

APPLICATION FOR PATENT: SPECIFICATION**TITLE**

Therapeutic Engineered Microbial Cell Systems and Methods for Treating Hyperuricemia and Gout

CROSS REFERENCE

This application is an original, non-provisional, utility application that claims priority benefit to the U.S. provisional application, 62/959,991, filed 12 January 2020, by inventor Christoph Geisler. Assignment of the provisional application from inventor Geisler to applicant Theraneutrics LLC was duly recorded on 05 January 2021, with the USPTO, thus giving the Applicant Theraneutrics ownership as the same person over both the priority application and present application at the time of filing this application.

STATEMENT REGARDING FEDERALLY SPONSORED**RESEARCH OR DEVELOPMENT**

This invention was made in part with government support under National Science Foundation Grant 2014679 awarded by the National Science Foundation. The government has certain rights in the invention. 35 USC §202 (c)(6).

BACKGROUND

[0001] Uric acid has been identified as a marker for a number of metabolic and hemodynamic abnormalities (Stack et al. Curr. Med. Res. Opin. Suppl 2:21-26 (2015)).

[0002] Gout is a painful, debilitating and progressive metabolic and inflammatory disease caused by abnormally elevated levels of uric acid in the blood stream. Gout is marked by recurrent attacks of red, tender, hot, and/or swollen joints. This leads to the deposition of painful, needle-like uric acid crystals in and around the connective tissue of the joints and in the kidneys, resulting in inflammation, the formation of disfiguring nodules, intermittent attacks of severe pain and kidney damage. In addition, evidence suggests that the chronic elevation of uric acid associated with gout, known as hyperuricemia, may also have systemic consequences, including an increased risk for kidney dysfunction and cardiovascular disease. After years of repetitive attacks, patients suffer the development of a chronic arthritis associated with the deposition of urate crystals and the build up to tophi in the joints (as well as in the tissues of the kidney and heart). The involved joints tend to become chronically deformed and painful and the risk for developing kidney stones, chronic renal insufficiency, and cardiovascular disease increases. This later stage, more involved clinical presentation is generally referred to as chronic tophaceous gout. Once patients reach this stage, they generally suffer multiple attacks every year.

[0003] Gout most often affects middle-aged to elderly men and postmenopausal women. The disease is typically associated with hyperuricemia (serum urate level ≥ 6.8 mg per deciliter, which is the upper limit of solubility) and painful episodic acute flares which generally resolve in one to two weeks. Disease prevalence is increasing, and the number of patients suffering could be as high as 6-8 million in the United States, although the relapsing and remitting nature of the disease makes it difficult to estimate a precise number. Prevalence increases with age and risk

factors include insulin resistance and obesity, as well as a purine rich diet (meat and seafood).

Gout is the most common form of inflammatory arthritis in men over the age of 40 and represents a significant unmet medical need with limited treatment options.

[0004] While many patients are well controlled with diet and lifestyle changes, as well as generic medications for acute attacks, many patients still experience poor urate control and progressive symptoms. Patients who experience two attacks per year, or who present with tophi are considered candidates for urate lowering therapy. Three classes of drugs are approved for lowering urate levels: xanthine oxidase inhibitors, uricosuric agents, and uricase agents.

[0005] The first line standard of care for chronic disease remains xanthine oxidase inhibition (e.g., febuxostat, allopurinol) which blocks uric acid synthesis, and for many this is an effective treatment option. Alternatively, uricosurics may be prescribed. Uricosuric agents (e.g., probenecid, lesinurad, benzbromarone) are oral drugs that inhibit the urate/anion exchanger URAT1, which is the transporter that mediates reuptake of uric acid from the proximal tubules of the kidney, and thus drive renal elimination of urate

[0006] Some patients fail all therapy and are thus considered chronic refractory. These patients are candidates for uricase (also known as urate oxidase) agents which break down uric acid directly. KRYSTEXXA® (pegloticase) is a pegylated engineered porcine/baboon hybrid uricase that was approved by the FDA for the treatment of chronic refractory gout in September 2010. Other uricases used to treat hyperuricemia and/or gout are non-engineered *Aspergillus flavus* uricase ('uricozyme') and engineered *Aspergillus flavus* uricase expressed in *S. cerevisiae* ('rasburicase').

[0007] Uricase converts uric acid into allantoin which is then excreted. While physicians describe Krystexxa as effective, in the pivotal program the primary endpoint was achieved in

only 42% of biweekly cohort and 35% of monthly cohort (v. 0% for placebo). Infusion reactions occurred in 26% of patients receiving q2 week dosing and 40% of patients receiving q4 dosing. Infusion reaction related discontinuation of therapy occurred in 11 and 13% and the label includes a boxed warning for anaphylaxis. Perhaps most concerning, there were eight serious cardiovascular events in patients in the Phase III trials versus one in the placebo arm. Krystexxa® administration is inconvenient with patients having to undergo a 4-hour premedication/infusion process once every two weeks.

[0008] Overall, treatment options for the majority of the chronic refractory gout population are limited. There remains a need in the art for improved ways to treat hyperuricemia and gout, and in particular, to treat chronic refractory gout.

SUMMARY OF THE INVENTION

[0009] The present invention provides microbial cells that have been engineered to comprise a uric acid degrading polypeptide. The engineered microbial cells of the invention are expected to overcome the limitations of existing therapies, and bring relief from debilitating and crippling pain to millions of patients suffering from hyperuricemia, gout, and in particular from refractory gout.

[0010] In particular, the present disclosure relates to non-pathogenic microbial cells that are engineered to comprise a uric acid degrading polypeptide (e.g., uricase), a uric acid transporter, or both a uric acid degrading polypeptide and a uric acid transporter. The engineered microbial cells can be probiotic cells. The engineered cells can be eukaryotic, e.g., fungal, e.g., *Saccharomyces boulardii*. The engineered cells can be bacterial, e.g., from the genus *Lactobacillus*, or can be archaeal. In one embodiment, the engineered microorganism constitutively expresses the polypeptide(s). In another embodiment, the microorganism is probiotic.

[0011] The engineered microbial cells are useful in the treatment of diseases and conditions associated with hyperuricemia, and in particular, gout. The present disclosure is based in part on the selection of a uric acid degrading polypeptide (e.g., uricase) and optionally together with a uric acid transporter that, when expressed in a microbial cell, increase uricolytic activity.

[0012] In some embodiments, pharmaceutical compositions comprising the engineered microbial cells described herein are administered to a subject (e.g., a human subject) for treatment of a disease or disorder. For example, the pharmaceutical composition may be administered orally to the subject. In some embodiments, the engineered microbial cells shield the uric acid degrading polypeptide and/or uric acid transporter from the harsh conditions encountered in the subject's

gastrointestinal tract, unlike current uricase treatments. Such harsh conditions include but are not limited to low pH, presence of proteases, bile acids, and other factors promoting the denaturation and degradation of proteins. These engineered microbial cells may act as metabolic factories in the gastrointestinal tract to effectively reduce serum uric acid levels in the subject, working longer and more effectively than naked uricase subjected to the conditions of the gastrointestinal tract.

[0013] In one aspect, the disclosure features a microbial cell engineered to degrade uric acid, comprising a first exogenous polypeptide comprising a uric acid degrading polypeptide, or a variant thereof. In one embodiment, the uric acid degrading polypeptide is a uricase, or a variant thereof.

[0014] In one embodiment, the engineered microbial cell is a fungal cell, e.g. *Saccharomyces boulardii*.

[0015] In one embodiment of the above aspects and embodiments, the uricase is a fungal uricase. In one embodiment, the fungal uricase is derived from *Candida utilis*. In one embodiment, the uricase derived from *Candida utilis* comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 1. In one embodiment, the fungal uricase is derived from *Aspergillus flavus*. In one embodiment, the uricase derived from *Aspergillus flavus* comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 2. In one embodiment of the above aspects and embodiments, the uricase is a bacterial uricase. In one embodiment, the bacterial uricase is derived from *Arthrobacter globiformis*. In one embodiment, the uricase derived from *Arthrobacter globiformis* comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 3. In one embodiment, the uricase is a porcine

/ baboon uricase chimera. In one embodiment, the porcine / baboon uricase chimera comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 4. In one embodiment, the fungal uricase is derived from *Schizosaccharomyces pombe*. In one embodiment, the uricase derived from *Schizosaccharomyces pombe* comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 5. In one embodiment, the bacterial uricase is derived from *Bacillus subtilis*. In one embodiment, the uricase derived from *Bacillus subtilis* comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 6. In one embodiment, the fungal uricase is derived from *Zygosaccharomyces parabailii*. In one embodiment, the uricase derived from *Zygosaccharomyces parabailii* comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 7.

[0016] In one embodiment, the fungal uricase is derived from *Spirosoma sp. KCTC 42546*. In one embodiment, the uricase derived from *Spirosoma sp. KCTC 42546* comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 8.

[0017] In one embodiment of the above aspects and embodiments, the uricase is a mutant uricase that retains the uricolytic activity of the wild type uricase. In one embodiment of the above aspects and embodiments, the first exogenous polypeptide is expressed inside the engineered microbial cell. In one embodiment of the above aspects and embodiments, the engineered microbial cell further comprises a second exogenous polypeptide comprising a uric acid transporter, or a variant thereof.

[0018] In one embodiment, the uric acid transporter is a fungal uric acid transporter. In one embodiment, the uric acid transporter is a bacterial uric acid transporter.

[0019] In one embodiment, the uric acid transporter is selected from the group consisting of:

Aspergillus nidulans UapA, *Aspergillus nidulans* UapC, *Aspergillus fumigatus* UapC, *Candida albicans* Xut1, *Schizosaccharomyces pombe* Q9HE12, *Bacillus subtilis* PucK, *Bacillus subtilis* PucJ, *Escherichia coli* YgfU, or *Zygosaccharomyces parabailii* AQZ18664, or *Spirosoma* sp. KCTC 42546 WP_142773020.

[0020] In one embodiment, *Aspergillus nidulans* UapA comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 9; wherein *Aspergillus nidulans* UapC comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 10; wherein *Aspergillus fumigatus* UapC comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 11; wherein *Candida albicans* Xut1 comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 12; wherein *Schizosaccharomyces pombe* Q9HE12 comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 13; wherein *Bacillus subtilis* PucK comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 14; wherein *Bacillus subtilis* PucJ comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 15; wherein *Escherichia coli* YgfU comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 16; wherein *Zygosaccharomyces parabailii* AQZ18664.1 comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 17; wherein *Spirosoma* sp. KCTC 42546 WP_142773020 comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO: 18.

[0021] In one embodiment, the second exogenous polypeptide is presented at the surface of the microbial cell.

[0022] In some embodiments, the uric acid transporter transports uric acid from outside the microbial cell to the inside of the microbial cell. In some embodiments of the above aspects and embodiments, the microbial cell when administered to a subject is capable of reducing serum uric acid level in the subject. In some embodiments, the level of serum uric acid is reduced to about 6.8 mg/dl or less.

[0023] In some embodiments of the above aspects and embodiments, the engineered microbial cell is a eukaryotic cell. In some embodiments of the above aspects and embodiments, the engineered microbial cell is a fungal cell. In some embodiments of the above aspects and embodiments, the engineered microbial cell is *Saccharomyces boulardii*. In some embodiments of all aspects of the invention, the uric acid degrading polypeptide is not uricase. In some embodiments of all aspects of the invention, the uric acid degrading polypeptide is not *Candida utilis* uricase.

[0024] In another aspect, the disclosure provides an engineered microbial cell comprising a first exogenous polypeptide comprising a uric acid transporter, or a variant thereof.

[0025] In some embodiments, the first exogenous polypeptide is presented at the surface of the engineered microbial cell.

[0026] In some embodiments, the uric acid transporter transports uric acid from outside the microbial cell to the inside of the microbial cell.

[0027] In some embodiments of the above aspects and embodiments, the engineered microbial cell is a fungal cell, e.g. *Saccharomyces boulardii*.

[0028] In another aspect, the disclosure provides an engineered microbial cell comprising a first exogenous polypeptide comprising a uricase, or a variant thereof, and a second exogenous polypeptide comprising a uric acid transporter, or a variant thereof.

[0029] In another aspect, the disclosure provides an engineered microbial cell comprising a first exogenous polypeptide comprising *Candida utilis* uricase, or a variant thereof, and a second exogenous polypeptide comprising *Aspergillus nidulans* UapA, or a variant thereof.

[0030] In another aspect, the disclosures provides an engineered microbial cell comprising a first exogenous polypeptide comprising *Candida utilis* uricase, or a variant thereof, and a second exogenous polypeptide comprising a uric acid transporter selected from the group consisting of *Aspergillus nidulans* UapA, *Aspergillus nidulans* UapC, *Aspergillus fumigatus* UapC, *Candida albicans* Xut1, *Schizosaccharomyces pombe* Q9HE12, *Bacillus subtilis* PucK, *Bacillus subtilis* PucJ, *Escherichia coli* YgfU, *Zygosaccharomyces parabailii* AQZ18664, or *Spirosoma sp.* KCTC 42546 WP_142773020.

[0031] In some embodiments of the above aspects, the engineered microbial cell is a fungal cell, e.g. *Saccharomyces boulardii*.

[0032] In another aspect, the disclosure provides a pharmaceutical composition comprising a plurality of the engineered microbial cells of any one of the above aspects and embodiments, and a pharmaceutically acceptable carrier. In some embodiments, the pharmaceutical composition comprises a therapeutically effective dose of the engineered microbial cells.

[0033] In another aspect, the disclosure provides a method of treating or preventing hyperuricemia in a subject, comprising administering to the subject the engineered microbial cell of any of the foregoing aspects and embodiments, in an amount effective to treat or prevent hyperuricemia in the subject. In some embodiments, the subject has a serum urate level greater

than about 6.8 mg/dl prior to administering the engineered microbial cell. In some embodiments, the subject has a serum urate level greater than about 8.0 mg/dl prior to administering the engineered microbial cell. In some embodiments, the subject has a serum urate level less than about 6.8 mg/dl after administering the engineered microbial cell. In some embodiments, the subject has a serum urate level of about 6.0 mg/dl after administering the engineered microbial cell. In some embodiments, the subject has been diagnosed with a disease selected from the group consisting of: gout, rheumatoid arthritis, osteoarthritis, cerebral stroke, ischemic heart disease, arrhythmia, and chronic renal disease. In a further embodiment, the gout is chronic refractory gout. In some embodiments, the subject has one or more risk factors for hyperuricemia selected from the group consisting of insulin resistance, obesity, a purine rich diet and advanced age. In some embodiments, the subject has been diagnosed with symptomatic gout with at least 3 gout flares in the previous 18 months. In some embodiments, the subject has been diagnosed with at least 1 gout tophus or gouty arthritis. In some embodiments, the subject has previously been treated with a urate lowering therapy, and failed to normalize level of serum uric acid to about 6.8 mg/dl or less. In some embodiments, the subject has a contraindication to allopurinol. In some embodiments, the subject has a failure to normalize uric acid to less than 6 mg/dL after at least 3 months of allopurinol treatment.

[0034] In some embodiments, the engineered microbial cell is administered to the subject about thrice daily. In some embodiments, the method further comprises administration of a second agent.

[0035] In another aspect, the disclosure provides an engineered microbial cell (e.g., engineered fungal cell), comprising a first exogenous polypeptide comprising a uric acid degrading polypeptide, or a variant thereof, produced by a process comprising introducing an exogenous

nucleic acid encoding the first exogenous polypeptide into a microbial cell and culturing the microbial cell under conditions suitable for production of the first exogenous polypeptide.

[0036] In another aspect, the disclosure provides an engineered microbial cell (e.g., engineered fungal cell), comprising a first exogenous polypeptide comprising a uric acid transporter, or a variant thereof, produced by a process comprising introducing an exogenous nucleic acid encoding the first exogenous polypeptide into a microbial cell (e.g., fungal cell); and culturing the microbial cell under conditions suitable for production of the first exogenous polypeptide.

[0037] In another aspect, the disclosure provides an engineered microbial cell (e.g., engineered fungal cell), comprising a first exogenous polypeptide comprising a uric acid degrading polypeptide, or a variant thereof, and a second exogenous polypeptide comprising a uric acid transporter, or a variant thereof, produced by a process comprising introducing an exogenous nucleic acid encoding the first exogenous polypeptide into a microbial cell (e.g., fungal cell); introducing an exogenous nucleic acid encoding the second exogenous polypeptide into a microbial cell (e.g., fungal cell); and culturing the microbial cell under conditions suitable for production of the first exogenous polypeptide and the second exogenous polypeptide.

[0038] In some embodiments, the uric acid degrading polypeptide is a uricase, or a variant thereof. In some embodiments, the uric acid degrading polypeptide is an allantoinase, or variant thereof. In some embodiments of the foregoing aspects, the exogenous nucleic acid comprises DNA or RNA. In some embodiments, the introducing step comprises electroporation or chemical transformation.

[0039] In some embodiments of the foregoing aspects, the introducing step comprises introducing the first exogenous nucleic acid encoding the first exogenous polypeptide by electroporation of an episomal vector. In some embodiments of the foregoing aspects, the

introducing step comprises introducing the first exogenous nucleic acid encoding the first exogenous polypeptide and the second exogenous nucleic acid encoding the second exogenous polypeptide by electroporation of an episomal vector, wherein the first exogenous nucleic acid and the second exogenous nucleic acid are contained in the same episomal vector.

[0040] In some embodiments of the foregoing aspects, the introducing step comprises introducing the first exogenous nucleic acid encoding the first exogenous polypeptide by electroporation of a first episomal vector, and introducing the second exogenous nucleic acid encoding the second exogenous polypeptide by electroporation of a second episomal vector.

[0041] In some embodiments of the foregoing aspects, the episomal vector comprises a promoter selected from the group consisting of *Saccharomyces boulardii* phosphoglycerate kinase 1 (PGK1), GPD (also known as TDH3 or GAPDH), GPM1, TPI1, or TEF1 promoter.

BRIEF DESCRIPTION OF DRAWINGS

[0042] Non-limiting and non-exhaustive examples of several of the various embodiments of the present subject matter are described with references to the following figures, and reference numbers refer to the same features throughout the various views and embodiments unless otherwise specified.

[0043] FIG. 1 is a genetic map of episomal plasmid used to transform *S. boulardii*, by way of an example embodiment, and provide it with the ability to degrade uric acid, as described in Example 1.

[0044] FIG. 2 shows the absorbance spectra of uric acid solutions in Phosphate Buffered Saline (PBS) with no addition of yeast, with non-modified wild-type *S. boulardii* cells added, and with modified *S. boulardii* cells expressing *Candida utilis* uricase and *Aspergillus nidulans* UapA uric acid transporter.

[0045] FIG. 3 shows the absorbance of: uric acid solutions in PBS, in PS with addition of non-modified wild-type *S. boulardii* cells, and in PBS with addition of modified *S. boulardii* cells expressing *Candida utilis* uricase and *Aspergillus nidulans* UapA uric acid transporter, observed over time at 293 nm.

[0046] FIG. 4 shows the urate consumption assay comparing urate uptake and breakdown capacity for probiotic strains produced as outlined in Example 1, Example 7, and Example 8.

DETAILED DESCRIPTION OF THE DRAWINGS

[0047] Now in reference to FIG. 1, it is a Genetic map of episomal plasmid used to transform **1** *S. boulardii* and provide it with the ability to degrade uric acid, as described in Example 1. The genetic map shows *Saccharomyces boulardii* GPD (TDH3) promoter [1]; *Candida utilis* uricase ORF [2]; *Saccharomyces boulardii* VPS13 terminator [3]; *Saccharomyces boulardii* TP11 promoter [4]; G418 – Resistance ORF [5]; *Saccharomyces boulardii* [6]; F1 Origin of replication [7]; Ampicilin Resistance ORF [8]; *Saccharomyces boulardii* 2 micron plasmid origin of replication [9]; *Saccharomyces boulardii* Pm9 terminator [10]; *Spergillus nidulans* UapA Uric acid transporter ORF [11]; and *Saccharomyces boulardii* Pgk1 promoter [12].

