cgtaggctgtt ttctgtaa 540
 gtgtgtgaaa ggcggggctt caacccggcg acggcacatg atactgcgag actagagtaa 600
 tggggggggg accggaaatc tcgggttagt agtggaaatgcg gttagatcg agaggaacac 660
 tcgtggccggc ggccgggttc tggatcttgc acgtggatgtt ggcacgggg ccagggggagc 720
 gaaagggtttt agataccctt gtatgttgcg cagtaaacgg tgcacgttgc gtgtgggggg 780
 aatcgacccc ctgcgtccgg gagaacgcg ttaagcgtgc gccttgggg gtaacggcgc 840
 aaattaaaaa ctcaaaagaaat ttggggggcc cccgcacaaat cgggtggatgttggcttaa 900
 ttctgttgcgaa cgcgaacatc tttaatggggg cttggatcttgc aatgaacaaat atgtgaaac 960
 atgcactct tcgggggggtt tacacagggtt ctgcacgttgc ctcgttgcgttgc 1020
 gatgtttgtt taatgttgcg aacgacgcgca accctgttgc ctagtttacca gcacgttgc 1080
 gtggggactt tcggggggactt gcccggatca acttggggggc aggtggggac gacgttgc 1140
 cgtatggcc ttatggcca ggggtgcaca cgtactacaa tgccccgtac agagggggcc 1200
 gaagccgcga ggccggggaa atcttaaaaaa ctggggcccg ttccggactgtt aggtgtcaac 1260
 ccgccttacac gaagccggaa tgcgttgcgatca gtcacggcgc cgttgcatacg 1320
 ttccgggttc ttgttacacac cgcggccatc atcatggaaat ctgggtcgac ccggaaatgttac 1380
 tgaagccaaac cgcaaggagg cagggttctca aggttgcggact ggttactggg atg 1433

SEQ ID NO: 107 moltype = DNA length = 1503
 FEATURE Location/Qualifiers
 misc_feature 1..1503
 note = NR_029231.1 Clostridium sporogenes strain McClung
 2004 16S ribosomal RNA, partial sequence
 source 1..1503
 mol_type = unassigned DNA
 organism = Clostridium sporogenes

SEQUENCE: 107
 gagagtttgc ttctggctca ggacgacgc tggggcgttg cttaacacat gcaagtgcag 60
 cgtatggact tccttcgggg aagtggatgtt cggccggacgg gtggatgttgc cgtgggttac 120
 ctgccttccaa tggtggggata gccttcggaa aggaaggata ataccgcata acataaggata 180
 atcgcgtatgt ttctttatca aagttttt gctttgtatgtt gttttgtatgttgc gacccggcc 240
 agttggtaat gtaacggctt accaaggca cgtatgttgc cgcacccgttgc aggggtatgt 300
 gcccacattgg aacttgcgaca cgggtccggac ttctacgggg ggcacggatgttgc 360
 cgcacatggg gaaaccctgtca cgcacgttgc cccgcgtgggtt gatgttgcgttgc ttccggatgttgc 420
 aaaggccctgtt ttctggggac gataatgttgc gtaccaggagg aggaaggccac ggcttaactac 480
 gtgtccggatgttgc cccggatgttgc acgtggatgttgc cggatgttgc tggggatgttgc 540
 ggggtgcgttgc gcccggatgttgc aagtggggatgttgc tggaaatcccc gggcttaacc tggggatgttgc 600
 attccaaactt ggtatgttgc agtgcaggatgttgc agggaaaggccatgttgc aatttgcgttgc 660
 aatgcgttgc gatttagggaa aacaccgttgc gcaaggccggc ttccgttgc tggaaatgttgc 720
 gtcggggccatgttgc gaaacgttgc gtagcaaaaca ggatttagata ccctggatgttgc ccacggccgttgc 780
 aacgcgttgc gtttttttttgcgttgc aactcccccgttgc cccggatgttgc aacacaataa 840

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|-------------|------------|------------|------------|-------------|------------|------|
| gtatccgc | tggggagtac | ggtcgcaaga | ttaaaactca | aaggattga | cggggcccg | 900 |
| cacaaggcgc | ggagcatgtg | gtttaattcg | aagcaacccg | aagaacctta | cctggacttg | 960 |
| acatccc | tttagtgc | catagctcg | atagatgtga | agcccttcgg | ggcaaggaga | 1020 |
| atgttgtcg | ttagtgcgt | tcgtgagatg | ttaggttaag | tcctgcaacg | agcgaaccc | 1080 |
| ttgttattag | ttgtcattat | taaggtagc | actctaata | gactgectgg | gtaccaggaa | 1140 |
| gaaagggtgg | gtatgttgc | aatcatcg | ccccctatgt | ccagggotac | acacgtgtca | 1200 |
| caatggtagg | tacaataaga | cgcaagaccc | tgaggtggat | aaaacttat | aaaacctatc | 1260 |
| tcaatccgg | ttgttagtgc | caactcgct | atcatgttgc | ggaggtgtca | gtatccgcg | 1320 |
| atcagaatgt | cgccgtgaat | acgttcccg | gcctgtaca | caccgeccgt | cacaccatga | 1380 |
| gagctgttgc | cccccaaggt | ccgtgaggta | accgttaagg | gcacageggc | gaaggtggga | 1440 |
| tttagtgcatt | gggtgttgc | gtatgttgc | gtaccagggt | agccgttagga | gaaacctggc | 1500 |
| tcc | | | | | | 1503 |

| | | | | | | |
|----------------|--|--------------|--------------|--------------|-------------|------|
| SEQ ID NO: 108 | moltype = DNA length = 1509 | | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1509 | | | | | |
| | note = NR_115155.1 Peptostreptococcus russellii strain | | | | | |
| | RT-10B 16S ribosomal RNA, partial sequence | | | | | |
| source | 1..1509 | | | | | |
| | mol_type = unassigned DNA | | | | | |
| | organism = Peptostreptococcus russellii | | | | | |
| SEQUENCE: 108 | | | | | | |
| gagagtttgc | ttctggctca | ggatgaacgc | tggccgcgtg | cttaaacat | gcaagtgcag | 60 |
| cgcggccct | ttgggtcttg | caccaaaagaa | gactgagccg | cgacgggtg | agtaacgcgt | 120 |
| gggttaacctg | ccctatacac | atggataaca | tgctgaaaag | catactaata | catgataaag | 180 |
| tacactgtat | gtatcttcgg | tgtatcaagg | cgtaggtggat | ataggatgga | cccgcgctcg | 240 |
| attagctgt | ttgtgtgggt | aaagcttac | aaggccacgg | tcatgttgcg | accttgagg | 300 |
| gtgtatgttgc | ccatggaaac | tgagacacgg | tccaaactcc | tacggggggc | agcagtgggg | 360 |
| aatattgcac | aatggggcga | agcctgtatgc | agcaacgcgg | cgtgaaccat | gaaggcttcc | 420 |
| ggatctgttgc | ttgtgttgc | aggggaaatg | aatgtgttgc | ccctgttgcg | aagcaccggc | 480 |
| taactactgt | ccaggcgttgc | cggtatatacg | taggtgttgc | gtgttgcgttgc | gattttactgg | 540 |
| gcgttaaagg | ttgtgttgc | gtcttc | tcgggtgttgc | aaaggctacgg | ctcaaccgt | 600 |
| ttaagccgc | gaaactggaa | gacttgcgt | caggagggaa | aagtggatt | ctcaactgt | 660 |
| cgggttgc | cgtagatatt | gagaagaaca | ccagtagcg | aggcggctt | ctggactgt | 720 |
| actgcacactg | aggcggcggaa | gcgttgcgttgc | caaacaggat | tagatacc | ggtagtccac | 780 |
| gcccgttgc | ataggatata | gggtgttgcgg | gttacccccc | tcgggtgcgc | agttacgc | 840 |
| ttaataatctc | ccctgttgcgg | gtacgcacgc | aaatgttgc | ctcaaaaggaa | ttgacgggaa | 900 |
| cccgccacaag | tagcggagca | tgtgtttaa | ttcgaagcaa | cgcgaagaa | cttacctaag | 960 |
| cttgcacatct | ttcagacccg | ttgtgttgc | tacccccc | tcgggtgttgc | gtatgcacgg | 1020 |
| gggtgcgttgc | tgtgtgtc | cgatgtgttgc | atgtgttgcg | ttaatgttgc | caacgcgc | 1080 |
| acccttgc | tttagtgc | agcattaaat | tgggcactt | agagagact | ccaggatata | 1140 |
| cctggaggaa | ggtggggatg | acgttacatc | atcatgtcccc | ttatgttgc | ggcttacacac | 1200 |
| gtgtcttacat | gggtgttgc | gagggtgttgc | aaagccgcgg | gtggagctaa | tcccttaaag | 1260 |
| ccattcttc | cgatgtgttgc | agggttgc | tcgttgc | aaatgttgc | ttactgttgc | 1320 |
| tcgcagatca | gtatgttgc | gtatgttgc | tccgggttgc | tgtatcc | gcccgttca | 1380 |
| ccatgttgc | ttggaaacc | cgaaaggccat | tatcttaccc | caaggaagaa | gtcgttgc | 1440 |
| gtgttgc | taacttaggt | gtatgttgc | aaaggatgttgc | gtatgttgc | gtcgttgc | 1500 |
| atcaccttc | | | | | | 1509 |

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|---------------------------|--|------------|------------|------------|--------------|-----|
| SEQ ID NO: 109 | moltype = DNA length = 1487 | | | | | |
| FEATURE | Location/Qualifiers | | | | | |
| misc_feature | 1..1487 | | | | | |
| | note = NR_025311.1 Mycolicibacterium smegmatis strain ATCC | | | | | |
| | 19420 16S ribosomal RNA, partial sequence | | | | | |
| misc_feature | 300 | | | | | |
| note = n is a, c, g, or t | | | | | | |
| misc_feature | 749 | | | | | |
| note = n is a, c, g, or t | | | | | | |
| misc_feature | 818 | | | | | |
| note = n is a, c, g, or t | | | | | | |
| misc_feature | 837 | | | | | |
| note = n is a, c, g, or t | | | | | | |
| misc_feature | 871 | | | | | |
| note = n is a, c, g, or t | | | | | | |
| source | 1..1487 | | | | | |
| | mol_type = unassigned DNA | | | | | |
| | organism = Mycolicibacterium smegmatis | | | | | |
| SEQUENCE: 109 | | | | | | |
| ggcggcggtgc | ttaacacat | caagtcgaa | ggaaaggccc | tttcgggggt | actcgatgttgc | 60 |
| cgaacgggttgc | actaaacat | gggtgtat | ccctgcactt | tgggataa | ctgggaaact | 120 |
| gggtcttaata | ccgaaat | cctgtgttgc | gtatgttgc | gtatgttgc | gtatgttgc | 180 |
| tgtggatgg | ccccggggcc | tatcgat | ttgtgttgc | gtatgttgc | caaggcgttgc | 240 |
| acgggtatgc | ggcctgttgc | ggtgcaccc | cacacttgc | ctgatgttgc | gcccgttgc | 300 |
| ctacgggg | cagcgttgc | gaatatt | caatggggcc | aagcctgtat | cagcgttgc | 360 |
| gcgttgc | tgatgttgc | ccgggttgc | accttgc | tcacac | gtcgttgc | 420 |
| acgttgc | caagaagg | accggcca | tacgttgc | cagcgttgc | aatacgttgc | 480 |

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|-------------|-------------|-------------|--------------|-------------|------------|------|
| gtccgagcgt | tgtccggaat | tactgggcgt | aaagagctcg | taggtggttt | gtcgctgtgt | 540 |
| tctgtaaaaac | tcacacgcta | actgtgggg | tgccggcgat | acgggcagac | taggtactg | 600 |
| caggggagac | tggatttcct | ggtgtagccg | tggaatgcgc | agatatcagg | aggaacaccg | 660 |
| gttgcgaagg | cgggctctg | ggcagtaact | gacgctgagg | acgcggaaacg | tggggagcga | 720 |
| acaggattag | ataccctggt | agtccacgn | gtaaacggtg | ggtacttaggt | gtgggttcc | 780 |
| ttccttggga | tccgtccgt | agctaaccgca | ttaagtanc | cgccctggga | gtacggnccg | 840 |
| aaggctaaaa | ctcaaaggaa | ttgacggggg | nccgcacaag | cgggggaca | tgtggattaa | 900 |
| ttcgatcoca | cgcgaagaac | cttaacttggg | tttgacatgc | acaggacccc | ggcagagatg | 960 |
| tcggttccct | tgtggctgt | gtcgggggtt | tgcgtggctg | tcgtcagctc | gtgtcgtgag | 1020 |
| atgttgggtt | aagtcccgca | acgacgcgaa | cccttgcctc | atgttgcac | cacgttatgg | 1080 |
| tggggactcg | tgagagactg | ccggggctaa | ctcggggaggaa | ggtggggatg | acgtcaagtc | 1140 |
| atcatgcccc | tstatgtccag | ggcttcacac | atgtcaata | ggccggta | aagggtctcg | 1200 |
| atgcgcgttag | gtggagcgaa | tccttcaaa | gcccgtct | gttcggatcg | gggtctgca | 1260 |
| ctcgaccctcc | tgaatcgccg | gtcgttagta | atcgacatgc | accaacgcgt | cggtgaatac | 1320 |
| gttcccgcc | cttgatcaca | ccggccgtca | cgtcatgaaa | gtcgttaaca | cccgaaacgg | 1380 |
| gtggccta | acccctgtgg | ggagccgtcg | aagggtggat | ccggcatttg | gacgaagtcg | 1440 |
| taacaaggt | gccgtacccg | aagggtcgcc | tggatcacct | cctttct | | 1487 |

SEQ ID NO: 110 moltype = DNA length = 1399
 FEATURE Location/Qualifiers
 misc_feature 1..1399
 note = NR_144609.1 Enterorhabdus muris strain WCA-131-CoC-2
 source 16S ribosomal RNA, partial sequence
 1..1399
 mol_type = unassigned DNA
 organism = Enterorhabdus muris

SEQUENCE: 110
 tggtcagga tgaacgctgg cggcgtgctt aacacatgca agtcgaacga ttaaaccgccc 60
 ctggggcgga catagactgg cgaacgggtg agtaacacgt gaccaacctg ccccgcgctc 120
 cggggacacc gctggaaacg gcggtataa ccggatactc cggggaggccc ccatggccct 180
 gccggaaag cggagacggc gccggatggg gtccggggccc attaggtaga cggcggggta 240
 acggccacc ctggccggca tggtagccg gactgagagg tcgacggccc acatgggac 300
 ttagataccg cccagactcc tacgggaggg agcagtgggg aattttcgcc aatgggggaa 360
 accctgacgc acgaacgccc cgtggggac gaaggccctc gggttgtaaa ccgcgttcag 420
 caagggaaac ttacacgccc tacccgtca aagaagctccg gctaactacg tgccagcagc 480
 cgcggtataa cgtagggggc gagcgttata cggatttttccggcataa cgcgcgttagg 540
 cggccgcctt aacgggaccc ctaaccccg cgtcaaccc cggggccgggt cccggactgg 600
 gccgctcgag tgccgttagag gagagcggaa ttcccggtgt agccgtggaa tgcgcagata 660
 tcggggaaac caccatgggg gaaaggccatc ctctggggcc tcactgacgc tgaggccgca 720
 aagctgggggg agcgaacagg attagatacc ctggtagtcc caggtgtaaa cgtatggccgc 780
 tagtgtggg gggacgatcc ctccgtccg cagccaaacgc attaagccgc ccgcgtgggg 840
 agtacggccg caaggctaaa actcaaaggaa attgacgggg gcccgcacaa gcagcggagc 900
 atgtggctta attcagaacg acgcgaagaa ctttaccagg gcttgcacatc ccgtgaaac 960
 cggggagacc cgggtggcca gagggtggcc gcaagggtgtt cgtcagtcg 1020
 tgcgtgaga tggtgggtt aatcccgca ctagcccaac ccccgccccg tggtggccagc 1080
 attcagtgg ggactcgcgg gggactgcgg gctgtcaaggc ggaggaaggt gggggcgcacg 1140
 tcaactatc atgccttggg tgcacacgtt ctacaatggc cggtagacag 1200
 ggttgcacc cccgggggg gaggccatcc cggaaaggcc gttcccaatc ggatcggagg 1260
 ctgcaacccg cttcgctgaa gcccggatgt cttagtaatcc cggatcggca cggccgggt 1320
 aatacgttcc cggcccttgtt acacacggcc cgtcacacca cccgagtcgt ctgcacccga 1380
 agccgcggc cgaaccccc 1399

SEQ ID NO: 111 moltype = DNA length = 1469
 FEATURE Location/Qualifiers
 misc_feature 1..1469
 note = NR_041609.1 Adlercreutzia equolifaciens strain
 FJC-B9 16S ribosomal RNA, partial sequence
 source 1..1469
 mol_type = unassigned DNA
 organism = Adlercreutzia equolifaciens

SEQUENCE: 111
 agagttttagt cttggctcag gatgaacgct ggccggctgc ttaacacatg caagtcaac 60
 gattaagacg gtttcggccg tgtatagat ggcgaacggg tgagtaacac gtgaccaacc 120
 tgcggccgcg tccgggacaa ccgtggataa cccgggtatac taccggatgc tccggggagg 180
 ccccatggcc tccggggaa agccccacgc gccggggatg ggggtcgccgc ccatttagta 240
 gacggccggg taacggccca ccgtggccgc gatgggtac cggactgaga ggtcgacccg 300
 ccacattggg actgagatac ggcccagact cttacgggg gcaaggatccg ggaatttgc 360
 gcaatggggg caacccgtac gcagcaacgc cgcgtgggg acgaaggcct tcgggttgc 420
 aaccgttttc aacggggaa acatagacgg tacctgcaga agaagctccg gctaactacg 480
 tgccagcgc cgggtataa cgtagggggg gagggttattc cggattttccggcataa 540
 cggcgcgttagg cggccgcctt aacggggaccc ctaatcccg ggtcaactt cggggccgggt 600
 tcggactgg ggggtcgag tgccgttagag gcaggccggaa ttcccggtgt agccgtggaa 660
 tgcgcagata tggggaaagaa caccgtggc gaaggccgac tgctggccgc ccactgacgc 720
 tgaggccgca aagctggggg agcgaacacgg attagatacc ctggtagtcc cagccgtaaa 780
 cgtatggccg taggtgtggg gggaccatcc cccgtgcggc cagccaaacgc attaagcgtc 840
 cccgcctgggg agtacggccg caaggctaaa actcaaaggaa attgacgggg gcccgcacaa 900

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| | | | | | | |
|-------------|-------------|-------------|-------------|------------|------------|------|
| gcagcggagc | atgtggctta | attcaagca | acgcgaagaa | ccttaccagg | gcttgacatg | 960 |
| cgagtgaagc | cgccggagacg | cggtggccga | gaggagctcg | cgccagggtg | gcatggctgt | 1020 |
| cgtcagtcg | tgtcgtgaga | tgttgggtta | agtcccccaa | cgagcgaac | ccccgtcccc | 1080 |
| tgttgcggc | attcaagttgg | ggactcgcgg | gagactcggc | gggtcaagcc | ggaggaaagg | 1140 |
| ggggacgacg | tcaagtcatc | atgcggctta | tgcctgggc | tgcacacgtg | ctacaatggc | 1200 |
| cggtagcagag | ggttgcaccc | ccggcgagggg | gaggcgatcc | cggaagccg | gtcccagg | 1260 |
| ggatcgcagg | ctgcaccccg | cctgcgtgaa | gtcgaggatgg | ctgataatcg | cgatcgacca | 1320 |
| tgcgcgggt | aatacgttcc | cgggcttgt | acacacccgc | cgtcacacca | cccgagtcgt | 1380 |
| ctgcaccccg | agccgcggc | cgaaccccttc | tggggcgag | gcgtcgaagg | tgtggagggt | 1440 |
| agggggggtt | aagtctgtaac | aaggttaacc | | | | 1469 |

SEQ ID NO: 112 moltype = DNA length = 1474
 FEATURE Location/Qualifiers
 misc_feature 1..1474
 note = NR_115868.1 Enterorhabdus caecimuris B7 16S
 ribosomal RNA, partial sequence
 source 1..1474
 mol_type = unassigned DNA
 organism = Enterorhabdus caecimuris

SEQUENCE: 112
 agagtttcatggcgtac gatgaacgc ggcggcgtgc ctaacacatg caagtcaac 60
 ggtaaaacccgc cctctggggc gacatacgt ggcgaacggg tgagtaaacac gtgaccaacc 120
 tgcggccgcg tccgggacaa ccgctggaa cggcggtctaa taccggatac tccggggccc 180
 ccgcatgggg gggcgccggaa agccccggcgc ggcggggatg ggtcgccgc ccattaggt 240
 gttaggcgggg tagaggccca cctagccgac gatgggtacg cggactgaga ggtcgatcg 300
 ccacattggg actgagatac gccccagat cctacgggg gcaagcgtgg ggaatttgc 360
 gcaatggggg gaaacctgac gcaacaaacgc cgctgtcggg acgaaggccc tcgggtcgta 420
 aaccgcgttc agcagggaag accttacgcg ggtacactgcg gaagaagctc cggctaacta 480
 cgtgccagca ggcgcggtaa tacgtgggg ggcagcgatcc tccggatcca ttggggctaa 540
 agcgcgcgtta ggccggccgc taagcgaaac ctctaaaccc ggggctcaac ctggggccgg 600
 gtcccgact gggcggtact agtgcgtgat aggagagcgg aattcccggt gttaggggtgg 660
 aatgcgcaga tatcggaag aacaccatg gcaaggcgg gcaactcgcc ctctctggc cgtcaactgac 720
 gctgaggcgc gaaagctggg ggagogaaca ggattagata ccctgttagt cccagccgt 780
 aacgatgggc gctaggtgtg gggggatccc ccctccgtgc cgcagccaaac gcattaagcg 840
 ccccgccctgg ggatcgacccg cgcacggta aaactcaaaag gaatttgcgg gggccgcac 900
 aagcagcggc gcatgtggc taattcgaag caacgcgaag aaccttacca gggcttgaca 960
 tgcgcctgaa gocgcggaga cgcgggtggc gagagggagg cgccgcgggt gtgcattggc 1020
 gtcgtcaget cgtgtcgta gatgtgggt taagtccgcg aacgcgcgcg acccccggtcc 1080
 cgtgtcgca gcatgtgggatggggactcg gggagactcg cggcgctcaag ccggaggaaag 1140
 gtggggacga cgtcaatc tcatggccct tatggccctgg gtcacacacg tgctacaatg 1200
 gccggtagac aggggttgcg ccccgccgg gggagcgatcc cccggaaagc cggcccccgt 1260
 tcggatcgca ggctgcaccc cgcctcggtg aagccggatg tgcttagtaat cgccggatcg 1320
 caccgcggc tgaatcggtt cccggccctt gtacacaccc cccgtcacac caccggatgc 1380
 gtctgcaccc gacggccggc gccgaaccccc cccctggggg cggaggcgatc gaagggtgtgg 1440
 agggtaaggc ggtgtaaaggc gtaacaagg 1474

SEQ ID NO: 113 moltype = DNA length = 1440
 FEATURE Location/Qualifiers
 misc_feature 1..1440
 note = NR_044049.1 Coprococcus eutactus strain ATCC 27759
 16S ribosomal RNA, partial sequence
 source 1..1440
 mol_type = unassigned DNA
 organism = Coprococcus eutactus