[0048] Now in reference to FIG. 2, it is an absorbance spectra of uric acid solutions in PBS with no addition (“No yeast”, left 3 panels), with non-modified wild-type *S. boulardii* cells added (“wild-type *S. boulardii*”, center 2 panels), and with modified *S. boulardii* cells expressing *Candida utilis* uricase and *Aspergillus nidulans* UapA uric acid transporter (“*S. boulardii* + AnUapA + CuUOX”, right 2 panels). Top row: before addition of yeast. Center row: after 10’ incubation at 37°C. Bottom row: after 40’ incubation at 37°C. X-axis: wavelength. Y-axis: absorbance. Uric acid is progressively degraded in the Uric acid solution with modified *S. boulardii* cells expressing *Candida utilis* uricase and *Aspergillus nidulans* UapA uric acid transporter added, as indicated by the progressive reduction of the peak at 293 nm. In contrast, Uric acid is not degraded in the Uric acid solution with non-modified wild-type *S. boulardii* cells added, as indicated by the fact the peak at 293 nm did not change over time. Uric acid also was not degraded in the Uric acid solution no *S. boulardii* cells added, as indicated by the fact no decrease in the peak at 293 nm was observed over time.

[0049] Now in reference to FIG. 3, it shows absorbance at 293 nm of uric acid solutions in PBS with no addition (“UA in PBS”, left 3 columns), with non-modified wild-type *S. boulardii* cells added (“UA in PBS + wild-type *S. boulardii*”, 4th and 5th columns), and with modified *S. boulardii* cells expressing *Candida utilis* uricase and *Aspergillus nidulans* UapA uric acid transporter (“UA in PBS + *S. boulardii* + AnUapA + CuUOX”, right 2 columns). X-axis: absorbance at 293 nm. Uric acid is progressively degraded in the Uric acid solution with modified *S. boulardii* cells expressing *Candida utilis* uricase and *Aspergillus nidulans* UapA uric acid transporter added, as indicated by the progressive decrease in Absorbance at 293 nm. In contrast, Uric acid is not degraded in the Uric acid solution with non-modified wild-type *S. boulardii* cells added, as indicated by the fact no decrease in Absorbance at 293 nm was observed over time. Uric acid also was not degraded in the Uric acid solution no *S. boulardii* cells added, as indicated by the fact no decrease in Absorbance at 293 nm was observed over time.

[0050] Now in reference to FIG. 4, it shows a Urate consumption assay comparing urate uptake and breakdown capacity for probiotic strains produced as outlined in Example 1, Example 7, and Example 8. *S. boulardii* cells expressing *Candida utilis* uricase and *Aspergillus nidulans* UapA uric acid transporter (“*C. utilis* UOX + *A. nidulans* Tporter”), produced as outlined in Example 1 most rapidly depleted urate in the assay buffer, followed by *S. boulardii* cells expressing *Candida utilis* uricase and *Zygosaccharomyces parabailii* uric acid transporter (“*C. utilis* UOX + *Z. parabailii* Tporter”), produced as outlined in Example 8, followed by *S. boulardii* cells expressing *Zygosaccharomyces parabailii* uricase and *Aspergillus nidulans* UapA uric acid transporter (“*Z. parabailii* UOX + *A. nidulans* Tporter”).

DETAILED DESCRIPTION OF THE INVENTION

[0051] In this Specification, which includes the figures, claims, and this detailed description, reference is made to particular and possible features of the embodiments of the invention, including method steps. These particular and possible features are intended to include all possible combinations of such features, without exclusivity. For instance, where a feature is disclosed in a specific embodiment or claim, that feature can also be used, to the extent possible, in combination with and/or in the context of other aspects and embodiments of the invention, and in the invention generally. Additionally, the disclosed architecture is sufficiently configurable, such that it may be utilized in ways other than what is shown.

[0052] The purpose of the Abstract of this Specification is to enable the U.S. Patent and Trademark Office and the public generally, and especially the scientists, engineers and practitioners of the art who are not familiar with patent or legal terms or phrasing, to determine quickly from a cursory inspection the nature and essence of the technical disclosure of the application. The Abstract is not intended to be limiting as to the scope of the invention in any way.

[0053] In the following description, numerous specific details are given in order to provide a thorough understanding of the present embodiments. It will be apparent, however, to one having ordinary skill in the art, that the specific detail need not be employed to practice the present embodiments. On other instances, well-known materials or methods have not been described in detail in order to avoid obscuring the present embodiments. When limitations are intended in this Specification, they are made with expressly limiting or exhaustive language.

[0054] Reference throughout this Specification to “one embodiment”, “an embodiment”, “one example” or “an example” means that a particular feature, structure, or characteristic described

in connection with the embodiment or example is included in at least one embodiment of the present embodiments. Thus, appearances of the phrases “in one embodiment”, “according to an embodiment”, “in an embodiment”, “one example”, “for example”, “an example”, or the like, in various places throughout this Specification are not necessarily all referring to the same embodiment or example. Furthermore, the particular features, structures, or characteristics may be combined in any suitable combinations and/or sub-combinations in one or more embodiments or examples.

[0055] The terms “comprises”, “comprising”, “includes”, “including”, “has”, “having”, “could”, “could have” or their grammatical equivalents, are used in this Specification to mean that other features, components, materials, steps, etc. are optionally present as a non-exclusive inclusion. For instance, a device “comprising” (or “which comprises” or “is comprised of”) components A, B, and C can contain only components A, B, and C, or can contain not only components A, B, and C but also one or more other components. For example, a method comprising two or more defined steps can be carried out in any order or simultaneously, unless the context excludes that possibility; and the method can include one or more other steps which are carried out before any of the defined steps, between two of the defined steps, or after all the defined steps, unless the context excludes that possibility.

[0056] Further, unless expressly stated to the contrary, “or” refers to an inclusive or and not to an exclusive or. For example, An embodiment could have optional features A, B, or C, so the embodiment could be satisfied with A in one instance, with B in another instance, and with C in a third instance, and probably with AB, AC, BC, or ABC if the context of features does not exclude that possibility.

[0057] Examples or illustrations given are not to be regarded in any way as restrictions on, limits to, or express definitions of any term or terms with which they are utilized. Instead, these examples or illustrations are to be regarded as being described with respect to one particular embodiment and as being illustrative only. Those of ordinary skill in the art will appreciate that any term or terms with which these example or illustrations are utilized will encompass other embodiments, which may or may not be given in this Specification, and all such embodiments are intended to be included within the scope of that term or terms. Language designating such nonlimiting examples and illustrations includes, but is not limited to “for example”, “for instance”, “etc.”, “or otherwise”, and “in one embodiment.”

[0058] The phrase “at least” followed by a number is used to denote the start of a range beginning with that number, which may or may not be a range having an upper limit, depending on the variable defined. For instance, “at least 1” means 1 or more.

[0059] In this specification, “a” and “an” and similar phrases are to be interpreted as “at least one” and “one or more.” In this specification, the term “may” or “can be” or “could be” is to be interpreted as “may, for example.” In other words, the term “may” is indicative that the phrase following the term “may” is an example of one of a multitude of suitable possibilities that may, or may not, be employed to one or more of the various embodiments.

[0060] The phrase “a plurality of” followed by a feature, component, or structure is used to mean more than one, specifically including a great many, relative to the context of the component.

[0061] It is the applicant’s intent that only claims that include the express language “means for” or “step for” be interpreted under 35 U.S.C. §112. Claims that do not expressly include the phrase “means for” or “step for” are not to be interpreted under 35 U.S.C. §112.

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[0063] The present disclosure is based on the development of microbial cells, e.g., fungal cells, that have been engineered to include a uric acid degrading polypeptide, a uric acid transporter, or both a uric acid degrading polypeptide and a uric acid transporter.

[0064] According to embodiments of the present disclosure, the engineered microbial cells are fungal, bacterial, or archaeal cells. According to embodiments of the present disclosure, the uric acid degrading polypeptide is located inside the cell (e.g., expressed in a microbial cell) and the uric acid transporter is located at the surface of the microbial cell, such that the uric acid transporter promotes uptake of uric acid into the cell.

[0065] The engineered microbial cells of the present invention provide advantages to, for example, non-engineered cells. In contrast to the microbial cells of the present invention, which are engineered to comprise a uric acid degrading polypeptide inside the cell, a non-engineered microbial cell is limited with respect to the levels of polypeptide that may be present in the cell. According to embodiments of the present disclosure, the engineered microbial cells are fungal cells (e.g., *Saccharomyces boulardii*).

[0066] Moreover, the engineered microbial cells of the invention confer protection to bile acid, proteolytic enzymes, and / or acid pH to the uric acid degrading polypeptide, and/or the uric acid transporter, as compared to when the uric acid degrading polypeptide, and/or the uric acid

transporter polypeptides are administered to a subject alone (i.e., not present in or on a microbial cell).

[0067] Many modifications and other embodiments of the inventions set forth herein will easily come to mind to one skilled in the art to which these inventions pertain having the benefit of the teachings presented in the foregoing descriptions and the associated drawings. Therefore, it is to be understood that the inventions are not to be limited to the specific embodiments disclosed and that modifications and other embodiments are intended to be included within the scope of the appended claims. Although specific terms are employed herein, they are used in a generic and descriptive sense only and not for purposes of limitation.

[0068] As used herein, the terms “about”, “approximate”, and “substantially” when referring to a measurable value such as an amount, a temporal duration, and the like; would be understood by a person of ordinary skill in the art that the given feature is close enough to the exact feature or value that the invention can still be practiced; i.e., that the difference is not so significant as to render the present invention inoperable. From a quantifiable perspective, it might be helpful to think of these terms as encompassing variations of $\pm 20\%$ or $\pm 10\%$, more preferably $\pm 5\%$, even more preferably $\pm 1\%$, and still more preferably $\pm 0.1\%$ from the specified value, as such variations are appropriate to perform the disclosed methods.

[0069] As used herein, any concentration range, percentage range, ratio range, or integer range is to be understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated.

[0070] As used herein, the terms “such as”, “for example” and the like are intended to refer to exemplary embodiments and not to limit the scope of the present disclosure.

[0071] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. Although any methods and materials similar or equivalent to those described herein can be used in the practice for testing of the present invention, preferred materials and methods are described herein.

[0072] As used herein, a “microbial cell”, or “microbe” refers to single-celled organisms, whether organized as colonies, suspensions, individual cells, or other configurations and collections; alive or dead or in a state of metabolic status or suspension; including but not limited to organisms such as Bacteria, Archaea, Fungi, or Protists. Clearly, cells capable of enzymatic activity are needed to transport and degrade uric acid, and thus practice the invention. For example, bacterial microbes may include e.g., *Lactobacillus casei*, and fungal microbes may include e.g., *Saccharomyces boulardii*.

[0073] As used herein, an “additional therapeutic” refers to any therapeutic that is used in addition to another treatment. For example, when the method is one directed to treatment with the engineered microbial cells described herein, and the method comprises the use of an additional therapeutic, the additional therapeutic is in addition to the engineered microbial cells described herein. Generally, the additional therapeutic will be a different therapeutic. The additional therapeutic may be administered at the same time or at a different time and/or via the same mode of administration or via a different mode of administration, as that of the other therapeutic. In preferred embodiments, the additional therapeutic will be given at a time and in a way that will provide a benefit to the subject during the effective treatment window of the other therapeutic. When two compositions are administered with a specific time period, generally the time period is measured from the start of the first composition to the start of the second

composition. As used herein, when two compositions are given within an hour, for example, the time before the start of the administration of the first composition is about an hour before the start of the administration of the second composition. In some embodiments, the additional therapeutic is another therapeutic for the treatment of gout or a condition associated with gout. As used herein, a "gout therapeutic" is any therapeutic that can be administered and from which a subject with gout may derive a benefit because of its administration. In some embodiments, the gout therapeutic is an oral gout therapeutic (i.e., a gout therapeutic that can be taken or given orally).

[0074] As used herein, "dose" refers to a specific quantity of a pharmacologically active material for administration to a subject for a given time. Unless otherwise specified, the doses recited refer to an engineered microbial cell comprising a uric acid degrading polypeptide as described herein, an engineered microbial cell comprising a uric acid transporter as described herein, or an engineered microbial cell comprising a uric acid degrading polypeptide and a uric acid transporter as described herein. In some embodiments, a dose of engineered microbial cells refers to an effective amount of engineered microbial cells. For example, in some embodiments a dose or effective amount of engineered microbial cells comprises at least 10^6 CFUs of engineered microbes per dose. In some embodiments, a dose or effective amount of engineered microbial cells refers to about 10^6 – 10^{12} engineered microbial cells per dose. When referring to a dose for administration, in an embodiment of any one of the methods, compositions or kits provided herein, any one of the doses provided herein is the dose as it appears on a label/label dose.

[0075] As used herein, a "drug-induced" gout flare refers to an occurrence of or increased incidence of a gout flare associated with initiation of therapy to treat gout and/or administration

of a therapeutic agent for the treatment of gout, for example, initiation of therapy with a xanthine oxidase inhibitor, urate oxidase, or a uricosuric agent. A gout flare is “associated” with initiation of gout therapy when the flare occurs contemporaneously or following at least a first administration of a therapeutic agent for the treatment of gout.

[0076] As used herein, an “elevated serum uric acid level” refers to any level of uric acid in a subject's serum that may lead to an undesirable result or would be deemed by a clinician to be elevated. In an embodiment, an elevated serum uric acid level refers to a level of uric acid considered to be above normal by the American Medical Association. In an embodiment, the subject of any one of the methods provided herein can have a serum uric acid level of >5 mg/dL, >6 mg/dL, or >7 mg/dL. Such a subject may be a hyperuricemic subject. Whether or not a subject has elevated blood uric acid levels can be determined by a clinician, and in some embodiments, the subject is one in which a clinician has identified or would identify as having elevated serum uric acid levels.

[0077] As used herein, the term “endogenous” is meant to refer to a native form of compound (e.g., a small molecule) or process. For example, in some embodiments, the term “endogenous” refers to the native form of a nucleic acid or polypeptide in its natural location in the organism or in the genome of an organism.

[0078] As used herein, the term “an engineered cell” is meant to refer to a genetically-modified cell or progeny thereof.

[0079] As used herein, the term “microbial” cell refers to a cell, e.g., a bacterial, fungal or archaeal cell, which may be a prokaryotic or eukaryotic cell. As used herein, a microbial cell includes a metabolically inactive spore or cell capable of germinating into or of being

reconstituted into a metabolically active cell. As used herein, a microbial cell includes freeze-dried, spray-dried, or otherwise dried microbial cell.

[0080] As used herein, the term “probiotic” refers to live microbial cells that, when administered in adequate amounts, may or may not confer a health benefit on the host, and do not exert harmful effects.

[0081] As used herein, the term “exogenous,” when used in the context of nucleic acid, includes a transgene and engineered nucleic acids.

[0082] As used herein, the term “exogenous nucleic acid” refers to a nucleic acid (e.g., a gene) which is not native to a cell, but which is introduced into the cell or a progenitor of the cell. An exogenous nucleic acid may include a region or open reading frame (e.g., a gene) that is homologous to, or identical to, an endogenous nucleic acid native to the cell. In some embodiments, the exogenous nucleic acid comprises RNA. In some embodiments, the exogenous nucleic acid comprises DNA. In some embodiments, the exogenous nucleic acid is integrated into the genome of the cell. In some embodiments, the exogenous nucleic acid is processed by the cellular machinery to produce an exogenous polypeptide. In some embodiments, the exogenous nucleic acid is not retained by the cell or by a cell that is the progeny of the cell into which the exogenous nucleic acid was introduced.

[0083] As used herein, the term “exogenous polypeptide” refers to a polypeptide that is not produced by a wild-type cell of that type or is present at a lower level in a wild-type cell than in a cell containing the exogenous polypeptide. In some embodiments, an exogenous polypeptide refers to a polypeptide that is introduced into or onto a cell, or is caused to be expressed by the cell by introducing an exogenous nucleic acid encoding the exogenous polypeptide into the cell or into a progenitor of the cell. In some embodiments, an exogenous polypeptide is a polypeptide

encoded by an exogenous nucleic acid that was introduced into the cell, or a progenitor of the cell, which nucleic acid is optionally not retained by the cell.

[0084] As used herein, the term “express” or “expression” refers to the process to produce a polypeptide, including transcription and translation. Expression may be, e.g., increased by a number of approaches, including: increasing the number of genes encoding the polypeptide, increasing the transcription of the gene (such as by placing the gene under the control of a constitutive promoter), increasing the translation of the gene, knocking out of a competitive gene, or a combination of these and/or other approaches.

[0085] As used herein, the term “transcription regulatory sequence” refers to a first nucleotide sequence that regulates transcription of a second nucleotide sequence to which it is operatively linked.

[0086] A “promoter” is a transcription regulatory sequence at least sufficient to promote the transcription of a nucleotide sequence in DNA into an RNA transcript. A transcript transcribed from a promoter typically includes sequences from the promoter downstream of the transcription start site, as well as downstream sequences that, in the case of mRNA, encode an amino acid sequence. Promoters are the best-characterized transcriptional regulatory sequences because of their predictable location immediately upstream of transcription start sites. Promoters include sequences that modulate the recognition, binding and transcription initiation activity of the RNA polymerase. These sequences can be cis acting or can be responsive to trans acting factors. Promoters, depending upon the nature of the regulation, can be constitutive or regulated. They are often described as having two separate segments: core and extended promoter regions.

[0087] The core promoter includes sequences that are sufficient for RNA polymerase recognition, binding and transcription initiation. The core promoter includes the transcriptional

start site, an RNA polymerase binding site, and other general transcription binding sites and is where the pre-initiation complex forms and the general transcription machinery assembles. The pre-initiation complex is generally within 50 nucleotides (nt) of the transcription start site (TSS).

[0088] The core promoter also includes a sequence for a ribosome binding site, necessary for translation of an mRNA into a polypeptide.

[0089] The extended promoter region includes the so-called proximal promoter, which extends to about 250 nucleotides upstream of the transcriptional start site (i.e. , -250 nt). It includes primary regulatory elements such as specific transcription factor binding sites. It has been found that many genes have transcription regulatory elements located further upstream. In particular, a fragment that includes most of the transcription regulatory elements of a gene can extend up to 700 nt or more up-stream of the transcription start site. In certain genes, transcription regulatory sequences have been found thousands of nucleotides upstream of the transcriptional start site.

[0090] As used herein, a nucleotide sequence is "operatively linked" or "operably linked" with a transcription regulatory sequence when the transcription regulatory sequence functions in a cell to regulate transcription of the nucleotide sequence. This includes promoting transcription of the nucleotide sequence through an interaction between a polymerase and a promoter.

[0091] As used herein, a first nucleotide sequence is "heterologous" to a second nucleotide sequence if the first nucleotide sequence is not operatively linked with the second nucleotide sequence in nature. By extension, a polypeptide is "heterologous" to an expression control sequence if it is encoded by nucleotide sequence heterologous the promoter.

[0092] As used herein, the terms "first", "second" and "third", etc. with respect to exogenous polypeptides are used for convenience of distinguishing when there is more than one type of

exogenous polypeptide. Use of these terms is not intended to confer a specific order or orientation of the exogenous polypeptides unless explicitly so stated.

[0093] As used herein, the term “fragment” refers to sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, and are at most some portion less than a full-length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice.

[0094] As used herein, the term “gene” is used broadly to refer to any segment of nucleic acid associated with expression of a given RNA or protein. Thus, genes include regions encoding expressed RNAs (which typically include polypeptide coding sequences) and, often, the regulatory sequences required for their expression. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have specifically desired parameters.

[0095] As used herein, the term “gout” generally refers to a disorder or condition associated with the buildup of uric acid, such as deposition of uric crystals in tissues and joints, and/or a clinically relevant elevated serum uric acid level. Accumulation of uric acid may be due to overproduction of uric acid or reduced excretion of uric acid. Gout may range from asymptomatic to severe and painful inflammatory conditions. A “disease, condition or disorder associated with gout” refers to any condition in a subject where the subject experiences local and/or systemic effects of gout, including inflammation and immune responses, and in which the condition is caused or exacerbated by, or the condition can result in or exacerbate, gout. A gout flare is an attack or exacerbation of gout symptoms, which can happen at any time. Gout flares

can include gout flares that occur after the administration of a uric acid lowering therapy. As used herein, the term “chronic refractory gout” refers to symptomatic gout in which conventional urate-lowering therapies are contraindicated or ineffective to control gout and/or hyperuricemia. Chronic refractory gout is often characterized by recurrent gout flares, chronic gout arthropathy with or without bony erosions, visible progressive tophi, physical disability, and/or poor health-related quality of life.

[0096] As used herein, the term “hyperuricemia” refers to the presence of high levels of uric acid in the blood. Hyperuricemia may occur because of decreased excretion. Hyperuricemia may also occur from increased production, or a combination of the two mechanisms.

[0097] As used herein the term “nucleic acid molecule” refers to a single or double- stranded polymer of deoxyribonucleotide or ribonucleotide bases. It includes chromosomal DNA and self-replicating plasmids, vectors, mRNA, tRNA, siRNA, etc. which may be engineered and from which exogenous polypeptides may be expressed when the nucleic acid is introduced into a cell.

[0098] The following terms are used herein to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) “reference sequence”, (b) “comparison window”, (c) “sequence identity”, (d) “percentage of sequence identity”, and (e) “substantial identity.”

[0099] The term “reference sequence” refers to a sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence

[0100] The term “comparison window” refers to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence may be compared to a reference sequence and wherein the portion of the polynucleotide sequence in the comparison window may

comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be at least 30 contiguous nucleotides in length, at least 40 contiguous nucleotides in length, at least 50 contiguous nucleotides in length, at least 100 contiguous nucleotides in length, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence, a gap penalty typically is introduced and is subtracted from the number of matches. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman, *Adv. Appl. Math.* 2:482 (1981); by the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.* 48:443 (1970); by the search for similarity method of Pearson and Lipman, *Proc. Natl. Acad. Sci.* 85:2444 (1988); by computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, Calif.; GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wis., USA; the CLUSTAL program is well described by Higgins and Sharp, *Gene* 73:237-244 (1988); Higgins and Sharp, *CABIOS* 5:151-153 (1989); Corpet, *Nucleic Acids Research* 16:10881-90 (1988); Huang, et al., *CABIOS*, 8:155-65 (1992), and Pearson, et al., *Methods in Molecular Biology*, 24:307-331 (1994). The BLAST family of programs, which can be used for database similarity searches, includes: BLASTN for nucleotide query sequences against nucleotide database sequences; BLASTX for nucleotide query sequences against protein database sequences; BLASTP for protein query sequences against protein database sequences; TBLASTN for protein query sequences against nucleotide database

sequences; and TBLASTX for nucleotide query sequences against nucleotide database sequences. See, Current Protocols in Molecular Biology, Chapter 19, Ausubel, et al, Eds., Greene Publishing and Wiley-Interscience, New York (2003). Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using the BLAST 2.0 suite of programs using default parameters. Altschul et al, Nucleic Acids Res. 25:3389-3402 (1997). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology-Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al, supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits then are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a word length (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length (W) of 3, an expectation

(E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff Proc. Natl. Acad. Sci. USA 89:10915 (1989)). In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90:5873-5887 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. BLAST searches assume that proteins may be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences which may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs may be employed to reduce such low-complexity alignments. For example, the SEG (Wootton and Federhen, Comput. Chem., 17:149-163 (1993)) and XNU (Claverie and States, Comput. Chem., 17:191-201 (1993)) low-complexity filters may be employed alone or in combination

[0101] The term “sequence identity” or “identity” in the context of two nucleic acid or polypeptide sequences is used herein to refer to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions that are not identical often differ by conservative amino acid substitutions, i.e., where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g. charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence

identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have “sequence similarity” or “similarity.” Means for making this adjustment are well-known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., according to the algorithm of Myers and Miller, CABIOS, 4:11-17 (1988) e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif., USA)

[0102] The term “percentage of sequence identity” is used herein mean the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e ., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

[0103] The term “substantial identity” of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 60% sequence identity, at least 70% sequence identity, at least 80% sequence identity, at least 90% sequence identity, or at least 95% sequence identity, compared to a reference sequence using one of the alignment programs described using standard

parameters. One of skill will recognize that these values may be adjusted appropriately to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 60%, at least 70%, at least 80%, at least 90%, or at least 95%. Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. However, nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides that they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is that the polypeptide that the first nucleic acid encodes is immunologically cross reactive with the polypeptide encoded by the second nucleic acid. Mutations may also be made to the nucleotide sequences of the present proteins by reference to the genetic code, including taking into account codon degeneracy.

[0104] As used herein, the term "probiotic composition" refers to a composition comprising probiotic microorganisms and a physiologically acceptable carrier. Typically, a probiotic composition confers a health or wellness benefit on the host subject to whom it is administered.

[0105] As used herein, the term "physiologically acceptable" refers to a carrier that is compatible with the other ingredients of a composition and can be safely administered to a subject. Probiotic compositions and techniques for their preparation and use are known to those of skill in the art in light of the present disclosure. For a detailed listing of suitable pharmacological compositions and techniques for their administration one may refer to texts such as Remington's Pharmaceutical Sciences, 17th ed. 1985; Brunton et al. , "Goodman and Gilman's The

Pharmacological Basis of Therapeutics," McGraw-Hill, 2005; University of the Sciences in Philadelphia (eds.), "Remington: The Science and Practice of Pharmacy," Lippincott Williams & Wilkins, 2005; and University of the Sciences in Philadelphia (eds.), "Remington: The Principles of Pharmacy Practice," Lippincott Williams & Wilkins, 2008.

[0106] The probiotic composition may be a liquid formulation or a solid formulation. When the probiotic composition is a solid formulation it may be formulated as a tablet, a sucking tablet, a chewing tablet, a chewing gum, a capsule, a sachet, a powder, a granule, a coated particle, a coated tablet, an enterocoated tablet, an enterocoated capsule, a melting strip or a film. When the probiotic composition is a liquid formulation it may be formulated as an oral solution, a suspension, an emulsion or syrup. Said composition may further comprise a carrier material independently selected from, but not limited to, the group consisting of lactic acid fermented foods, fermented dairy products, resistant starch, dietary fibers, carbohydrates, proteins, and glycosylated proteins.

[0107] As used herein, the probiotic composition could be formulated as a food composition, a dietary supplement, a functional food, a medical food or a nutritional product as long as the required effect is achieved, e.g. treatment or prevention of an alcohol hangover. Said food composition may be chosen from the group consisting of beverages, yogurts, juices, ice creams, breads, biscuits, crackers, cereals, health bars, spreads, gummies and nutritional products. The food composition may further comprise a carrier material, wherein said carrier material is chosen from the group consisting of lactic acid fermented foods, fermented dairy products, resistant starch, dietary fibers, carbohydrates, proteins and glycosylated proteins. As used herein, the terms "polypeptide", "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more

amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers. The essential nature of such analogues of naturally occurring amino acids is that, when incorporated into a protein, that protein is specifically reactive to antibodies elicited to the same protein but consisting entirely of naturally occurring amino acids. The terms “polypeptide”, “peptide” and “protein” also are inclusive of modifications including, but not limited to, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation, and ADP-ribosylation. It will be appreciated, as is well known and as noted above, that polypeptides may not be entirely linear. For instance, polypeptides may be branched as a result of ubiquitination, and they may be circular, with or without branching, generally as a result of posttranslational events, including natural processing event and events brought about by human manipulation which do not occur naturally. Circular, branched and branched circular polypeptides may be synthesized by non-translation natural processes and by entirely synthetic methods, as well. According to some embodiments, the peptide is of any length or size.

[0108] As used herein, polypeptides referred to herein as “engineered” refers to polypeptides which have been produced by engineered DNA methodology, including those that are generated by procedures which rely upon a method of artificial recombination, such as the polymerase chain reaction (PCR) and/or cloning into a vector using restriction enzymes.

[0109] “Engineered” polypeptides are also polypeptides having altered expression, such as a naturally occurring polypeptide with engineeredly modified expression in a cell, such as a host cell.

[0110] As used herein, the terms “subject”, “individual”, “host”, “recipient”, “person”, and “patient” are used interchangeably herein and refer to any mammalian subject for whom

diagnosis, treatment, or therapy is desired, particularly humans. The methods described herein are applicable to both human therapy and veterinary applications. In some embodiments, the subject is a mammal, and in particular embodiments the subject is a human.

[0111] As used herein, the phrase “subject in need” refers to a subject that (i) will be administered an engineered microbial cell (or pharmaceutical composition comprising an engineered microbial cell) according to the described invention, (ii) is receiving an engineered microbial cell (or pharmaceutical composition comprising an engineered microbial cell) according to the described invention; or (iii) has received an engineered microbial cell (or pharmaceutical composition comprising an engineered microbial cell) according to the described invention; or (iv) is in need of and/or would benefit from administration of an engineered microbial cell (or pharmaceutical composition comprising an engineered microbial cell) according to the described invention, unless the context and usage of the phrase indicates otherwise

[0112] As used herein, the term “suppress”, “decrease”, “interfere”, “inhibit” and/or “reduce” (and like terms) generally refers to the act of reducing, either directly or indirectly, a concentration, level, function, activity, or behavior relative to the natural, expected, or average, or relative to a control condition.

[0113] As used herein, the terms “therapeutic amount”, “therapeutically effective amount”, an “amount effective”, or “pharmaceutically effective amount” of an active agent (e.g. an engineered microbial cell as described herein) are used interchangeably to refer to an amount that is sufficient to provide the intended benefit of treatment. However, dosage levels are based on a variety of factors, including the type of injury, the age, weight, sex, medical condition of the patient, the severity of the condition, the route of administration, and the particular active agent

employed. Thus the dosage regimen may vary widely, but can be determined routinely by a physician using standard methods. Additionally, the terms “therapeutic amount”, “therapeutically effective amounts” and “pharmaceutically effective amounts” include prophylactic or preventative amounts of the compositions of the described invention. In prophylactic or preventative applications of the described invention, pharmaceutical compositions or medicaments are administered to a patient susceptible to, or otherwise at risk of, a disease, disorder or condition in an amount sufficient to eliminate or reduce the risk, lessen the severity, or delay the onset of the disease, disorder or condition, including biochemical, histologic and/or behavioral symptoms of the disease, disorder or condition, its complications, and intermediate pathological phenotypes presenting during development of the disease, disorder or condition. It is generally preferred that a maximum dose be used, that is, the highest safe dose according to some medical judgment. The terms “dose” and “dosage” are used interchangeably herein.

[0114] As used herein the term “therapeutic effect” refers to a consequence of treatment, the results of which are judged to be desirable and beneficial. A therapeutic effect can include, directly or indirectly, the arrest, reduction, or elimination of a disease manifestation. A therapeutic effect can also include, directly or indirectly, the arrest reduction or elimination of the progression of a disease manifestation.

[0115] For any therapeutic agent described herein the therapeutically effective amount may be initially determined from preliminary in vitro studies and/or animal models. A therapeutically effective dose may also be determined from human data. The applied dose may be adjusted based on the relative bioavailability and potency of the administered agent. Adjusting the dose to achieve maximal efficacy based on the methods described above and other well-known methods is within the capabilities of the ordinarily skilled artisan. General principles for determining

therapeutic effectiveness, which may be found in Chapter 1 of Goodman and Gilman's The Pharmacological Basis of Therapeutics, 12th Edition, McGraw-Hill (New York) (2001) are summarized below.

[0116] Pharmacokinetic principles provide a basis for modifying a dosage regimen to obtain a desired degree of therapeutic efficacy with a minimum of unacceptable adverse effects. In situations where the drug's plasma concentration can be measured and related to the therapeutic window, additional guidance for dosage modification can be obtained.

[0117] As used herein, the terms “treat”, “treating”, and/or “treatment” include abrogating, substantially inhibiting, slowing or reversing the progression of a condition, substantially ameliorating clinical symptoms of a condition, or substantially preventing the appearance of clinical symptoms of a condition, obtaining beneficial or desired clinical results. Treating further refers to accomplishing one or more of the following: (a) reducing the severity of the disorder; (b) limiting development of symptoms characteristic of the disorder(s) being treated; (c) limiting worsening of symptoms characteristic of the disorder(s) being treated; (d) limiting recurrence of the disorder(s) in patients that have previously had the disorder(s); and (e) limiting recurrence of symptoms in patients that were previously asymptomatic for the disorder(s).

[0118] Beneficial or desired clinical results, such as pharmacologic and/or physiologic effects include, but are not limited to, preventing the disease, disorder or condition from occurring in a subject that may be predisposed to the disease, disorder or condition but does not yet experience or exhibit symptoms of the disease (prophylactic treatment), alleviation of symptoms of the disease, disorder or condition, diminishment of extent of the disease, disorder or condition, stabilization (i.e., not worsening) of the disease, disorder or condition, preventing spread of the disease, disorder or condition, delaying or slowing of the disease, disorder or condition

progression, amelioration or palliation of the disease, disorder or condition, and combinations thereof, as well as prolonging survival as compared to expected survival if not receiving treatment.

[0119] As used herein, a “disease or disorder associated with hyperuricemia” refers to a disease or disorder typically associated with elevated levels of uric acid, including, but not limited to a metabolic disorder, e.g., metabolic syndrome, hyperuricemia, gout (e.g., chronic refractory gout, gout tophus and gouty arthritis), tumor-lysis syndrome, Lesch-Nyhan syndrome, cardiovascular disease, diabetes, hypertension, renal disease, or uric acid nephrolithiasis. Such disorders may optionally be acute or chronic. Elevated levels refer to levels that are higher than levels that are considered normal by the American Medical Association, although significantly lower levels are common in vegetarians due to a decreased intake of purine-rich meat.

[0120] As used herein, “uric acid”, also known as urate (the two terms are used interchangeably herein), refers to an end product of purine metabolism. Humans produce large quantities of uric acid. In human blood, uric acid concentrations between 3.6 mg/dL (~214 pmol/L) and 8.3 mg/dL (~494 pmol/L) (1 mg/dL = 59.48 pmol/L) are considered normal by the American Medical Association. Uric acid concentrations can be measured in samples from a subject, e.g., blood or urine samples, using known methods.

[0121] As used herein, a “uric acid degrading polypeptide” or “uric acid degrading enzyme” refers to any polypeptide (enzyme) that is involved in catabolizing or degrading uric acid. Examples of uric acid degrading polypeptides include urate oxidase (also known as uricase), allantoinase and allantoinase. Other examples of uric acid degrading polypeptides are described herein and are not intended to be limiting. In an embodiment, a uric acid degrading polypeptide

has uric acid as its substrate. In an embodiment, a uric acid degrading polypeptide catalyzes the hydrolysis of uric acid.

[0122] As used herein, “uricolytic activity” refers to the activity of degradation of uric acid.

Uricolytic activity is measured in units, where one unit of activity is defined as degradation of 1 umol of uric acid per minute. In an embodiment, a uric acid degrading polypeptide alone has uricolytic activity. In an embodiment, two or more uric acid degrading polypeptides contribute to uricolytic activity.

[0123] As used herein, the term “variant” refers to a polypeptide which differs from the original protein from which it was derived (e.g., a wild-type protein) by one or more amino acid substitutions, deletions, insertions (i.e., additions), or other modifications. In some embodiments, these modifications do not significantly change the biological activity of the original protein. In many cases, a variant retains at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 100% of the biological activity of original protein. The biological activity of a variant can also be higher than that of the original protein. A variant can be naturally-occurring, such as by allelic variation or polymorphism, or be deliberately engineered. For example, a variant may comprise a substitution at one or more amino acid residue positions to replace a naturally-occurring amino acid residue for a structurally similar amino acid residue. Structurally similar amino acids include: (I, L and V); (F and Y); (K and R); (Q and N); (D and E); and (G and A). In some embodiments, variants include (i) polymorphic variants and natural or artificial mutants, (ii) modified polypeptides in which one or more residues is modified, and (iii) mutants comprising one or more modified residues. Variants may differ from the reference sequence (e.g., by truncation, deletion, substitution, or addition) by no more than 1, 2, 3, 4, 5, 8, 10, 20, or 50

residues, and retains (or encodes a polypeptide that retains) a function of the wild-type protein from which they were derived.

[0124] The amino acid sequence of a variant is substantially identical to that of the original protein. In many embodiments, a variant shares at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, or more global sequence identity or similarity with the original protein. Sequence identity or similarity can be determined using various methods known in the art, such as Basic Local Alignment Tool (BLAST), dot matrix analysis, or the dynamic programming method. In one example, the sequence identity or similarity is determined by using the Genetics Computer Group (GCG) programs GAP (Needleman-Wunsch algorithm). The amino acid sequences of a variant and the original protein can be substantially identical in one or more regions, but divergent in other regions. A variant may include a fragment (e.g., a biologically active fragment of a polypeptide). In some embodiments, a fragment may lack up to about 1, 2, 3, 4, 5, 10, 20, 30, 40, 50, or 100 amino acid residues on the N-terminus, C-terminus, or both ends (each independently) of a polypeptide, as compared to the full-length polypeptide.

Engineered Microbial Cells

[0125] The present disclosure features engineered microbial cells that are engineered to include at least one exogenous polypeptide comprising a uric acid degrading polypeptide, a uric acid transporter, or both. In some embodiments the microbial cell is a fungal cell.

[0126] The present disclosure provides microbial cells that are engineered to degrade uric acid by expression of a uric acid degrading polypeptide, a uric acid transporter, or both a uric acid degrading polypeptide and a uric acid transporter. In some embodiments the microbial cell is a fungal cell.

[0127] The engineered cells may be advantageously used to reduce uric acid concentration in the milieu surrounding the cell (e.g., in vitro or in vivo). For example, the engineered cells provided herein may be administered to a subject (e.g., a human subject) to reduce the concentration of uric acid in the subject (e.g., in the intestinal lumen, in the digestive tract, blood, plasma, or serum of the subject, or elsewhere in the subject).

[0128] In some embodiments, the disclosure provides an engineered microbial cell comprising at least one (e.g., one, two, three, four, or more) exogenous polypeptides, wherein each exogenous polypeptide may comprise either at least one uric acid degrading polypeptide, at least one uric acid transporter, or both a uric acid degrading polypeptide and a uric acid transporter.

[0129] Any condition, disease or disorder in which a reduction of uric acid levels is desired may be treated by administering the engineered cells provided herein.

[0130] In some embodiments of any of the aspects herein, the engineered microbial cell is a fungal cell.

Uric Acid

[0131] Uric acid is an end product of purine metabolism in humans. Xanthine oxidase oxidizes oxypurines such as xanthine and hypoxanthine to uric acid. In humans and higher primates, uric acid is the final oxidation product of purine catabolism. In most other mammals, uricase (uricase) further oxidizes uric acid to 5-hydroxyisourate, which is then further catabolized to allantoin.

[0132] In contrast to other mammals, humans lack the capacity to metabolize urate by hepatic uricase, due to mutational silencing of the enzyme. The loss of uricase in higher primates parallels the similar loss of the ability to synthesize ascorbic acid. This may be because in higher primates, uric acid partially replaces ascorbic acid. Both uric acid and ascorbate are strong reducing agents and potent antioxidants. In humans, about half the antioxidant capacity of

plasma comes from urate. The urate body pool is about 1-1.2g, with daily turnover being approximately 0.6-0.7g. Two-thirds of the newly produced uric acid is excreted in urine, while the remaining one third has a biliary or intestinal elimination or undergoes bacterial uricolysis. It emerges, therefore, that in typical healthy human adults the kidney is the main regulator of uric acid balance.

[0133] Humans produce large quantities of uric acid. In human blood, uric acid concentrations between 3.6 mg/dL (-214 pmol/L) and 8.3 mg/dL (-494 pmol/L) (1 mg/dL = 59.48 pmol/L) are considered normal by the American Medical Association, although significantly lower levels are common in vegetarians due to a decreased intake of purine-rich meat. Uric acid is a weak organic acid of molecular weight 168 Daltons, with dissociation constants $pK_{a1} = 5.75$ and $pK_{a2} = 10.3$ [I]. Therefore, at physiological blood pH, almost all the urate species are in the form of monovalent-anion. The solubility of urate in blood is about 7.0 mg/dL, above which it may deposit in tissues as monosodium-urate-monohydrate.

[0134] Only about 4-5% of urate is bound to plasma proteins. Relative to other mammals, humans have high urate levels in plasma, ranging between 3.5 and 7.5 mg/dL (200-450 pmol/L), males having 1.2 times greater urate levels than healthy females.

[0135] Disorders associated with high uric acid levels (hyperuricemia) include metabolic syndrome, hyperuricemia, gout (e.g., chronic refractory gout, gout tophus and gouty arthritis), tumor lysis syndrome, Lesch-Nyhan syndrome, cardiovascular disease, diabetes, hypertension, renal disease, metabolic syndrome, or uric acid nephrolithiasis. Such disorders can be treated with an engineered microbial cell of the invention comprising a uric acid degrading polypeptide, a uric acid transporter polypeptide, or an engineered microbial cell comprising a uric acid degrading polypeptide and a uric acid transporter polypeptide, e.g., a composition (e.g., a

pharmaceutical composition) comprising said engineered microbial cells, as described herein. In addition, such disorders can be treated by a combination of the engineered microbial cells described herein, and another agent (e.g., a xanthine-oxidase inhibitor and/or a uricosuric and/or an antacid and/or a proton pump inhibitor). The treatment of various diseases and disorders associated with hyperuricemia is described herein.