SEQUENCE: 113
 gatgaacgcg ggcggcgtgc ttaacacatg caagtcaac gattgaagct ggaggttgct 60
 cccggccatt tagtggcga cgggtgatgta acgcgtgggt aacctgcctc atacagggg 120
 atagcagttg gaaacgactg gtaaaaccgc ataagcgcac rgtatcgcat gatacagtgt 180
 gaaaacactc cgggtgtatg agatggaccc ggcgtctgtg agcttagttgg tgaggtaacg 240
 gcccaccaag ggcgcgtca gtagccggcc tgaggggtg aacggccaca ttggggactga 300
 gacacggccccc aaactcctac gggaggcgcg agtggggaaat atgcacaaat gggggaaacc 360
 ctgtatcgac gacgcggcgt gactgtggaa gtattccgtt atgtaaagct ctatcagcag 420
 ggaagataat gacggtaacct gactaagaag caccggctaa atacgtgcgca gcagccgcgg 480
 taatacgatg ggtcaacggc ttactcggtt taaagggtgc gttaggtggca 540
 aggcaagtct gaaatggaaa tccgggctc aacccggaaat ctgggttggaa aactgttttag 600
 cttagatcaca ggagggatgg tggaaatcc tagtgcgtcg gtggaaatgcg tagatattag 660
 gaggaaacacc agtggcgaag ggcacttact ggactgtac tgacactgag gcacgaaagc 720
 gtggggacga aacaggatta gataccctgg tagtccacgc cgtaaaacgtat gaatactagg 780
 tgggggttc caaaggactc cgggtccgtc gcaaacgcatt taagtattcc acctggggag 840
 tacgttcgca agaatggaaa tcaaaaggat tgacggggac ccgcacaagc ggtggagcat 900
 gtgtttat tccaaaggcaca ggcggaaaacc ttaccaacgt ttgacatctt gatgcacgtt 960
 ccttaacccgg aacttctt cggagcatca gagacagggt gtgcacatgggtt gtcgtcagct 1020
 cgtgtcgatc gatgtgggt taagtccgcg aacgagcgcac accccattt ccagttagcca 1080
 gcagtaatcg gggactctg gagagactcg cggggataac cggggaggaaat gtggggatgt 1140
 cgtcaatc tcatggccct tatgtttgg gtcacacacg tgctacaatg gcgttacaa 1200
 agagaagcra acctgtgaag cgcagcaac ctcaaaaagg ctgtctcgtt cgccattgtt 1260

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gtctgcact cgactacatg aagctggat cgcttagtaat cgcagatcg catgtgcgg 1320
tgaatacggtt cccgggtctt gtacacaccc cccgtcacac catggggatc ggtaacgcc 1380
gaagtcatgtg acccaacccgc aaggaggag ctggcgaagg caggatcgat aactgggtg 1440
```

```
SEQ ID NO: 114 moltype = DNA length = 1453
FEATURE Location/Qualifiers
misc_feature 1..1453
note = NR_044048.1 Coprococcus comes ATCC 27758 16S
source ribosomal RNA, partial sequence
1..1453
mol_type = unassigned DNA
organism = Coprococcus comes
```

```
SEQUENCE: 114
gtgaacgct ggcggcgtgc ttaacacatg caagtgcac gaagcactta tmcttgattc 60
ttcggatgaa grggtttgtc actgagtggc ggacgggtga gtaacgcgtg ggttaacctgc 120
ctcatacagg gggataacag tttagaatga ctgctaatac cgcataagac cacrgagcc 180
catggctcg tggaaaaaac tccgggtgtt tgagatggc cccggtctga ttagtagtt 240
ggtgtggtaa cggcctacca agccaaacatc cagtagccga cctgagaggg tgaccggca 300
cattgggact gagacacggc ccaaactct acggggaggc gcaatggggg atattgcaca 360
atggggaaa ccctgtatgc ggcacggcgtc gtgagcgaag aagtatccg gtagttaag 420
cttcatacgc agggagaaaa atgacggtaatc ctgactaaga agcaccggct aaatacg 480
cagcagccgc ggttaatacgat atgggtcaag cgttataccgg attactggg tgtaaaggga 540
gctgttagcggc ctgtgtaaatc ctgtagtggaa agccccccggg gactgttttgc 600
gaaactatgc agcttagtgc tcggagaggat aagtggaaatc cccagtgtatc cggtaatgc 660
cgttagatatt gggagaaaca ccagtggcga aggccgttta ctggacgatc actgacgtt 720
aggctcgaaa gctgtggggag caaacaggat tagataccct ggttagtccac gccgtaaacg 780
atgactacta ggtgtgggggg agcaagacttcc ttgggtgcggc cagcaacacg aataatgt 840
ccacctgggg agtacgttcg caagaatggaa actccaaaggat attgacgggg accccgcacaa 900
ggegtggagc atgtggtttta attcgaagca acgcgaagaa ccttacccgc tcttgacatc 960
ccgggtgaccgc gctgtatgc acgccttttcc ttccggacac cgggtacagg tggtgcattt 1020
ttgtcgatcg ctccgtgtcgat gagatgttttgc gtagtgcggc gcaacggcgg caaccctt 1080
cttcagtagc cagcaatttcg gatggggact ctggagagac tgccggggat aacctggagg 1140
aagggtggggaa tgacgtcaaa tcacatgc ccttatgacg agggttacac acgtgttaca 1200
atggcgtaaa caaagggaag cgagcctgcg agggtaagca aatctcaaaa ataacgttcc 1260
agttcgatttgc atgtgtatgc actgactacta atgaaatgttgc aatcgtatg aatcgcgaaat 1320
cagcatgtcg cggtaatc gttccgggtt cttgtacaca ccggccgtca caccatggga 1380
gttggtaacgc cccgaaatgc gtagccaaatc cgttaaggagg gagctgcgcg aggtgggacc 1440
gataactggg gtg 1453
```

```
SEQ ID NO: 115 moltype = AA length = 477
FEATURE Location/Qualifiers
REGION 1..477
note = misc_feature - Tryptophan decarboxylase (EC
4.1.1.105) Ruminococcus gnavus HB-40
source 1..477
mol_type = protein
organism = Ruminococcus gnavus
```

```
SEQUENCE: 115
MIGTEYILNS TQLEEAIKSF VHDFAEKHE IHDQPVVVEA KEHQEDKIKQ IKIPEKGRPV 60
NEVVSEMMNE VYRYRGDAH PRFFSFVPGP ASSVSWLGDII MTSAYNIHAG GSKLAPMVNC 120
IEQEVLWLA KQVGTGNPG GVVFVSGGMSA NITALTAARD NKLTDINLHL GTAYISDQTH 180
SSVAKGLRII GITDSRIRRI PTNSHFQMDT AKLEEVIEAD KKSGYIPFVV IGTAGTTNTG 240
SIDPLTEISA LCKKHDMWFH IDGAYGASVLLSPKYKSLLN GTELADSIW DAHKWLFLQTY 300
GCAMVLVKDI RNLFHSFHVN PEYLKDLEND IDNVNTWDIG MELTRPARGL KLWLTQVLG 360
SDLIGSAIEH GFQLAVWAEE ALNSKKDWEI VSPAQMAMIN FRYAPKDLTK EEQDILNEKI 420
SHRILESGYA AIFTTVLNGK TVLRICAIHP EATQEDMQHT IDLLDQYGRE IYTEMKG 477
```

```
SEQ ID NO: 116 moltype = AA length = 477
FEATURE Location/Qualifiers
REGION 1..477
note = misc_feature - Tryptophan decarboxylase (EC
4.1.1.105) Ruminococcus gnavus HB-516
source 1..477
mol_type = protein
organism = Ruminococcus gnavus
```

```
SEQUENCE: 116
MIGTEYILNS TQLEEAIKSF VHDFAEKHK IHDQPVVVEA KEHQEDKIKQ IKIPEKGRPV 60
NEVVSEMMNE VYRYRGDAH PRFFSFVPGP ASSVSWLGDII MTSAYNIHAG GSKLAPMVNC 120
IEQEVLWLA KQVGTGNPG GVVFVSGGMSA NITALTAARD NKLTDINLHL GTAYISDQTH 180
SSVAKGLRII GITDSRIRRI PTNSHFQMDT AKLEEVIEAD KKSGYIPFVV IGTAGTTNTG 240
SIDPLTEISA LCKKHDMWFH IDGAYGASVLLSPKYKSLLN GTELADSIW DAHKWLFLQTY 300
GCAMVLVKDI RNLFHSFHVN PEYLKDLEND IDNVNTWDIG MELTRPARGL KLWLTQVLG 360
SDLIGSAIEH GFQLAVWAEE ALNSKKDWEI VSPAQMAMIN FRYAPKDLTK EEQDILNEKI 420
SHRILESGYA AIFTTVLNGK TVLRICAIHP EATQEDMQHT IDLLDQYGRE IYTEMKG 477
```