[0136] Uric acid, a weak organic acid, has very low pH-dependent solubility in aqueous solutions. About 70% of urate elimination occurs in urine, the kidney standing as a major determinant of plasma levels. The complex renal handling results in a fractional clearance of less than 10%. Recently identified urate-specific transporter/channels are involved in tubular handling and extracellular transport. Extracellular fluid, rather than urine output, is the main regulator of urate excretion. A number of interfering agents, including widely used drugs such as aspirin, losartan, diuretics, may decrease or increase urate elimination.

[0137] Hyperuricemia induced by hypouricosuria often accompanies metabolic syndrome, and insulin resistance has been hypothesized as the common underlying defect. Hyperuricosuria, associated with dehydration or exercise, results in acute uric acid nephropathy, and causes an obstructive acute renal failure (ARF).

Uric Acid Degrading Enzymes

[0138] In one aspect, the present disclosure provides a microbial cell engineered to degrade uric acid, comprising an exogenous polypeptide comprising at least one uric acid degrading polypeptide, or a variant thereof. In some embodiments, the microbial cell comprises more than one (e.g., two, three, four, five, or more) exogenous polypeptides, each comprising at least one uric acid degrading polypeptide, or a variant thereof. In some embodiments, the engineered cells described herein comprise more than one type of exogenous polypeptide, wherein each

exogenous polypeptide comprises a uric acid degrading polypeptide, and wherein the uric acid degrading polypeptides are not the same (e.g., the uric acid degrading polypeptides may comprise different types of uric acid degrading polypeptides, or variants of the same type of uric acid degrading polypeptide). For example, in some embodiments, the engineered cell may comprise a first exogenous polypeptide comprising a uricase, or a variant thereof, and a second exogenous polypeptide comprising a uric acid degrading polypeptide that is not a uricase. In addition, an exogenous polypeptide may comprise more than one (e.g., one, two, three, four, five, or more) uric acid degrading polypeptide (e.g., two different uricases).

[0139] Many uric acid degrading polypeptides are known in the art and may be used as described herein. For example, the uric acid catabolism pathway includes several uric acid degrading enzymes. Urate oxidase is the first of three enzymes to convert uric acid to S-(+)-allantoin (allantoin). After uric acid is converted to 5-hydroxyisourate by urate oxidase, 5-hydroxyisourate (HIU) is converted to 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline (OHCU) by HIU hydrolase, and then to S-(+)-allantoin (allantoin) by 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase (OHCU decarboxylase). Allantoin is converted to allantoate by allantoinase. Allantoate is converted to urea by allantoinase. (Lee et al. 2013 PloS ONE 8(5):e64292). Any one or more of the enzymes involved in uric acid catabolism (i.e., uric acid degrading polypeptides) can be included in the microbial cells described herein.

[0140] In some embodiments, the at least one uric acid degrading polypeptide is any enzyme that is capable of degrading uric acid (e.g., a uricase). In some embodiments, the at least one uric acid degrading polypeptide is any enzyme having uric acid as a substrate. In some embodiments, the at least one uric acid degrading polypeptide is any enzyme that is involved in uric acid catabolism, for example, an enzyme that degrades HIU (e.g., an HIU hydrolase), an enzyme that

degrades OHCU (e.g., an OHCU decarboxylase), an enzyme that degrades allantoin (e.g., an allantoinase), or an enzyme that degrades allantoate (e.g., an allantoicase).

[0141] In some embodiments, the at least one uric acid degrading polypeptide, or variant thereof, can be derived from any source or species, e.g., mammalian, fungal, plant or bacterial sources, or can be engineeredly engineered. In some embodiments, the uric acid degrading polypeptide can be a chimeric uric acid degrading polypeptide, e.g., derived from two different species.

[0142] The exogenous polypeptides included in the engineered cells provided herein may comprise an exogenous polypeptide comprising any uric acid degrading polypeptide. In some embodiments, the uric acid degrading polypeptide comprises a uricase, or a variant thereof.

[0143] Uricases (also referred to as urate oxidase), and variants thereof, are described in detail below.

[0144] In some embodiments, the uric acid degrading polypeptide comprises or consists of a variant of the wild-type uric acid degrading polypeptide having at least 60%, sequence identity to the amino acid sequence of a corresponding wild-type uric acid degrading polypeptide.

Uricase

[0145] The disclosure provides, in one aspect, a microbial cell engineered to degrade uric acid, comprising a first exogenous polypeptide comprising a uricase, or a variant thereof. In some embodiments, the microbial cell comprises more than one (e.g., two, three, four, or five) exogenous polypeptide comprising a uricase.

[0146] Uricase (also referred to as UO, urate oxidase, urate:oxygen oxidoreductase (E.C.1.7.3.3)) is an enzyme in the purine degradation pathway that catalyzes the oxidation of uric acid to 5-hydroxyisourate. Uricase is the first in a pathway of three enzymes to convert uric acid to S-(+)-allantoin. After uric acid is converted to 5-hydroxyisourate by urate oxidase, 5-

hydroxyisourate (HIU) is converted to 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline (OHCU) by HIU hydrolase, and then to S-(+)-allantoin by 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase (OHCU decarboxylase). Without HIU hydrolase and OHCU decarboxylase, HIU will spontaneously decompose into racemic allantoin.

[0147] Uricase is an enzyme endogenous to most mammals, with the exception of humans and certain other primates, and is also found in plants, fungi, yeast, and bacteria. Humans do not produce enzymatically active uricase as a result of mutations in the gene for uricase acquired during the evolution of higher primates (see Wu, et al, J Mol Evol 34:78-84 (1992)). As a consequence, in susceptible individuals, excessive concentrations of uric acid in the blood (hyperuricemia) and in the urine (hyperuricosuria) can lead to gout, disfiguring urate deposits (tophi), renal failure, and other related disorders, as described herein.

[0148] An engineered microbial cell of the disclosure may comprise an exogenous polypeptide comprising a uricase, or variant thereof, wherein the uricase is derived from any source(s) known in the art, including mammalian, plant or microbial sources, as well as by engineered technologies.

[0149] In some embodiments, the uricase, or uricase variant, is obtained from a fungal (including yeast) source. In some embodiments, the uricase is derived from *Candida utilis* (e.g., as described in Koyama et al, J. Biochem., 120:969-973 (1996)). In some embodiments, the uricase is derived from the fungus *Aspergillus flavus*. In some embodiments, the uricase is the *Aspergillus flavus* uricase contained in rasburicase (ELITEK®; FASTURTEC®, Sanofi Genzyme). Other fungal sources of uricases can include, for example, *Schizosaccharomyces* (e.g. *Schizosaccharomyces pombe*) or *Zygosaccharomyces* (*Zygosaccharomyces parabailii*).

[0150] In some embodiments, the uricase, or uricase variant, is derived from a bacterium, such as *Arthrobacter* (e.g., *Arthrobacter globiformis*) or *Bacillus* (e.g., *Bacillus subtilis*)

[0151] In some embodiments, the uricase is a chimeric uricase, in which portions of the uricase are derived from different sources. For example, a portion of the chimeric uricase may be obtained (e.g., derived) from one organism and one or more other portions of the chimeric uricase may be obtained (e.g., derived) from another organism. In some embodiments, a portion of the chimeric uricase is obtained from a pig and another portion of the chimeric uricase is obtained from a baboon. In some embodiments, the chimeric uricase may contain portions of porcine liver and/or baboon liver uricase. For example, the chimeric uricase may comprise all or a portion of a porcine uricase (*Sus scrofa* NP_999435) sequence, wherein the sequence contains the mutations R291K and T301S (PKS uricase). Alternatively, the uricase may comprise all or a portion of a baboon liver uricase (*Papio hamadryas* A36227) sequence in which tyrosine at amino acid residue 97 has been replaced by histidine, whereby the specific activity of the uricase may be increased by at least about 60% as compared to the wild-type uricase from which it was derived (i.e., lacking the amino acid substitution). In some embodiments, the chimeric uricase comprises a chimeric uricase described in U.S. Patent No. 6,783,965, or comprises pegloticase (KRYSTEXXA®) (Horizon Rheumatology, Inc.). In some embodiments, the chimeric uricase comprises or consists of the amino acid sequence set forth in SEQ ID NO: 4.

[0152] Alternatively, in some embodiments, the uricase, or uricase variant, may comprise an invertebrate uricase, a plant uricase, a mammalian uricase.

[0153] In some preferred embodiments of the disclosure, the uricase (or variant thereof) comprises or consists of a uricase selected from those set forth in Table 1, below, including a uricase derived from *Candida utilis*, *Aspergillus flavus*, *Arthrobacter globiformis*,

Baboon/porcine (chimera), *Schizosaccharomyces pombe* (Fission yeast), *Bacillus subtilis*, or *Zygosaccharomyces parabailii*. In some embodiments, the uricase comprises an amino acid sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:8.

[0154] In some embodiments, the uricase comprises the *Candida utilis* uricase comprising the amino acid sequence set forth in SEQ ID NO: 1. In some embodiments, the uricase comprises the *Aspergillus flavus* uricase comprising the amino acid sequence set forth in SEQ ID NO:2. In some embodiments, the uricase comprises the *Arthrobacter globiformis* uricase comprising the amino acid sequence set forth in SEQ ID NO:3. In some embodiments, the uricase comprises the baboon/porcine chimeric uricase comprising the amino acid sequence set forth in SEQ ID NO:4. In some embodiments, the uricase comprises the *Schizosaccharomyces pombe* (Fission yeast) uricase comprising the amino acid sequence set forth in SEQ ID NO:5. In some embodiments, the uricase comprises the *Bacillus subtilis* uricase comprising the amino acid sequence set forth in SEQ ID NO:6. In some embodiments, the uricase comprises the *Zygosaccharomyces parabailii* uricase comprising the amino acid sequence set forth in SEQ ID NO:7. In some embodiments, the uricase comprises the Spirosoma sp. KCTC 42546 uricase comprising the amino acid sequence set forth in SEQ ID NO:8.

[0155] In some embodiments, the uricase comprises a variant of a wild-type uricase having at least 60% sequence identity to the amino acid sequence of any one of SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8. In some embodiments, the uricase variant possesses a function of the uricase from which it was derived (e.g., the ability to catalyze the oxidation of uric acid (urate) to 5-hydroxyisourate).

[0156] In a particular embodiment, the uricase consists of the amino acid sequence of any one of SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.

[0157] In some embodiments, the uricase, or variant thereof, is engineered to delete a peroxisome targeting signal (e.g., a native peroxisome targeting signal). In some embodiments, the uricase, or variant thereof, lacks a peroxisome targeting signal.

[0158] In general, a variant uricase, from any origin, may be produced, for example, to enhance production of the protein in an engineered cell, to improve turnover/half-life of the protein or mRNA encoding the protein, and/or to modulate (enhance or reduce) the enzymatic activity of the uricase. The uricase, whatever the source, may also be in a form that is truncated, either at the amino terminal, or at the carboxyl terminal, or at both terminals.

[0159] In some embodiments, the invention provides an engineered microbial cell (e.g. an engineered fungal cell) comprising a nucleic acid sequence encoding a uric acid degrading polypeptide as described herein. In some embodiments, the invention provides an engineered microbial cell prepared by using a nucleic acid sequence encoding a uric acid degrading polypeptide (e.g. a uricase) as described herein. In some embodiments, the nucleic acid sequence encodes a uricase as described herein.

[0160] In some embodiments, the exogenous polypeptide is a fusion polypeptide comprising a uricase, or a variant thereof, linked to a heterologous protein sequence (e.g., via a linker).

Uric Acid Transporters

[0161] In one aspect, the disclosure provides an engineered microbial cell comprising a first exogenous polypeptide comprising a uric acid transporter, or a variant thereof. In some embodiments, the disclosure provides an engineered microbial cell comprising at least one (e.g.,

one, two, three, four, or more) exogenous polypeptide comprising a uric acid transporter. In some embodiments, the disclosure provides an engineered microbial cell comprising more than one exogenous polypeptide, each comprising a uric acid transporter.

[0162] In another aspect, the disclosure provides a microbial cell engineered to degrade uric acid, wherein the cell comprises a first exogenous polypeptide comprising a uric acid degrading polypeptide, e.g., uricase, or a variant thereof, and further comprises a second exogenous polypeptide comprising a uric acid transporter, or a variant thereof.

[0163] In yet another aspect, the disclosure provides an engineered cell comprising at least one (e.g., one two, three, four, or more) exogenous polypeptide, wherein the exogenous polypeptide comprises both a uric acid degrading polypeptide (or a variant thereof) and a uric acid transporter (or a variant thereof). Without wishing to be bound by any particular theory, engineered cells comprising an exogenous polypeptide that comprises both a uric acid degrading polypeptide and a uric acid transporter may improve turnover of uric acid (e.g., the catalysis of uric acid) by facilitating the transfer of uric acid from the uric acid transporter to the uric acid degrading polypeptide, thereby microcompartmentalizing the channeling and catalysis of uric acid.

[0164] In humans, uric acid transporters regulate uric acid transport in the kidney and thereby regulate plasma uric acid levels (see, So and Thorens, *J. Clin. Investigation*, 120:1791-1799 (2010)).

[0165] Uric acid transporters capable of excreting or re-absorbing uric acid are also expressed in the intestine in humans, and thereby contribute to the regulation of plasma uric acid levels (Xu, et al, *Pharmaceutical Biology*, 54:3151-3155 (2016)).

[0166] In microbes, uric acid transporters contribute to the uptake of uric acid from the environment (See e.g., Pantazopoulou and Diallinas, *FEMS Microbiology Reviews*, 31:657-675

(2007)). Typically, microbial uric acid transporters enable the use of uric acid as a carbon and / or nitrogen source, and / or as an energy source, enabling growth and division of the microbe (Middelhoven, et al, Antonie van Leeuwenhoek, 50:369-378 (1984)).

[0167] Microbial uric acid transporters include archaeal, fungal, and bacterial uric acid transporters. It is expected any microbial organisms whose genome encodes gene products predicted to be involved in uric acid degradation (e.g., uricase) will also have uric acid transporters encoded in their genome. In some prokaryotes, these would be multipass transmembrane proteins encoded in the same operon that encodes the uricase.

[0168] Microbial uric acid transporters may be able to transport other purine or purine metabolites (e.g., Xanthine), in addition to uric acid, from outside the cell to inside the cell. These other purines may be transporter in preference to uric acid, with about the same preference, or may be less preferred.

[0169] Well characterized microbial uric acid transporters that could be used to engineer microbial cells of the present invention in order to improve uric acid transport and facilitate uric acid degradation include, but are not limited to: *Bacillus subtilis* PucK (genbank accession number O32140) and PucJ (genbank accession number O32139), as described by Schultz et al, Journal of Bacteriology 183:3293-3302 (2001); *Aspergillus nidulans* UapA (genbank accession number Q07307) and UapC (genbank accession number P487777), as described by Diallynas et al, The EMBO journal 17:3827-3837 (1998), Gorfinkiel et al, J Biol Chem 268:23376-23381 (1993), Alguel et al, Nature Communications 7:11336 (2016), and Kryptou and Diallynas, Fungal Genetics and Biology 63:1-8 (2014); *Aspergillus fumigatus* UapA (genbank accession number XP748919), as described by Goudela et al, Fungal Genetics and Biology. 45:459-472 (2008). *Candida albicans* Xut1 (genbank accession number AAX2221), as described by Goudela

et al, Molecular membrane biology, 22:263-275 (2005), *Escherichia coli* YgfU (genbank accession number EFJ59310), as described by Papakostas et al, Journal of Biological Chemistry, 287:15684-15695 (2012).

[0170] In some embodiments, a microbial cell of the disclosure comprises an exogenous polypeptide comprising a uric acid transporter selected from the group consisting of *Aspergillus nidulans* UapA, *Aspergillus nidulans* UapC, *Aspergillus fumigatus* UapC, *Candida albicans* Xut1, *Schizosaccharomyces pombe* Q9HE12, *Bacillus subtilis* PucK, *Bacillus subtilis* PucJ, *Escherichia coli* YgfU, *Zygosaccharomyces parabailii* AQZ18664, or Spirosoma sp. KCTC 42546 WP_142773020.

[0171] In some embodiments, the engineered microbial cell provided herein comprises at least one exogenous polypeptide comprising a uric acid transporter selected from the group consisting of *Aspergillus nidulans* UapA, *Aspergillus nidulans* UapC, *Aspergillus fumigatus* UapC, *Candida albicans* Xut1, *Schizosaccharomyces pombe* Q9HE12, *Bacillus subtilis* PucK, *Bacillus subtilis* PucJ, *Escherichia coli* YgfU, *Zygosaccharomyces parabailii* AQZ18664, Spirosoma sp. KCTC 42546 WP_142773020, or a variant thereof. In some embodiments, the uric acid transporter is derived from or is a microbial uric acid transporter.

[0172] In some preferred embodiments, the microbial cell of the disclosure comprises an exogenous polypeptide comprising a uric acid transporter selected from those set forth in Table 2, below, comprising or consisting of the amino acid sequence of any one of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO: 18, or a variant thereof. In some embodiments, the uric acid transporter comprises a *Aspergillus nidulans* UapA comprising the amino acid sequence set forth in SEQ ID NO: 9. In some embodiments, the uric acid transporter

comprises a *Aspergillus nidulans* UapC comprising the amino acid sequence set forth in SEQ ID NO: 10. In some embodiments, the uric acid transporter comprises a *Aspergillus fumigatus* UapC comprising the amino acid sequence set forth in SEQ ID NO: 11. In some embodiments, the uric acid transporter comprises a *Candida albicans* Xut1 comprising the amino acid sequence set forth in SEQ ID NO: 12. In some embodiments, the uric acid transporter comprises a *Schizosaccharomyces pombe* Q9HE12 comprising the amino acid sequence set forth in SEQ ID NO: 13. In some embodiments, the uric acid transporter comprises a *Bacillus subtilis* PucK comprising the amino acid sequence set forth in SEQ ID NO: 14. In some embodiments, the uric acid transporter comprises a *Bacillus subtilis* PucJ comprising the amino acid sequence set forth in SEQ ID NO: 15. In some embodiments, the uric acid transporter comprises a *Escherichia coli* YgfU comprising the amino acid sequence set forth in SEQ ID NO: 16. In some embodiments, the uric acid transporter comprises a *Zygosaccharomyces parabailii* AQZ18664 comprising the amino acid sequence set forth in SEQ ID NO: 17. In some embodiments, the uric acid transporter comprises a *Spirosoma* sp. KCTC 42546 WP_142773020 comprising the amino acid sequence set forth in SEQ ID NO: 18.

[0173] In some embodiments, the uric acid transporter comprises a variant of a wild-type uric acid transporter having at least 60% sequence identity to the amino acid sequence of any one of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16 or SEQ ID NO: 17, or SEQ ID NO: 18. In some embodiment the variant of the uric acid transporter possesses a function of the wild-type uric acid transporter from which it was derived (e.g., the ability to transport uric acid).

[0174] In a particular embodiment, the uric acid transporter consists of the amino acid sequence of any one of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, or SEQ ID NO: 18.

[0175] In general, a variant uric acid transporter, may be produced, for example, to enhance production of the protein in an engineered cell, to improve turnover/half-life of the protein or mRNA encoding the protein, and/or to modulate (enhance or reduce) the activity of the uric acid transporter. The uric acid transporter may also be in a form that is truncated, either at the amino terminal, or at the carboxyl terminal, or at both terminals.

[0176] In some embodiments, the invention provides an engineered microbial cell (e.g. an engineered fungal cell) comprising a nucleic acid sequence encoding a uric acid transporter as described herein. In some embodiments, the invention provides an engineered microbial cell prepared by using a nucleic acid sequence encoding a uric acid transporter as described herein. In some embodiments, the nucleic acid sequence encodes a uric acid transporter (*Aspergillus nidulans* UapA, *Aspergillus nidulans* UapC, *Aspergillus fumigatus* UapC, *Candida albicans* Xut1, *Schizosaccharomyces pombe* Q9HE12, *Bacillus subtilis* PucK, *Bacillus subtilis* PucJ, *Escherichia coli* YgfU, *Zygosaccharomyces parabailii* AQZ18664, or *Spirosoma* sp. KCTC 42546 WP_142773020) as described herein.

Polypeptides and Nucleic Acids

[0177] In one aspect, the disclosure provides isolated uric acid degrading polypeptides (e.g., uricase) and uric acid transporters described herein. In some embodiments, the uric acid degrading polypeptides comprise an amino acid sequence having at least 60% sequence identity to the amino acid sequences of a uric acid degrading polypeptide described herein. In some embodiments, the uric acid transporters comprise an amino acid sequence having at least 60%

sequence identity to the amino acid sequences of a uric acid transporter described herein. In some embodiments, the uric acid degrading polypeptides and uric acid transporters are engineered. Methods for producing engineered proteins are known in the art and described herein.

[0178] In another aspect, the disclosure provides nucleic acids (e.g., DNA or RNA (e.g., mRNA)) encoding a uric acid degrading polypeptide described herein. In another aspect, the disclosure provides nucleic acids (e.g., DNA or RNA (e.g., mRNA)) encoding a uric acid transporter described herein. In some embodiments, the nucleic acids are codon-optimized for expression in a desired cell type (e.g., a bacterial or fungal or archaeal cell).

[0179] Furthermore, any of the genes encoding the foregoing enzymes (or any others mentioned herein (or any of the regulatory elements that control or modulate expression thereof)) may be optimized by genetic/protein engineering techniques, such as directed evolution or rational mutagenesis, which are known to those of ordinary skill in the art. Such action allows those of ordinary skill in the art to optimize the enzymes for expression, activity, stability, or other desirable parameters.

Populations of Engineered Microbial Cells

[0180] In one aspect, the invention features cell populations comprising the engineered microbial cells of the invention, e.g., a plurality or population of the microbial cells. In various embodiments, the engineered microbial cell population comprises predominantly fungal cells.

[0181] It will be understood that during the preparation of the engineered microbial cells of the invention, some fraction of cells may not contain the exogenous polypeptide or be transformed to express an exogenous polypeptide. Accordingly, in some embodiments, a population of engineered microbial cells provided herein comprises a mixture of engineered microbial cells

and unmodified microbial cells, i.e., some fraction of cells in the population will not comprise, present, or express an exogenous polypeptide.

Urate Consumption Assays

- [0182]** Urate consumption assays can be used to quantify uptake and/or biodegradation of uric acid from media surrounding intact cells.
- [0183]** The reduction of absorbance at wavelengths between 290 and 295 nm has been used to measure uric acid concentrations by converting urate into 5-hydroxyisourate through addition of purified uricase enzyme (Prætorius and Poulsen, *Scandinavian Journal of Clinical and Laboratory Investigation*, 5273-280 (1953)). Urate consumption by intact cells can be measured by quantifying growth of microbial strains on culture media containing uric acid as the sole nitrogen source as compared to growth on culture media containing alternative nitrogen sources, as outlined for example in Martzoukou et al, *J. Molec. Biol.* 427:2679-2696 (2015), or in Schultz et al, *Journal of Bacteriology* 183:3293-3302 (2001). Assays that quantify urate consumption by intact cells can also rely on the use of expensive and hazardous radiolabeled compounds, e.g., ^3H -labeled or ^{14}C -labeled uric acid, as outlined for example in Goudela et al, *Molecular membrane biology*, 22:263-275 (2005).
- [0184]** The invention contemplates a much simpler, faster, easier and safer assay that quantifies uric acid consumption by intact cells by spectrophotometrically tracking depletion of uric acid in medium or buffer surrounding said cells. Intact cells require a uric acid transporter to transport urate into cells, where it is broken down by a uricase enzyme. Both a functional uric acid transporter and a functional uricase are required. Uric acid is depleted over time in a culture medium or buffer containing uric acid if intact cells are added that have the ability to take up uric acid from the culture medium or buffer and break it down to allow continued importation of uric

acid from the medium or buffer surrounding cells into said intact cells. The rate of uric acid depletion is dependent on the rate of uric acid consumption by the intact cells, allowing uric acid consumption to be quantified. The uric acid concentration can be tracked spectrophotometrically by measuring absorbance at a wavelength where urate strongly absorbs, preferably between 275 nm and 350 nm, most preferably 293 nm, following separation of the intact cells from the medium or buffer.

Methods of Obtaining Engineered Microbial Cells

[0185] Various methods of obtaining genetically engineered microbial cells, e.g., fungal cells, are contemplated by the present disclosure.

[0186] Methods of manufacturing microbial cells comprising an exogenous agent (e.g., a polypeptide) are described, e.g., in Yeast Protocols Handbook, Clontech Laboratories, Mountain View, USA, 2009.

[0187] In one aspect, the disclosure features an engineered microbial cell (e.g., engineered fungal cell), comprising a first exogenous polypeptide comprising a uric acid degrading polypeptide, or a variant thereof, produced by a process comprising introducing an exogenous nucleic acid encoding the first exogenous polypeptide into a microbial cell; and culturing the microbial cell under conditions suitable for production of the first exogenous polypeptide.

[0188] In another aspect, the disclosure features an engineered microbial cell (e.g., engineered fungal cell), comprising a first exogenous polypeptide comprising a uric acid transporter, or a variant thereof, produced by a process comprising introducing an exogenous nucleic acid encoding the first exogenous polypeptide into a microbial cell; and culturing the microbial cell under conditions suitable for production of the first exogenous polypeptide.

[0189] In another aspect, the disclosure features an engineered microbial cell (e.g., engineered fungal cell), comprising a first exogenous polypeptide comprising a uric acid degrading polypeptide, or a variant thereof, and a second exogenous polypeptide comprising a uric acid transporter, or a variant thereof, produced by a process comprising introducing an exogenous nucleic acid encoding the first exogenous polypeptide into a microbial cell; introducing an exogenous nucleic acid encoding the second exogenous polypeptide into a microbial cell; and culturing the microbial cell under conditions suitable for production of the first exogenous polypeptide and the second exogenous polypeptide.

[0190] In some embodiments, the uric acid degrading polypeptide is a uricase, or a variant thereof. In some embodiments, more than one uric acid degradation polypeptide, or variant thereof, may be combined in one or more microbial cells, as described herein.

[0191] The processes of making the engineered microbial cells are described in more detail below.

Probiotic Cells

[0192] Provided herein are engineered microbial cells, and methods of making the engineered microbial cells.

[0193] As used herein, the term “probiotic” refers to a live microbial cells that, when administered in adequate amounts, may or may not confer a health benefit on the host, and do not exert harmful effects on the host. Probiotic cells may be referred to or sold using alternative designations, for example as “nutraceuticals”, “dietary supplements”, “supplements”, “food additives”, “dietary ingredients”, “food ingredients”, and “ingredients”.

[0194] The engineered microbial cells can be probiotic cells. The engineered probiotic cells can be eukaryotic, e.g., fungal, e.g. *Saccharomyces boulardii*, e.g., *Candida utilis*, e.g. from the

genus Kluyveromyces, bacterial, e.g. from the genus Lactobacillus, or can be archeal. The engineered microbial cell can be from the genus Escherichia, e.g., *Escherichia coli* Nissle. The engineered microbial cell can be from the genus Bacteroides, e.g., *Bacteroides ovatus*, *Bacteroides fragilis*, *Bacteroides thetaiotaomicron*, *Bacteroides vulgatus*, *Bacteroides ovatus*, or *Bacteroides uniformis*. The engineered microbial cell can be from the genus Clostridium. The engineered microbial cell can be from the genus Bacillus.

Expression of Exogenous Polypeptides

- [0195] In some embodiments, the engineered microbial cells described herein are generated by contacting a suitable isolated cell, e.g., a microbial cell, with an exogenous nucleic acid encoding a polypeptide of the disclosure (e.g., a uricase and/or a uric acid transporter).
- [0196] In some embodiments, the exogenous polypeptide is encoded by a DNA, which is contacted with a microbial cell. In some embodiments, the exogenous polypeptide is encoded by an RNA, which is contacted with a microbial cell.
- [0197] An exogenous polypeptide may be expressed from a transgene introduced into an microbial cell, e.g. by electroporation, chemical or polymeric transfection; an exogenous polypeptide that is over-expressed from the native locus by the introduction of an external factor, e.g., a transcriptional activator, transcriptional repressor, or secretory pathway enhancer.
- [0198] In certain embodiments, the introducing step comprises electroporation. In some embodiments, the introducing step comprises chemical transformation (e.g., PEG-mediated transformation).
- [0199] In some embodiments, the introducing step comprises introducing the first exogenous nucleic acid encoding the first exogenous polypeptide by electroporation of an episomal plasmid.

[0200] Exogenous polypeptides (e.g., a uricase or a uric acid transporter) can be introduced by transfection of single or multiple copies of genes, transformation, or electroporation in the presence of DNA or RNA. Methods for expression of exogenous proteins in microbial cells are well known in the art.

[0201] In some embodiments, when there is more than one polypeptide (e.g., two or more), the polypeptides may be encoded in a single nucleic acid, e.g., a single vector. When both the uricase and uric acid transporter are encoded in the same vector, there are multiple possible sub-strategies useful for this method of co-expression. In some embodiments, the single vector has a separate promoter for each gene, or any other suitable configuration. In some embodiments, the engineered nucleic acid comprises a gene encoding a first exogenous polypeptide, wherein the first exogenous polypeptide is uricase, or a variant thereof, and a gene encoding a second exogenous polypeptide, wherein the second exogenous polypeptide is a uric acid transporter, or a variant thereof.

[0202] For dual expression via 2 promoters, the PGK1 promoter may be used as promoter #1 and the GPD (TDH3) promoter as promoter #2, although the disclosure is not to be limited by these two exemplary promoters. Another strategy is to express both uricase and uric acid transporter proteins by inserting an internal ribosome entry site (IRES) between the two genes. Still another strategy is to express uricase and uric acid transporter as direct peptide fusions separated by a linker.

[0203] In some embodiments, the two or more polypeptides are encoded in two or more nucleic acids, e.g., each vector encodes one of the polypeptides.

[0204] In certain embodiments, the expression vector comprises a promoter selected from the group consisting of *Saccharomyces* PDC1p, FBA1p, TEF2p, PGK1p, PGI1p, ADH1p, TDH2p,

PYK1p, ENO2p, GPDp, GPM1p, TPI1p, TEF1p, and HXT7p promoters, as described in Sun et al, *Biotechnology and Bioengineering* 109:2082-2092 (2012).

[0205] Nucleic acids such as DNA expression vectors or mRNA for producing the exogenous polypeptides may be introduced into progenitor cells that are suitable to produce the exogenous polypeptides described herein. In some instances, the expression vectors can be designed such that they can incorporate into the genome of cells by homologous or non-homologous recombination by methods known in the art.

[0206] According to some embodiments, one or more exogenous polypeptides may be cloned into plasmid constructs for transfection. Methods for transferring expression vectors or genes into cells that are suitable to produce the engineered microbial cells described herein include, but are not limited to, transformation, chemical or polymeric transformation.

[0207] According to some embodiments, engineered DNA encoding each exogenous polypeptide may be cloned into a suitable integrative plasmid for integration into microbial cells. In some embodiments, the episomal or integrative vector comprises DNA encoding a single exogenous polypeptide for integration into microbial genomes. For example, in some embodiments, the episomal or integrative vector comprises DNA encoding a uricase polypeptide for integration into microbial cells. In some embodiments, the episomal or integrative vector comprises DNA encoding a uric acid transporter for integration into microbial cells. In other embodiments, the episomal or integrative vector comprises two, three, four or more exogenous polypeptides as described herein for integration into microbial cells. For example, in some embodiments, the episomal or integrative vector comprises DNA encoding a uricase polypeptide and a uric acid transporter polypeptide for integration into microbial cells. According to some embodiments, engineered DNA encoding the one or more exogenous polypeptides may be

cloned into a plasmid DNA construct encoding a selectable trait, such as an antibiotic resistance gene or an auxotrophy complementation gene. According to some embodiments, engineered DNA encoding the exogenous polypeptides may be cloned into a plasmid construct that is adapted to stably express each engineered protein in the microbial cells.

[0208] In some embodiments, the engineered microbial cell is generated by contacting a suitable isolated microbial precursor cell with an exogenous nucleic acid encoding one or more exogenous polypeptides. In some embodiments, the exogenous polypeptide is encoded by a DNA, which is contacted with a microbial precursor cell.

[0209] The one or more exogenous polypeptides may be genetically introduced into a microbial cell (e.g., fungal cell), using a variety of DNA techniques, including transient or stable transfections and gene transfer approaches. The exogenous polypeptides may be expressed on the surface and/or in the cytoplasm and/or in other subcellular compartments of the engineered microbial cells.

[0210] Optionally, electroporation methods may be used to introduce a plasmid vector into suitable microbial cells. Electroporation allows for the introduction of various molecules into the cells including, for example, DNA and RNA. As such, microbial cells are isolated and cultured as described herein.

[0211] Electroporation may be done using, for example, a MicroPulser Electroporator or Gene Pulser (Bio-Rad), as described in Benatuil et al, Protein Eng Des Sel. 23:155-159 (2010), Supplementary Methods.

[0212] Microbial cells may be transformed with an integrative expression vector which is unable to self-replicate. Alternatively, microbial cells may be transformed with a vector which may persist as autonomously replicating genetic units without integration into chromosomes. These

vectors (e.g., plasmids) may exploit genetic elements derived from plasmids that are normally extrachromosomally replicating in cells. Such plasmids include, for example, the episomal *Saccharomyces* 2 micron plasmid. Self-replicating vectors may also include chromosomal elements that allow for independent replication. Such self-replicating vectors exploit the cell's endogenous replication and chromosome segregation machinery to persist like mini-chromosomes. Chromosomal elements that can be used to produce self-replicating vectors include, for example, an autonomously replicating sequence (ARS) and a centromere (CEN), as described for example in Gnügge and Rudolf, *Yeast* 34:205-221 (2017).

[0213] Exogenous nucleic acids encoding one or more exogenous polypeptides may be assembled into expression vectors by standard molecular biology methods known in the art, e.g., restriction digestion, overlap-extension PCR, and Gibson assembly.

[0214] In certain embodiments, the engineered microbial cell is a microbial cell that presents a first exogenous polypeptide that is conjugated with a second exogenous polypeptide.

Methods of Use and Treatment

[0215] The present disclosure provides methods of treating or preventing hyperuricemia in a subject, comprising administering to the subject the engineered microbial cell as described herein, in an amount effective to treat or prevent hyperuricemia in the subject.

[0216] Methods of administering engineered microbial cells comprising (e.g., presenting) exogenous agents (e.g., polypeptides) are described, e.g., in Govender et al, *Aaps PharmSciTech* 15:29-43 (2014).

[0217] In embodiments, the engineered microbial cells described herein (e.g., engineered fungal cells) are orally administered to a subject, e.g., a mammal, e.g., a human. The methods described herein are applicable to both human therapy and veterinary applications.

[0218] In one aspect, the present disclosure provides a method of treating or preventing hyperuricemia in a subject, comprising orally administering to the subject an engineered microbial cell as described herein (e.g. an engineered microbial cell comprising a uric acid degrading polypeptide, e.g., uricase, an engineered microbial cell comprising a uric acid transporter, an engineered microbial cell comprising a uric acid degrading polypeptide, e.g., uricase and a uric acid transporter), in an amount effective to treat or prevent hyperuricemia in the subject.

[0219] The normal range of uric acid in blood is between 3.4 mg/dL and 7.0 mg/dL in men, between 2.4 mg/dL and 6.0 mg/dL in premenopausal women, and from 2.5 mg/dL to 5.5 mg/dL in children. Urate crystal formation/precipitation typically occurs in men at levels of 6.6 mg/dL or higher and in women at levels of 6.0 mg/dL or higher. Also, what may be in the normal range for the population as a whole may be elevated for the individual.

[0220] Cardiovascular and other consequences of elevated uric acid can occur with blood levels well within these “normal” ranges. Therefore, a diagnosis of hyperuricemia is not necessarily a prerequisite for the beneficial effects of the engineered microbial cells of the invention.

[0221] In some embodiments, the subject has a serum urate level greater than about 6.8 mg/dl prior to administering the engineered microbial cell.

[0222] In some embodiments, the methods described herein comprise selecting a subject having a serum urate level greater than about 6.8 mg/dl, and administering an engineered microbial cell described herein.

[0223] In some embodiments, the subject has a serum urate level less than about 6.8 mg/dl, after administering the engineered microbial cell. In some embodiments, the subject has a serum urate level of about 6.0 mg/dl after administering the engineered microbial cell, for example 6.0, 5.9,

5.8, 5.7, 5.6, 5.5, 5.4, 5.3, 5.2, 5.1, 5.1 mg/dL or less, after administering the engineered microbial cell.

Hyperuricemia

[0224] Hyperuricemia is the presence of high levels of uric acid in the blood. Hyperuricemia may occur because of decreased excretion. Hyperuricemia may also occur from increased production, or a combination of the two mechanisms. Underexcretion accounts for the majority of cases of hyperuricemia. Overproduction accounts for only a minority of patients presenting with hyperuricemia. Consumption of purine-rich diets is one of the main causes of hyperuricemia. Other dietary causes are ingestion of high protein and fat, and starvation. Starvation results in the body metabolizing its own muscle mass for energy, in the process releasing purines into the bloodstream. Purine bases composition of foods varies. Foods with higher content of purine bases adenine and hypoxanthine are suggested to be more potent in exacerbating hyperuricemia.

[0225] Humans lack uricase, an enzyme which degrades uric acid. Increased levels predispose for gout and, if very high, renal failure. Apart from normal variation (with a genetic component), tumor lysis syndrome produces extreme levels of uric acid, mainly leading to renal failure. The Lesch-Nyhan syndrome is also associated with extremely high levels of uric acid. The Metabolic syndrome often presents with hyperuricemia, while a hyperuricemic syndrome is also common in Dalmatian dogs. A uric acid degrading polypeptide, e.g., uricase, described herein and a pH increasing agent, alone or in combination with another agent, e.g., another agent described herein, can be used to treat hyperuricemia.

[0226] Asymptomatic hyperuricemia is the term for an abnormally high serum urate level, without gouty arthritis or nephrolithiasis. Hyperuricemia is defined as a serum urate

concentration greater than about 6.8 mg per dL, the approximate level at which urate is supersaturated in plasma. Serum uric acid levels above 360 uM are considered pathogenic.

[0227] Although gouty arthritis characteristically occurs in patients with hyperuricemia, hyperuricemia is not necessarily associated with clinical gout. Researchers from the Normative Aging Study followed 2,046 initially healthy men for 15 years by taking serial measurements of serum urate levels. The five-year cumulative incidence rates of gouty arthritis were 2.0 percent for a serum urate level of 8.0 mg per dL (475 pmol per L) or lower, 19.8 percent for urate levels from 9.0 to 10.0 mg per dL (535 to 595 pmol per L) and 30 percent for a serum urate level higher than 10 mg per dL (595 pmol per L). Hyperuricemia predisposes patients to both gout and nephrolithiasis, but therapy is occasionally not warranted in the asymptomatic patient. Recognizing hyperuricemia in the asymptomatic patient, however, provides the physician with an opportunity to modify or correct underlying acquired causes of hyperuricemia.

Hyperuricosuria

[0228] Hyperuricosuria is defined as urinary excretion of uric acid greater than 800 mg/d in men and greater than 750 mg/d in women. This may be due to either excess dietary intake of purine-rich foods or endogenous uric acid overproduction. Hyperuricosuria may be associated with hyperuricemia.

Gout

[0229] Gout is a condition that results from crystals of uric acid depositing in tissues of the body. Gout is characterized by an overload of uric acid in the body and recurring attacks of joint inflammation (arthritis). Chronic gout can lead to deposits of hard lumps of uric acid in and around the joints, decreased kidney function, and kidney stones.