```
SEQ ID NO: 117 moltype = AA length = 490
```

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| FEATURE REGION | Location/Qualifiers |
|--|---|
| | 1..490 |
| | note = misc_feature - Tryptophan decarboxylase (EC 4.1.1.105) Ruminococcus gnavus ATCC 29149 |
| source | 1..490 |
| | mol_type = protein |
| | organism = Ruminococcus gnavus |
| SEQUENCE: 117 | |
| MSQVIKKR NTFMIGTEYIL NSTQLEEAIK SFVHDFCAEK HEIHDQPVV EAKEHQEDKI | 60 |
| KQIKIPEKGR PVNEVSEMM NEVRYRGRDA NHPRFFFSFVP GPASSVSWLG DIMITSAYNIH | 120 |
| AGGSKLAPMV NCIEQEVLKW LAKQVGFEN PGGVFVSGGS MANITALAA RDNLKTDINL | 180 |
| HIGTAYISDQ THSSVAKGLR IIGITDSRIR RIPTNSHQM DTTKLEEAIE TDJKSGYIPF | 240 |
| VVIGTAGTTN TGSIDPLTEI SALCKKHDMW FHIDGAYGAS VLLSPKYKSL LTGTGLADSI | 300 |
| SWDAHKWLFO TYGCAMVLV DIRNLFHSHF VNPEYFLKDLE NDIDVNNTWD IGMELTRPAR | 360 |
| GLKLWLTLQV LGSDLIGSAI EHGFQALAVWA EEALNPKKDW EIVSPAQMAM INFYRAPKDL | 420 |
| TKEEQDILNE KISHRILESG YAAIFTTVLN GKTVLRICAI HPEATQEDMQ HTIDLDDQYG | 480 |
| REIYTEMKKA | 490 |
| SEQ ID NO: 118 | moltype = AA length = 477 |
| FEATURE REGION | Location/Qualifiers |
| | 1..477 |
| | note = misc_feature - Tryptophan decarboxylase (EC 4.1.1.105) Enterocloster lavalensis (Clostridium lavalense) HB452c |
| source | 1..477 |
| | mol_type = protein |
| | organism = Enterocloster lavalensis |
| SEQUENCE: 118 | |
| MDSFMEAQTQ RAGELMERFI GQTLDFYENI KREDVFRKAD GAAISRLKK GIPQKGRPVD | 60 |
| EYVREMMDDV YANTSIVQHP RCFACIPSPV SLEFSWMGDVM TNAFDPHAGC VMNASAAGCI | 120 |
| ERELIRWMCG LAGYPKGCG LFVSGGSMAN LTALTAARDL RLTEAERALA VAYVSDQTHS | 180 |
| STAKGLHIG PRADQVRKIP SDTNFCMDME TLRAAVRADL AAGRKPFAVI ATAGTTNTGS | 240 |
| VDPLPEIAEI CRTYGMWMHV DGAFGASILL SSNERKRLDG IEYSDLSWD AHKWLQTYG | 300 |
| CSMVLVRDQS HLVRSPFAVHP EYLTDAGAFN EADPFWDLGP ELTRPARSLK LWITLQVMGS | 360 |
| EAMGQMIDHG CAMARLTEL IRRYPGWEIV SPARLGIVNF RCAPVNIPPS RIDRLNQDIA | 420 |
| REVTDSGYAQ ILTTELNGKR VLRCMTHPE TTEEDIRNTV RLLCESRAAS MGQCRTA | 477 |
| SEQ ID NO: 119 | moltype = AA length = 610 |
| FEATURE REGION | Location/Qualifiers |
| | 1..610 |
| | note = misc_feature - Tryptophan decarboxylase (EC 4.1.1.105) Enterococcus durans HB-48 |
| source | 1..610 |
| | mol_type = protein |
| | organism = Enterococcus durans |
| SEQUENCE: 119 | |
| MKDMDIKAVF IGDKAENGAV YKMLLNKMVD EHLGWRENYL PGDLPAISEE DKLAPRYIAT | 60 |
| RERMMVTLDE VSERMRAGSI PWHSAGRYWG QMNAETLMPM LLAYNYAMLW NPNNVALESS | 120 |
| MATSQMEADEV QODFADLFNM TDGWHITAD GS1ANLEGLW YARCIKSIPL AVKEVPEKV | 180 |
| ENKTEWELLN LSVEEILEMI EKFTDEELDA VKAASSRSKG HIQELGKWLW PQTKHYSWMK | 240 |
| ALDICGVGLD QMIAIIPVQED YRMDVAELEK TIRELAEQK1 PILGVVAVVG TTEEQQVDSV | 300 |
| DKIVELREKLQ YRGEIYFYLH DVAAYGGYAR SLFLNEAGEF VPYESLTEFF EEHQVFHQV | 360 |
| KIDKSVYDGF KAITEADSVI IDPHKMGYVP YAAGGIVIKH KNMRNIISYY APYVFEKSVK | 420 |
| APDMLGAYIL EGSKAGATAA AWVTAHRVLP LNVTYGYQLI GASIEAAQRF REFLGQLSFT | 480 |
| VIGKTIEVHP LNHPDPNMFD WVFVKVQDCTD LKKINDLNEK MPDVSSYMDG DVYDERFIT | 540 |
| HTTFTKADYG DSPVKFIESL GLSKEEWQKE QQVTLLRAAI MTPYLNDDKI FKFYTDAITK | 600 |
| AIEKKLNELL | 610 |
| SEQ ID NO: 120 | moltype = AA length = 285 |
| FEATURE REGION | Location/Qualifiers |
| | 1..285 |
| | note = misc_feature - Putative Tryptophan hydroxylase (EC 1.14.16.4) Ruminococcus gnavus HB-40 |
| source | 1..285 |
| | mol_type = protein |
| | organism = Ruminococcus gnavus |
| SEQUENCE: 120 | |
| MGLGLRYKNE EQIFQEQYTE PPYLEYPMFR ETGIVKHGFS TRIGGVSKGC FSSLNLSTFR | 60 |
| GDEEEAVREN PRRIGSAMGI RCEDMVFTHQ THTINVRRVTT EADRGCGIVK PRTYSVDVGL | 120 |
| VTDIPGICLV TFYADCVPLY FVDPVKVIG LSHSGWRGTV GKIGKVTVET MCREFKSRPE | 180 |
| DILAAVGPSI CQDCYEVSED VIROFRKNFPF EDCWDALFYQ KENQKYQLNL WKANELIFRE | 240 |
| AGILPEHIAV TNLCTHCNSE ILYSHRQAGD ARGNLCAFLA LDQEV | 285 |
| SEQ ID NO: 121 | moltype = AA length = 324 |
| FEATURE REGION | Location/Qualifiers |
| | 1..324 |

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note = misc_feature - Putative Tryptophan hydroxylase (EC
      1.14.16.4) Enterococcus durans HB-48
source 1..324
mol_type = protein
organism = Enterococcus durans

SEQUENCE: 121
MDTQIRGIHH VTAMTSSATK IYRFFTDILG MRLVKKTVNQ DDIETYHLYF TDEHGAPGTD 60
MTFDDFPNQA KGKKRTDTIS RASFRVPNDE ALTFWLERFE KYGITHSEIK ERFSKKYLEF 120
EDFDSDQAYQL ISDENNHGIA SGIPWKNSNV PSKYGITGLG PVFVRVKNLD HIRVILENIL 180
GFKETAHADA FYQFEVGEGG NGASIIIEHR TDLPDAIEGF GNIHHHLALRV ADKEALEHWI 240
RLINKVLDPLN SGFVDRFYFQ SEYFLAASHV LFELATDPGF FFGDEPTETA GEILSLPPFL 300
EKKRAEIEEY VRPFDTSDAN KKRE 324

SEQ ID NO: 122      moltype = AA length = 95
FEATURE Location/Qualifiers
REGION 1..95
note = misc_feature - Putative Tryptophan hydroxylase (EC
      1.14.16.4) Enterococcus durans HB-48
source 1..95
mol_type = protein
organism = Enterococcus durans

SEQUENCE: 122
MIVINAKFSI KPEKRNEFLA EVKNLIEATK KEDGCLSYKL FESIDTENEF VMIENWRDQQ 60
AVEGHNQSPL LQKLFHSMPE YSSKSEIVV SKTID 95

SEQ ID NO: 123      moltype = AA length = 288
FEATURE Location/Qualifiers
REGION 1..288
note = misc_feature - Putative Tryptophan hydroxylase (EC
      1.14.16.4) Enterocloster lavalensis (Clostridium
      lavalense) HB452c
source 1..288
mol_type = protein
organism = Enterocloster lavalensis

SEQUENCE: 123
MKIQWKYKND LEIFETKGQE STPYLSFRAL DLLGMVKNGF STRMGGASRG KFATMNFSYS 60
RGDDPDHVLE NFTRMAAALG VERDRMVASY QTHTTNVRRT TEEDLGKGVV RTRDYRDVG 120
LTINLPGVTL VFIFYADCVPL YLVPDKVKAI GLSHSGWRGT VARMGRETVE AMKREFGTDP 180
GDLVACIGPS ICEDCFEVGG EVVEAFQCQAF APEQHPALFR QGVGPGKYQL DLWAANRIIL 240
KEAGVPAKQI HTTNICTKCN SDYLFSHRTV GEERGNLAAF LCLKGGAL 288

SEQ ID NO: 124      moltype = AA length = 493
FEATURE Location/Qualifiers
REGION 1..493
note = misc_feature - Putative Tryptophan hydroxylase (EC
      1.14.16.4) Bacillus velezensis SB-9
source 1..493
mol_type = protein
organism = Bacillus velezensis

SEQUENCE: 124
MKTQVAIIGG GPVGLMLASE LALAGVKTTV IERLKKTVPY SKALIMHprt LEFLFAMRGIL 60
ERFVDQGKTV SSGHFSMLDT RLDFSRLLDKT QNYSLMLPQA ETERMLEEYA SSLGANIIRG 120
AEAVAVQTQD DGVETVFRDE SGIGTLHSLY AAGTDGAGSI VRKQAGIAFS GTDADLTGTL 180
CDAALKHPPF SSFFSTCRLE GSVVIPLTD GLFRVLIVSP HPVQKRKEER VTEDELKEDL 240
RRICGTDFGL SDPVWMSRFG NAERQAEQYR SGRIFVAGDA AHIHFPAAGGQ GLNTGLQDAV 300
NLGWKLAAQM KGKAAPHLLD SYHQRHSTG KEVLHNKIQTQ IKLMDFTESG MALRETMAL 360
LDFQESNRLL AGKVSALDLH YEPDAELPPH TLNGKRLPDI ELTLHDGRPA RLYDFLRKGG 420
FVLLSLRGSI PAGIDTDSVA AVRAELAETR ADWNDVHTVL IRPDGHAAWA AGGSGREAAEE 480
AVLAGLERWG LFI 493

SEQ ID NO: 125      moltype = AA length = 482
FEATURE Location/Qualifiers
REGION 1..482
note = misc_feature - Putative Tryptophan hydroxylase (EC
      1.14.16.4) Bacillus velezensis SB-9
source 1..482
mol_type = protein
organism = Bacillus velezensis

SEQUENCE: 125
MMGIINGKMF IDRLNQLGNE IWLDGEKIEG QISEHPAFKG LLETKRSLYD LQTKPDMKDQ 60
MTYSLPGKKE RAGLSYLQPK TKDDVKRRRN MFEHWARHTH GMMGRSPDYM NTVLMFASS 120
AALLKDRHEC FPEHQVQALYE RAAAQDLSFT HTFIFTQVNVR SQMGVNVSPT PISAKVVDKN 180
EKGLIIHGCAR ILATQGLTD EVLVVSLPKM YFESDEAFAF SIPSNTKGVK FICRESFVLG 240
KSAFDYPPLSS RYEEMDSIVV FDHVLPWER VFFYNYYEAA FDFNMKSSFN AFAFHQVITR 300
QIVKTEFLLG LAQTLVEAID VGEYQHQAK MAEIITGLET MKALLEKSEN DAETDEWGYM 360
RPSVTPLRVC SAIFPDYIYPR FTEIIQLIGA SGMVTLPTEK AFRSDIRGDL DQYQLQAAELN 420

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|--|---|
| AEDRVKVFLR AWDLTMSPFG TRQTQYERYF FGDPVRLTSH LYRSYPKEEQ TAVIKEFLHI HK | 480 482 |
| | |
| SEQ ID NO: 126 | moltype = AA length = 373 |
| FEATURE | Location/Qualifiers |
| REGION | 1..373 |
| | note = misc_feature - Putative Tryptophan hydroxylase (EC 1.14.16.4) Chromobacterium sp. IIBBL 274-1 |
| source | 1..373 |
| | mol_type = protein |
| | organism = Chromobacterium sp. |
| SEQUENCE: 126 | |
| MKILVIGAGP AGLVFASQMK QARPQWTIDI VEKNDEQEVL GWGVVLPKGP GQHPANPLSY LDAPERLSPQ FLEEFKLVHH NEPSLMSTGV LLCGVERRGL VHALRKCRS QGISIRFESP LLERGELPLA DYDLVLLANG VNWKTSHFTE ALAPQVDYGR NKYIWYGTQS LFDQMNLVFR THGKDVFIAH AKYKSDTMSF VNVCESEETY ARTRLGEMSD EASAEVVAKV FQAEGLGGHGL ASQPGIGWRN FMTLSHDRCH DGKLVLLGDA LQSGHFSIGH GTTMAVVVAQ LLVKALCAED GVPAALRSFE ERALPLVQLF RGHADNSRVW FETVDERMH SSAEFVQSF DARRKSLPPMP EALAQNLRYA LQR | 60 120 180 240 300 360 373 |
| | |
| SEQ ID NO: 127 | moltype = AA length = 481 |
| FEATURE | Location/Qualifiers |
| REGION | 1..481 |
| | note = misc_feature - tr^A401WSJ6^A401WSJ6_ACEPA Aromatic-L-amino-acid decarboxylase OS=Acetobacter pasteurianus NBRC 3188 OX=1226663 GN=NBRC3188_0995 PE=3 SV=1 |
| source | 1..481 |
| | mol_type = protein |
| | organism = Acetobacter pasteurianus |
| SEQUENCE: 127 | |
| MAGLDPEPNWE ELRTLGHMRML DDMLESIKNV AKGPVWQPMP DTLRQNFKQA PLPHGAQPLE GLYEQFANTV QPYAVGNRHP RFMGWVHGGG TAQGMLAEML AAGLNANLGG RNHAPVEVER MVIWRAAEMF GFPDTASGVL VTGSSMANFI AILTASRAVP DGTALREQGV AGRKLVGYAA QTAHGCVARA FDMAGLGMKA LRRVWDGAAF RMDMQALRRM VAQDRADGYE PFLVVGTTAGT VDTGSVDPLD ELADYAEAEK LWFHVVDGAFG ALAQLAPDYA PLLKGLERAD SLAFDFHKWA QVPYDAGCVL VREQGRQAAAT FAQSLAYLSR EDRGLAADAP WFCDFGPCLS RGFRALKVWF TLAGFGTEGL CNVVAQSCTV AQYLASRVVA TPGLTLLAPV TLNIVCFRVD MPDVGDLDTL NAELVKDLQE SGIAAPSTTR IHGKLAIRAA IVNHRTTTED ADIMLAGLAD MVQARLGRPL A | 60 120 180 240 300 360 420 480 481 |
| | |
| SEQ ID NO: 128 | moltype = AA length = 472 |
| FEATURE | Location/Qualifiers |
| REGION | 1..472 |
| | note = misc_feature - tr^A4P5SJ26^A4P5SJ26_9ACTN Aromatic-L-amino-acid decarboxylase OS=Actinobacteria bacterium OX=1883427 GN=LBMAG12_16630 PE=3 SV=1 |
| source | 1..472 |
| | mol_type = protein |
| | organism = Actinobacteria bacterium |
| SEQUENCE: 128 | |
| MDAQEFRANG QAVIELIAQY LETIEERPVT ADVKPGDVRH QLPAHPPTAP ESFESVLAADV SNIIVPGLTH WQHPNFFAFF PGNSYPSIL ADLLTAGLGV QGMSWLSSPA CTEVETLMLD WMQELLGLPE SFRSTTASGG GVIQGSASEA TLSSILAARW RITEGHVNRD GDTTKLIAYC TSQSHSSIEK GLRIAGIGTQ NIRIIEHDS FAMVADALEA QILADQAAGL IPFWVCSTHG TTSSGAFDPT SAIGAITQRH HLWLVHDAAAM HGIAALALAEY RWVNDGLELA DSYCTNPWKW MGVNFDCCDLF WTQDRASLLG ALSILPEYLR SAAAETGAII DYRDWQIPLG RRFRSLKLWF AIRCDGTAVF QEIIIRRHIQI TQEELADLVAQ DHRFEIMAPH PLNLLCIRLR GESPQDGAR TDALIEANA TRSVFFTTRTI LEGRSVLRFs IGGRTTHGQH ALSAWGLLRS FA | 60 120 180 240 300 360 420 472 |
| | |
| SEQ ID NO: 129 | moltype = AA length = 480 |
| FEATURE | Location/Qualifiers |
| REGION | 1..480 |
| | note = misc_feature - trDFJ0DFJ0_BACAT Aromatic-L-amino-acid decarboxylase OS=Bacillus atrophaeus OX=1452 PE=3 SV=1 |
| source | 1..480 |
| | mol_type = protein |
| | organism = Bacillus atrophaeus |
| SEQUENCE: 129 | |
| MSENLQLSAE EMRQLGYQAV DLIIDHMNHL KSKPVSETID SDILRNKLT SIPENGSDPK ELLHFLNRNV FNQITHVDHP HFLAFVPGPN NYGVVVADFL ASGFNVFTA WIAGAGAEQI ELTTINWLKS MLGFPDSAEG LFVSGGSMAN LTALTVAQRQA KLNNNDIENAV VYFSDQTHFS VDRALKVLGF KHHQICRIET DEHLRISVSA LKKQIKEDRT KGKKPFCVIA NAGTTNCGAV DSLNEELADLC NDEDVWLHAD GSYGAPAILS EKGSAMLQGI HRADSLTLDP HKWLFQPYDV GCVLIRNSQY LSKTFRMMPE YIKDSETNVE GEINFGECEGI ELSRRFRALK VWLSPKVFGV | 60 120 180 240 300 360 |

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| | |
|--|---|
| AAFRQAIIDHG IMLAEQVEAF LGKAKDWEVV TPAQLGIVTF RYIPSELAST DTINEINKKL | 420 |
| VEKEITHRGFA MLSTTELKEK VVIRLCSINP RTTTEEMLQI MMKIKALAEE VSISYPCVAE | 480 |
| | |
| SEQ ID NO: 130 | moltype = AA length = 454 |
| FEATURE | Location/Qualifiers |
| REGION | 1..454 |
| | note = misc_feature - tr^A136NI40^A136NI40_9BACT |
| | Aromatic-L-amino-acid decarboxylase OS=Bacteroidetes |
| | bacterium OLB10 OX=1617421 GN=UZ10_BCD003001760 PE=3 SV=1 |
| source | 1..454 |
| | mol_type = protein |
| | organism = Bacteroidetes bacterium |
| | |
| SEQUENCE: 130 | |
| MQBAERNIT DAVTSYTNHF IAGLKHKVKGF QQNELNSLAI DNKKKTIEEL LSIYQKEVAE | 60 |
| NGINAASGTH LGYIPGGVF TGAVADFIAA VTNPFAVYY ASPGAAMVEN EVVNWLKRVF | 120 |
| SFPESATGCL SSGGSISTLI AFTAARDHQ VKNERVRKSV VYLSQVHHS TQKALRIIGL | 180 |
| EDVLIRYVPL DSHHRIQVDA LEQLIAKDTA QGLIPFLIVA TAGTTDGAI DPLNDIADLA | 240 |
| KKYHTWPHVD AAYGGFFILT SRKSLFKGIE RADSMIVDPH KGMFLPYGVG AVLKDISH | 300 |
| LHSNYYEANY MQDAADELELA KSPANLSPPE TKHFRGLRVW LPLQYHGIEP FIACLEEKLL | 360 |
| LVKYFRQOLQ ERGFwigpep DLSVSYFRYP FEKDADRKNQ QLMNEIHADG DVFLSSSVIE | 420 |
| GKFVIRIAIL AFRTKKETVD RAVAMIERCL KKVK | 454 |
| | |
| SEQ ID NO: 131 | moltype = AA length = 461 |
| FEATURE | Location/Qualifiers |
| REGION | 1..461 |
| | note = misc_feature - tr^A1N7QKD0^A1N7QKD0_9RHOB |
| | Aromatic-L-amino-acid decarboxylase OS=Gemmobacter |
| | megaterium OX=1086013 GN=SAMN05421774_1143 PE=3 SV=1 |
| source | 1..461 |
| | mol_type = protein |
| | organism = Gemmobacter megaterium |
| | |
| SEQUENCE: 131 | |
| MNHDDDLRWDW KRAADWAHHY HAGLDRPVR ATIAPGSLRD ALPAAAPEAG EPMEQIWKDF | 60 |
| QALVPPDMTH WQHPRFFAYF PANAAPVSMI AEQLANAMAA QAMLWQTAPA ATEI EQAMMV | 120 |
| WLRKAIGLPA RFTGTIHDSA TSATLSAVLT MRERALGWWRG IAEGLSGAPR LRLYASAETH | 180 |
| SSVDKAARLA GIGQDNLVKV PTDASLMDP AALADAISAD RAAGALPIGV VICAGGTSVG | 240 |
| AFDRVGDVIA VARTEGLPTH VDAAWAGSAM ICPEFRALWA GVEGADSLVF NPHKWLGQF | 300 |
| DCAVQFIADP GAQIERTMGLR PTYLETLPDE EIVNFNEWTV PLGRRFRALK LWFLLRAHGL | 360 |
| EDLRQRIRNH VAWAHQARDA LAALPGVIEV TEPSLSSLFSF ALRDGDAATE ALLRRINDDG | 420 |
| RIYLTQTRHG GRYVIRVQVG AFDCTRADVE VIAQVQDLDL P | 461 |
| | |
| SEQ ID NO: 132 | moltype = AA length = 477 |
| FEATURE | Location/Qualifiers |
| REGION | 1..477 |
| | note = misc_feature - tr^A1R4J257^A1R4J257_9MICC |
| | Aromatic-L-amino-acid decarboxylase OS=Micrococcus lyliae |
| | OX=1273 GN=PM125_05970 PE=3 SV=1 |
| source | 1..477 |
| | mol_type = protein |
| | organism = Micrococcus lyliae |
| | |
| SEQUENCE: 132 | |
| MTPEEFRTHG HALIDIWADY RAALHERPVM SPLRPGEVAA QLPAAAPETG EDPATVLLADL | 60 |
| DRVILPGLSL WQHPEFFHFF PANAAELSSVL GDIASTGLGV LGLSWESSPA LSEVEIRTMD | 120 |
| WMRRLLGLSG AWRGVVQDSA SGCALTAMIE ARERASGFAM HAGGTDQGRD RMVYVCAAQA | 180 |
| HSSVPKAMLL AGFGRONVRE VPVDAFYAMD AQALRAIAVE DRAAGLRPAA VVATCGTTAT | 240 |
| TALDPLAEG RIAQDEDLWF HVDAAMAGSA MLLPECRWMM EGVELADSLV VNAHKWLGV | 300 |
| FDCSLFFFVKD PVFLEKVMAT HPSYLQSSH EDVNVLRDWG VPLGRRFRAL KLWFMRLMEG | 360 |
| AEALRARLRR LDNAAWLAA QVDAAEQWER VAPTPLQTVC VRHVPAGLDP ADPADTEAID | 420 |
| AHTRAWAQAV NASGKAAVSL ATLEGGRWMVR LSVGALGGTE REHVERLWKV LGEAVAR | 477 |
| | |
| SEQ ID NO: 133 | moltype = AA length = 470 |
| FEATURE | Location/Qualifiers |
| REGION | 1..470 |
| | note = misc_feature - tr^A059UV10^A059UV10_PSEPU |
| | Aromatic-L-amino-acid decarboxylase OS=Pseudomonas putida |
| | OX=303 GN=DW66_2355 PE=3 SV=1 |
| source | 1..470 |
| | mol_type = protein |
| | organism = Pseudomonas putida |
| | |
| SEQUENCE: 133 | |
| MTPEQFRQYG HQLIDLIADY RQTVGERPVM AQVEPGYLNKA ALPAQAPRQG EPFAAILDDV | 60 |
| NQLVMPGLSH WQHPDFYGYF PSNGTLSSVL GDFLSTGLGV LGLSWQSSPA LSELEETTLD | 120 |
| WLRQLLGLSG QWSGVIQDTA STSTLVALIC ARERASDYAL VRGGLQAQAK PLIVVVSABA | 180 |
| HSSVDKAALL AGFGRDNIRL IPTDERYALR PEALQVIAEQ DLAAGNQPCA VVATTGTTAT | 240 |
| TALDPLRPIG EIAQAHGLWL HVDSAMAGSA MILPECRWMM DGIELADSLV VNAHKWLGV | 300 |
| FDCSIYYVRD PQHLIRVMST NPSYLSQSAVD GEVKNLRDWG IPLGRRFRAL KLWFMRLSEG | 360 |

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|---|-----|
| VEALQARLRR DLDNAQWLAG QIGAAAEWEV LAPVQLQTLC IRHRPAGLEG EALDAHTKGW | 420 |
| AEERLNASGDA YTPTPATLDGR WMVRVSIGAL PTEREHVBOQ WARLQEVVKG | 470 |

| | |
|--|--|
| SEQ ID NO: 134 | moltype = AA length = 962 |
| FEATURE | Location/Qualifiers |
| REGION | 1..962 |
| | note = misc_feature - trNN89NN89_9PROT Steroid C25 |
| | dehydrogenase alpha subunit OS=Sterolibacterium |
| | denitrificans OX=157592 GN=s25dA PE=3 SV=1 |
| source | 1..962 |
| | mol_type = protein |
| | organism = Sterolibacterium denitrificans |
| SEQUENCE: 134 | |
| MQISRROFIV GSAVAAGLG LYSLRPKHVV PAAPRPADKP GIPAKKVYN DYSDIWRKEW | 60 |
| KWDRVVKGTH TRANCIGACIS WDYYVKDGIW WREEQAAIYE PHRPDIPDFN PRGCQKGACY | 120 |
| THLQVNESRI KYPLKRVGER GEGKWKRITW DEALTEIADK LIDAAVAEGT ESIIFFDDGTT | 180 |
| NAGYGPETAG DVFATLSQT TKIDSWAGVS DMPMGLVQWT GMYNCEGTSD DWFRSDYIVI | 240 |
| WVGNPIYTRI PEAHFLHEAR YRGAKLWVIA PDLNPSVTWA DTWLKINPET DAALGLAAAO | 300 |
| VMITENLIKK DYVLEQTDMP FLVRKDDDKRF LRGADMVKGG ADNAVYIWDE AKQAAVAVPG | 360 |
| CEDGEGGGRS LKLNGIKPAL SGTFTVKLAN GESVEVHTVF DMLKEKLDT EYTPELAEKV | 420 |
| GIHPNVIRTF AREMAAAPNA MIYCSWGAACK HHHSDLYQRA MALLMTFTGN QGKPGSGV | 480 |
| AAWWGVGDME AMTAGLFSTM DKIKLIPKAI KGLTPRDYED LFIDISDREA NTPMIVFLYV | 540 |
| HGGYKEMWDK PHLQDPALPR NLAEMYRESI DKGWTKVYP ENRSPKAYIF TGCNPPLRRWP | 600 |
| SPQIAKVLW PKFDVVVSVR FMRSTSTMF A DVYLPVAGYV EKYGIKYGS YVPYLITS | 660 |
| ATEPLGESKS DWEVFGLLSK TIAERAKARN IPPVRGFKDR PHDLTKVYDI HTENGLYDPT | 720 |
| HPEPDPKLLED AIFEQPSPLG ANSGREALEM GAVPIISTGR PSLIYQNYTD YDPKDTHWPH | 780 |