- [0230] Gout is generally divided into four categories based upon progressively more severe symptoms:
- [0231] Asymptomatic. Elevated uric acid levels in the blood, but no overt symptoms.
- [0232] Acute gouty arthritis: Sudden onset of symptoms, often in a single joint (commonly a big toe), and then involving other joints. Symptoms include pain, swelling, redness and fever.
- [0233] Intercritical gout: Asymptomatic phases between gout attacks.
- [0234] Chronic tophaceous gout: A chronic condition that may include frequent attacks, constant mild pain and inflammation of joints, destruction of cartilage and bone, development of uric acid crystal deposits, kidney dysfunction and kidney stones.
- [0235] Excess serum accumulation of uric acid can lead to a type of arthritis known as gout (gouty arthritis). Gouty arthritis is usually an extremely painful attack with a rapid onset of joint inflammation. The joint inflammation is precipitated by deposits of uric acid crystals in the joint fluid (synovial fluid) and joint lining (synovial lining). Intense joint inflammation occurs as white blood cells engulf the uric acid crystals and release chemicals of inflammation, causing pain, heat, and redness of the joint tissues.
- [0236] The small joint at the base of the big toe is the most common site of an acute gout attack. Other joints that can be affected include the ankles, knees, wrists, fingers, and elbows. Acute gout attacks are characterized by a rapid onset of pain in the affected joint followed by warmth, swelling, reddish discoloration, and marked tenderness.
- [0237] Hyperuricemia and gout are particularly significant issues in organ transplant recipients (Stamp et al, Drugs 65:2593-2611 (2005)). Uric acid is often elevated in patients with renal transplants, and common immunosuppressive drugs such as cyclosporine can cause particularly severe hyperuricemia. In transplant patients, allopurinol is contra indicated due to interactions

with some immunosuppressants such as azathioprine, and due to bone marrow failure caused by the combination. Furthermore, elevated uric acid may contribute to graft failure (Armstrong et al, Transplantation 80:1565-1571 (2005)).

Lesch-Nyhan syndrome

[0238] Lesch-Nyhan syndrome (LNS), also known as Nyhan's syndrome, is a rare, inherited disorder caused by a deficiency of the enzyme hypoxanthine-guanine phosphoribosyltransferase (HGPRT). LNS is an X-linked recessive disease: the gene is carried by the mother and passed on to her son. LNS is present at birth in baby boys. Patients have severe mental and physical problems throughout life. The lack of HGPRT causes a build-up of uric acid in all body fluids, and leads to problems such as severe gout, poor muscle control, and moderate mental retardation, which appear in the first year of life.

[0239] Abnormally high uric acid levels can cause sodium uric acid crystals to form in the joints, kidneys, central nervous system and other tissues of the body, leading to gout-like swelling in the joints and severe kidney problems. Neurological symptoms include facial grimacing, involuntary writhing, and repetitive movements of the arms and legs similar to those seen in Huntington's disease. The direct cause of the neurological abnormalities remains unknown. Because a lack of HGPRT causes the body to poorly utilize vitamin B 12, some boys may develop a rare disorder called megaloblastic anemia.

[0240] The symptoms caused by the buildup of uric acid (arthritis and renal symptoms) respond well to treatment with drugs such as allopurinol that reduce the levels of uric acid in the blood. There is no cure, but many patients live to adulthood. LNS is rare, affecting about one in 380,000 live births.

Uric Acid Nephrolithiasis

[0241] Uric acid stones account for about 5% to 10% of all kidney stones in Western countries and Japan. The stones can be composed of uric acid alone or admixed with calcium oxalate. Sex distribution indicates a male to female ratio of more than one, which tends to diminish in the post-menopausal age. Kidney stones, also called renal calculi, are solid concretions (crystal aggregations) of dissolved minerals in urine; calculi typically form inside the kidneys or ureters. The terms nephrolithiasis and urolithiasis refer to the presence of calculi in the kidneys and urinary tract, respectively.

[0242] The formation of uric acid stones is associated with conditions that cause high blood uric acid levels, such as gout, leukemias/lymphomas treated by chemotherapy (secondary gout from the death of leukemic cells), and acid/base metabolism disorders where the urine is excessively acid resulting in uric acid precipitation.

Vascular conditions

[0243] Diseases related to elevated soluble uric acid often involve vascular problems: hypertension (Sundstrom et al, Hypertension 45:28-33 (2005)), prehypertension (Syamela et al, J Hypertens 25:1583-1589 (2007)), atherosclerosis (Ishizaka et al, Arterioscler Thromb Vase Biol 5:1038-1044 (2005)), peripheral artery disease (Shankar, et al, Atherosclerosis 196:749-755 (2007)), vascular inflammation (Zoccali et al, J Am Soc Nephrol. 17:1466-1471 (2006)), heart failure (Strasak et al, Clin Chem. 54:273-284 (2008); Pascual-Figal et al, Eur J Heart Fail 9:518-524 (2006); Çengel et al, Acta Cardiol 60:489-492 (2005)), myocardial infarctions (Strasak et al, Clin Chem. 54:273-284 (2008); (Bos et al, Stroke 37:1503-1507 (2006)), renal dysfunction

(Cirillo et al, J Am Soc Nephrol 17(12 Suppl 3):S165-S168 (2006)), and strokes (Bos et al, Stroke 37:1503-1507 (2006)). Uric acid directly causes endothelial dysfunction (Kanellis et al, Semin Nephrol. 25:39-42 (2005); Khosla et al, Kidney Int. 67:1739-1742 (2005)). In children, early-onset essential hypertension is associated with elevated serum uric acid, and reduction of uric acid with allopurinol reduced blood pressure in a small cohort of patients (Feig and Johnson, J Ren Nutrition 17:79-83 (2007)). Hyperuricemia is an independent risk factor in all of these conditions.

Diabetes

[0244] Elevated levels of uric acid are associated with prediabetes, insulin resistance, the development of Type 2 diabetes, and an increased probability of a variety of undesirable conditions in people with diabetes, such as peripheral artery disease, strokes, and increased mortality risk. Studies have shown that high serum uric acid is associated with higher risk of type 2 diabetes independent of obesity, dyslipidemia, and hypertension. Serum uric acid is a strong predictor of stroke in patients with non-insulin dependent diabetes mellitus.

Metabolic Syndrome

[0245] Metabolic syndrome is a cluster of conditions that occur together, increasing the risk of heart disease, stroke and diabetes. Metabolic syndrome involves having several disorders related to metabolism at the same time, including: obesity; elevated blood pressure; an elevated level of triglycerides; a low level of high-density lipoprotein (HDL) cholesterol; high blood pressure and/or high insulin levels. Hyperuricemia is associated with components of metabolic syndrome, and may play a pathogenic role in the metabolic syndrome.

Inflammatory Responses

[0246] Elevated soluble uric acid is also associated with or directly induces inflammatory responses. For example, uric acid is transported into vascular smooth muscle cells via organic acid transporters, especially the uric acid transporter URAT1, and then stimulates vascular smooth muscle cells to produce C-reactive protein, MCP-1 and other cytokines, thereby stimulating proliferation and other changes associated with atherosclerosis (Price et al, J Am Soc Nephrol 17:1791-1795 (2006); Kang et al, Am J Nephrol. 25:425-433 (2005); Yamamoto et al, Hypertens. Res. 29:915-921 (2006), stimulates human mononuclear cells to produce IL-1 b, IL-6 and TNF-a, causes marked increases in TNF-a when infused into mice, activates endothelial cells and platelets, and increases platelet adhesiveness (Coutinho et al, Amer. J. Hypertens. 20:83-89 (2007); Levya et al, Eur. Heart J. 19:1814-1822 (1998)). Uric acid has also been shown to inhibit bioavailability of endothelial nitric oxide and activate the renin-angiotensin system.

Cognitive Impairment

[0247] Hyperuricemia is also associated with cognitive impairment and other forms of central nervous system dysfunction. (Schretlen et al, Neuropsychology 21:136-140 (2007); Watanabe et al, J. Health Science 52:730-737 (2006)).

[0248] An engineered microbial cell as described herein (e.g. an engineered microbial cell comprising a uric acid degrading polypeptide, e.g., uricase, an engineered microbial cell comprising a uric acid transporter, or an engineered microbial cell comprising a uric acid degrading polypeptide, e.g., uricase and a uric acid transporter), alone or in combination with another agent, e.g., another agent described herein, can be used to treat hyperuricemia, asymptomatic hyperuricemia, hyperuricosuria, gout, refractory gout, Lesch-Nyhan syndrome, kidney stones and nephrolithiasis, e.g., kidney stones and/or nephrolithiasis caused by, or associated with, elevated uric acid concentrations, cardiovascular disease caused by, or

associated with, elevated uric acid concentrations, diabetes caused by, or associated with, elevated uric acid concentrations, metabolic syndrome caused by, or associated with, elevated uric acid concentrations, inflammatory responses caused by, or associated with, elevated uric acid concentrations, cognitive impairment caused by, or associated with, elevated uric acid concentrations.

[0249] In some embodiments, a subject has refractory gout if they have demonstrated contraindication to allopurinol, or have a medical history of failure to normalize uric acid (e.g., to less than 6 mg/dL) with at least 3 months of allopurinol treatment at the maximum medically appropriate dose.

Dosing

[0250] In one embodiment, a dose of engineered microbial cells as described herein comprises about 10^6 – 10^{12} engineered microbial cells per dose.

[0251] In one example, administration of the engineered microbial cell is initiated at a dose which is minimally effective, and the dose is increased over a pre-selected time course until a positive effect is observed. Subsequently, incremental increases in dosage are made limiting to levels that produce a corresponding increase in effect while taking into account any adverse effects that may appear.

[0252] Any one of the doses provided herein for an engineered microbial cell as described herein can be used in any one of the methods or kits provided herein. Generally, when referring to a dose to be administered to a subject the dose is a label dose. Thus, in any one of the methods provided herein the dose(s) are label dose(s).

[0253] Also provided herein are a number of possible dosing schedules. Accordingly, any one of the subjects provided herein may be treated according to any one of the dosing schedules

provided herein. As an example, any one of the subject provided herein may be treated with an engineered microbial cell as described herein. In certain embodiments, the engineered microbial cell comprises a first exogenous polypeptide comprising uricase, or a variant thereof, and a second exogenous polypeptide comprising a uric acid transporter, or a variant thereof.

[0254] Each dose of engineered microbial cells can be administered at intervals such as thrice, twice, or once daily, once weekly, twice weekly, once monthly, or twice monthly. In some embodiments, a subject is dosed on a monthly dosing schedule.

[0255] The mode of administration for the composition(s) of any one of the treatment methods provided may be by oral administration, such as a capsule containing (freeze-)dried microbes, a powder containing (freeze-)dried microbes, or a suspension containing live microbes, prior to, during, or after a meal. Additionally, any one of the methods of treatment provided herein may also include administration of an additional therapeutic, as described in more detail below. The administration of the additional therapeutic may be according to any one of the applicable treatment regimens provided herein.

[0256] In some embodiments of any one of the methods provided herein, the level of uric acid is measured in the subject at one or more time points before, during and/or after the treatment period.

[0257] The methods described herein are intended for use with any subject that may experience the benefits of these methods. Thus, "recipients" "subjects," "patients," and "individuals" (used interchangeably) include humans as well as non-human subjects, particularly domesticated animals. Subjects provided herein can be in need of treatment according to any one of the methods or compositions or kits provided herein. Such subjects include those with elevated serum uric acid levels or uric acid deposits. Such subjects include those with hyperuricemia. It is

within the skill of a clinician to be able to determine subjects in need of a treatment as provided herein.

[0258] In some embodiments, the subject and/or animal is a mammal, e.g., a human. In some embodiments, the human is a pediatric human. In other embodiments, the human is an adult human. In other embodiments, the human is a geriatric human. In other embodiments, the human may be referred to as a patient.

[0259] In other embodiments, the subject is a non-human animal, and therefore the disclosure pertains to veterinary use. In a specific embodiment, the non-human animal is a household pet. In another specific embodiment, the non-human animal is a livestock animal. In certain embodiments, the subject is a human cancer patient that cannot receive chemotherapy, e.g. the patient is unresponsive to chemotherapy or too ill to have a suitable therapeutic window for chemotherapy (e.g. experiencing too many dose- or regimen-limiting side effects). In certain embodiments, the subject is a human subject having gout or another disease or condition associated with hyperuricemia. In other certain embodiments, the subject is a human subject having chronic refractory gout.

[0260] In some embodiments, any one of the subjects for treatment as provided in any one of the methods provided has gout or a condition associated with gout or another condition as provided herein. In some embodiments, any one of the subjects for treatment as provided in any one of the methods provided has been diagnosed with a disease selected from the group consisting of gout, rheumatoid arthritis, osteoarthritis, cerebral stroke, ischemic heart disease, arrhythmia, and chronic renal disease. In some embodiments, any one of the subjects for treatment as provided in any one of the methods provided has chronic refractory gout. In some embodiments, any one of the subjects for treatment as provided in any one of the methods provided the subject has had or

is expected to have gout flare. In some embodiments, any one of the subjects for treatment as provided in any one of the methods provided has one or more risk factors for hyperuricemia selected from the group consisting of insulin resistance, obesity, a purine rich diet and advanced age. In some embodiments, any one of the subjects for treatment as provided in any one of the methods provided has been diagnosed with symptomatic gout with at least 3 gout flares in the previous 18 months. In some embodiments, any one of the subjects for treatment as provided in any one of the methods provided has been diagnosed with at least 1 gout tophus or gouty arthritis. In some embodiments, any one of the subjects for treatment as provided in any one of the methods provided has a contraindication to allopurinol. Contraindications to allopurinol include extreme loss of body water, chronic heart failure, allergic reaction causing inflammation of blood vessels, liver problems and moderate to severe kidney impairment. In some embodiments, any one of the subjects for treatment as provided in any one of the methods provided has a failure to normalize uric acid to less than 6 mg/dL after at least 3 months of allopurinol treatment.

[0261] In some embodiments, the subject has or is at risk of having an elevated uric acid level, e.g., an elevated plasma or serum uric acid level. When blood levels of uric acid may exceed the physiologic limit of solubility, the uric acid may crystallize in the tissues, including the joints, and may cause gout and gout-associated conditions.

[0262] In some embodiments, serum uric acid levels >5 mg/dL, >6 mg/dL, or >7 mg/dL are indicative that a subject may be a candidate for treatment with any one of the methods or compositions or kits described herein.

[0263] In some embodiments, the subject has, or is at risk of having, hyperuricemia. In some embodiments, the subject has, or is at risk of having, gout, acute gout, acute intermittent gout,

gouty arthritis, acute gouty arthritis, acute gouty arthropathy, acute polyarticular gout, recurrent gouty arthritis, chronic gout (with or without tophi), tophaceous gout, chronic tophaceous gout, chronic advanced gout (with or without tophi), chronic polyarticular gout (with or without tophi), chronic gouty arthropathy (with or without tophi), idiopathic gout, idiopathic chronic gout (with or without tophi), primary gout, chronic primary gout (with or without tophi), refractory gout, such as chronic refractory gout, axial gouty arthropathy, a gout attack, a gout flare, podagra (i.e., monarticular arthritis of the great toe), chiragra (i.e., monarticular arthritis of the hand), gonagra (i.e., monarticular arthritis of the knee), gouty bursitis, gouty spondylitis, gouty synovitis, gouty tenosynovitis, gout that affects tendons and ligaments, lead-induced gout (i.e., saturnine gout), drug induced gout, gout due to renal impairment, gout due to kidney disease, chronic gout due to renal impairment (with or without tophi), chronic gout due to kidney disease (with or without tophi), erosive bone disease associated with gout, stroke associated with gout, vascular plaque associated with gout, cirrhosis or steatohepatitis associated with gout, liver-associated gout, incident and recurrent gout, diabetes associated with damage to pancreas in gout, general inflammatory diseases exacerbated by gout, other secondary gout, or unspecified gout.

[0264] In some embodiments, the subject has, or is at risk of having, a condition associated with the renal system, for example, calculus of urinary tract due to gout, uric acid urolithiasis, uric acid nephrolithiasis, uric acid kidney stones, gouty nephropathy, acute gouty nephropathy, chronic gouty nephropathy, urate nephropathy, uric acid nephropathy, and gouty interstitial nephropathy.

[0265] In some embodiments, the subject has, or is at risk of having, a condition associated with the nervous system, for example, peripheral autonomic neuropathy due to gout, gouty neuropathy, gouty peripheral neuropathy, gouty entrapment neuropathy, or gouty neuritis.

[0266] In some embodiments, the subject has, or is at risk of having, a condition associated with the cardiovascular system, for example, metabolic syndrome, hypertension, obesity, diabetes, myocardial infarction, stroke, dyslipidemia, hypertriglyceridemia, insulin resistance/hyperglycemia, coronary artery disease/coronary heart disease, coronary artery disease or blockage associated with gout or hyperuricemia, heart failure, peripheral arterial disease, stroke/cerebrovascular disease, peripheral vascular disease, and cardiomyopathy due to gout.

[0267] In some embodiments, the subject has, or is at risk of having, a condition associated with the ocular system including, for example, gouty iritis, inflammatory disease in the eye caused by gout, dry eye syndrome, red eye, uveitis, intraocular hypertension, glaucoma, and cataracts.

[0268] In some embodiments, the subject has, or is at risk of having, a condition associated with the skin including, for example, gout of the external ear, gouty dermatitis, gouty eczema, gouty panniculitis, and miliarial gout.

[0269] In some embodiments, the subject is selected for treatment with an microbial cell engineered to degrade uric acid of the present disclosure. In some embodiments, the subject is selected for treatment of hyperuricemia with an engineered microbial cell of the present disclosure. In some embodiments, the subject is selected for treatment of gout with an engineered microbial cell of the present disclosure. In some embodiments, the subject is selected for treatment of chronic refractory gout with an engineered microbial cell of the present disclosure.

[0270] In certain embodiments, the methods of the present disclosure provide treatment of gout and diseases or disorders associated with hyperuricemia to human patients suffering therefrom.

The treatment population is thus human subjects diagnosed as suffering from gout or hyperuricemia. The invention encompasses the treatment of a human subject at risk of suffering from a recurrent gout episode or for developing hyperuricemia or gout.

[0271] The present disclosure also encompasses treating a population of patients with drug-induced gout flares, including flares induced by gout therapeutics such as xanthine oxidase inhibitors, such as allopurinol and febuxostat; flares induced by urate oxidase, for example, uricase, rasburicase and pegylated uricase; and flares induced by uricosuric agents, such as probenecid, sulfinpyrazone, benzbromarone, and fenofibrate. By “drug-induced” gout flare is meant occurrence of or increased incidence of a gout flare associated with initiation of therapy to treat gout and/or administration of a therapeutic agent for the treatment of gout, for example, initiation of therapy with a xanthine oxidase inhibitor, urate oxidase, or a uricosuric agent. A gout flare is “associated” with initiation of gout therapy when the flare occurs contemporaneously or following at least a first administration of a therapeutic agent for the treatment of gout.

Pharmaceutical Compositions

[0272] The present disclosure encompasses the preparation and use of pharmaceutical compositions comprising an engineered microbial cell (e.g., engineered fungal cells) of the disclosure as an active ingredient. Such a pharmaceutical composition may consist of the active ingredient alone, as a combination of at least one active ingredient (e.g., an effective dose of an engineered fungal cell) in a form suitable for administration to a subject, or the pharmaceutical composition may comprise the active ingredient and one or more pharmaceutically acceptable carriers, one or more additional (active and/or inactive) ingredients, or some combination of these.

[0273] In some embodiments, a pharmaceutical composition comprises a plurality of the engineered fungal cells described herein, and a pharmaceutically acceptable carrier. In further embodiments, the pharmaceutical composition comprises a therapeutically effective dose of the engineered microbial cells.

[0274] In some embodiments, the pharmaceutical composition comprises between 10^6 and 10^{12} engineered microbial cells.

[0275] Pharmaceutical compositions of the present disclosure may be administered in a manner appropriate to the disease to be treated (or prevented). The quantity and frequency of administration will be determined by such factors as the condition of the patient, and the type and severity of the patient's disease, although appropriate dosages may be determined by clinical trials.

[0276] The administration of the pharmaceutical compositions may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The compositions of the present disclosure may be administered to a patient orally.

[0277] As used herein, the term "pharmaceutically acceptable carrier" means a chemical composition with which the active ingredient may be combined and which, following the combination, can be used to administer the active ingredient to a subject.

[0278] The formulations of the pharmaceutical compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology. In general, such preparatory methods include the step of bringing the active ingredient into association with a carrier or one or more other accessory ingredients, and then, if necessary or desirable, shaping or packaging the product into a desired single- or multi-dose unit.

[0279] Although the descriptions of pharmaceutical compositions provided herein are principally directed to pharmaceutical compositions which are suitable for ethical administration to humans, it will be understood by the skilled artisan that such compositions are generally suitable for administration to animals of all sorts. Modification of pharmaceutical compositions suitable for administration to humans in order to render the compositions suitable for administration to various animals is well understood, and the ordinarily skilled veterinary pharmacologist can design and perform such modification with merely ordinary, if any, experimentation. Subjects to which administration of the pharmaceutical compositions of the disclosure is contemplated include, but are not limited to, humans and other primates, mammals including commercially relevant mammals such as non-human primates, cattle, pigs, horses, sheep, cats, and dogs.

[0280] Pharmaceutical compositions that are useful in the methods of the disclosure may be prepared, packaged, or sold in formulations suitable for oral, or another route of administration.

[0281] A pharmaceutical composition of the disclosure may be prepared, packaged, or sold in bulk, as a single unit dose, or as a plurality of single unit doses. As used herein, a "unit dose" is discrete amount of the pharmaceutical composition comprising a predetermined amount of the active ingredient. The amount of the active ingredient is generally equal to the dosage of the active ingredient which would be administered to a subject or a convenient fraction of such a dosage such as, for example, one-half or one-third of such a dosage.

[0282] The relative amounts of the active ingredient, the pharmaceutically acceptable carrier, and any additional ingredients in a pharmaceutical composition of the disclosure will vary, depending upon the identity, size, and condition of the subject treated and further depending upon the route by which the composition is to be administered. By way of example, the composition may comprise between 0.1% and 100% (w/w) active ingredient.

[0283] In addition to the active ingredient, a pharmaceutical composition of the disclosure may further comprise one or more additional pharmaceutically active agents.

[0284] Controlled- or sustained-release formulations of a pharmaceutical composition of the disclosure may be made using conventional technology.

[0285] The pharmaceutical compositions may be prepared, packaged, or sold in the form of a capsule or pill containing (freeze-)dried or metabolically active engineered microbes, a powder containing (freeze-)dried or metabolically active engineered microbes, or a suspension containing (freeze-)dried or metabolically active live microbes. These solids or liquids may be formulated according to the known art, and may comprise, in addition to the active ingredient, additional ingredients such as the dispersing agents, wetting agents, or suspending agents described herein. Such formulations may be prepared using a non-toxic orally-acceptable substance, such as cellulose, for example.

[0286] Other acceptable substances include, but are not limited to, guar gum, hypromellose (hydroxypropyl methylcellulose), inulin, fructooligosaccharides, gelatin, magnesium stearate, Silicon dioxide, rice bran extract, and lactose.

[0287] Formulation methods are described by e.g., Martins et al, Letters in Applied Microbiology 49:738-744 (2009), and by Joshi and Thorat, Drying Technology, 29:749-757 (2011).

[0288] The engineered microbial cell of the disclosure can be administered to an animal, e.g., a human. Where the engineered microbial cell are administered, they can be administered in an amount ranging from about 10^6 to about 10^{12} cells wherein the cells are administered to the animal, preferably, a human patient in need thereof. While the precise dosage administered will

vary depending upon any number of factors, including but not limited to, the type of animal and type of disease state being treated, the age of the animal and the route of administration.

[0289] The engineered microbial cell may be administered to an animal as frequently as several times daily, or it may be administered less frequently, such as once a day, once a week, once every two weeks, once a month, or even less frequently, such as once every several months or even once a year or less. The frequency of the dose will be readily apparent to the skilled artisan and will depend upon any number of factors, such as, but not limited to, the type and severity of the disease being treated, the type and age of the animal, etc.

[0290] An engineered microbial cell may be co-administered with the various other compounds (e.g. other therapeutic agents). Alternatively, the compound(s) may be administered in advance of or after administration of the engineered microbial cell. The frequency and administration regimen will be readily apparent to the skilled artisan and will depend upon any number of factors such as, but not limited to, the type and severity of the disease being treated, the age and health status of the animal, the identity of the compound or compounds being administered, the route of administration of the various compounds and the engineered microbial cell, and the like.

[0291] In some embodiments, the disclosure features a pharmaceutical composition comprising a plurality of the engineered microbial cells described herein, and a pharmaceutical carrier. In other embodiments, the disclosure features a pharmaceutical composition comprising a population of engineered microbial cells as described herein, and a pharmaceutical carrier. It will be understood that any single engineered microbial cell, plurality of engineered microbial cells, or population of engineered microbial cells as described elsewhere herein may be present in a pharmaceutical composition of the invention.

[0292] In some embodiments, the pharmaceutical compositions provided herein comprise engineered (i.e. modified) microbial cells and unmodified microbial cells. For example, a single unit dose of microbial cells (e.g., modified and unmodified microbial cells) can comprise, in various embodiments, about, at least, or no more than 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%), 85%, 90%, 95%, or 99% engineered microbial cells, wherein the remaining microbial cells in the composition are not engineered.

[0293] In some embodiments of the above aspects and embodiments, the engineered microbial cell is a fungal cell, e.g. *Saccharomyces boulardii*.

Combination Therapies

[0294] According to some embodiments, the disclosure provides methods that further comprise administering an additional agent (e.g. an additional therapeutic) to a subject. In some embodiments, the disclosure pertains to co-administration and/or co-formulation.

[0295] Additional therapeutics for elevated uric acid levels, gout, gout flares, or conditions associated with gout, may be administered to any one of the subjects provided herein, such as for the reduction of uric acid levels and/or gout treatment and/or gout flare prevention. Any one of the methods provided herein may include the administration of one or more of these additional therapeutics. In some embodiments, any one of the methods provided herein do not comprise the concomitant administration of an additional therapeutic. Examples of additional therapeutics include, but are not limited to, the following. Other examples will be known to those of skill in the art.

[0296] Additional therapeutics include anti-inflammatory therapeutics (i.e., any therapeutic that can act to reduce inflammation). Anti-inflammatory therapeutics include, but are not limited to, corticosteroids or derivatives of cortisol (hydrocortisone). Corticosteroids include, but are not

limited to, glucocorticoids and mineralocorticoids. Still other examples of corticosteroids include, but are not limited to, those that are natural and those that are synthetic. Corticosteroids, particularly glycocorticoids, have anti-inflammatory and immunosuppressive effects that may be effective in managing symptoms, including pain and inflammation associated with gout, gout flare, and/or conditions associated with gout.

[0297] Administration of corticosteroids may also aid in reducing hypersensitivity reactions associated with one or more additional therapies, for example uricase replacement therapy.

[0298] Still other non-limiting examples of corticosteroids include prednisone, prednisolone, Medrol, and methylprednisolone.

[0299] Additional therapeutics include short term therapies for gout flare or pain and inflammation associated with any of the symptoms associated with gout or a condition associated with gout include nonsteroidal anti-inflammatory drugs (NSAIDS), colchicine, and oral corticosteroids. Non-limiting examples of NSAIDS include both over-the-counter NSAIDS, such as ibuprofen, aspirin, and naproxen, as well as prescription NSAIDS, such as celecoxib, diclofenac, diflunisal, etodolac, indomethacin, ketoprofen, ketorolac, nabumetron, oxaprozin, piroxiam salsalate, sulindac, and tolmetin.

[0300] Colchicine is an anti-inflammatory agent that is generally considered as an alternative for NSAIDs for managing the symptoms, including pain and inflammation associated with gout, gout flare, and/or conditions associated with gout.

[0301] Further examples of additional therapeutics include xanthine oxidase inhibitors, which are molecules that inhibit xanthine oxidase, reducing or preventing the oxidation of xanthine to uric acid, thereby reducing the production of uric acid. Xanthine oxidase inhibitors are generally classified as either purine analogues or other types of xanthine oxidase inhibitors. Examples of

xanthine oxidase inhibitors include allopurinol, oxypurinol, tisopurine, febuxostat, topiroxostat, inositols (e.g., phytic acid and myo-inositol), flavonoids (e.g., kaempferol, myricetin, quercetin), caffeic acid, and 3,4-dihydrox-5-nitrobenzaldehyde (DHNB).

[0302] Still other examples of additional therapeutics include uricosuric agents. Uricosuric agents aim to increase excretion of uric acid in order to reduce serum levels of uric acid by modulating renal tubule reabsorption. For example, some uricosuric agents modulate activity of renal transporters of uric acid (e.g., URAT1/SLC22A12 inhibitors). Non-limiting examples of uricosuric agents include probenecid, benzbromarone, lesinurad, and sulfinpyrazone. Other additional therapeutics may also have uricosuric activity, such as aspirin.

[0303] Additional therapeutics also include other uricase-based therapies, which include pegylated uricase. Such therapies, such as when infused into humans, have been shown to reduce blood uric acid levels and improve gout symptoms. Rasburicase (ELITEK), an unpegylated engineered uricase cloned from *Aspergillus flavus*, is approved for management of uric acid levels in patients with tumor lysis syndrome. KRYSTEXXA (pegloticase) is a engineered uricase (primarily porcine with a carboxyl-terminus sequence from baboon) bound by multiple 10 kDa PEG molecules approved for the treatment of chronic refractory gout.

[0304] The treatments provided herein may allow patients to switch to oral gout therapy, such as with xanthine oxidase inhibitors, unless and until such patients experience a subsequent manifestation of uric acid deposits at which time a new course of treatment as provided herein according to any one of the methods provided is then undertaken. Any one of the methods provided herein, thus, can include the subsequent administration of an oral gout therapeutic as an additional therapeutic after the treatment regimen according to any one of the methods provided is performed. It is believed that oral therapy may not completely prevent the buildup over time of

uric acid crystals in patients with a history of chronic tophaceous gout. As a result, it is anticipated that treatment as provided herein is likely to be required intermittently in such patients. Thus, in such subjects, the subject is also further administered one or more compositions according to any one of the methods provided herein.

[0305] The treatments provided herein may allow patients to subsequently be treated with a uric acid lowering therapeutic, such as a uricase.

[0306] Treatment according to any one of the methods provided herein may also include a pre-treatment with an anti-gout flare therapeutic, such as with colchicine or NSAIDS.

[0307] Accordingly, any one of the methods provided herein may further comprise such an anti-gout flare therapeutic whereby the anti-gout flare therapeutic is concomitantly administered with the composition comprising uricase and the composition comprising synthetic nanocarriers comprising an immunosuppressant.

[0308] Monitoring of a subject, such as the measurement of serum uric acid levels and/or ADAs, may be an additional step further comprised in any one of the methods provided herein. In some embodiments, should such subject develop an undesired immune response, the subject is further administered one or more compositions according to any one of the methods provided herein. In some embodiments of any one of the methods provided herein, the subject is monitored with dual energy computed tomography (DECT), that can be used to visualize uric acid deposits in joints and tissues. Imaging, such as with DECT, can be used to assess the efficacy of treatment with any one of the methods or compositions provided herein. As a result, any one of the methods provided herein can further include a step of imaging, such as with DECT. In some embodiments of any one of the methods provided herein, the subject is one in which the gout,

such as chronic tophaceous gout, or condition associated with gout has been diagnosed with such imaging, such as with DECT.

Identifying Uric Acid Degradation

[0309] A method to identify uric acid degrading polypeptides can comprise the steps of functionally expressing a candidate uric acid degrading polypeptide by operably linking it to a promoter in a cell functionally expressing one or more of the uric acid transporters of SEQ ID NO: 9-18, or polypeptide having uric acid transporter activity as identified in [[CLAIM Y]]; identifying cells with increased urate consumption by quantifying urate uptake and biodegradation of cells from step 1. using a urate consumption assay and comparing their urate consumption to cells functionally expressing only the one or more of the uric acid transporters of SEQ ID NO: 9-18 or polypeptide having uric acid transporter activity as identified in [[CLAIM Y]]. The cells that show increased urate consumption functionally express a uric acid degrading polypeptide, thereby confirming the candidate uric acid degrading polypeptide can functionally break down uric acid and encodes a uricase (EC 1.7.3.3).

[0310] A method to identify uric acid transporters can comprise the steps of functionally expressing a candidate uric acid transporting polypeptide by operably linking it to a promoter in a cell functionally expressing one or more of the uricases of SEQ ID NO: 1-8, or polypeptide having uricase activity as identified in CLAIM X; identifying cells with increased urate consumption by quantifying urate uptake and biodegradation of cells from step 1. using a urate consumption assay and comparing their urate consumption to cells functionally expressing only the one or more of the uricases of SEQ ID NO:1-8 or polypeptide having uricase activity as identified in CLAIM X. The cells that show increased urate consumption functionally express a uric acid transporter polypeptide, thereby confirming the candidate uric acid transporting

polypeptide can functionally transport uric acid from outside the cell to inside the cell and encodes a uric acid transporter.

[0311] An assay to quantify urate uptake and biodegradation by cells can comprise collecting cells followed by resuspension in assay buffer containing dissolved uric acid with A₂₉₃ between 0.0 and 3.0; incubating resuspended cells under conditions suitable for uric acid uptake and biodegradation; removing aliquots at designated intervals; collecting the supernatant; and spectrophotometrically determining the reduction in urate concentration by measuring absorbance at a wavelength where urate strongly absorbs, preferably between 275 nm and 350 nm, most preferably 293 nm.

Example 1

[0312] Example 1: “*Saccharomyces boulardii* cells genetically engineered to comprise *Candida utilis* uricase and *Aspergillus nidulans* UapA uric acid transporter”

[0313] Episomal expression vector encoding *Candida utilis* uricase and *Aspergillus nidulans* UapA uric acid transporter:

[0314] An episomal plasmid shuttle vector was constructed encoding genes for the expression of *Candida utilis* uricase (SEQ ID NO: 1) (CuUOX) and *Aspergillus nidulans* UapA uric acid transporter (SEQ ID NO: 9) (AnUapA). A schematic drawing of the map is provided in Figure 1. The sequence of this episomal plasmid shuttle vector is included in SEQ ID NO: 19

[0315] This vector is able to replicate in *E. coli* cells grown in the presence of Ampicillin by virtue of the Ampicillin resistance gene (β -Lactamase) and the bacterial F1 origin of replication. The vector is able to replicate in *S. boulardii* cells grown in the presence of G418 disulphate by virtue of the bacterial aminoglycoside phosphotransferase (from transposon Tn903) and the *S. cerevisiae* 2 micron plasmid origin of replication.

- [0316] The vector encodes *Candida utilis* uricase under control of the *S. boulardii* GPD (aka TDH3) promoter, and *Aspergillus nidulans* UapA uric acid transporter under control of the *S. boulardii* Pgk1 promoter.
- [0317] Salient features of SEQ ID:19 include: GPD (TDH3) promoter in the 13-663 nucleotides; *Candida Uricase* in the 687 – 1598 nucleotides; VPS13 terminator in the 1599 - 1701 nucleotides; TPI1 promoter in the 1714 - 2163 nucleotides; EM7 promoter in the 2164 – 2231 nucleotides; KanR in the 2232 - 3041 nucleotides; *Ashbya gossypii* TEF terminator in the 3047 – 3244 nucleotides; Pgk1 promoter in the 9925 - 9388 (antisense) nucleotides; UapA UA transporter in the 9387- 7663 (antisense) nucleotides; Prm9 terminator in the 7662 - 7413 (antisense) nucleotides; yeast 2 μ plasmid origin of replication in the 6033 – 7378 nucleotides; AmpR in the 5403 - 4543 (antisense) nucleotides; F1 Origin of replication in the 4372 - 3784 (antisense) nucleotides.
- [0318] The vector was amplified in *E. coli* DH5 α cells (Cat no. 18265017, Thermo Fisher Scientific, Grand Island, NY 14072, USA), and extracted using methods well known in the art, as described e.g. in Sambrook and Russell, Molecular cloning: a laboratory manual. Ed. 3. Cold spring harbor laboratory press, 2001. The vector DNA was further purified using silica spin columns.
- [0319] *Saccharomyces boulardii* cells (Kirkman, Lake Oswego, OR 97035) were grown in YPD medium by transferring the content of a capsule into 50 mL YPD medium in a 125 mL shake flask. The *S. boulardii* starter culture was grown on a platform shaker at 225 rpm and 30°C to stationary phase (OD 600 to or about 3) overnight. The next morning, a 5 mL aliquot of the overnight culture was inoculated into 100 mL YPD media in a 250 mL shake flask to initiate a culture at approx. OD600 0.3. The inoculated cells were grown in a shaking incubator at 30 °C

and 225 rpm until OD600 was approximately 1.6. Yeast cells were pelleted by centrifugation at 3000 rpm for 5 minutes and the media was aspirated. Cell were resuspended in 20 mL ice cold water, and pelleted again by centrifugation at 3000 rpm for 5 min. The supernatant was aspirated, and cells were resuspended in 20 mL ice cold water, and pelleted again by centrifugation at 3000 rpm for 5 min. The supernatant was aspirated, and cells were resuspended in 50 mL ice-cold electroporation buffer (1 M Sorbitol / 1 mM CaCl₂ in distilled water), and pelleted again by centrifugation at 3000 rpm for 5 min.

[0320] Cells were resuspended in 20 mL 0.1 M LiOAc / 10 mM DTT, transferred to a 125 mL shake flask and shaken at 100 rpm for 30 minutes at 30 °C. Cells were pelleted by centrifugation at 3000 rpm for 3 min, the supernatant removed, and cells were gently resuspended in 20 mL ice-cold electroporation buffer. Cells were pelleted by centrifugation at 3000 rpm for 3 min and the supernatant removed. Cells were resuspended in electroporation buffer to reach a final volume of 1 mL. 40 µL DNA solution was transferred into a pre-chilled electroporation cuvette (2 mm electrode gap) on ice, and 400 µL resuspended electrocompetent yeast cells was added. The cuvette was kept on ice for 5 minutes until electroporation. The cells were electroporated at 2.5 kV, 25 µF and 200 Ohm. Electroporated cells were transferred from each cuvette into 10 mL of 1:1 mix of 1 M Electroporation buffer : YPD medium. The cells were recovered by incubation on a platform shaker at 225 rpm and 30°C for 2 hours. The cells were pelleted by centrifugation, the supernatant removed, and the cells resuspended in 1 mL YPD medium. Cells were pelleted again, the supernatant removed, and cells were resuspended in 200 µL YPD medium. Cells were plate on YPD plates with 600 µg / mL G418 disulphate, taped shut with parafilm, and incubate at 30°C for 2 days. Colonies were picked used to inoculate liquid YPD cultures with 200 600 µg / mL G418 sulphate, and cells were grown for 48 hours to approximately stationary phase.

[0321] A control culture consisting of parental, untransformed *S. boulardii* was grown in YPD medium without antibiotics, and these cells were also grown for 48 hours to approximately stationary phase. 1 mL of cell suspension was removed from the culture, transformed cells were pelleted in a 1.7 mL Eppendorf tube by centrifugation. The supernatant was removed, and cells were resuspended in 1 mL of phosphate buffered saline, pH 7.4, to wash the cells. Cells were then resuspended in 1 mL phosphate buffered saline containing uric acid at a concentration yielding an optical density at 293 nm (OD₂₉₃) of approximately A₂₉₃ = 1.0. A control consisted of uric acid solution in PBS without any cells. The suspensions were then incubated on a tumbler at 37°C for 10 minutes.

[0322] Following incubation, cells were pelleted again, 500 µL of supernatant was assayed spectrophotometrically using a quartz glass cuvette with 1 cm pathlength in a Nanodrop spectrophotometer (see Prætorius and Poulsen, Scandinavian Journal of Clinical and Laboratory Investigation, 5:273-280 (1953)). The cell pellet was resuspended in the remaining supernatant, and cells were incubated for an additional 30 minutes on a tumbler at 37°C. Following the second incubation, cells were pelleted again, and the remaining 500 µL of supernatant was assayed spectrophotometrically using a quartz glass cuvette with 1 cm pathlength in a Nanodrop spectrophotometer. It should be noted uric acid has an absorbance peak at 293 nm, where the degradation product as produced by uricase does not absorb at this wavelength.

[0323] Results are shown in FIG. 2 (absorbance spectra 200 - 350 nm) and FIG. 3 (absorbance at 293 nm). Results showed that uric acid in the suspension containing *S. boulardii* engineered with the shuttle vector (SEQ ID: 19) was partially degraded after 10 minutes, and essentially completely degraded after 40 minutes. In contrast, uric acid in the suspension containing wild-

type *S. boulardii* was not degraded, as was uric acid in the solution without *S. boulardii*. In both of the latter, uric acid levels were the same as before treatment.