| GDFVTKKTAW PTLTGRQQFY IDHPWFLEGG ESLPTHKPP HAGSKYPLRI YGGHNRWSIH | 840 |
| AIWRDVKLLL RLQRGQPACW LNPLEAEKRG IKDGDMLRY NHHGEFECMV KVAPITAPGE | 900 |
| VIVYHAWEPY QFKNWKGQNQE PAEAPWKALH LAGGYHQIHY RMYYGGPSHA PRGVPIEIEK | 960 |
| VK | 962 |

| | |
|--|--|
| SEQ ID NO: 135 | moltype = AA length = 256 |
| FEATURE | Location/Qualifiers |
| REGION | 1..256 |
| | note = misc_feature - tr^A2N0V092^A2N0V092_9FIRM |
| | Tryptophan synthase alpha chain OS=Ruminococcus bromii |
| | OX=40518 GN=trpA PE=3 SV=1 |
| source | 1..256 |
| | mol_type = protein |
| | organism = Ruminococcus bromii |
| SEQUENCE: 135 | |
| MTDIKSFAQN GKAFIPFVTA GDPDLETTEK LLIEMSKNGA DIIIEIGIPFS DPTAEGVVIQ | 60 |
| EADLRSLSAG TTTDKIFDMV KRIRPQIDAV LAVMTYMNPI FVYGTERFMA KCQECGISAV | 120 |
| IVPDTPYEEK HELTDYSGKY GIDVISLIAP TSHERIKMIA KEAEGFVYCV SSMGVTGVRS | 180 |
| ELTTDVGMV RLVKSVKDIP CAIGFGISTP EQAKKMSESA DGVIVGSAIV KIIAKYGD | 240 |
| VKPVCDYVKS MKEAIS | 256 |

| | |
|----------------|--|
| SEQ ID NO: 136 | moltype = AA length = 256 |
| FEATURE | Location/Qualifiers |
| REGION | 1..256 |
| | note = misc_feature - 136trPTA4PTA4_ACESD Tryptophan |
| | synthase alpha chain OS=Acetoanaerobium sticklandii |
| | (strain ATCC 12662 / DSM 519 / JCM 1433 / NCIMB 10654) |
| | OX=499177 GN=trpA PE=3 SV=1 |
| source | 1..256 |
| | mol_type = protein |
| | organism = Acetoanaerobium sticklandii |
| SEQUENCE: 136 | |

| | |
|---|-----|
| MNNIERVEKNN KKAFAIFITC ADPNLETTRE IIFELVKNGA DIIIELGIPFS DPTAEGEVIQ | 60 |
| SANTRALLNG VTTDEILDFV QEVKKNLSTV LVFMTYANVI FSYGAEKFKI RCSEIGIEGI | 120 |
| IVPDLPYEEK NEFYPFCKKY EVNLISMIAP TSEDRISMIA KEAEGFLYIV SSMGVTGERT | 180 |
| NITTDLKEII NIAKLNKDIP CAVGFGISTP SQVSKILEIA DGVIVGSAIV KIIEKHSINS | 240 |
| AKYVGEFVKQ MKSEIK | 256 |

| | |
|----------------|---|
| SEQ ID NO: 137 | moltype = AA length = 256 |
| FEATURE | Location/Qualifiers |
| REGION | 1..256 |
| | note = misc_feature - tr[D6]D4J0[D6]D4J0_9BACE Tryptophan |
| | synthase alpha chain OS=Bacteroides xylanisolvens XB1A |
| | OX=657309 GN=trpA PE=3 SV=1 |
| source | 1..256 |
| | mol_type = protein |
| | organism = Bacteroides xylanisolvens |
| SEQUENCE: 137 | |

| | |
|--|-----|
| MNRINQLFNS NKKDILSIYF CAGTPTLGDT ANVIRITLEKH GVSMIEIGIP FSDPMADGIV | 60 |
| IQNAATQALR NGMSLKLLFE QLDIRKDVK IPLVFMGYLN PIMQFGFENF CRKCVECGID | 120 |

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|--|--|
| SEQ ID NO: 138 | moltype = AA length = 250 |
| FEATURE | Location/Qualifiers |
| REGION | 1..250 |
| | note = misc_feature - tr^A367CA00^A367CA00_9ENTE |
| | Tryptophan synthase alpha chain OS=Enterococcus durans |
| | OX=53345 GN=trpA PE=3 SV=1 |
| source | 1..250 |
| | mol_type = protein |
| | organism = Enterococcus durans |
| SEQUENCE: 138 | |
| MPKPLTYLЕН QTTKPLFIPY IMAGAQGLEH LPEEIEMLAK SGATAIELGI PFSDPVADGP 60 | |
| IIQEAGLNAF KHQVTLKKII AVLQDYHSPV PLILMGYSNS FFHYGVKQLV DDLKDCHVQG 120 | |
| VIIPDLPYEH RDLVLPDLGD IALIQLVSLT SPSERIDTLV KEAEGFIYAV TINGTTGVNK 180 | |
| TYQONLTEHL KEIKEKSAIP VLAGFGISKA EHVRRAFQCC DGVVVGSKIV HSLQVDGLTK 240 | |
| TQELIGELLR 250 | |
| SEQ ID NO: 139 | moltype = AA length = 291 |
| FEATURE | Location/Qualifiers |
| REGION | 1..291 |
| | note = misc_feature - tr.A1I9.A1I9_BIFAA Tryptophan |
| | synthase alpha chain OS=Bifidobacterium adolescentis |
| | (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a) |
| | OX=367928 GN=trpA PE=3 SV=1 |
| source | 1..291 |
| | mol_type = protein |
| | organism = Bifidobacterium adolescentis |
| SEQUENCE: 139 | |
| MNTATSTSPTP GQPLGISHKP SPTETMFDEF KAADKPAFIG YLPYGFPPDPD YSLKAFRTMV 60 | |
| EHGVAVEIG LPYSDPVMGD PVIQAASQIA IDNGEKIANV FKAVETVANA GGVLVMSYW 120 | |
| NLIFHYGVER FARDFENAGG AGLITPDLIP DEAGEWIEAS DRHGLDRIFL VSPDSTEDRL 180 | |
| KVADNARGF VYAAARMGVT GERSTIDASP KELVARTRKA GAKNVCVGIG VSTAEQGARV 240 | |
| GSYADGVIVG SALVHTMIDE SGKHAVDEAT GLKALAAKTE ELAEIGHNR N 291 | |
| SEQ ID NO: 140 | moltype = AA length = 394 |
| FEATURE | Location/Qualifiers |
| REGION | 1..394 |
| | note = misc_feature - tr^A413K7N7^A413K7N7_9FIRM |
| | Tryptophan synthase beta chain OS=Ruminococcus bromii |
| | OX=40518 GN=trpB PE=3 SV=1 |
| source | 1..394 |
| | mol_type = protein |
| | organism = Ruminococcus bromii |
| SEQUENCE: 140 | |
| MTYGKFGIWG GQFVPETLMN AINEFEEAYN RYKDDPEFVA ELDTLMREYA GRPSLLYYAE 60 | |
| KMTKDLGGAK IYLKREDLNH TGSHKLNNCL GQCLLAKERMG KTRVIAETGA GQHGVTATAV 120 | |
| AALLGLECEI FMGKEDTIRQ ALNVYRMKLL GAKVNAVETG TMTLKDAVNE AMREWTRNRS 180 | |
| DTHYVLMGSV GPHPFPTVVE DFQSVIGKEI KSQMLEKEGR LPDVVMACVG GGSNAMGAFY 240 | |
| EPIKDENVKL IGCEAAGLGT DTPKTAATIA TGTLGIFHGM KSYFCQNEYG QIAPVYSISA 300 | |
| GLDYPGIGPE HANLADTGRA SYVPTDEEA VNafeYLSRT EGIPIAIESA HAVAHCICKIA 360 | |
| PTMDKDKIIV VNLSGRGDKD VAAIARYRG E DLHD 394 | |
| SEQ ID NO: 141 | moltype = AA length = 395 |
| FEATURE | Location/Qualifiers |
| REGION | 1..395 |
| | note = misc_feature - trPT95PT95_ACESD Tryptophan |
| | synthase beta chain OS=Acetoanaerobium sticklandii (strain |
| | ATCC 12662 / DSM 519 / JCM 1433 / NCIMB 10654) OX=499177 |
| | GN=trpB PE=3 SV=1 |
| source | 1..395 |
| | mol_type = protein |
| | organism = Acetoanaerobium sticklandii |
| SEQUENCE: 141 | |
| MERNNGYFGQ FGGAFVPEEL KNVLKDVEEA FYKYIEDEF LSELAYYQRQ YIGRENPLYL 60 | |
| AKRLSEQLGG AKIYLKREDL NHTGAHKINN AMQGVLLAKR MGKKRIIAET GAGQHGVTATA 120 | |
| TCALMGLEC IIYMGAIK RQELNVFRME MLGAKVVPVT TGTATLKDAV DEALADFVAN 180 | |
| AHDFTYLLGS AVGPHPYPTM VREFQSVIGK EARKQILEVE GKLPDYIVAC VGGGSNAIGL 240 | |
| FAPFVDDLSV KIVGVEPGGE GLDTNEHAAS ISKGSGVVIH GFKCYTLQDE NGEPLPVHSI 300 | |
| AAGLDYPGVG PEHSYYKESN RAEYIAITDD EAMQAFFLLS RTEGIIPAIE SAHAVAYAVK 360 | |
| LAATLSSLKDQT IIVNLNSGRGD KDVNQVKEMN LLDKN 395 | |
| SEQ ID NO: 142 | moltype = AA length = 395 |
| FEATURE | Location/Qualifiers |

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| | |
|--|---|
| REGION | 1..395 |
| | note = misc_feature - tr[D6]D4J6[D6]D4J6_9BACE Tryptophan synthase beta chain OS=Bacteroides xylosoisolvans XB1A OX=657309 GN=trpB PE=3 SV=1 |
| source | 1..395 |
| | mol_type = protein |
| | organism = Bacteroides xylosoisolvans |
| SEQUENCE: 142 | |
| MKSFLVDQDG YYGEFGGAYV PEILHKCVEE LTNKYLEVIE SEDFKKEFDQ LLRDYVGGRPS | 60 |
| PLYLAKRLSE KYGCKLYLKR EDLNHTGAHK INNTIGQILL ARRMGKKRII AETGAGQHGV | 120 |
| ATATVCALMD MECIVYMGKT DVERQHINVE PVTSGNMMLK DATNEAIRDW | 180 |
| CCHPADTYII IGSTVGHPHY PDMVARLQSV ISEBIKKQLQ EKEGRDYPDY LIACVGGGSN | 240 |
| AAGTIYHYIN DERVGILAE AGGKGietGM TAATIQLGM GIIHGARTYV IQNEDGQIEE | 300 |
| PYSISAGLDY PGIGPIHANL AAQSRANVL INDEAIEAA YELTKLEGII PALESAHALG | 360 |
| ALKKLKFKE DIVVLTVSQR GDKDIETYLS FNEQL | 395 |
| SEQ ID NO: 143 | moltype = AA length = 395 |
| FEATURE | Location/Qualifiers |
| REGION | 1..395 |
| | note = misc_feature - tr^A367CAD3^A367CAD3_9ENTE Tryptophan synthase beta chain OS=Enterococcus durans OX=53345 GN=trpB PE=3 SV=1 |
| source | 1..395 |
| | mol_type = protein |
| | organism = Enterococcus durans |
| SEQUENCE: 143 | |
| MYQQPNBQGF YYGEFGGQFV ETLMYAVKEL TETYEEETKTD EEFQKEFAYV LKQVVGREN | 60 |
| LYPAQRLEH LGGAKIYLKR EDLNHTGAHK INNALGQVLL AKRMGKKVV AETGAGQHGV | 120 |
| ATATAAAALFG MECTIFMGEI DVKRQELNVF RMELLGAKVV SVTSGSKTLK DAVNEALRYW | 180 |
| VEHVVEDTHYV MGGSVILGPHPF PEIVRVDYQSV IGTTEARRQIL EAEGRLPDVA IACIGGGSNS | 240 |
| MGLFYPPFLND PVRLIGVEAS GHGLDTNEHA ASINKGSVGV LHGAKMHLQ DDDGQVIEAF | 300 |
| SISAGLDYPG ICPEHSYLYT SGRAEYAAIT DREAVEAPHL LSEKEGIIPA LESSHALAHV | 360 |
| MKLAPTMKAQ ELIVVCLSGR GDKDVQQIKE MEEQA | 395 |
| SEQ ID NO: 144 | moltype = AA length = 697 |
| FEATURE | Location/Qualifiers |
| REGION | 1..697 |
| | note = misc_feature - tr_A1I8.A1I8_BIFAA Multifunctional fusion protein OS=Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a) OX=367928 GN=trpBC PE=3 SV=1 |
| source | 1..697 |
| | mol_type = protein |
| | organism = Bifidobacterium adolescentis |
| SEQUENCE: 144 | |
| MSVLDDELVAG AVEDQRSREN NVPLAEVKRM AFEASAPIDA RQWLKKADGI PVIAEIKRAS | 60 |
| PSKGHLSDIP DPAALAREYE QGGASAISVL TEGRRFLGSSL EDFDKVRAAV RIPVLRKDFI | 120 |
| VTEYQIWEAR AHGADLVLLI VAALDDVULKL SLDDLHSLN MTVLVETHTR EEIQRRAINAG | 180 |
| AKVIGINARN LKDLKVDVNK YNELAADLPD DVIRVAESGV FGSVELEDYA RAGADAVLVG | 240 |
| EGVATAANHE QAVERLVKAG ARVKASEQTP LASHEGPYFG QFGGRYVPEA LITALDELER | 300 |
| VTEAKADPE PHKELARLNQ QYVGRPSPLT EAPRFAQRNLK EKTGLDARVE LKREDLNHTG | 360 |
| AHKINNALGQ ALLVKRMGKT RVIAETGAGQ HGVTATVCA MLGLKCRIM QOIDARRQAL | 420 |
| NVARMRMLGA EVVEVTLGDE ILKDAINEAL RDWVTVNKDT HYLLGTVAGH HPFPMVRDF | 480 |
| QKIIIGEEAKQ QLQDWYGIDH PDAICACVGG GSNAIGIMNA FLDDERVNLY GYEAGGNP | 540 |
| SGRHAIKFAP CTGEGLGMFQG AKSYLLENPE GOTLDTYSIS AGLDYASVGP EHAWLKDIGR | 600 |
| VNYSWATDQE AMSAFKDLCE TEGIIPAIIES SHAVAGAYKA AADLAKAKGYE HPVMIINISG | 660 |
| RGDKDMNTAG KWFGYLTDEQ AKALESNQGA GNNADGE | 697 |
| SEQ ID NO: 145 | moltype = AA length = 260 |
| FEATURE | Location/Qualifiers |
| REGION | 1..260 |
| | note = misc_feature - tr^A2N0UX30^A2N0UX30_9FIRM Indole-3-glycerol phosphate synthase OS=Ruminococcus bromii OX=40518 GN=trpC PE=3 SV=1 |
| source | 1..260 |
| | mol_type = protein |
| | organism = Ruminococcus bromii |
| SEQUENCE: 145 | |
| MILETTIADAN RVRYEEIEKQ VPLEVIKQKA LSMETDNEFP FEKALAGKDI SFICEVKKAS | 60 |
| PSKGIIAEDF PYVQIAKDYE NAGASAISVL TEPKWFKGEN AFLEEISKNV SIPLLRKDFT | 120 |
| VCEYQIYEAK TIGASAVLLI CSLLDDTIR RWIKLCDSLG LSALVEAHTA DEVYSAIAAG | 180 |
| ARIVIGVNNRN LRDFTVDINN CTKLRLVPD NIIFVAESGI KTRDDIKVLE NAGVNAVLIG | 240 |
| ETLMRNPDKK AALDELSGRK | 260 |
| SEQ ID NO: 146 | moltype = AA length = 262 |
| FEATURE | Location/Qualifiers |

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REGION          1..262
note = misc_feature - trPTA8PTA8_ACESD
Indole-3-glycerol phosphate synthase OS=Acetoanaerobium
sticklandii (strain ATCC 12662 / DSM 519 / JCM 1433 /
NCIMB 10654) OX=499177 GN=trpC PE=3 SV=1
source          1..262
mol_type = protein
organism = Acetoanaerobium sticklandii
SEQUENCE: 146
MNNILKEIVG YTAKFRIEDEEK MKISLEKTIE LAFSIQTESN FRFENALKTK EISLICECKK 60
ASPSMGIIDY NYNYINIARE YEASGASCIS VLTEPKWMG SDDHLVDVVK NVSIPCIRKD 120
FIVDEYMIYQ SKIIGASAVAL LICSVLSDKS LRRLYLRICQD LGLSALVEHV TENEIDIALE 180
VGARIIGVNN RNLKDFSVDI RTSERLRKVV PSDVLFVSES GIKTESDVRR LIEIGVDAML 240
IGEAFMKSND KSKLIDSWRG KK 262

SEQ ID NO: 147      moltype = AA length = 260
FEATURE          Location/Qualifiers
REGION           1..260
note = misc_feature - trUUT1UUT1_9BACE
Indole-3-glycerol phosphate synthase OS=Bacteroides
xylanisolvens CL03T12C04 OX=997892 GN=trpC PE=3 SV=1
source          1..260
mol_type = protein
organism = Bacteroides xylanisolvens
SEQUENCE: 147
MDILSEIIIA NKRFEVDLQK QAISIEQLQE GISESPTLRS MKQALASSAS GIIAEFKRRS 60
PSKGWIQEEA CPEEIVPSYA AAGASALSIL TDEKFFGGSL KDIREARPVL EIPILRKDFI 120
IDEBYQLYQAK IVGADAVLLI AAALPEPKCN ELAEKAHELG MEVLLIEHSS EELAYINKGI 180
DMVGINNRNL GTFFTDVENS FRLAGQLPD SVLVSESGIS DPEIVKRLRA AGFRGFLIGE 240
TFMKTQRPGE TLQNFLQAIQ 260

SEQ ID NO: 148      moltype = AA length = 252
FEATURE          Location/Qualifiers
REGION           1..252
note = misc_feature - tr^A367CBM8^A367CBM8_9ENTE
Indole-3-glycerol phosphate synthase OS=Enterococcus
durans OX=53345 GN=trpC PE=3 SV=1
source          1..252
mol_type = protein
organism = Enterococcus durans
SEQUENCE: 148
MDFLEKILKE KANEVNNLTP VEKRVEKQRP SFYQTVKGNP KKVHIIIGEIK RASPSKGLIN 60
GTVDILQOAK TYEKSGVSAI SVLTDPVFFN GTIHDLTAVA QVVDVPVLCK DFIIDEQQIV 120
RAKQAGASLI LLIVAALPKV RLKELHEYAT ELGLEVLVET HDAQELAIAK EIGATIIGVN 180
NRNLKTRQVS LQTSIDLSPQ EGQCIYISES GFKTAQDVEK ISQNYQGILV GETLMRAGNV 240
EEKVKELQVS RR 252

SEQ ID NO: 149      moltype = AA length = 336
FEATURE          Location/Qualifiers
REGION           1..336
note = misc_feature - tr^A2NOV079^A2NOV079_9FIRM
Anthranilate phosphoribosyltransferase OS=Ruminococcus
bromii OX=40518 GN=trpD PE=3 SV=1
source          1..336
mol_type = protein
organism = Ruminococcus bromii
SEQUENCE: 149
MIKEAIKKLV AGNDLTFDEA AQVMDEMFSQ TATQSQMAAY LTALRIKGET IDEITASAQV 60
MREKALHIKP NRDVLDIVGT GGDGTGTFNI STTAAFTIAA AGIPVAKHGN RSMSSKSGSA 120
DCLEQLGINI NITPEKAVLW LNKAGACMF AQGYHSSMKY VGPVKEIGI RNIFNVLGPL 180
TNPAGADLQV TGVYSEALVE PIAQVFSNLG VKKGYVFYGM DGMDEVTLTT TTKVCEIDNG 240
KFNTFILNPE DYGLKLCAPE DLAGGDGKEN AEITKEILSG EIKDAKRDIV VLNAALGLCT 300
GGKADSIQDG IKLANEIIDS GKAYAKIEEF AKASNE 336

SEQ ID NO: 150      moltype = AA length = 338
FEATURE          Location/Qualifiers
REGION           1..338
note = misc_feature - trPTA9PTA9_ACESD Anthranilate
phosphoribosyltransferase OS=Acetoanaerobium sticklandii
(strain ATCC 12662 / DSM 519 / JCM 1433 / NCIMB 10654)
OX=499177 GN=trpD PE=3 SV=1
source          1..338
mol_type = protein
organism = Acetoanaerobium sticklandii
SEQUENCE: 150
MIKDVIKLV NKQDISYQET YEVISQIISG KSTMVQNAAF LTALSTKNTK SETIEEILGA 60

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|--|--|
| ALAVRDNALE IKHDMEVLDI VGTGGDNSGS FNISTTSAAV LAAGGIKVAK HGNRAASSKC | 120 |
| GTADCLEAQN ININLSPPEK CTTLEEKIGIC FIFQAQNYHES MKNVAQVRKE LGFRTIFNVI | 180 |
| GPLANPSKPS IQFLGVYDES LVEPMAKVLA SLGVERGMVV YGHDKLDEIS ISSETTICEF | 240 |
| AGKQINKYLI KPEDFGLRRY KKEDIFGGNP KENADILKSI LEGEQGARRD IVSINAGACF | 300 |
| YSAGKVGSIS NGISLANQII DSGLALKKLE EFRKMSNE | 338 |
| SEQ ID NO: 151 | moltype = AA length = 331 |
| FEATURE | Location/Qualifiers |
| REGION | 1..331 |
| | note = misc_feature - tr[D4]VH46 [D4]VH46_9BACE Anthranilate |
| | phosphoribosyltransferase OS=Bacteroides xylinisolvans SD |
| | CC 1b OX=702447 GN=trpD PE=3 SV=1 |
| source | 1..331 |
| | mol_type = protein |
| | organism = Bacteroides xylinisolvans |
| SEQUENCE: 151 | |
| MKQILYKLFE HQYLGRDEAR TILQNIQAGK YNDVQVVASL I TVFLMRNISV EELCGFRDAL | 60 |
| LEMIRIPVDSL DFAPIDIVGT GGDGKNTFNII STASCFVAG AGFPVVKHGN YGATSVGAS | 120 |
| NVMEQHQGVKF TSDVDQLRRS MEKCNCLAYLH APLFNPALKA VAPVVKGLAV RTFFNMGLGPL | 180 |
| VNPVLPAVQYL LGVYNLPPLL RLYTYTYQESK TKPAAVHSLS QYDEISLTNE FKVATSDHEK | 240 |
| IYTPESLGFS RYKDIDLDGG QTPEDAAKIF DHIMNNNTATE AQKNVVIVNS AFIAHVIRPE | 300 |
| KTIEECIALA KESLESGRAL ATLKKFIELN S | 331 |
| SEQ ID NO: 152 | moltype = AA length = 333 |
| FEATURE | Location/Qualifiers |
| REGION | 1..333 |
| | note = misc_feature - tr[A377L8Z1_A377L8Z1_9ENTE |
| | Anthranilate phosphoribosyltransferase OS=Enterococcus |
| | durans OX=53345 GN=trpD2 PE=3 SV=1 |
| source | 1..333 |
| | mol_type = protein |
| | organism = Enterococcus durans |
| SEQUENCE: 152 | |
| MQQLFERIYQ QKDLSQAEME QLATAMFDQE VTANQISGVL IGLKVKGAST EELTGLAHVM | 60 |
| QRRAPIPMKA PTGVMMDNCGT GGDHSQSPNI STTAAAFVLAG GGIPMAKHGN RSISSRSSGA | 120 |
| DVLEALGVTI TNSKEQIDHL LKNVGIAFLF APAMHPAMRA VMSVRKELAT PTIFNLIGGPL | 180 |
| INPYPLEYQL MGTYAGDSLA STAETLGKLG RKQALVLHGQ QGMDEANLGG KTHCAFYQSG | 240 |
| KVSEFSFSPE EVGLESPLPT AITGGDVQKN KEILLSVLKG EKTPYYETVL LNAGLGFLAG | 300 |
| AKVQSIREGI KEAEQVIQSG AAFDTLQNLN KEQ | 333 |
| SEQ ID NO: 153 | moltype = AA length = 377 |
| FEATURE | Location/Qualifiers |
| REGION | 1..377 |
| | note = misc_feature - tr,A267,A267_BIFAA Anthranilate |
| | phosphoribosyltransferase OS=Bifidobacterium adolescentis |
| | (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a) |
| | OX=367928 GN=trpD PE=3 SV=1 |
| source | 1..377 |
| | mol_type = protein |
| | organism = Bifidobacterium adolescentis |
| SEQUENCE: 153 | |
| MGERPIVTIG GIRTTIKACD SAKEGIMAEI TWKSILTKLV GGDHLSAEE EWFVDDLMNG | 60 |
| NADPAAVGAV LATQQQLGLT PDEVRGAAKA MVAHAIPLHI DGETTDIVGT GGDGASTVNL | 120 |
| SSMGAVVAAA AGVKVVKHGN RAASSKCGTA DCFEALGLPM DLTPEQVSEV GNECGIAFAF | 180 |
| ARTFHPAMRF VGPPIRAALGV PCVFNVLGPL TNPASPCKHMA VGCANRKMSPI MAAYVAANG | 240 |
| QIGMVYTSHE GLDEMAPTGP VSIWEFKDGK VTEKFDPVTI ELGLAKVTIA DLKGGEP TLN | 300 |
| AQLARDFFAG KDVSFRTTAL LNAASAIVAD GHLVPGDASL ADRFKAAAYA AEQTVDSGKA | 360 |
| TALLDKWIAT AQAAKKA | 377 |
| SEQ ID NO: 154 | moltype = AA length = 486 |
| FEATURE | Location/Qualifiers |
| REGION | 1..486 |
| | note = misc_feature - tr[A2NOULMO_A2NOULMO_9FIRM |
| | Anthranilate synthase component 1 OS=Ruminococcus bromii |
| | OX=40518 GN=trpE PE=3 SV=1 |
| source | 1..486 |
| | mol_type = protein |
| | organism = Ruminococcus bromii |
| SEQUENCE: 154 | |
| MIKPSYDEVL NLKDNYSVIP IYKEIYADAF TPINLLRKIA GKSDKFFLLE SIEGGEKWAR | 60 |
| YSFIGFNPKA RLSYKNGTLT VTGEGARVVK TAKPYDALRE YLADYKTPHF KDIPPTGGL | 120 |
| VGYFGYAMIS VAEPVRLKR GDTNDFDMLM FDKIIAYDH KKEKLIIVNM KTNDTKAQYE | 180 |
| LAKKDDIAII STITSPEPLP KLESDGNVEF TSTYSKEEFC KMVEKTKYEI FDGDIFQCVV | 240 |
| SRRFEADYKN SLINAYRVLR STNPSPYMVY MSIDGDEII TSPETLVKLQ NGVLNTFPPIA | 300 |
| GSRPRGKTD EDNALADELI HDEKLAEHN MLVDLGRNDI GKISEFNSVK VTKYQEVLRY | 360 |
| SKIMHICSEV EGKLKDGLDA FDAIESLLPA GTLSGAPKIR ACEIIEELER TPRGVYGGAL | 420 |

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|---|--|
| GYVDFNGNLD TCIAIRMAVK KNDKVYVQAG AGIVADSVPE SEYEETYNAK LAVMNAVKN | 480 |
| GEVNAL | 486 |
| SEQ ID NO: 155 | moltype = AA length = 484 |
| FEATURE | Location/Qualifiers |
| REGION | 1..484 |
| | note = misc_feature - trPTB1PTB1_ACESD Anthranilate synthase component I OS=Acetoanaerobium sticklandii (strain ATCC 12662 / DSM 519 / JCM 1433 / NCIMB 10654) OX=499177 GN=trpE PE=4 SV=1 |
| source | 1..484 |
| | mol_type = protein |
| | organism = Acetoanaerobium sticklandii |
| SEQUENCE: 155 | |
| MIKPDFKLLK ELSKQGKF DI TPVSISFKSN SKPIDVFNL KEKTECTFIL DWDDEYGN YD 60 | |
| RYTFIGFNPK MKVSKCDSNM CLGEKRIFTK KPSEVLRGIL KENRSPKFDF LPPFTGGFAG 120 | |
| YFSYDYFKYI EPSVKFTSDN TCNFNDLELF LFDKIVVLDN LNNLITIIVN TSLLEIEKNY 180 | |
| TKTIEDLNCI KOIIQSENEN LMKGKGLKSE FSPAVSKNDY MQLMEKSNSH IFEGDIFQIV 240 | |
| LSNKVEAEFE GSLLNVYENL RLINPSPYIF YLSTEDIEIA GASPETLVKL KDKTLNTYPL 300 | |
| AGTRPRGKTA EEDFNLEKEL LLDEKEVAEH NMLVDSLGRND LGKISKEPNSV EVEKYKMVER 360 | |
| YSHVMHIASS VKGEICDGKD ALDAIEAVLP AGTLGAPKI KAVELIDKLE KDRRGIGYGA 420 | |
| LGYISFTGDM DMCIGIRLAY KKGDKVFVRS GAGIVSDSIP ESEYNECINK SGAMIATINL 480 | |
| LKEG | 484 |
| SEQ ID NO: 156 | moltype = AA length = 468 |
| FEATURE | Location/Qualifiers |
| REGION | 1..468 |
| | note = misc_feature - tr4SX84SX8_BACPR Anthranilate synthase component I OS=Bacteroides fragilis (strain YCH46) OX=295405 GN=BF2651 PE=4 SV=1 |
| source | 1..468 |
| | mol_type = protein |
| | organism = Bacteroides fragilis |
| SEQUENCE: 156 | |
| MNAFNYTT HS KQVLGDLHTP VSIYLKVRDM YPQSALMESS DYHAGENSLS FIALCPLASI 60 | |
| GINSGIVTTT YPDNTRREEP LSQSFRVENA LNRFINRPVH EGDDKKFCGL YGYTTFNAVK 120 | |
| YFEHIPVKES HDEQNDAPDL LYIILKYIIV FNHFKNELTL VEMLAEGEES NLSQLESAIE 180 | |
| NRNYASYNFS VIGPVTTIT DEEHKANVRK GIAHCLRGDV FQIVLSSRFI QPYAGDDFKV 240 | |
| YRALPSNPS PYLFYDFGG YRIFGSSPTEY HCKVESGQAY IDPIAGTTRR TGDTIKDKE 300 | |
| TEALLADPK NAEHVMLVDL ARNLDLSRNCH DVRVVFYKEP QYYSHVIHLV SRVSGALNN 360 | |
| ANPLKTFIDT PPAGTLGAP KVRAQMOLISE IEPHNRGAYG GCIGFIGLNG ELNQAITIRT 420 | |
| FVSRNNELWQ QAGGGIVARS QDEYELQE VN NKLGALKKAI DLAVKLKN | 468 |
| SEQ ID NO: 157 | moltype = AA length = 454 |
| FEATURE | Location/Qualifiers |
| REGION | 1..454 |
| | note = misc_feature - tr ^A 367CCZ ₈ ^A 367CCZ ₈ _9ENTE Anthranilate synthase component 1 OS=Enterococcus durans OX=53345 GN=trpE PE=3 SV=1 |
| source | 1..454 |
| | mol_type = protein |
| | organism = Enterococcus durans |
| SEQUENCE: 157 | |
| MRKTKKINGD CLTPINLYYR LRDEKSCSLL SIPREKENG R YSVIAFEPAH HVKYAEGEFS 60 | |
| FDETTTYRKCD PLKELEKYV VEEELHEELP FQGGAIGYVG YDIAACYEET GTIPEDELGL 120 | |
| PDMQFYLYES FVIYDHQQQE ITVVVSNSYS HETEEVLAQR S LDFEQKIRT MNEAEGSEL 180 | |
| SLSLQFKSNF SQEKFRQIVA EAQKQIREGD LFQVVPSSRL SVDFTDIPFD YYRQLRVTS 240 | |
| SSYLYFLPP QATIIGSSPE SLVRVKGEIV TTNPPIAGTRK RGASKELDDQ LAKELISDPK 300 | |
| ETAAEHQMLVD LGRNDLGKVA QHGSVTVPFL MTVERYRFVM HIVSLVQARL KTGFSA DAL 360 | |
| KATLPGATVS GAPKIRAMTR IYEWEPVKRS IYAGAVGYZS QDNQADFAIA IRTMVVKGKK 420 | |
| AVVQAGAGIV YDSDPTSEYF ETLQKAKGLL EVRK | 454 |
| SEQ ID NO: 158 | moltype = AA length = 518 |
| FEATURE | Location/Qualifiers |
| REGION | 1..518 |
| | note = misc_feature - tr ^A 1I7 ₁ I7_BIFAA Anthranilate synthase component 1 OS=Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a) OX=367928 GN=trpE PE=3 SV=1 |
| source | 1..518 |
| | mol_type = protein |
| | organism = Bifidobacterium adolescentis |
| SEQUENCE: 158 | |
| MSECsvQTLK WGATWPSREQ FHELAQGYR VIPIVRRLLA DSLTPVGFYE RLAGGRSGTF 60 | |
| ILESAAFGGA WSRYSFIVGH SIAQLRSNNG KADWLGVQPV GVPTDGDVVE VAHAALKTLK 120 | |
| APHVEGLPNL TSGLVGTVGW DSIRHWEPTL RAEAPNETGQ PETVLALATD IAVVHDHS 180 | |

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|---|---------------------------|
| VWLIANAVNV DDRPTRADAA YDEALARLDD MQRKAAAPVE NEARVNVLDE SVGQPQLRFR | 240 |
| TEKSDYERSV EEAKRHHIIDG DVFCQVISQR LDIDSPADPF DVYRVRLTLN PSPYPMYFMAL | 300 |
| TDAQGRDFNV IGSSPETLIK VDNGHAMSFP IAGSRPRGAT PEEDERLAKE LLADPKERSE | 360 |
| HIMLVDLARN DLSRVCRPES VEVVSLMDIK RFSHIMHICS TVTGQVDPHM TAFDVFTSAF | 420 |
| PAGTLGAKP PRAEIIDEL EPADRGYIYGG TVGYFDFSGN LDMAIAIRTA FIRDHEASVQ | 480 |
| AGAGIVLDSV PASEWQETRN KAEASVEAVQ IAAQLRQL | 518 |
| SEQ ID NO: 159 | moltype = AA length = 202 |
| FEATURE | Location/Qualifiers |
| REGION | 1..202 |
| note = misc_feature - tr^A2N0UU08^A2N0UU08_9FIRM | |
| N-(5'-phosphoribosyl)anthranilate isomerase | |
| OS=Ruminococcus bromii OX=40518 GN=trpF PE=3 SV=1 | |
| source | 1..202 |
| mol_type = protein | |
| organism = Ruminococcus bromii | |
| SEQUENCE: 159 | |
| MVKKICGTT AEDIKIVNAC EPDFAGFVMF FPKSKRNLSP ETAKSLIEML DKNVLSVAVT | 60 |
| VSPITLEQVKT AYDCGFDYIQ IHGEVGGDVL SNPYLKVIRA FNVSDELEKFE EYRMNPNIVG | 120 |
| YVFDHAHEPGS GKTFDWTMLE NLPRDDKLFM LAGGLNPETV AKAVKAVKPD GVDVSSGVEN | 180 |
| SNGNGKDFEK VKKFIISARS EN | 202 |
| SEQ ID NO: 160 | moltype = AA length = 201 |
| FEATURE | Location/Qualifiers |
| REGION | 1..201 |
| note = misc_feature - trPTA7PTA7_ACESD | |
| N-(5'-phosphoribosyl)anthranilate isomerase | |
| OS=Acetoanaerobium sticklandii (strain ATCC 12662 / DSM | |
| 519 / JCM 1433 / NCIMB 10654) OX=499177 GN=trpF PE=3 SV=1 | |
| source | 1..201 |
| mol_type = protein | |
| organism = Acetoanaerobium sticklandii | |
| SEQUENCE: 160 | |
| MSNLKIKICG LKHNE DIEYV NSVDIDYVGF VFVEKSSRFI TAIKAKELKN KLSPTIKAVG | 60 |
| VFVDKPIEYI VELANNNIID MIQLHGNENE KYILDLKKIT DKSIKAFQV NSSEDLIKAE | 120 |
| KSSADYILLD CGGGGSGICI DWSIIYELDR PFFLAGGLNA DNVARAVSIV NPYAVDVSSG | 180 |
| VEVDSKKLDL EIKKFVIAAR R | 201 |
| SEQ ID NO: 161 | moltype = AA length = 209 |
| FEATURE | Location/Qualifiers |
| REGION | 1..209 |
| note = misc_feature - tr[D6]D4J1[D6]D4J1_9BACE | |
| N-(5'-phosphoribosyl)anthranilate isomerase OS=Bacteroides | |
| xylanisolvens XB1A OX=657309 GN=trpF PE=3 SV=1 | |
| source | 1..209 |
| mol_type = protein | |
| organism = Bacteroides xylanisolvens | |
| SEQUENCE: 161 | |
| MINGKIIKVC GMREAENIQL VEAIEGIDML GFIFYPKSPR CVYELPAYLP THARRGVVF | 60 |
| NEDKQVVSMY ADRFGLNDVQ LHGNESPEYC RSLHSTGLKI IKAFSVDRPK DLKKVYDYEK | 120 |
| VCDLFLFDTK CEQYGGSGNQ FDWSILHTYN RDVPFLLSGG INSYSANALK EFKHPRLAGY | 180 |
| DLNRSRFETKP GEKDPERIRT FLNELKSSL | 209 |
| SEQ ID NO: 162 | moltype = AA length = 200 |
| FEATURE | Location/Qualifiers |
| REGION | 1..200 |
| note = misc_feature - tr^A367C9T6^A367C9T6_9ENTE | |
| N-(5'-phosphoribosyl)anthranilate isomerase | |
| OS=Enterococcus durans OX=53345 GN=trpF PE=3 SV=1 | |
| source | 1..200 |
| mol_type = protein | |
| organism = Enterococcus durans | |
| SEQUENCE: 162 | |
| MTEIKICGLT TTKTAIDAAIQ SGASYLGFVF AESPRKITPE NVRALTQDLP EKVKKVGVFV | 60 |
| SPTKEFVEEI VKIAQLDFVQ IHGEKKFQQI DVPIIRAKSV TKNVSLTVAT GEDFLLLDAP | 120 |
| PTKYMGGNGQ RFDWSAVAVQ QLEKEKLWLA GGLTAENVGE AIVYFQPKVV DVSSGVETDG | 180 |
| KKDLAKISAF CEAVERIADNS | 200 |
| SEQ ID NO: 163 | moltype = AA length = 241 |
| FEATURE | Location/Qualifiers |
| REGION | 1..241 |
| note = misc_feature - sp.A2H2-S4_BIFAA | |
| 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Bifidobacterium | |
| adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / | |
| E194a) OX=367928 | |

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source          1..241
               mol_type = protein
               organism = Bifidobacterium adolescentis

SEQUENCE: 163
MSLTLLPAVD VRDGKAVRLR QGESGSETDY GSPLEAARTW VESGAEWIHL VDLDAAFGTG  60
NNRDQLRAIV KELGDVKVIE MSGGVRDDAS LDAALEAGAA RVNIGTAALE NPDWTASVIK 120
KYGDRRAVGL DVRGHTLAAR GWVKEGGDLF ETMKFLDSVG CSRYVVTDVA RDGMMSGPNI 180
ELLREVASRT DAKVTASGGI SKLDDLRNIK ELAELGVDA ILGKSLYARA FTLEEALEVA 240
R                                         241

SEQ ID NO: 164      moltype = AA length = 377
FEATURE
REGION           1..377
note = misc_feature - trQ917Q917_ACIIR Acyl-CoA
dehydrogenase OS=Acidaminococcus intestini (strain
Ryc-MR95) OX=568816 GN=bcd PE=3 SV=1
source          1..377
               mol_type = protein
               organism = Acidaminococcus intestini

SEQUENCE: 164
MDFALTEEQL ELQAMVREFV EKEIVPYTDE MDKNNACRPE IIKKAGDMGL LNLVVPEEYG  60
GPGGLDSVIA MIYEELGKG C VGVATSIAAN ALASYPILIA CNDEQKKYQC DLLNNNGGLAA 120
FALTEPDAGS DAGGVSTKAV KEGDHYVLNG SKVFITNGGI ADSFLVFANT RKTGGIRGLT 180
CFIVPKGTG FSVGKRKEDKM GIRPSNTCEL ILEDVVVPES MRVGREGQQF RIAMQTLDSA 240
RPFVASVAVG VAQSALDIAA HYARERRQFG QPISSFQLIQ GMVADMAMKV HGARLMVQQA 300
CWMRDQGLEF GMEAAMSCKF ASDVAMEVTT DAVQIMGGY YMKDYPMEKK MRDAKILQIY 360
EGTNQIQRLV IANKILY                                         377

SEQ ID NO: 165      moltype = AA length = 568
FEATURE
REGION           1..568
note = misc_feature - tr^A139KHX6^A139KHX6_BACUN
Acyl-CoA dehydrogenase OS=Bacteroides uniformis OX=820
GN=Bun01g_18050 PE=3 SV=1
source          1..568
               mol_type = protein
               organism = Bacteroides uniformis

SEQUENCE: 165
MANFYTEVPE LKYHLLNNSMM ERICELKERG YQDKDKYDYA PQDYADAMDS FDKVLEITGE  60
ITGEIIIAPNA EGVDEEGPHC ANGRVEYASG TKQNLDAMVK AGLNGMTMPR RFGLGNFPIT 120
PYTMCAEIVAAADAGFGNIW SLQDCIETLY EFGNEDQHSR FIPRVCAGET MSMDLTEPDA 180
GSDLQSVMLK ATYDEANNCW RLNGVKRFIT NGDANLHVL ARSEEGTKDG RGLSMFIYDK 240
NEGGVDRRI ENKLGIGHGSP TCELYVYKNAK AELCGDRKLG LIKYVMALMN GARLGIAAQ 300
VGLSQAYAYNE GLAYAKDRKQ FGKAIIEFPV VYDMLAIMKA KLDAGRSLLY QTSRYVDIYK 360
ALLDIARERK LTPEERQEQQ KYAKLADAPT PLAKGMMSEY ANQNAVDSIQ IHGGSGFMLE 420
YACQRIYRDA RITSIYEGTT QLQTVAAIRY VTNGSYSATL RDYEQVPCSE EMQPLMDRIK 480
EMTNKFEACT NAVKEAQNQE LLDFVARRLY EMAAVCIMSH LIIQDATKAP ELFGKSALVY 540
VNYYAEAEVEK HFNFIRKFKA EELEYSYRK                                         568

SEQ ID NO: 166      moltype = AA length = 499
FEATURE
REGION           1..499
note = misc_feature - tr^A564RYK6^A564RYK6_BIFLI
Acyl-CoA reductase OS=Bifidobacterium longum subsp.
infantis OX=1682 GN=luxC PE=3 SV=1
source          1..499
               mol_type = protein
               organism = Bifidobacterium longum

SEQUENCE: 166
MPTADEVSQ AIDVFHLPSC ADVSDYEIYD VATSDGVKRL RYPRLDGPKV TSLAKQLADV  60
RNRTLAAAMSV NDILDIVADA AQLWADPDE LRRQAEILLIP AITGYEPDMV RIELKRYMRQ 120
FRRRELLRFL DSEIGQPSML DEFRPNKAGG YSKYVGPALT YQVFSSNVPG IPVWSMAMTL 180
LVKGAILGKS SFSEPVMPAF FARSIAMVNS DLADAIAVVP WKGGSQQLED SAIDVADAVI 240
VYGSQQITKL IAGKVAGSKP CLGYGAKVGL AFIGREALRP DTYADTVHRV AVDIATYDQQ 300
SCLAPQTVFV ETDGALTARE VAQLLGGELE NQQRKYPRSV LSDAENVVAIQ RARTDAEMRA 360
LMGKAAVFA SGHSTAWSVL YRELDGSGAD EDVASLMSPL NRTVNVVAVP DLLDAARRLT 420
SCRGWLQSCG VAVDSTRFLFG LADILAEAGV NRICPLGEMD RAKSGWHDG GFNLIDLLRA 480
VDVERGSDAY GDSFDMDME                                         499

SEQ ID NO: 167      moltype = AA length = 451
FEATURE
REGION           1..451
note = misc_feature - tr7GS87GS8_CLOAB Acyl-CoA
reductase OS=Clostridium acetobutylicum (strain ATCC 824 /
DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) OX=272562
GN=CA_C2287 PE=3 SV=1

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source          1..451
               mol_type = protein
               organism = Clostridium acetobutylicum
SEQUENCE: 167
MKLEFTCGEE ITIKEVNKLK LELMTSGKGD VEKELERLKK NKNKVHDIKT EETIDLLRC 60
AKLWLDDNYS KKHIETLAQI TNQSFELVNY EFKSMMQMML RENIQNTIKR ELGEVDILDS 120
WHKTNYGYEH RQPRGIIFHN ISGNNAFVVIP MSISMGLLSK NCNLVVKSKD EPYFAYAFYK 180
SLCELDETVK DRSLVLYFDS SKTEIYDTIV KNSDGVIHWG GEYSSRIIGE MCAKYQKHM 240
MHGAKISFEV VDKCDDLNVK SEEIAKDIIC WEQKACLSPR VFVLNDKIDV DEFSHCLAS 300
LRKITEVIPK AYLSEWNSV TIQDRQYCTL KYGMKNERRF KVYSSFNADY TVILSDGMPE 360
KEDINKCFYR FIFVCPISSK SDVNVNVSEN LDKYLQTMGY SGNDEFIEK MTLLGVSVIT 420
KPGKMSLHEP GTSHDGIHNL KEFTFLVSRQ I                                451

SEQ ID NO: 168      moltype = AA length = 389
FEATURE
REGION          1..389
               note = misc_feature - tr^A0M6WEG7^A0M6WEG7_9FIRM
               Acyl-CoA dehydrogenase OS=[Eubacterium] rectale OX=39491
               GN=DW001_08475 PE=3 SV=1
source          1..389
               mol_type = protein
               organism = Eubacterium rectale
SEQUENCE: 168
MDPTLDQKHE MARDLFKQFA ETEVKPLAQE TDETEVFPAA TVAKMGKYGF MGIPVPKEYG 60
GQQCDPLTYV MCVEELSKVC GTTGVIVSAH TSLCIDPIMT FGTEEQKKY VPDLASGKKI 120
GAGFLTEPGA GTDAQPGCQTK AVLDGDEWVL NGSKCFITNG KVADVYIIIA ITSITEDKRG 180
RKKKNFSAFI VDKGTGPGFSF GTKEKKMGR GSSTYELIFE DARIPKDALL GKEGRGPPIA 240
MHTLDGGRIG IAAQALGIAE GALERTIEYT KERKQFGRSI AQQQNTQFKL ADMATRIDAA 300
KYLVYAAAMK KAEFAKNPKV SYSVDAAKAK LFAAETAMAV TTECVQLFGG YGYIREYDVE 360
RMMRDRAKITE IYEGTSEVQR MVISGSLLR                                389

SEQ ID NO: 169      moltype = AA length = 381
FEATURE
REGION          1..381
               note = misc_feature - tr[D6]EA99[D6]EA99_9ACTN Acyl-CoA
               dehydrogenases OS=Gordonibacter pamelaeae 7-10-1-b
               OX=657308 GN=GPA_25140 PE=3 SV=1
source          1..381
               mol_type = protein
               organism = Gordonibacter pamelaeae
SEQUENCE: 169
MDFKKTEEQE LLLDSLKTVM ERGNFEDYFK ECDRNHEYPO QAVDALVEAG FTTLGIPEEF 60
GGPTPTDLTQ VMVAEEAHAL GYPSLCWINT ATEVDDILTF GNKEQQEKIL GYALEGKCPF 120
TLGFTEPQAG SDSAAMATTA TKRDGKVYIN GNKTFNTSD RAPYMLCVCR SGVNESPYKD 180
FSMYLFPMDR PGVAIEKLDK IGNMMCGTYE VHLDLVCEEE SDLVGEECKG FYQLMKNFEV 240
ERLTICAANV GMARCMAYDEA LRYAAQRMQF GKIIGSFQLV QEKLVDMRIK IENMQNLLYK 300
TAWKKDNGES IMIDSSLVKK YTQQAFAFEVI DDAMQIMGGI GYTHDCRISR LWRDQRVYRI 360
MAGTEEMIVH TAGRALIKEA Q                                381

SEQ ID NO: 170      moltype = AA length = 408
FEATURE
REGION          1..408
               note = misc_feature - tr^A1E3KW51^A1E3KW51_LACPN
               Acyl-CoA dehydrogenase OS=Lactobacillus plantarum OX=1590
               GN=GPJ80_14625 PE=3 SV=1
source          1..408
               mol_type = protein
               organism = Lactobacillus plantarum
SEQUENCE: 170
MEATETAPYE PTKKLVHTKP GTKMTDEEFA LYLKQIKHLA ENEFDYLOQE VEVTNRFPKK 60
FFELAIDNDL YRFALPLKYG GFGLSCKQIF QVQEMFSRGP GGMRMHLHYA ADLNWRIMDE 120
FGRPELKAEV MPKLQDKSIF TCFALTEESG GTGADLHTTA VKDGDYYILN GEKTLISHTD 180
CSDAAYVIAV TDPDAEGSKR LSAFYVPVDT PGYEIVPMFH MMGCRGAGHA GLKFTNMVRN 240
KKYLLGEEGD GLHVAIASL ISRAHIAASN LGMSQRMLEM AIARAKDRV FGKPLAKRQA 300
IQQEIADMGT EIFALRTMLH NLADQYDRGE DIEEKAAMCK LFSINTVKLV SDYCLEIFGG 360
IGYFEDNPYVG PVERMYRDCR AMWLEEGPRS VQLTAARKL IANDGIIE                                408

SEQ ID NO: 171      moltype = AA length = 376
FEATURE
REGION          1..376
               note = misc_feature - tr^A415S9V5^A415S9V5_RUMGN
               Acyl-CoA dehydrogenase OS=Ruminococcus gnavus OX=33038
               GN=DWZ50_08895 PE=3 SV=1
source          1..376
               mol_type = protein
               organism = Ruminococcus gnavus

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SEQUENCE: 171
 MNMNVMDDKL PYNEIKEFAR NYLDKQNSNE KHLWERLGEF GILGLSIDEK YGGLGESYRM 60
 CAEILEILGY TCWNNGLIFS INNHIWMAQN LINLYGSTWL KNKYVGNMVA GEKIGAFALT 120
 EPDAGSDPYS MKTCAIRAGD YYIINGRKT VSNGPIADFV IVFAITSQTE MKKITAFVVD 180
 KTMPGVТИK NIEKMGLECS PTSDICFENC EVPADNLGK VLGNNILDA ALEWERCFEF 240
 IPIHIGSMKRI MEYCICKSNE RKQFGKRINE NQSHKIAN MSMKIELAKN LMYRIVDLKE 300
 QGKSSYYESS IFKVVFSESY VETCRDAIQI LGAYGYTKEY PVEKELRDAI ASTIYSGTNE 360
 MQRNNIFNIE SIRNMV 376

SEQ ID NO: 172 moltype = AA length = 544
 FEATURE Location/Qualifiers
 REGION 1..544
 note = misc_feature - Tryptophanase (indole production) (EC
 4.1.99.1) Enterocloster lavalensis HB-452c
 source 1..544
 mol_type = protein
 organism = Enterocloster lavalensis

SEQUENCE: 172
 MKNYPLNVEA PKSYSYVKRN IPNVTVQRE RALKSTHYNE FAFFPAGMLTV DMLSDSGTTA 60
 MTDVQWSAMF LGDESYGRNK GYYVLMDAFR DVPERGDDQK RVINLVRTDC QDIDKMMDEM 120
 YLCEYEGGLF NGGAQAMERP NTFIMPQGRA AESVLFAMVS KILGERHPGK NFTIPSNGHF 180
 DTTEGNIKQM GSTPRNCFDK QLLWEVPEGG VYEKNPFGKN MDTAKLEALI QEAGPENVPL 240
 VYTTITNTV RESRIAHKY GIPFMMLDAAR WAENCYFIKV NEEGYGDKSI 300
 FAIAKEFLSY CCGFTASLKK DGHANMGGIL AFRDKGLFWK NFSDFDAEGN VVTDVILLK 360
 VKQISSYGN SYGGMSGRDI MALAAGLYEC GRVEYLKERV EQCEYLAQGF YKNGVKGVVL 420
 PAGGHGVYIN MDEFDFDGKRG HQSFGAGFS LELIRRYGIR VSELGDFSMY YDLKTPEQQK 480
 EVCNVVRPAI NRSQLSREHL DYVIAAVTEL YKDRKSIPNM KITLGHKLPM RHFHALEPY 540
 EAEE 544

SEQ ID NO: 173 moltype = AA length = 412
 FEATURE Location/Qualifiers
 REGION 1..412
 note = misc_feature - Cinnamoyl-CoA:phenyllactate
 CoA-transferase fldA (EC 2.8.3.17) Clostridium sporogenes
 source 1..412
 mol_type = protein
 organism = Clostridium sporogenes

SEQUENCE: 173
 MENNTNMFVG VKVIELANFI AAPAAGRFFA DGGAEVIIKIE SPAGDPLRYT APSEGRPLSQ 60
 EENTTYDLEN ANKKAIVLNL KSEKGKKILH EMLAEADILL TNWRTKALVK QGLDYETLKE 120
 KYPKLVFAQI TGYGEKGPDK DLPGFDYTAF FARGGVSGTL YEKGTVPPNV VPGLGDHQAG 180
 MFLAAGMAGA LYKAKTTGQQ DVKTVSLMHs AMYGLGIMIQ AAQYKDHALV YPINRNETPN 240
 PFIGSYKSKD DYFVQVCMPP YDVFYDRFMT ALGREDLVGD ERYNKIENLK DGRAKEVYI 300
 IEQQMVTKTK DEWDNIFRDA DIPFAIAQTW EDLLEDEQAW ANDLYLYMKY PTGNERALVR 360
 LPVFFKEAGL PEYNQSPQIA ENTVEVLKEM GYTEQEIEEL EKDKDIMVRK EK 412

SEQ ID NO: 174 moltype = AA length = 407
 FEATURE Location/Qualifiers
 REGION 1..407
 note = misc_feature - (R)-3-(aryl)lactoyl-CoA dehydratase,
 alpha subunit fldB (EC 4.2.1.175) Clostridium sporogenes
 source 1..407
 mol_type = protein
 organism = Clostridium sporogenes

SEQUENCE: 174
 MSDRNKEVKE KKAHKHYLREI TAKHYKEALE AKERGEKVGW CASNFPQEIA TTLGVKVYP 60
 ENHAAAAAAR CNGQNMCEHA EAMGFSNDVC GYARVNLLAVM DIGHSEDQPI PMPDFVLCCN 120
 NICNQMIKWKY EHIATKLDIP MILIDIPYNT ENTVSQDRIK YIRAQFDDAI KQLEEITGKK 180
 WDENKFEEVM KISQESAKQW LRAASYAKVK PSPFSGFDLF NHMAVAVCAR GTQEAADAFK 240
 MLADEYEENV EKQKSTYRG EKQKSTYRG ACWPYLRHKL TKLSEYGMNV TATVYAEAFG 300
 VIYENMDLEM AAYNKVPNSI SFENALKMRL NAVTSTNTEG AVIHINRSCK LWSGFLYELA 360
 RRLEKETGIP VVSFDGDQAD PRNFSEAQYD TRIQGLNEVM VAKKEAE 407

SEQ ID NO: 175 moltype = AA length = 373
 FEATURE Location/Qualifiers
 REGION 1..373
 note = misc_feature - (R)-3-(aryl)lactoyl-CoA dehydratase,
 beta subunit fldC (EC 4.2.1.175) Clostridium sporogenes
 source 1..373
 mol_type = protein
 organism = Clostridium sporogenes

SEQUENCE: 175
 SNSDKFFNDF KDIVENPKKY IMKHMEQTGQ KAIGCMPLYT PEELVLAAGM FPVGWGSNT 60
 ELSKAKTYFP AFICSILOTT LENALNGEYD MLSGMMITNY CDSLKCMQN FKLTVENIEF 120
 IPVTVPQNRK MEAGKEFLKS QYKMNIEQLE KISGNKITDE SLEKAIEIYD EHRKVMNDFS 180
 MLASKYPGII TPTKRNVYVMK SAYYMDKKEH TEKVRQLMDE IKAIPEKPFE GKRVITTGII 240

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| | |
|--|--|
| ADSEDLKLIL EENNIAIVGD DIAHESRQYR TLTPEANTPM DRLAEQFANR ECSTLYDPEK | 300 |
| KRGQYIVEMA KERKADGIIF FMTKFCDPPEE YDYPQMKDF EEAGIHPVLI ETDMQMKNYE | 360 |
| QARTAIQAFS ETL | 373 |
| SEQ ID NO: 176 | moltype = AA length = 264 |
| FEATURE | Location/Qualifiers |
| REGION | 1..264 |
| | note = misc_feature - (R)-phenyllactate dehydratase |
| | activating ATPase fldI, archerase (EC 5.6.1.9) Clostridium |
| | sporogenes |
| source | 1..264 |
| | mol_type = protein |
| | organism = Clostridium sporogenes |
| SEQUENCE: 176 | |
| MADIYTMGVG IGSTASKTVV LKNGKEIVSQ AVISVGAGTS GPKRAIDSVL KDAKLSIEDL | 60 |
| DYIVVSTGYGR NSFDFANKQI SELSCHAKGV YFDNNKARTV IDIGGQDIKV LKLADSGRLL | 120 |
| NFIMNDKCAA GTGRFLDVMS RVIEVPVDEL GKKALESKNP CTISSTCTVF AESEVISQLA | 180 |
| RGVKTEDLIA GICKSVASRV ASLAKRSGIE ELVVMMSGVVA KNIGVVKAME AELGRDIYIS | 240 |
| KNSQLNGALG ASLYAYESFQ KERS | 264 |
| SEQ ID NO: 177 | moltype = AA length = 412 |
| FEATURE | Location/Qualifiers |
| REGION | 1..412 |
| | note = misc_feature - putative Cinnamoyl-CoA:phenyllactate |
| | CoA-transferase fldA (EC 2.8.3.17) Peptostreptococcus |
| | russellii |
| source | 1..412 |
| | mol_type = protein |
| | organism = Peptostreptococcus russellii |
| SEQUENCE: 177 | |
| MSTRKQPLKG IKVIELANFI AAATTGRFLA DLGADVIKIE SAKGDPLRYT APTEGRPLDM | 60 |
| YENTTWELEN ANKRCISLNW KDPAGKEAFF KLLDDADVLI TNWRVQALER AGLDYETLK | 120 |
| KYPSLVYALC TGYGEFGPDK DLPGFDFTAF FARGGYLENL RQKSDVPMNV VPGLGDHNVG | 180 |
| INLAAGVLAA LYHAKLTGEG EKVETSLFES AIPNMGMIIQ AAQYPDHGKV YPINIREASN | 240 |
| PFNACWRTSE GRYIQTCPMD YNTYQTKPLT ALGLTDMVED ERFFPVQNLH ENGLGTTVYD | 300 |
| RVMSTFEEQKS HEEWAQILTE ADIPPFALAKT WEELEDDQA WANDCFHKMQ YPNGERVLVK | 360 |
| HPIKFAEMGP TPYNKGPMSG EHGVEVMKEL GYNEDQINEM IENKTLYIWE DK | 412 |
| SEQ ID NO: 178 | moltype = AA length = 412 |
| FEATURE | Location/Qualifiers |
| REGION | 1..412 |
| | note = misc_feature - putative (R)-3-(aryl)lactoyl-CoA |
| | dehydratase, alpha subunit fldB (EC 4.2.1.175) |
| | Peptostreptococcus russellii |
| source | 1..412 |
| | mol_type = protein |
| | organism = Peptostreptococcus russellii |
| SEQUENCE: 178 | |
| MSNTGMEEK PAKKMLGEIV AKHYQEAWDA KERGEKVGWC ASNFPQEIFFE TLDIKVVYPE | 60 |
| NQAAAISAKG GGQRQLCEVAE NNGYSNDICA YARISLAYMD VKDAPELNMP QPDFVACCNN | 120 |
| ICNCMIKYWE NIAKELNIP1 ILIDVPYNNE YEAGDDRVEYL LKGQFDYAIK QLEDLTGKKW | 180 |
| DEDKFNEVME VSQRTFRAWL KATGYAKTP SPFSGFDVFN HMAVAVCARG KLESALAFEK | 240 |
| LAEEFDQNVK EGKSTFKADE KYRIVFEGIA CWPHLRHTFK QLKDNGVNVC GTVYADAFGY | 300 |
| IYNNTYELMQ AYCGBTNAIS YERATDMRLK LLEENNIDGM LFHINRSCKQ WSAIMYEMER | 360 |
| EIREKTIPIAT ATFDGDQADP RNFSEAQYDT RVQGLIEVME ASKAKEBAQR HE | 412 |
| SEQ ID NO: 179 | moltype = AA length = 372 |
| FEATURE | Location/Qualifiers |
| REGION | 1..372 |
| | note = misc_feature - putative (R)-3-(aryl)lactoyl-CoA |
| | dehydratase, beta subunit fldC (EC 4.2.1.175) |
| | Peptostreptococcus russellii |
| source | 1..372 |
| | mol_type = protein |
| | organism = Peptostreptococcus russellii |
| SEQUENCE: 179 | |
| MSNINLLLEK LDVCPLEQLD KYTNDGKKVI GCAPVYAPEE LVYAGMIPM GIWGAEGEVT | 60 |
| SAKEYFPFY AAPILRLMDL GLEGKLDKMS GMIIGGLSDG LKGLSQNWKR AVKNVPCLYI | 120 |
| GYGQNRIKKA SIDYNEKQYI KLKKELEEIA GCKIEDSKVE EAIVLYNNHR KAMSEFNQLA | 180 |
| STHLNTITPT LRARVMSSAY FFDKAELHAI LEEINNILKS TPEEKFEGKK IVTTGILANS | 240 |
| PDIMKILEEF KLGINDDVN HESQFQDYLV DEATDNPVRA LAKWISDIEG SALLYDPSKL | 300 |
| RGQIVIDKVK KHADGVLYL MTKFSESDEF DYPIIRDELN EAGIMNILVE VDQQMTNFEQ | 360 |
| AKTALQTFAD MI | 372 |
| SEQ ID NO: 180 | moltype = AA length = 262 |
| FEATURE | Location/Qualifiers |

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REGION          1..262
note = misc_feature - putative (R)-phenyllactate
dehydoratase activating ATPase fldI, archerase (EC 5.6.1.9)
Peptostreptococcus russellii

source          1..262
mol_type = protein
organism = Peptostreptococcus russellii

SEQUENCE: 180
MSEIYTMGID IGSTSSKCVI LKNGKDIVSK GVVNLGAGTK GVDRVIDEVI KKANLTLKDI 60
EVIVSTGYGR NSYDDAKKTM SELSCHAKGG SYIFGDVRTI IDIGGQDIKV LKLNKKQQLM 120
NFLMNDKCAA GTGRFLEVMC GVLVLEGLD GLKDEQATEK TPISSTCTVF AESEVISCM 180
KKIPIPNIVK GIHYSVASRV AGLAKRGGLT QPVAMTGGVT KNSGIVRALS GELETEIMIS 240
EDSQMAGAIG AALYYAYEEYL KS 262

SEQ ID NO: 181      moltype = AA length = 321
FEATURE          Location/Qualifiers
REGION          1..321
note = misc_feature - Putative tryptophan
N-methyltransferase Mycolicibacterium smegmatis

source          1..321
mol_type = protein
organism = Mycolicibacterium smegmatis

SEQUENCE: 181
MTLSLANYLA ADSAAEALRR DVRAGLTAAP KSLPPKWFYD AVGSDLFDQI TRLPEYYPTR 60
TEAQILRTRS AEIIIAAGAD TLVELSGTS EKTRMLLDAM RDAELLRFI PFDVDAGVLR 120
SAGAAIGAEGY PGIEIDAVCG DFEELHGKIP HVGRRLVVF GSTITGNLTPA PRAEFLSTLA 180
DTLQPGDSLL LGTDLVKDTG RLVRAYDDAA GTVAAFNRNV LAVVNRELSA DFDLDAFEHV 240
AKWNSDEERI EMWLRARTAQ HVRVAALDLE VDFAAGEEML TEVSCKFRPE NVVAELAEAG 300
LRQTHWWTDP AGDFGGLSLAV R 321

SEQ ID NO: 182      moltype = AA length = 247
FEATURE          Location/Qualifiers
REGION          1..247
note = misc_feature - Putative amino acid
N-methyltransferase Akkermansia muciniphila

source          1..247
mol_type = protein
organism = Akkermansia muciniphila

SEQUENCE: 182
MDWNADLYEN KHDFVAEYGR DLLSHVPENP GQAILEDLGCG TGTLTHALLE KSTSVVGLDA 60
SPEMIGKARQ LYPGMDFRVL DACLMPWNW FDVIFSNAAF HWIPDHGALL KAISRALKPQ 120
GKLICEFGAH RNILRIREAF RPSLERMNL P YKTRFYFPTV EYRSMSLEQA GLRPBVMDF 180
DRPTPLKDPG DGLRNWARQF FWADLKCLHE KRRVRIFEEM EKALRDELWD GTQWVADYRR 240
IRVIASK 247

SEQ ID NO: 183      moltype = AA length = 247
FEATURE          Location/Qualifiers
REGION          1..247
note = misc_feature - Putative amino acid
N-methyltransferase Adlercreutzia equolifaciens

source          1..247
mol_type = protein
organism = Adlercreutzia equolifaciens

SEQUENCE: 183
MTIDTATGLE APAELSSERV RDIFSHIARK YERFNALSSF GAYKLWLAGM MRQAPIDESH 60
DVLDIAGGTG DVTFTVARTK HPSHIQCTDL VPEMLDVARM HIDEGDGAGV PIDFEVVDQ 120
DIPYADASYD VITMAYGIRN MPDRPRALSE MFRVLKPGGS LVCLEFSTPP NGAWRALYHF 180
YLRHLIPFWG GLVTGDKDGF VYLAKSIRAF PDQEGLAEMM REAGFTDTVW KNYTGGIAAV 240
HVAKKPE 247

SEQ ID NO: 184      moltype = AA length = 254
FEATURE          Location/Qualifiers
REGION          1..254
note = misc_feature - Putative amino acid
N-methyltransferase Enterorhabdus sp. NM05_H27

source          1..254
mol_type = protein
organism = Enterorhabdus sp.

SEQUENCE: 184
MSIDTATGLE APPELSSERV RDIFSAIARK YERFNAISSF GAYKLWLAGM MRQAPIAEHH 60
DVLDIAGGTG DVTFTVARTK HPAHIQCTDL VPEMLDVARM HVDEGDGAGV PIDFQVVDQ 120
DIPYADAAYD VITMAYGIRN MPDRPRALAE MFRVLKPGGS LVCLEFSTPP NRIWRALYHF 180
YLRHLIPFWG GLITGDKEGF VYLAKSIRAF PDQEGLAALM GEAGFTDTVW KNYTGGIAAV 240
HVARKPASGA SGRS 254

SEQ ID NO: 185      moltype = AA length = 417

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| | |
|----------------|---|
| FEATURE | Location/Qualifiers |
| REGION | 1..417 |
| 63 | note = misc_feature - Tryptophan_decarboxylase[0anc]Tr;; C_sporogenes_ATCC_15579_(POSITIVE_CONTROL) |
| source | 1..417 |
| | mol_type = protein |
| | organism = Clostridium sporogenes |
| SEQUENCE: 185 | |
| MKEPWRKYTQQ | EKTMNYDNTK TIGIPGTTKLD DTVFYDDHSF VKHSPYLRTF 60 |
| IQNPNHIGCH | GTFDIERELI QLLAIDVLNG NDEEFDGVT QGGTEANIQA 120 |
| MWVYRNYFKK | ERAKAKHEEIA IITSADTHYS AYKGSDLLNI DIIKVPVDFY SRKIQENTL 180 |
| SIVKEAKEIG | KKYFIVVISNM GTTMFGSVDD PDLYANIFDK YNLEYKIHD GAFGGFIYPI 240 |
| DNKECKTDFS | NKVNVSITLD GHKMLQAPYG TGIFVSRKLN IHNTLTKEAT YIENLDVTLS 300 |
| GSRSGSNSAVA | IWMVLASYGP YGWMEKINKL RNRTKWLCQK LNDMARIKYK EDSMNIVTIE 360 |
| EQYVNKEIAE | KYFLVPEVHN PTNNWYKIVV MEHVELDILN SLVYDLRKFN KEHLKAM 417 |
| SEQ ID NO: 186 | moltype = AA length = 490 |
| FEATURE | Location/Qualifiers |
| REGION | 1..490 |
| 63 | note = misc_feature - Tryptophan_decarboxylase[0anc]Tr;; Ruminococcus_gnavus_(strain ATCC_29149/_VPI_C79)_ (POSITIVE _CONTR OL) |
| source | 1..490 |
| | mol_type = protein |
| | organism = Ruminococcus gnavus |
| SEQUENCE: 186 | |
| MSQVIKKKR | TPMIGTEYIL NSTQLEEEAIK SFVHDFCAEK HEIHDQPVVV EAKEHQEDKI 60 |
| KQKIPIKEKGR | PVNEVVSSEMM NEVYRYRGDA NHPRFFSFVP GPASSVSWLG DIMTSAYNIH 120 |
| AGGSKLAPMV | NCIEQBVWKW LAKQVGFTEN PGGVFVSGGS MANITALTAA RDNLKLTINL 180 |
| HILGTAYISDQ | THSSVAKGLR IIGITDSRIR RIPTNSHFQDM DTTKLEEAE TDKKSGYIPF 240 |
| VVIGTAGTTN | TGSSIDPLTEI SALCKKHDMW FHIDGAYGAS VLLSPKYKSL LTGTGLADSI 300 |
| SWDAHKWLFO | TYGCAMVLVK DIRNLFHFSFH VNPEYLKDL NDIDNVNTWD IGMELTRPAR 360 |
| GLKLWLTLQV | LGSDLIGSAI EHGFQLAVWA EAALNPKKDW EIVSPAQMAM INFYAPKDL 420 |
| TKEEQDILNE | KISHRILESG YAAIFTTVLN GKTVLRICAI HPEATQEDMQ HTIDLDDQYG 480 |
| REIYTEMKKA | 490 |
| SEQ ID NO: 187 | moltype = AA length = 491 |
| FEATURE | Location/Qualifiers |
| REGION | 1..491 |
| 63 | note = misc_feature - UbiD_family_decarboxylase[0anc]Tr;; Enterococcus_durans_HB48 |
| source | 1..491 |
| | mol_type = protein |
| | organism = Enterococcus durans |
| SEQUENCE: 187 | |
| MTEQPYDLRK | VIEELKTLPG QYHETDLEID PEADLSGVYR YIGAGGTVKR PTQEGPAMTF 60 |
| NNIKGFPGKR | VNIGTMASRK RVGQILHHDY RALGRFLKDA VEHPLPKVKV DKADAPAQEV 120 |
| VHLATDADFD | IRNLIPAKPN TPEDAGPYIT MGVVVLGSDPE KTMSDVTIHR MVLEDKDITG 180 |
| MYIMPGRGH | CHFQKQFEAL NQPMPIITINI GLDPAAIAIGT TFEPPPTPLG YNELWCAGAL 240 |
| RNEPIQLVDG | VAVNEVGIAR AEFIIIEAEIM PNQTMQEDIN TNSGKAMPEF PGYTGDANPA 300 |
| VNVVKVKAIT | HRKDNPIMQT TIGPSEEHVS MAGIPTEASI LALVDAKAIPG KVNVVNPPA 360 |
| GGGKLMTIMQ | IRKENEADEG IQRQAAILAL SAFKELKTVI LVDEDVDFID MNDVMWTFNT 420 |
| RFQGDKDIIV | 1PGMRNHPLD PSELPOQYNPG VIRFRGMSAK TIFDGTVPFD MKEHFIRAQF 480 |
| KEVDNWKDYL | N 491 |
| SEQ ID NO: 188 | moltype = AA length = 191 |
| FEATURE | Location/Qualifiers |
| REGION | 1..191 |
| 63 | note = misc_feature - Lysine_decarboxylase_family[0anc]Tr;; Enterococcus_durans_HB48 |
| source | 1..191 |
| | mol_type = protein |
| | organism = Enterococcus duran |
| SEQUENCE: 188 | |
| MKLTVFCSR | PGNKESYKFI AQMLGKYMAG ENIELVYGGG DSGIMGIFSQ TVLENNGKVT 60 |
| GIYPTGLFEL | ETPKEEVTTF IPTDSIDERK VLLFEKGDAV LIFPGGLGTL EEFSQLLSWI 120 |
| AIGLTPDKPI | GILDIGGYYS GLQTLLETFA KEGFMDAKWL NRIFFSNNPPL KLVDLLREET 180 |
| TGLSTLLKEA | K 191 |
| SEQ ID NO: 189 | moltype = AA length = 477 |
| FEATURE | Location/Qualifiers |
| REGION | 1..477 |
| 63 | note = misc_feature - Pyridoxaldependent_decarboxylase[0anc]Tr;; Clostridium_asparagiforme_HB452c |
| source | 1..477 |
| | mol_type = protein |
| | organism = Clostridium asparagiforme |

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SEQUENCE: 189
 MDSFMEAQTQ RAGELMERFI GQTLDFYENI KREDVFRKAD GAAISRLLKK GIPOKGRPWD 60
 EVYREMMDDV YANTS LVQHP RCFACIPSPV SLFSWMGDVM TNAFDPHAGC VMNASAAGCI 120
 ERELIRWMCG LAGYPKGCGG LFVSGGSMAN LTALTAARDL RLTEAERALA VAYVSDQTHS 180
 SIAKGLHIIG PRADQVRKIP SDTNFCMDME TLRAAVRADL AAGRKPFAVI ATAGTTNTGS 240
 VPDLPLPEAEI CRYGMWMHV DGAFFASILL SSNERKRLDG IEYSDSLSWD AHKWLRTQYG 300
 CSMVLVRDQS HLVRSAFAVHP EYLTDAGAFN EAPDFWDLGP ELTRPARSLK LWITLQVMS 360
 EAAMQMDIDHG CAMARLTEL IRYPGWEIV SPARLGIVNF RCAPVNIPPS RIDRLNQDIA 420
 REVTDSGYAQ ILTTELNGKR VLRMCTLHPE TTEEDIRNTV RLLCESRAAS MGQCRTA 477

SEQ ID NO: 190 moltype = AA length = 421
 FEATURE Location/Qualifiers
 REGION 1..421
 note = misc_feature -
 Diaminopimelate_decarboxylase_(EC_4.1.1.20) [0anc] Tr;;
 63 Clostridium_asparagiforme_HB452c
 source 1..421
 mol_type = protein
 organism = Clostridium asparagiforme

SEQUENCE: 190
 MDKPKPFVTL EKLEEVKDYP TPFHLYDEKG IRENAMKLQ AFAWNKGKFE YFAVKATPNP 60
 FILQLLKECG CGTDCSSMT E LMLSEACFGS GEIIMFSSND TPPEEFAYAA RLGAIIINLDD 120
 FTHIQFLEDT LGYIPETISC RFNPNGVFKI SNDIMDNPGD SKYGMTEQM FEAFKILKAK 180
 GAKRFGIHAF LASNTVTNEY YPLLARQLFE LAVKLKEETG AHIAFINLSG GIGIPYRPDQ 240
 EPNDILVIGE GVRNAYQDVL VPAGMGDVAL CTELGRFLMLG PFGCLVTRAI HEKHTYKEYV 300
 GVDACAVNLM RPAMYGAYHH VTVMGKENLP CDHMYDVUGS LCENNNDKFAI DRMLPKVDKG 360
 DLLVIHDTGA HGFAMGYN YN GKLKAELL KEDGSVQMR RAETPKDYFV TFDPCDILKN 420
 D 421

SEQ ID NO: 191 moltype = AA length = 389
 FEATURE Location/Qualifiers
 REGION 1..389
 note = misc_feature -
 NADP-dependent_malic_enzyme_(EC_1.1.1.40) [0anc] Tr;;
 63 Clostridium_asparagiforme_HB452c
 source 1..389
 mol_type = protein
 organism = Clostridium asparagiforme

SEQUENCE: 191
 MDVNKAISLD HYELAGKIEV VSRKKIETRE DLSSLAYTPGV AEPCRVIAKD YEQSFKLTRR 60
 SNLVAVITDG TA VGLGLGDIG PAAGMPVMEG KCVLFKEFAD VDAFPPLCIDS KDTDTIVQTI 120
 HLI SKFGGI MLIEDTAAPRC FEIERTRLBEI CDIPVFLHDQ HGTAIVVAAA LINAIKVVTGK 180
 EMGKIKIVIN GAGAACIAIG KLLISMGFGN VVMDINGI CEGDEGLNAG QEEISHISNL 240
 NEKHGKLADA LKGADAFVGV SRPNLVTKEM VASMNNGIVF AMANPTPEIM PDEARAGGAA 300
 VI GTGRSDFP NQINNNLVFP GIFKGALSVR AKEITETMKQ RAAYAIAISMI PDEELNAENI 360
 IPSPLNKVA AVVAKAVADT AVEEGIARI 389

SEQ ID NO: 192 moltype = AA length = 386
 FEATURE Location/Qualifiers
 REGION 1..386
 note = misc_feature -
 Oxaloacetate_decarboxylase_beta_chain_(EC_4.1.1.3) [0anc] Tr;;
 63 Clostridium_asparagiforme_HB452c
 source 1..386
 mol_type = protein
 organism = Clostridium asparagiforme

SEQUENCE: 192
 MEFLLDGIMA VLGP GGWKM AMYIVGIALI VLAVKKEYEP SLLLPLGF GA ILVNL PYSGV 60
 IDQLVQN KVE AAGIIQWLFF VGIEASEAMP ILLFIGIGAM IDFGPLLSQP VLFLFGAAQ 120
 FGIFAA ILIA CLMGFDLKDA ASIGIIGAAD GPITSILVSQV LGSNYMGPIA VAAYSY MALV 180
 PIIQPFAIKL VTTKKERCIH MQYNPGDVS R GMRIAFPIAV TII VGFISPQ SVALVGFLMF 240
 GNLRLREC GLV HSLSQAQNE LANIITLLIG ITISFSMRAE QFVNPA TLM MALGLVAFVF 300
 DTIGGV FAK VVNVFLK MAG PCKVNP MIGG CGISAFPMSS RVVQKMAA EEPGNIILMQA 360
 AGTNVSCQVA SVIAGGLVIS IVTQYI 386

SEQ ID NO: 193 moltype = AA length = 363
 FEATURE Location/Qualifiers
 REGION 1..363
 note = misc_feature -
 L-threonine_30phosphate_decarboxylase_(EC_4.1.1.81) [0anc] Tr;;
 63 Clostridium_asparagiforme_HB452c
 source 1..363
 mol_type = protein
 organism = Clostridium asparagiforme

SEQUENCE: 193
 MEYQHGGDIY SQEV DLD FSA NLNP FGL PEA VRRAA AD SLG NCTV VPDS SSS RKLTA ALAAY 60
 HGVPQEQVIC GNGAADLIFG LALALKPERA LVTAPAFSEY EQALASV DCR VSWL DLRE KD 120

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|--|---|
| GFRLTPRELL EKLSGEPEQLL FLCNPNNPTG VSIPREDMEW VAGVCRKQGV RLVVDECFCD FLDAPGACSL IPLLKYPNV FVLKAFTKLY AMAGLRIGYG LCADGELMER LKQVRQPWSV SSVAQAAGLA ALGETGYVRA STEAIARERR WLTGELTRLG LTVYGSQANY IFFRDPAGAD GSARGRLYEA LLERRILIRS CANYRGLDHT YYRVCVRLHE DNEILIRELK RILTGRDHLE RQE | 180 240 300 360 363 |
| SEQ ID NO: 194 FEATURE REGION 63 source SEQUENCE: 194 | moltype = AA length = 389 Location/Qualifiers 1..389 note = misc_feature - NADH-dependent_butanol_dehydrogenase_A_(EC_1.1.1.) [Oanc] Tr;; Clostridium_asparagiforme_HB452c 1..389 mol_type = protein organism = Clostridium asparagiforme |
| SEQ ID NO: 195 FEATURE REGION 63 source SEQUENCE: 195 | moltype = AA length = 379 Location/Qualifiers 1..379 note = misc_feature - 4-carboxymuconolactone_decarboxylase_(EC_4.1.1.44) [Oanc] Tr;; Clostridium_asparagiforme_HB452c 1..379 mol_type = protein organism = Clostridium asparagiforme |
| SEQ ID NO: 196 FEATURE REGION 63 source SEQUENCE: 196 | moltype = AA length = 390 Location/Qualifiers 1..390 note = misc_feature - NADP-dependent_malic_enzyme_(EC_1.1.1.40) [Oanc] Tr;; Clostridium_asparagiforme_HB452c 1..390 mol_type = protein organism = Clostridium asparagiforme |
| SEQ ID NO: 197 FEATURE REGION source SEQUENCE: 197 | moltype = AA length = 483 Location/Qualifiers 1..483 note = misc_feature - Acetylcoenzyme_A_carboxyl_transferase_alpha_chain_(EC_6.4.1 .2)[\m]Clostridium_asparagiforme_HB452c 1..483 mol_type = protein organism = Clostridium asparagiforme |
| MSNSAQASAS SRIAALLDEN SFVEVGAYIT ARTTDFNMTE QETPADGVVT GYGTIEGCLV YVYSQDASVL CGSMGEMHAK KISNIYSMAM KMGAvgVIGLI DCAGLRLQEA TDALAGFGQV YLNQTMASGV IPQISAIFGT CGGGMAVSAA ITDFTFMEDK SAKLFVNAPN ALKGNYTSCK DTSSAAQOSA EAGLVDFTGD EASTLGQIRR LVSILPSNNE DDMSYGECDQ DLNRISGELA GCAGDTALAL SIISDNNNFFM EVKKNYDPSM VTGFIRLNQ TVGCVANRSE VYENGEKTAE YPEVLSAKGC DKAADFINFO DSFNIPVLSL VNVKGYKASK CTEKLIAKAA GRLTYAYANA SVPKVTVIVK DALGSAYLTM GSKSIGADVV YAWENAAIGM MDPAEAVKIM YAKEIEAAED | 60 120 180 240 300 360 390 |

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SVALISEKTA QYAALQSSAL AAARRGYIDD IIKAGETRQR VIAAFEMLFT KREDRPSKKH 480
GTV 483

SEQ ID NO: 198      moltype = AA length = 381
FEATURE          Location/Qualifiers
REGION           1..381
note = misc_feature -
Oxaloacetate_decarboxylase_beta_chain_(EC_4.1.1.3)_MethylmalonylC oA_decarboxylase_beta_chain_(EC_4.1.1.41)[0anc]Tr;;
Clostridium_asparagiforme_HB452c
63 source        1..381
mol_type = protein
organism = Clostridium asparagiforme

SEQUENCE: 198
MDPGTIVNNL LDQMAFFHLQ PGNYAMIGVA LVFLFLAIKK GFEPLLLIPI SFGMILLVNIY 60
PEIMYSPEQT SNGTGGLLWY FFQLDEWSIL PSLIFLGVGIA MTDFGPLIAN PISFLMGAAA 120
QVGIYSAYFF AILLGFNGKE AAAISIIGGA DGPTSLFLCS KLGQSQIMGP IAVAAYSYMA 180
LVPIIQPQVM KLLTTTEKERK IKMBQLRPVS KLEKILFPII VTIVVCLILP STAPLVGMLM 240
LGNLFRECGV VKQLAETASN ALMYIVVILL GTSVGATTSA EAFLNWTLIK IVGLGLVAFI 300
FTGAGGVLLG KLLCKITGGK INPLIGSAGV SAVPMAARVS QKVGAEADPT NFLLMHAMGP 360
NVAGVIGTAV AAGTFMAIFG V 381

SEQ ID NO: 199      moltype = AA length = 470
FEATURE          Location/Qualifiers
source           1..470
mol_type = protein
organism = Clostridium asparagiforme

SEQUENCE: 199
MAEIEKKPKV IVETVLRDAH QSLLATRMST DQMLPIVDKM DQVGYYAVEC WGGATFDSC 60
RFLKEDPWER LRKLRLAGFKN TKLQMLFRQW NILGYNHYAD DVVEYFVQKS IANGIDIRI 120
FDCLNDIRNL RTAVKATNKE KGHAQIACRY TLGDAYTLDY WKNIAREIED MGADSLCIKD 180
MAGLLTPYAA AELVTALKEG TSLPIDLHTH YTSGVASMTY LKAVEAGCDI IDCAMSPLAL 240
GTSQPATEVM VETFRGTPYD TGYDQTLLAE IADHFQPIRD QALKSGLLNP KVGVNIKTL 300
QYQVPGGMLS NLVNQNLKEAG QEDKYRQVLE EIPRVRKDFG EPPLVTPSSQ IVGTOAVLNV 360
IMGERYKMPV KESKIMLGE FGQTVKPFNP EVQKKIIGDE TPITCRPADL IEPQLPQFEK 420
DCAQWKQQDE DVLSYALFPQ VAKDFFIYRE AQQTKVDQTV ADKNSKAYPV 470

SEQ ID NO: 200      moltype = AA length = 116
FEATURE          Location/Qualifiers
REGION           1..116
note = misc_feature -
4-carboxymuconolactone_decarboxylase_(EC_4.1.1.44)[0anc]Tr;;
Clostridium_asparagiforme_HB452c
63 source        1..116
mol_type = protein
organism = Clostridium asparagiforme

SEQUENCE: 200
MKDVRTMLND FVGGGLGKLGE TNEAHVQAFM NLLGTNYAEG ALSVKTKELI SVAIGAYNRC 60
EYCIVYHVYK AYEAGATREE IIEAMIAVA FGGGPMAYS VTTLMADVNE FEHDFD 116

SEQ ID NO: 201      moltype = AA length = 295
FEATURE          Location/Qualifiers
REGION           1..295
note = misc_feature -
Phosphatidylserine_decarboxylase_(EC_4.1.1.65)[0anc]Tr;;
Clostridium_asparagiforme_HB452c
63 source        1..295
mol_type = protein
organism = Clostridium asparagiforme

SEQUENCE: 201
MKHNASTNAG PRDGFQDKLL QLIYNHALGR ALILPFTHPV ISKIGGYCMD SSLSRILIPS 60
FIRTAHIDLQ CELPAGGRY RSFNFDFTRR LLPQARPFPDP DPLTLASPCD ARLTAYSIISP 120
RRVFHIKQTA YRLEDLRLDP KLARRFAGGT ALVFRRLCVDD YHRYAWPDGG LRAHYRKIPG 180
RLHTVNPVAN DHFPIYKENC REYTVVRSPQH FTGTYLMMEVG ALMVGRKIVNH HTGYTRLDM 240
RGQEKGYFAF GGSTIVLLFM PGAVELDEPI LQASARGEET RVRMGQRIGR AARRQ 295

SEQ ID NO: 202      moltype = AA length = 395
FEATURE          Location/Qualifiers
REGION           1..395
note = misc_feature -
NADH-dependent_butanol_dehydrogenase_A_(EC_1.1.1.1)[0anc]Tr;;
Clostridium_asparagiforme_HB452c_Assembly
63 source        1..395
mol_type = protein
organism = Clostridium asparagiforme

SEQUENCE: 202
MNNFEFYPTPT RMIFGRGTHL QVGKIVKEYG FKKVLVHPGG ASAKKTGLLD AVCGALEAEG 60

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|-------------|-------------|------------|------------|------------|-------------|-----|
| IGYVQLGGVQ | ANPTLSMAKK | GIELCLAEKA | DFVLAVGGGS | VIDSAKCIAD | GAGNPGVDW | 120 |
| KFFTKEAAPA | GALPGVGTILT | LSASGSEMSA | SCVITNEENG | LKRGFNSTH | RPLFSICNPE | 180 |
| LYTYTVNRQQT | CGCTVTDIMMH | TLERYMGGTT | KETPLTDRIA | EGLLKTVAEA | GAVALDRPEN | 240 |
| YEARATLMWA | GSLSHNDLTS | AGRAFMMQVH | QMBEHELSGY | PQIAHAGGLS | ALWPWSWARYV | 300 |
| CAAWPERFAQ | YAVRVWNLEM | NFENPMETAL | AGIKVTEDYF | KSLNMPTNIR | DLGVEPEKID | 360 |
| EMAEKCTNFG | TRTLPGIREL | GKAEMMEIYR | MAMEA | | | 395 |

| | | | | | |
|--------------------------------------|--|--------------|------------|-------------|-----|
| SEQ ID NO: 203 | moltype = AA | length = 504 | | | |
| FEATURE | Location/Qualifiers | | | | |
| REGION | 1..504 | | | | |
| note = misc_feature - | | | | | |
| 63 | UbID_family_decarboxylase_Lactobacillus_brevis_type[0anc]Tr;; | | | | |
| source | Clostridium_asparagiforme_HB452c_Assembly | | | | |
| 1..504 | | | | | |
| mol_type = protein | | | | | |
| organism = Clostridium asparagiforme | | | | | |
| SEQUENCE: 203 | | | | | |
| MQNQINDLRS A LELLRNLPQG | LAETDVPVPD | MAELAGGVYR | VGAGGTVMP | TKEGPAMIFN | 60 |
| NIKGHPGARI AIGLLASRDR | VAALFGCKPQ | QLSRTLLEAV | EHPIPPVLTA | KVPPCQQVHH | 120 |
| LASDPDPFDLR TLI PAPNTNP | VDAGPYLTIG | MCYATHPDIG | ESDVTIHRMC | ILGRDELSIF | 180 |
| FTP GIGRIGHA MALRAEELGR | PLPIISISIVG | DPVIEISSCF | EPPTTPLGFD | ELSIAGALRG | 240 |
| EPVQMCRLT VEEKAIAANAE | YVLEGEIIPG | VRVTEDCNTH | TGYAMPFFPG | YTGPSSECC | 300 |
| LIKVKAVTHR ENPIMQTCIG | PSEEHVSMTG | ICTEASILAM | AEKAMPGKLT | NICCPSSGGG | 360 |
| KYMAVLQFKK SVPSDEGRQR | QAALLAFAAF | SELKHVFLVD | EDVDCFDMDK | VFWAMSTRFQ | 420 |
| ADQDVIAIPG VRCHPLDPSN | DPGFSPSIRD | HGIACKAIFD | CTVPYDQKAR | FKRAEFLEVD | 480 |
| PSRWLEKTAG SPQWQEVKAC | AQND | | | | 504 |
| SEQ ID NO: 204 | moltype = AA | length = 526 | | | |
| FEATURE | Location/Qualifiers | | | | |
| REGION | 1..526 | | | | |
| note = misc_feature - | | | | | |
| 63 | Arginine_decarboxylase_(EC_4.1.1.19)_Lysine_decarboxylase_(| | | | |
| source | EC_4.1 .1.18)_Ornithine_decarboxylase_(EC_4.1.1.17) [0anc]Tr;; | | | | |
| 1..526 | Clostridium_asparagiforme_HB452c | | | | |
| mol_type = protein | | | | | |
| organism = Clostridium asparagiforme | | | | | |
| SEQUENCE: 204 | | | | | |
| MRREERLISR LKAYNETDMY | PFHMPGHKRL | AGAGDGEDEM | LEFPNPFTVD | IITEIEGFNDL | 60 |
| HPPEGILRES MEWAAGVYGA | DRTYYLVNGS | SGGILAAISA | AAGFESRILT | ARNCHKSVYH | 120 |
| AVYLNRLKPV YLYPQTVPGL | GIQGGILPED | VEKSLRQYPD | TRAVMVVSPT | YDGIVSDIHK | 180 |
| IAEIVHRAGL PLIVDEAHGA | HFRYGRFPQ | SALELGADLV | IQSIIKTLPS | LTQTAILLHVN | 240 |
| LNRDKGGPVY DGRLERFLQ | IYQSSSPSYV | LMASIENAVW | LMERLRLDRG | APGNAIDRYM | 300 |
| ERMGRRLRDNL SKMRCRLLAG | EWLKGSCGVW | DTDMSKVVIS | TAGTGMTGTE | LDGILRELYH | 360 |
| LEMEMCPEY ATAITSVMDS | GEGLDRLEAA | VMKIDRELAQ | KLEKTGNPNQ | GGWAGTGGAD | 420 |
| AAANSPALPL ASQTCAPFP | LRSIIMPIASA | MDKDLERVAL | RESGGRISGE | YIYIYPPGIP | 480 |
| IVAPGEEISG EALDLVLRFM | EQGLPVQGPQ | DRALEWLVV | RQNIDR | | 526 |
| SEQ ID NO: 205 | moltype = AA | length = 131 | | | |
| FEATURE | Location/Qualifiers | | | | |
| REGION | 1..131 | | | | |
| note = misc_feature - | | | | | |
| 63 | Biotin_carboxyl_carrier_protein_methylmalonylCoA_decarboxyl | | | | |
| source | ase[\m]Clostridium_asparagiforme_HB452c | | | | |
| 1..131 | | | | | |
| mol_type = protein | | | | | |
| organism = Clostridium asparagiforme | | | | | |
| SEQUENCE: 205 | | | | | |
| MKSYTITVNG KAYAVTVEEG | AASGVAAAPA | AAVAVAPAPA | APAPAAAPAP | APAAAPAGAA | 60 |
| GAVKVTAAMP GKVGVKASA | GQAVKKGDTI | LVLEAMKMEN | DIVAPQDGTV | ASINVSTGDS | 120 |
| VESGAVLATL N | | | | | 131 |
| SEQ ID NO: 206 | moltype = AA | length = 305 | | | |
| FEATURE | Location/Qualifiers | | | | |
| REGION | 1..305 | | | | |
| note = misc_feature - | | | | | |
| 63 | Orotidine_5'-phosphate_decarboxylase_(EC_4.1.1.23) [0anc]Tr;; | | | | |
| source | Clostridium_asparagiforme_HB452c | | | | |
| 1..305 | | | | | |
| mol_type = protein | | | | | |
| organism = Clostridium asparagiforme | | | | | |
| SEQUENCE: 206 | | | | | |
| MJQQOLIEKIK KTKAPICVGL | DPMMLNYIPEH | ILKKSYSEFG | ETLEGAADAI | WQFNKEIVDH | 60 |
| TYDLIPSVKP QIAMYEQFGI | EGLKSYQKTV | DYCQEKGLLV | IGDAKRGDIG | STSAAyatgh | 120 |
| LGKVQVGKGT YSGFHTDFLT | VNPYLGTDGV | KPFVDCNSD | DKGLFVLVKT | SNPSSGEFQD | 180 |
| LGIDGRPLYE LVAEKVVEWG | DTCMGDYDSN | VGA VVGATYP | EMSKVLRKLM | PRTYFLVPGY | 240 |
| GAQGGTAADL AHCFNEDGLG | AVVNSSRGII | AA YRQEKYKQ | FGPEHFAEAS | RQAVIDMVAD | 300 |

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| | |
|--|---|
| INSVL | 305 |
| SEQ ID NO: 207 | moltype = AA length = 395 |
| FEATURE | Location/Qualifiers |
| REGION | 1..395 |
| | note = misc_feature - |
| | <i>Phosphopantothenoylcysteine_decarboxylase_(EC_4.1.1.36)_/_P</i> |
| | <i>phospho pantothenoylcysteine_synthetase_(EC_6.3.2.5) [Oanc]Tr; ;</i> |
| 63 | <i>Clostridium_asparagiforme_HB452c</i> |
| source | 1..395 |
| | mol_type = protein |
| | organism = <i>Clostridium asparagiforme</i> |
| SEQUENCE: 207 | |
| MLKDKTVLLG VTGSIAAYKI ASLASMLVKQ GAKVQVLMTNATNFINPIT FETLTGRKCL | 60 |
| VDTFDRNFEF SVEHVSIAKA ADVVMIAVAS ANVIAKLAHG LADDMLTTV LACRCKIIA | 120 |
| PAMINTNMYEN PIVQDNLKVC ERYGMEVIAP ATGYLACGDT GAGKMPEPEV LFYEIVREIA | 180 |
| FGKDLAGKRV LVTAGPTRES IDPVRFITNR STGKMGYAVA RAAAYRGARV TLVTGPVNWK | 240 |
| PPMFVDVVPV ESAREMFEAV TSRSGEMDMI VKSAAVADYR PGTVGAEKIK KSDGDMSIAL | 300 |
| ERTDDILGWL GSHRREGQIL CGFSMETQNM LENSAAKLEK KHVDIMIVANN LKVSGAGFGT | 360 |
| DTNVVTFITK DGAEELPLIT KDEVAHRLLD RLMGL | 395 |
| SEQ ID NO: 208 | moltype = AA length = 482 |
| FEATURE | Location/Qualifiers |
| REGION | 1..482 |
| | note = misc_feature - <i>Arginine_decarboxylase_(EC_4.1.1.19) [Oanc]Tr; ;</i> |
| 63 | <i>Ruminococcus_gnavus_HB40</i> |
| source | 1..482 |
| | mol_type = protein |
| | organism = <i>Ruminococcus gnavus</i> |
| SEQUENCE: 208 | |
| MKNLSQENAP IYEALERFRR MRIVPFDPVG HKHGRGNKEL VELLGERCVS IDVNSMKPLD | 60 |
| NLCHPVSVIK DAEQLAAEAF HASHAFLMVG GTTSSVQAMV LSCCKKGDKI ILPRNVHRSV | 120 |
| INALVLCGAI PIYVNDVDH DLGISLGMKV SOVERAIQKH PDAVAVFVNN PTYYGICSDL | 180 |
| RSIVKKAAAH GMVKVLVDEAH GTHPYFGENL PVSAMEAGAD MASVSMHKSG GSLTQSSFL | 240 |
| VGPSMHAGVV RQIINLTQTT SGSSYLLSSL DISRRRNLLVR GKESFARVAA LADYAREEIN | 300 |
| RIGGYYAFSK ELINGDSIYD FDTTKLSIHT LEIGLAGIEV YDILRDEYDI QIEFGDIGNI | 360 |
| LAYLSIGDRI QEIERLVSAL AEVKKRKYQKD KTGMLSQBYI EPEVIMSPQD SFYABKEAVP | 420 |
| IREESEGRICS EFVMCYPPGI PILAPGEKIT KDVIEYILYA KEKGCSMTGP EDDAAIEYLN | 480 |
| LV | 482 |
| SEQ ID NO: 209 | moltype = AA length = 385 |
| FEATURE | Location/Qualifiers |
| REGION | 1..385 |
| | note = misc_feature - |
| | <i>209NADHdependent_butanol_dehydrogenase_A_(EC_1.1.1.) [Oanc]Tr; ;</i> |
| 63 | <i>Ruminococcus_gnavus_HB40_Assembly_20200511.fasta_[Oanc]Tr; ;</i> |
| 63 | <i>33038.681</i> |
| REGION | 1..385 |
| | note = misc_feature - |
| | <i>NADHdependent_butanol_dehydrogenase_A_(EC_1.1.1.) [Oanc]Tr; ;</i> |
| 63 | <i>Ruminococcus_gnavus_HB40_Assembly_20200511.fasta_[Oanc]Tr; ;</i> |
| 63 | <i>33038.681</i> |
| source | 1..385 |
| | mol_type = protein |
| | organism = <i>Ruminococcus gnavus</i> |
| SEQUENCE: 209 | |
| MENFNFCVGT RILFGKGQEE KLPPELLRPYG NKVLLTYGGG SIKRTGLYDR IKNLLHEFEI | 60 |
| FELGGIEPNP RIESVYAGAE ICREEDIDVI LAVGGGSTID CSKAIAAAAY YEGDAWDLIL | 120 |
| HDPRIEKALP ICTVLTLSAT GSEMDNGGV1 TNLKTKEKLG FGNPLLPPKA SVLNENTFT | 180 |
| VSASQTAAGS ADIMSHILEV YFDTRRAAVP DRISEGLLKT VIQYAPIAVR EPENYEARAE | 240 |
| LWMTSSLAIN GICSTGKDCA WSCHPMEHEL SAYDITHGV GLAILTPRWM RYILNEHTVE | 300 |
| KFAEYAKNVW GIEEKADLFE TANAGIDATE EFLKSLGIPM TLSEVGITEE YFTEMAEHAV | 360 |
| IFGGLSEAYV PLKAEDVVNI YRMCM | 385 |
| SEQ ID NO: 210 | moltype = AA length = 382 |
| FEATURE | Location/Qualifiers |
| REGION | 1..382 |
| | note = misc_feature - <i>L-threonine_phosphate_decarboxylase [Oanc]Tr; ;</i> |
| 63 | <i>Ruminococcus_gnavus_HB40</i> |
| source | 1..382 |
| | mol_type = protein |
| | organism = <i>Ruminococcus gnavus</i> |
| SEQUENCE: 210 | |
| MTNSEKALQM HEQWNGKLET AAKAHVNSRE DLAIAYTPGV AEPCKVIAKD PEAAYKYTIK | 60 |
| SNTVAVVSDG SAVLGLGNIG ALAAMPVMEG KAVLFKEFGG VNAPVICLDT QDTEEIITV | 120 |
| VNIAPAFGGI NLEDISAPRC FEIEERLKEL LDIPVFHDDQ HGTAIVVLAG IINALKVTGK | 180 |
| KKEDCRVVVN GAGSAGVAIT KLLLTYGFH ITMCDINGII SSASPNLNWQ QKKMTEVTNL | 240 |

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ENKTGSLTDA MRGADIFVGV SAPGIVTKEM VASMNSDAIL FAMANPVEI MPDLAKEAGA 300
RVVGTGRSDF PNQVNINNVAF PGIFKGALEG RATQITEEMK LATANAIASL VSDEELNENN 360
ILPEAFDSRV ADVVSKAVKE LI 382

SEQ ID NO: 211      moltype = AA length = 371
FEATURE           Location/Qualifiers
REGION            1..371
note = misc_feature - L-threonine_phosphate_decarboxylase[0anc]Tr;;
63                 Ruminococcus_gnavus_HB40
source             1..371
mol_type = protein
organism = Ruminococcus gnavus

SEQUENCE: 211
MNTKLEFHGS DIEKVCEHYG LKKDDIVNFG ANVNPLGLQE QVKKALAAHL DLLSSYPDRS 60
YTSLRNLST YCQIPADFL PGNGSSELIS LLTEERRPKH TMILGPTYSE YSRELGFSDS 120
TIDCFYKLPE QDFQLSVEEL CLALAKKQID FLILCNPNNP TSSAIFHPEL IKLLEFCQDH 180
NIFVMIDETY VEFAPDVDAV TAVPLTQNFPQ NLMLVRGVSK FFAAPGMRFQ YGITGNAEFL 240
KLLKSKQIPW SLNSLGAFAG ELLFQDKKEYI KKTRNLILSE REYMYTKLRE LPFFYVYPAY 300
ANFLLVQIQK DGLTSSDVFE ACIREGLMIR DCSSFTGLEG EFVRCIMDP EDNRRLLTVF 360
QKISQSARKQ V 371

SEQ ID NO: 212      moltype = AA length = 289
FEATURE           Location/Qualifiers
REGION            1..289
note = misc_feature -
63                 Phosphatidylserine_decarboxylase_(EC_4.1.1.65) [0anc]Tr;;
source             1..289
Ruminococcus_gnavus_HB40
mol_type = protein
organism = Ruminococcus gnavus

SEQUENCE: 212
MKLADRRGNI EECSSGQDRL LEWIYTHETG RFLMKGLINP HISEIGAAFL DSRASRVLIA 60
WFIRKNKIPM YQYEQKKYRS FNEFFKRKAL PGARRIIREP ERLISPDCGR LSVYKIEENS 120
RFQIKHTSYS TESLLKNEGL AKRYAGGYAW VFRLCVEDYH RYIYVDDGVK SENVKIPGVL 180
HTVNPVANDS PFIYKENARE FSLLCSHENFG TVLMMEVGAM MVGKINRHQ AARVRRGQEKG 240
GNFAFGGSTI ILLTQKGKAM PDPIWENSL NGIETKVRLG ESVGRGKRR 289

SEQ ID NO: 213      moltype = AA length = 155
FEATURE           Location/Qualifiers
REGION            1..155
note = misc_feature -
63                 Uroporphyrinogen_decarboxylase_(UROD) [0anc]Tr;;
Ruminococcus_gnavus_HB40
1..155
mol_type = protein
organism = Ruminococcus gnavus

SEQUENCE: 213
MLDKMKGCKN FILAPGCDMP YDVPVENAIG VAQAVYETDS VREMLKNYVA EDEDIEVELP 60
DYEHLEKPLV EVFTLDSATC AACTYMMGAA NEAKKTFGDA IDMVEYKFTL KENIARCKKM 120
GVPNLPSMYI NGELKFRSLV PSKEELEGAI RAAMK 155

SEQ ID NO: 214      moltype = AA length = 471
FEATURE           Location/Qualifiers
REGION            1..471
note = misc_feature -
63                 Oxaloacetate_decarboxylase_alpha_chain_(EC_4.1.1.3)_Methylm
alonyl CoA_decarboxylase_alpha_chain_(EC_4.1.1.41) [0anc]Tr;;
Ruminococcus_gnavus_HB40
1..471
mol_type = protein
organism = Ruminococcus gnavus

SEQUENCE: 214
MAEIAKKPIK ITETILRDAH QSLIATRMTT EQMMPPIVDKMK DVGYHAVEC WGGATFDASL 60
RFLHEDPWER LRKFRDGFKN TKLQLMLFRGQ NILGYRPYAD DVVEYFVQKS AANGIDIIRI 120
FDCMNDMRNL QTAVTAANKE KAHAQVAMS YTLGDAYTLE WVELAKRIED MGANSICVKD 180
MAGLLCPYQA TELVTALKEA VEIPIEMHTH YTSGVASMTY LKSVEAGADI IDTAMSPFAL 240
GTSQPATEVM VETFKGTPYD TGQLDNLLAE IADYFRPIRD EALESGLNLP KNLGVNIKTL 300
LYQVPGGMLS NLTSQLKEQQ AEDKPYEVLE EVPRVRKD LG EPPLVTPSSQ IVGTOAVFN 360
LMGERYKMAT KETKDVLSGK YGATAKPFNP EVQKKVIGED AEVITCRPAD LIPNELDTLR 420
KECAQYSQD EDVLTYALFP QVATDFFKYL DAQQTKVDAK VADTEDGAYP V 471

SEQ ID NO: 215      moltype = AA length = 383
FEATURE           Location/Qualifiers
REGION            1..383
note = misc_feature -
Oxaloacetate_decarboxylase_beta_chain_(EC_4.1.1.3)_Methylma

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63                               lonylC oA_decarboxylase_beta_chain_(EC_4.1.1.41) [Oanc]Tr;;
source                         Ruminococcus_gnavus_HB40
1..383
mol_type = protein
organism = Ruminococcus gnavus

SEQUENCE: 215
MEYISNTLGN LVEQTAFMNL TFGNLIIMAV ACFFLYLAIR HGFEPLLLVP IAFGMLLVNI 60
YPDIMALHAED SANGTGGGLY YFYVLDWEWI LPSLIFLGVG AMTDFGPLIA NPKSFLLGAA 120
AQPGIFAAYL GAMAMGFSDK AAAAISIIGG ADGPTSIFLA GKLQQTAILG PIAVAAYSYM 180
SLVPIIQPPI KMLLTTEER KIKMEQLRPV SKLERILFPI IVTIVVCTIL PTTAPLVGML 240
MILGNLFKESG VVRQLTETAS NALMYIVVIL LGTSVGVATTES AEAFLNMDTL KIVALGLIAF 300
AFGTAAGVLF GKLMCWATKG KVNPPLIGSAG VSAVPMAARV SQKVGAEADP TNFLLMHAMG 360
PNVAGVIGTA VAAGTFMAIF GVK 383

SEQ ID NO: 216      moltype = AA length = 258
FEATURE           Location/Qualifiers
REGION            1..258
note = misc_feature -
63                           MethylmalonylCoA_decarboxylase_deltasubunit_(EC_4.1.1.41) [Oanc]Tr;;
source                         Ruminococcus_gnavus_HB40
1..258
mol_type = protein
organism = Ruminococcus gnavus

SEQUENCE: 216
MKKKLSSLVL ACALTLGVSG CGSEADTTTS NEKESMVSYSS EAIVSSFSQQT PDEVFDQYEE 60
MSELQLDDML LNTGLPVDE NFLSMIEAWK AGEAEKGAFK SYGEFETEMT SSGIVVSTEA 120
EYENKTADIE PTFDDEEQMDT SLTINAHYST AEILKKAGLN TILGMGTVFV VLIFISFIIS 180
LFRFPIPELEK KFKNKKTAEP AKAPAPAPVP VAEPAEEDDS DDAELVAVIS AAIAAAEGTS 240
ADGFVVRSIK RRKSNKWN 258

SEQ ID NO: 217      moltype = AA length = 477
FEATURE           Location/Qualifiers
REGION            1..477
note = misc_feature - Pyridoxaldependent_decarboxylase [Oanc]Tr;;
63                           Ruminococcus_gnavus_HB40
1..477
mol_type = protein
organism = Ruminococcus gnavus

SEQUENCE: 217
MIGTEYILNS TQLEEAIKSF VHDPCAEKHE IHDPQVVEA KEHQEDKIKQ IKIPEKGRPV 60
NEVVSEMMNE VVRYRGDAH PRFFSFVPGP ASSVSWLGDII MTSAYNIHAG GSKLAPMVNC 120
IEQEVLKWLA KQVGFTGNPG GFVVGGSMA NITALTAARD NKLTDINLHL GTAYISDQTH 180
SSVAKGLRII GITDSRIRRI PTNSHFQMDT AKLEEVIEAD KKSGYIPFVV IGTAGTTNTG 240
SIDPLTEISA LCKKHDMWFH IDGAYGASVL LSPKYKSLLN GTELADSIW DAHKWLQFTY 300
GCAMVLVKDI RNLFHFSFHVN PEYLKDLEND IDNVNTWDIG MELTRPARGL KLWLTLQVLG 360
SDLIGSAIEH GFQLAVWAEE ALNSKKDWEI VSPAQMAMIN FRYAPKDLTK EEQDILNEKI 420
SHRILESGYA AIFFTTLNGK TVLRICAIHP EATQEDMQHT IDLLDQYGRE IYTEMKG 477

SEQ ID NO: 218      moltype = AA length = 155
FEATURE           Location/Qualifiers
REGION            1..155
note = misc_feature -
63                           Uroporphyrinogen_decarboxylase_(UROD) [Oanc]Tr;;
source                         Ruminococcus_gnavus_HB40
1..155
mol_type = protein
organism = Ruminococcus gnavus

SEQUENCE: 218
MLDKMKGCNN FILAPGCDMP YDVPVENAIG VAQAVYETDS VREMLKNYVA EDEDIEVELP 60
DYEHLEKPLV EVFTLDSATC AACTYMMGAA NEAKKTFGDA IDMVEYKFTL KENIARCKKM 120
GVPNLPSMYI NGELKPRSLV PSKEELEGAI RAAMK 155

SEQ ID NO: 219      moltype = AA length = 372
FEATURE           Location/Qualifiers
REGION            1..372
note = misc_feature -
63                           Carboxynorspermidine_decarboxylase_(EC_4.1.1.96) [Oanc]Tr;;
source                         Ruminococcus_gnavus_HB40
1..372
mol_type = protein
organism = Ruminococcus gnavus

SEQUENCE: 219
MKREELRPC YVIMESEMKK NLQILQEIRQ QSGCKILLAQ KAFSMYSCYP LIGEYLDGTT 60
ASGLYEAQLG KECMGKENHI FSPAYREDEF EEVLESCEHL VFNSFSQLER FGERAAKAGK 120
SVGIRVNPEC STQGEHAIYD PCAPGSRLGI LVSEFPETLP SYVEGLHFHT LCEQNADALE 180
ITLKAVEEKF GKWMKQLKWW NFGGHHITR ADYDRELLIS CVRRIQDTYN VQVYLEPGEA 240
VALNAGHLIT TVEDIVHNDI AVLDVSAACH MPDVIEMPYR PPLFDSGEAK EKEYTYLLGG 300

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PTCLAGDVIG SYSFDQPLKV GDRLTGDMIA IYTTVKNNTF NGMRLPDIVW ERESGECEIV 360
KSFGYEDFKC RL 372

SEQ ID NO: 220      moltype = AA length = 397
FEATURE          Location/Qualifiers
REGION           1..397
note = misc_feature -
    Phosphopantothenoylcysteine_decarboxylase_(EC_4.1.1.36)_/_P
    phospho pantothenoylcysteine_synthetase_(EC_6.3.2.5) [0anc]Tr;;
    Ruminococcus_gnavus
63               1..397
source          mol_type = protein
                organism = Ruminococcus gnavus
SEQUENCE: 220
MLKGKTVVLA VSGSIAAYKI ASLASALKKL HANVQVLMTK NAVNFINPIT FESLTGNKCL 60
VDTFDRNFQY SVEHVALAKQ ADVVLVAPAS ANVIGKIAHG IADDMLTTV MACKCKKIIA 120
PAMNTNMPDN PILQDNLKIL EHYGYEVISP AVGYLACGDT GAGKMPPEL LLQYLREIA 180
YEKDMQGKRV LVTAGPTQES IDPVRFITNH STGKMGYAIKA KMCMRLGAEV TLVSGPTSTA 240
KPEFVHVVDV VTAKEEMYEEV TKRAKDQDII IKAAAVADYR PKSVSSEKMK KKDDDLAIPM 300
ERTDDILKFL GEHKKEHQFL CGFSMETENM LENSRKKLEK KHLDIMIVANN LKVEGAGFAG 360
DTNVVTIITG QEEVSLGKMT KEETALRILD EILKATN 397

SEQ ID NO: 221      moltype = AA length = 424
FEATURE          Location/Qualifiers
REGION           1..424
note = misc_feature -
    Diaminopimelate_decarboxylase_(EC_4.1.1.20) [0anc]Tr;;
    Ruminococcus_gnavus_HB40
63               1..424
source          mol_type = protein
                organism = Ruminococcus gnavus
SEQUENCE: 221
MNKTPFVTKP QLDEIVKTYP TPFHLYDEMG IRENVKALRE AFSWNNECYKE YFAVKACPNP 60
FLIDILCPYD CGCDCSSYSTE LMLMSDAIGVK GQDIMFSSND TPADEVYVLAE KLGAIINLDD 120
FTHIDFLEKT IGYIPETISC RYNPGGLFKI SNDIMDNPGD AKYGMTEQL FEAFKVLKSK 180
GAKEFGIHAIF LASNTVTNDY YPMPLAKVLFE QAVKLQKETG VHVKFINLSG GIGIPYTPDQ 240
EPNDIRVIGE GVRRVYEEVL VPAGMDVAI YTELGRFMMG PYGCLVTTAI HEKHHTKEYI 300
GVDACAVDLM RPAMYGAYHH ITVMGKEDAP HDHKYDVTGS LCENNNDKFAI DRMLPEIEKG 360
DYLVIHDTGA HGFAMGYSYN GKLKHAELLL KEDGSVQMMIR RAERPADYFA TFDCFDIGKK 420
LIKN 424

SEQ ID NO: 222      moltype = AA length = 321
FEATURE          Location/Qualifiers
REGION           1..321
note = misc_feature -
    Orotidine_5phosphate_decarboxylase_(EC_4.1.1.23) [0anc]Tr;;
    Ruminococcus_gnavus_HB40
63               1..321
source          mol_type = protein
                organism = Ruminococcus gnavus
SEQUENCE: 222
MFCFPFLENRE EEKMINKLVA KIKETKAPIV VGLDPMLNYI PEHVQKKAFA EFGETLEGAA 60
EAIWQFNKEI VDKTYDLIPA VKPQIAMYEQ FGVPVGIEAFK KTVDYCKSKD LVVIGDIKRG 120
DIGSTSAAYA VGHGLGSVKVG SKEYVPFDED FATVNPYLGSS DGVNPFIDVC KEHKKGLFIL 180
VKTSNPSSGE PQDQLIDGKP LYELVGEKVA QWGADCAGDE YSYIGAVVGA TYPEMGKVLR 240
KVMPKSYILV PGYGAQGGQQG KDLVHFFNED GLGAIVNSSL GIIAAYQEA YAKFGAENFG 300
DASRAAVEAM VADIQALEA R 321

SEQ ID NO: 223      moltype = AA length = 122
FEATURE          Location/Qualifiers
REGION           1..122
note = misc_feature -
    Biotin_carboxyl_carrier_protein_methylmalonylCoA_decarboxyl
    ase_Bi_otin_carboxyl_carrier_protein[0anc]Tr;;
    Ruminococcus_gnavus_HB40
63               1..122
source          mol_type = protein
                organism = Ruminococcus gnavus
SEQUENCE: 223
MNYYTITVNG NYYDVTVEEK GAGAVPVAPT VPKAAPKAAP APAPKAAPAG AGSIQVKAGA 60
AGKVFSDAS VGQAVKAGDA IVTVEAMKME IPVVAPEDEGT VASIDVAVGD AVESGAVLAT 120
LN 122

SEQ ID NO: 224      moltype = AA length = 478
FEATURE          Location/Qualifiers
REGION           1..478
note = misc_feature -

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source          Acetylcoenzyme_A_carboxyl_transferase_alpha_chain_(EC_6.4.1.
                .2) /
                Acetylcoenzyme_A_carboxyl_transferase_beta_chain_(EC_6.4.1.
                2) [\m] Ruminococcus_gnavus_HB40
SEQUENCE: 224
MSNNATENSA SRRIATLLDG GSFVEIGSAV TARNTDFNLQ EKETPADGVI TGYGVIDGNL 60
VVVYSQDASV LKGAI GEMHA KKI NAYDMA MKMGAPVIGL IDCAGLRLQEQ ATDALEAFGS 120
LYPKQAMASV VIPQITAVFG MCGGLAVVP GLTDFTFMEN KEKGKLFVNSP NALDGNIDS 180
CINTASABYQS KTAGLVDAAG TEEEILGQIR SLICMLPANF EDDASYDECT DDLNRVCADL 240
ANAAEADTGIA LATISDNNIF FETKREYAKE MVTGFIRLNG MTVGAVANRS KKYDAEGNAE 300
SYGQVLTVDG CKKAADFNFN CDAFSIPVLS LTNTVGFTEAT LEEAKDMARA VAKLTYAFAN 360
ASVPKVNVIV GKAYGSAYIA MNSKSIGADL VYAWPTAEIG MMDASMAAKI MYADADAETL 420
KEKAAEYKEL QSSPVSAARQ GYVDAIIDAA DTRKYVIGAF EMLFLTKREDR PAKKHGT 478

SEQ ID NO: 225      moltype = AA length = 610
FEATURE           Location/Qualifiers
REGION            1..610
source             note = misc_feature - decarboxylase_putative[0anc] Tr;;
                  Enterococcus_durans_HB48
1..610
mol_type = protein
organism = Enterococcus durans

SEQUENCE: 225
MKMDMDIKAVF IGDKAENGAV YKMLLNKMDV EHLGWRENYL PGDLPAISEE DKLAPRYIAT 60
RERMMMTVLDE VSERMRAGS  PWHSAGRYWG QMNAETLMP S LLAYNYAMLW NPNNVALESS 120
MATSQMEAEV GQDFADLFNM TDGWHGHTAD GSIA NLEGWLW YARCIKSIPL AVKEVFPKV 180
ENKTEWELLN LSVEEILLEM 1 EKFTDEELDA VKAASSRSRK HIQELGKWLW PQTKHYSWMK 240
ALDICGVGLD QMIAIPVQED YRMDVAELEK TIRELAEQK  PILGVVAVVG TTEEGQVDSV 300
DKIVELREKL RGEGLYFYHL VDAAGGGYAR SLFLNEAGEF VPYESLTEFV EEHQVFHVQ 360
KIDKSVYDGF KAITEADSVT IDPHKMGYVP YAAGGIVIKH KNMRNIISYF APYVFEKSVK 420
APDMLGAYIL EGSKAGATAA AVWTAHVRVLP LNVTGYGOLI GASIEAAQRF REFLQLSFT 480
VKGKTIEVHP LNHPDFNMF D WVFKVQDCTD LKKINDLNEK MFDVSSYMDG DVYDERFITS 540
HTTFTKADYG DSPVKPIESL GLSKEEWQKE QQVTLRAAI MTPYLNDDKI FKFYTDAITK 600
AIEKLLNELL 610

SEQ ID NO: 226      moltype = AA length = 188
FEATURE           Location/Qualifiers
REGION            1..188
source             note = misc_feature - Lysine_decarboxylase_family[0anc] Tr;;
                  Enterococcus_durans_HB48
1..188
mol_type = protein
organism = Enterococcus durans

SEQUENCE: 226
MKITIFCGAS NGNNNPIYSQR TVELGEWMIK NNHD L VYGG KVGLMGVIAD TIINNGGGQAI 60
GVMPTFLKDR EIAHINLSEL IVVENMPQRK GKMMALGEAF IALPGGPGLT EEISEVISWS 120
RIGQNDSPCV LYNIDGYFNH LRNMPDHMVS EGFLSQDDR N ILFSDDIIIE IESFIKDYKS 180
PTIRKYSN 188

SEQ ID NO: 227      moltype = AA length = 300
FEATURE           Location/Qualifiers
REGION            1..300
source             note = misc_feature - RALTA_RS15325 phenylalanine
                  4-monoxygenase [ Cupriavidus taiwanensis LMG 19424 ] Gene
                  ID: 29760330
1..300
mol_type = protein
organism = Cupriavidus taiwanensis

SEQUENCE: 227
MSIAMATEAP GAFQGTLTDK LKEQFDAGLL SGQELRPDFT IAQPVHRYTS IDHAIWRKLY 60
ERQAEMLRGR VSDEFQGLA TLGMKEDRVP DFQQLNETLM RATGWQVVAV PGLVPDEVFF 120
EHLANRRFP A SWWMRKPEQL DYLQEPDCFH DVFGHVPLLI NPVFA DYM EA YGKGLKAAG 180
LGALDMLSRL YWYTVEFGLI RTEQGLR IYG AGIVSSQGES IYSLDSASP RIGFDVRRIM 240
RTRYRIDTFQ KTYFVIDSFE QLFDATRPDF APLYEELRAQ PTLGAGDVAP GDQVLNVGTR 300

SEQ ID NO: 228      moltype = AA length = 321
FEATURE           Location/Qualifiers
REGION            1..321
source             note = misc_feature - Mycolicibacterium smegmatis (strain
                  ATCC 700084 / mc(2)155); Histidine
                  N-alpha-methyltransferase, uniprot A0R5M8
1..321
mol_type = protein
organism = Mycolicibacterium smegmatis

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SEQUENCE: 228
MTLSLANYLA ADSAAEALRR DVRAGLTAAP KSLPPKWFYD AVGSDLFQI TRLPEYYPTR 60
TEAQILRTRS AEIIAAAGAD TLVELGSGTS EKTRMLLDAM RDAELLRFI PFDVDAGVLR 120
SAGAAIGAEY PGIEIDAVCG DFEEHLGKIP HVGRRLVVFL GSTIGNLTPA PRAEPLSTLA 180
DTLQPGDSLL LGTDLVKDTG RLVRAYDDAA GVTAAFNRNV LAVVNRELSA DFDLDAFEHV 240
AKWNSDEERI EMWLRARTAQ HVRVAALDLE VDPAAGEEML TEVSCKFRPE NVVAELAEAG 300
LRQTHWWTDP AGDFGLSLAV R 321

SEQ ID NO: 229      moltype = AA length = 206
FEATURE          Location/Qualifiers
REGION           1..206
note = misc_feature - Putative aromatic amino acid
        N-methyltransferase (EC 2.1.1.-) A0A139TQU2 Akkermansia
        sp. KLE1798 tr_A139TQU2_A139TQU2_9BACT
        Uncharacterized protein OS=Akkermansia sp. KLE1798
        OX=1574265 GN=HMPREF3039_01924 PE=4
source            1..206
mol_type = protein
organism = Akkermansia sp.

SEQUENCE: 229
MNTHAKSLNE RLRTLISLIF GLFIGCALLF GETRWETSPV VEESLMLIAC FMAGIGAFGR 60
IWCSLYIAGY KNVLVIEGP YSMCRNPLYF FSFIGGVGA CATEFTVPL LTALAFGIYY 120
PAIIRREQER LISLFGNAYR DYCRTVPSFI PSLSLLKPPP ATYSVNPATF THNIFDALWF 180
IWFIGIFEFI SGLHDAGILP VWFFIP 206

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What is claimed is:

1. A therapeutic composition for increasing serotonin level in a mammalian subject in need thereof, the composition comprising an amount of a live isolated serotonin-increasing bacterial species, dead isolated serotonin-increasing bacterial species, conditioned medium from an isolated, cultured serotonin-increasing bacterial species, cell pellet of an isolated serotonin-increasing bacterial species, a purified metabolite produced by an isolated serotonin-increasing bacterial species, a purified protein produced by an isolated serotonin-increasing bacterial species, or a combination thereof sufficient to increase serotonin level in the subject, and an excipient or carrier suitable for delivery to the gut.
 2. The therapeutic composition of claim 1, wherein the isolated serotonin-increasing bacterial species increases serotonin in at least one of the following ways: production of serotonin; production of secreted metabolites or secreted proteins that induce serotonin production; production of ligands that induce serotonin production; or production of an agonist of a serotonin receptor or the trace amine-associated receptor (TAAR).
 3. The therapeutic composition of claim 1, wherein the isolated serotonin-increasing bacterial species comprises *Bifidobacterium adolescentis*.
 4. The therapeutic composition of claim 1, wherein the serotonin increasing bacterial species comprises one or more species selected from *Enterococcus durans*, *Clostridium lavalense*, and *Clostridium asparagiforme*.
 5. The therapeutic composition of claim 1, wherein the serotonin-producing bacterial species comprises one or more species selected from *Enterococcus durans* HB-48, *Clostridium lavalense* HB-452c, and *Bifidobacterium adolescentis* HB-179.
 6. The therapeutic composition of claim 1, wherein the serotonin increasing bacterial species comprises a 16S sequence at least 95% identical to a 16S sequence selected from SEQ ID NOs: 3, 4, and 12.
 7. The therapeutic composition of claim 1, wherein the serotonin-producing bacterial species produces serotonin under conditions found in the mammalian gut.
8. The therapeutic composition of claim 1, wherein the mammalian subject is a human subject.
 - 9-34. (canceled)
 35. A pharmaceutical composition comprising the therapeutic composition of claim 1, and a pharmaceutically acceptable carrier.
 36. A method of increasing serotonin level in a mammalian subject in need thereof, the method comprising administering a composition of claim 35 to the subject, whereby a serotonin level is increased.
 37. The method of claim 36, wherein the administering is to the gut of the subject.
 38. The method of claim 36, wherein the level of serotonin in the gut is increased.
 39. The method of claim 36, wherein the level of serotonin in circulation is increased.
 40. A method of treating a disease or disorder involving or characterized by low serotonin in a subject in need thereof, the method comprising administering a composition of claim 35 to the subject, whereby the disease or disorder is treated.
 41. The method of claim 40, wherein the administering is to the gut of the subject.
 42. The method of claim 40, wherein the level of serotonin in the gut is increased.
 43. The method of claim 40, wherein the level of serotonin in circulation is increased.
 44. The method of claim 40, wherein the disease or disorder is selected from the group consisting of constipation, IBS-C, depression, anxiety, addiction, a neurodegenerative disorder, autism spectrum disorder, a sleep disorder, attention deficit hyperactivity disorder (ADHD), memory loss (e.g., dementia), learning difficulties, osteoporosis, heartburn, a dermatological condition (e.g., eczema and itch), GERD, and a pain disorder.
 45. The method of claim 40, wherein the disease or disorder is not a gut disease or disorder.
 46. The method of claim 40, wherein the disease or disorder is selected from the group consisting of depression, anxiety, addiction, a neurodegenerative disorder, autism spectrum disorder, a sleep disorder, attention deficit hyper-

activity disorder (ADHD), memory loss (e.g., dementia), learning difficulties, osteoporosis, a dermatological condition (e.g., eczema and itch), and a pain disorder.

47-153. (canceled)

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