Example 2

[0324] Example 2. “*Escherichia coli* strain Nissle cells genetically engineered to overexpress *Escherichia coli* YgfU uric acid transporter and *Arthrobacter globiformis* uricase induced by low oxygen conditions”

[0325] A synthetic plasmid encoding an expression cassette comprising the *Arthrobacter globiformis* uricase operably linked to a promoter induced by the oxygen level-dependent FNR protein from *N. gonorrhoeae* (see, e.g., Isabella et al, BMC Genomics 12:1471-2164 (2011)) (a promoter that is induced by low-oxygen or anaerobic conditions); and, with translation terminated by the synthetic Bba_B1002 terminator, and with said operon flanked by 50 bps sequences facilitating homologous recombination into the malE/K locus, e.g. as set forth in SEQ ID NO: 20, is obtained from a synthetic DNA vendor, e.g. Twist Bioscience (San Francisco, CA) or Integrated DNA Technologies (Coralville, IA). The fragment may additionally comprise antibiotic selection markers or other selectable markers.

[0326] This fragment is flanked by appropriate unique NotI restriction sites. This fragment is excised from a large scale preparation of the plasmid, purified, and used to transform *E. coli* Nissle cells.

[0327] A synthetic plasmid encoding an expression cassette comprising the *Escherichia coli* YgfU uric acid transporter operably linked to a promoter induced by the oxygen level-dependent FNR protein from *N. gonorrhoeae* (see, e.g., Isabella et al, BMC Genomics 12:1471-2164 (2011)) (a promoter that is induced by low-oxygen or anaerobic conditions); and, with translation terminated by the synthetic Bba_B1006 terminator, and with said operon flanked by 50 bps

sequences facilitating homologous recombination into the lacZ locus, eg as set forth in SEQ ID NO: 21, is obtained from a synthetic DNA vendor, e.g. Twist Bioscience (San Francisco, CA) or Integrated DNA Technologies (Coralville, IA). The fragment may additionally comprise antibiotic selection markers or other selectable markers.

[0328] This fragment is flanked by appropriate unique NotI restriction sites. This fragment is excised from a large-scale preparation of the plasmid, purified, and used to transform *E. coli* Nissle cells.

[0329] Lambda red recombination is used to make chromosomal modifications, e.g., to express *Escherichia coli* YgfU uric acid transporter and *Arthrobacter globiformis* uricase in *E. coli* Nissle. Lambda red recombinase mediated recombineering is a procedure using recombination enzymes from a bacteriophage lambda to insert a piece of custom (e.g., synthetic) DNA into the chromosome of *E. coli*.

[0330] pKD46 (CGSC# 7669, Yale Coli Genetic Stock Center, Dept. of Molecular, Cellular, and Developmental Biology, Yale University, New Haven, CT 06520, USA) is a temperature-sensitive plasmid that encodes the lambda red recombinase genes. The pKD46 plasmid is transformed into the *E. coli* Nissle host strain (PZN: 03840841, Mutaflor®, ArdeyPharm, Herdecke, Nordrhein-Westfalen, Germany). *E. coli* Nissle cells are grown overnight in LB media. The overnight culture is diluted 1:100 in 5 mL of LB media and grown until it reaches an OD600 of 0.4-0.6. All tubes, solutions, and cuvettes are pre-chilled to 4° C. The *E. coli* cells are centrifuged at 2,000 rpm for 5 min. at 4° C., the supernatant is removed, and the cells are resuspended in 1 mL of 4° C. water. The *E. coli* are centrifuged at 2,000 rpm for 5 min. at 4° C., the supernatant is removed, and the cells are resuspended in 0.5 mL of 4° C. water. The *E. coli* are centrifuged at 2,000 rpm for 5 min. at 4° C., the supernatant is removed, and the cells are

resuspended in 0.1 mL of 4° C. water. The electroporator is set to 2.5 kV. 1 ng of pKD46 plasmid DNA is added to the *E. coli* cells, mixed by pipetting, and pipetted into a sterile, chilled cuvette. The dry cuvette is placed into the sample chamber, and the electric pulse is applied. 1 mL of room-temperature SOC media is immediately added, and the mixture is transferred to a culture tube and incubated at 30°C. for 1 hr. The cells are spread out on a selective media plate containing antibiotics and incubated overnight at 30°C.

[0331] DNA sequences comprising the desired urate catabolism genes and transporters, e.g., those shown above are ordered from a gene synthesis company. The lambda enzymes are used to insert this construct into the genome of *E. coli* Nissle through homologous recombination. The construct is inserted into a specific site in the genome of *E. coli* Nissle based on its DNA sequence. In one example, the construct encodes *Escherichia coli* YgfU uric acid transporter, which is inserted at the lacZ site in the *E. coli* Nissle genome. In another example, the construct encodes *Arthrobacter globiformis* uricase, which is inserted at the MalE/Ksite in the *E. coli* Nissle genome.

[0332] The homologous sequences are ordered as part of the synthesized gene. Alternatively, the homologous sequences may be added by PCR. The construct is used to replace the natural sequence in the *E. coli* Nissle genome. The construct may include an antibiotic resistance marker that may be removed by recombination.

[0333] The constructs comprising the desired urate catabolism genes and transporters are transformed into *E. coli* Nissle comprising pKD46. All tubes, solutions, and cuvettes are pre-chilled to 4° C. An overnight culture is diluted 1:100 in 5 mL of LB media containing ampicillin and grown until it reaches an OD600 of 0.1. 0.05 mL of 100× L-arabinose stock solution is added to induce pKD46 lambda red expression. The culture is grown until it reaches an OD600

of 0.4-0.6. The *E. coli* cells are centrifuged at 2,000 rpm for 5 min. at 4° C., the supernatant is removed, and the cells are resuspended in 1 mL of 4° C. water. The *E. coli* are centrifuged at 2,000 rpm for 5 min. at 4° C., the supernatant is removed, and the cells are resuspended in 0.5 mL of 4° C. water. The *E. coli* are centrifuged at 2,000 rpm for 5 min. at 4° C., the supernatant is removed, and the cells are resuspended in 0.1 mL of 4° C. water. The electroporator is set to 2.5 kV. 0.5 µg of the constructs comprising the desired urate catabolism genes and transporters is added to the cells, mixed by pipetting, and pipetted into a sterile, chilled cuvette. The dry cuvette is placed into the sample chamber, and the electric pulse is applied. 1 mL of room-temperature SOC media is immediately added, and the mixture is transferred to a culture tube and incubated at 37° C. for 1 hr. The cells are spread out on an LB plate and incubated overnight.

[0334] The presence of the mutation is verified by colony PCR. Colonies are picked with a pipette tip and resuspended in 20 µl of cold ddH₂O by pipetting up and down. 3 µL of the suspension is pipetted onto an index plate with appropriate antibiotic for use later. The index plate is grown at 37° C. overnight. A PCR master mix is made using 5 µL of 10× PCR buffer, 0.6 µL of 10 mM dNTPs, 0.4 µL of 50 mM MgSO₄, 6.0 µL of 10× enhancer, and 3.0 µL of ddH₂O (15 µL of master mix per PCR reaction). A 10 µM primer mix is made by mixing 2 µL of primers unique to the *argA* mutant construct (100 µM stock) into 16 µL of ddH₂O. For each 20 µL reaction, 15µL of the PCR master mix, 2.0 µL of the colony suspension (template), 2.0 µL of the primer mix, and 1.0 µL of Pfx Platinum DNA Pol are mixed in a PCR tube. The PCR thermocycler is programmed as follows, with steps 2-4 repeating 34 times: 1) 94°C at 5:00 min., 2) 94°C at 0:15 min., 3) 55°C at 0:30 min., 4) 68°C at 2:00 min., 5) 68°C at 7:00 min., and then cooled to 4°C. The PCR products are analyzed by gel electrophoresis using 10 µL of each

amplicon and 2.5 μ L 5 $\times$ dye. The PCR product only forms if the mutation has inserted into the genome.

[0335] Next, the antibiotic resistance is removed by transforming cells with pCP20 plasmid (CGSC# 14177, Yale Coli Genetic Stock Center, Dept. of Molecular, Cellular, and Developmental Biology, Yale University, New Haven, CT 06520, USA)

[0336] pCP20 has the yeast F1p recombinase gene, FLP, chloramphenicol and ampicillin resistant genes, and temperature sensitive replication. Bacteria are grown in LB media containing the selection antibiotic at 37°C until OD600 reaches 0.4-0.6. 1 mL of cells are pelleted at 16,000 $\times$ g for 1 min, the supernatant is discarded and the pellet is resuspended in 1 mL ice-cold 10% glycerol. This wash step is repeated 3 times. The pellet is then resuspended in 70 μ L ice-cold 10% glycerol. Next, cells are electroporated with 1 μ g pCP20 plasmid DNA, and 1 mL SOC supplemented with 3 mM thymidine is immediately added to the cuvette. Cells are resuspended and transferred to a culture tube and are grown at 30°C for 1 hour. Cells are then pelleted at 10,000 $\times$ g for 1 minute, the supernatant is discarded, and the cell pellet is resuspended in 100 μ L LB containing 3 mM thymidine and spread on LB agar plates containing 3 mM thy and 100 μ g/mL carbenicillin. Cells are grown at 30°C for 16-24 hours. Next, transformants are colony purified non-selectively (in the absence of antibiotics) at 42°C.

[0337] To test the colony-purified transformants, a colony is picked from the 42°C plate with a pipette tip and resuspended in 10 μ L LB. 3 μ L of the cell suspension is pipetted onto a set of 3 plates: Cam, (37°C: tests for the presence/absence of CamR gene in the genome of the host strain), Amp, (30°C: tests for the presence/absence of AmpR from the pCP20 plasmid) and LB only (37°C, desired cells that have lost the chloramphenicol cassette and the pCP20 plasmid).

Colonies were considered cured if there is no growth in neither the Cam or Amp plate, picked, and re-streaked on an LB plate to get single colonies, and grown overnight at 37°C.

Example 3

[0338] Example 3: “Bacteroides cells genetically engineered to comprise Spirosoma uricase and uric acid transporter”

[0339] Adding urate-degradation capabilities to a member of the genus Bacteroides can be accomplished by addition of transgenes from other organisms (e.g. species from the Bacteroidetes phylum, e.g. a species from the Spirosoma genus).

[0340] A synthetic conjugative plasmid containing an expression cassette comprising a synthetic operon encoding a Spirosoma uricase (SEQ ID NO: 8) and Spirosoma urate transporter SEQ ID NO: 18), operably linked to a phage derived promoter, e.g. P_{BFP1E6} (as described in Russ et al, WO2020123483), e.g. as set forth in SEQ ID NO: 22, is obtained from a synthetic DNA vendor, e.g. Twist Bioscience (San Francisco, CA) or Integrated DNA Technologies (Coralville, IA). The plasmid may carry an NBU2 integrase gene, which catalyzes genomic integration of the plasmid at the 3' end of a serine-tRNA gene in the Bacteroides genome. The plasmid may additionally comprise antibiotic selection markers or other selectable markers. Multiple selective markers (such as tetracycline, erythromycin, or chloramphenicol) can be used to deliver multiple constructs into a single Bacteroides strain. The plasmid has the RK2/RP4 transfer origin.

[0341] The plasmid is transformed into Escherichia coli S17-1 donor cells (Catalog number 47055, ATCC). The RK2 conjugative machinery allows for conjugative transfer of plasmids bearing an RP4 transfer origin to a variety of species, including Bacteroides. DNA is transformed with addition of 20 µL of chemically competent E. coli S17-1 cells (mid-log cells resuspended 1:20 in TSS/KCM: LB medium with 8.3% PEG-3350, 4.2% DMSO, 58 mM MgCl₂, 167 mM

CaCl₂ and 457 mM KCl), followed by a 90 second heat shock at 42°C, recovery at 37 °C for 30 minutes, a dilution into 600 µL LB medium with Ampicillin in a deep well 96-well plate (Corning 07-200-700) and aerobic growth at 37°C. A *Bacteroides* culture is prepared with overnight anaerobic growth in trypticase yeast extract-glucose (TYG) growth medium. At mid to late log growth, 200 µL of the transformed S17-1 cells are spun down, resuspended with 10 µL of a 1:10 concentration of the *Bacteroides* culture, and added to a deep well 96-well plate containing 400 µL of solidified Brain Heart Infusion Blood Agar (BHI-BA) per well. After at least 16 hours, the lawn of S17-1 and *Bacteroides* are resuspended in 400 µL of TYG by vortex or pipetting, 200 µL of the resuspension are spun down and resuspended in 15 µL TYG and several dilutions in TYG are made. 3 µL of the resuspension and its dilutions are spotted onto a 120 x 120 mm square petri dish containing BHI-BA plus the appropriate antibiotics (200 µg/mL gentamycin, and 25 µg/mL erythromycin or 2 µg/mL tetracycline). *Bacteroides* colonies can be picked after a 24 hour anaerobic incubation at 37 °C.

Example 4. “*Bacillus* cells genetically engineered to overexpress uricase and / or uric acid transporter”

[0342] Various bacterial species in the genus *Bacillus*, e.g. *B. subtilis*, appear to endogenously comprise genes involved in uric acid catabolism genes, including uricase and / or one or (putative) more uric acid transporter(s). The ability of *Bacillus* cells to take up and break down uric acid may be improved by overexpression of uricase, e.g. PucL, and / or uric acid (purine) transporters, e.g. PucJ and / or PucK (see e.g. Schultz et al, Journal of Bacteriology 183:3293-3302 (2001)). The flgM gene may be removed to yield a *Bacillus* strain with enhanced gene expression from the hag promoter (as described in Abbott, US 2020/0345793 A1). Deletion of

flgM greatly enhances constitutive expression and activity of SigD, and consequently results in higher and more constitutive transcription of the flagellar operon and specifically the hag gene.

[0343] The *B. subtilis* strain PY79 from the Bacillus Genetic Stock Center is used (strain 1A747) for all manipulations. The CsrA-binding site in the Bacillus hag promoter may be mutated to constitutively enhance promoter activity (as described in Abbott, US 2020/0345793 A1). Bacteria are grown in LB medium (1% tryptone, 0.5% yeast extract, 0.5% sodium chloride, with addition of 1.5% agar for solid media. For MLS resistance selection, 1 µg/mL erythromycin and 25 µg/mL lincomycin are used. For transformation experiments, bacteria are grown in modified competence (MC) medium (100 mM phosphate buffer, 2% glucose, 3 mM trisodium citrate, 22 mg/L ferric ammonium citrate, 0.1% casein hydrolysate, 0.16% glutamic acid, 3 mM magnesium sulfate). The plasmid used to make genetic modifications may be pMiniMAD (Catalog #ECE765, Bacillus Genetic Stock Center, Biological Sciences 556, 484 W. 12th Ave, Columbus, OH 43210-1214) as described in Patrick and Kearns, Mol. Microbiol. 70:1166-1179 (2008). The hag (flagellin) gene is replaced with an operon encoding uric acids transporter(s) and urate catabolism genes.

[0344] A synthetic plasmid encoding an expression cassette comprising a partial Puc operon comprising the Bacillus PucJ and PucL purine transporters (SEQ ID. NO: 14 and SEQ ID. NO: 15), the Bacillus PucL uricase / OHCu decarboxylase fusion protein (SEQ ID. NO: 6), and a Bacillus HIUHase operably linked to a Bacillus hag promoter, flanked by 800 base pairs 5' and 3' of the hag gene (as described in Abbott, US 2020/0345793 A1), e.g. as set forth in SEQ ID NO: 23, is obtained from a synthetic DNA vendor, e.g. Twist Bioscience (San Francisco, CA) or Integrated DNA Technologies (Coralville, IA).

[0345] This fragment is excised using the BamHI restriction enzyme, subcloned into the pMiniMAD plasmid linearized with BamHI and dephosphorylated with Calf intestinal phosphatase as recommended by the manufacturer (New England Biolabs). Plasmid DNA is used as the DNA source for chromosomal modifications. A single colony of *Bacillus* strain PY79 is picked, and inoculated in 2 mL of MC medium in a 15 mL test tube. The culture is grown at 37°C with shaking at 275 rpm for 4.5 hours, or approx. 1 hour after the end of the exponential growth phase. 400 uL of the culture is transferred to a new 15 mL test tube, and 1 µg of pMiniMAD plasmid containing the fragment from SEQ ID NO: 23 is added. The culture with DNA is returned to the 37°C shaker for 1.5 hours. Cultures are plated on LB agar with 1 µg/mL erythromycin and 25 µg/mL lincomycin, and incubated overnight at 37°C. Isolated colonies are screened for mutant allele via PCR using primer pairs where one primer anneals to a region outside the insert, and the other anneals to a region inside the insert. If the insert has recombined into the chromosome at the expected locus, PCR products of the expected size are obtained. A positive colony is then inoculated in 3 mL LB broth without antibiotics. This culture is grown overnight at room temperature with shaking at 275 rpm. 10 uL of the overnight culture is streaked on LB without antibiotics and grown at 37° C. overnight. Because of the lack of antibiotic selection, the plasmid is lost during overnight replication. The observed stability of this plasmid is about 90%, with about 1 colony in 10 losing the plasmid at this stage. Isolated colonies are duplicate streaked on LB plates with and without selection antibiotics (1 µg/mL erythromycin and 25 µg/mL lincomycin), and grown overnight at 37° C. Antibiotic sensitive colonies are screened again with the same primer pairs to identify strains with the mutant allele.

Example 5. “*Kluyveromyces* cells genetically engineered to comprise *Candida utilis* uricase and *Aspergillus nidulans* UapA uric acid transporter”

- [0346] Kluyveromyces cells such as *K. lactis* or *K. marxianus* may be engineered to express uricase and / or uric acid transporter polypeptides using protocols and methods described in eg. Rajkumar et al, Front. Bioeng. Biotechnol. 7:97, doi: 10.3389/fbioe.2019.0009 (2019).
- [0347] A synthetic integrative plasmid encoding two expression cassettes, one comprising a Kluyveromyces PGK1 promoter driving expression of the *Aspergillus nidulans* AnUapA uric acid transporter, with transcription terminated by the Kluyveromyces INU1 terminator, and the other comprising a Kluyveromyces PDC1 promoter driving expression of the *Candida albicans* uricase, with transcription terminated by the Kluyveromyces PGK1 terminator, flanked by 878 base pairs 5' and 3' of the LAC4 β -galactosidase gene (as described in Rajkumar et al, Front. Bioeng. Biotechnol. 7:97, doi: 10.3389/fbioe.2019.0009 (2019)), and a kanMX antibiotic resistance marker, e.g. as set forth in SEQ ID NO: 24, is obtained from a synthetic DNA vendor, e.g. Twist Bioscience (San Francisco, CA) or Integrated DNA Technologies (Coralville, IA).
- [0348] Kluyveromyces may be transformed using the LiOAc/PEG method as outlined by Gietz, Yeast Protocols 33-44. Humana Press, New York, NY, 2014.
- [0349] Kluyveromyces cells are grown in 3 mL YPD at 250 rpm and 30°C overnight. The following day, cultures are diluted in 50 mL YPD and allowed to grow until they reach an OD600 of approx. 0.8. Cells from 50 mL YPD cultures are collected by centrifugation (2700 rcf, 2 min, 25°C). The cells are washed with 50 mL sterile water and collected by centrifugation at 2700 rcf for 2 min at RT. The cells are washed again with 25 mL sterile water and collected by centrifugation at 2700 rcf for 2 min at RT. The cells are resuspended in 1 mL 100 mM lithium acetate and transferred to a 1.5 mL Eppendorf tube. The cells are collected by centrifugation for 10 sec at 18,000 rcf at RT. The cells are resuspended in a volume of 100 mM lithium acetate that is approximately 4× the volume of the cell pellet.

[0350] The expression cassette is excised from the integrative plasmid using AscI (New England Biolabs). A volume of 10-15 μ L of DNA, 72 μ L 50% PEG 3350, 10 μ L 1 M lithium acetate, 3 μ L denatured salmon sperm DNA, and sterile water is combined to a final volume of 100 μ L for each transformation. In a 1.5 mL tube, 15 μ L of the cell suspension is added to the DNA mixture and the transformation suspension is vortexed with 5 short pulses. The transformation is incubated for 30 min at 30°C, followed by incubation for 22 min at 42°C. The cells are collected by centrifugation for 10 sec at 18,000 rcf at RT. The cells are resuspended in 400 μ L of an appropriate medium and spread on YPGal (2% galactose, 2% peptone, 1% yeast extract) plates containing 200 μ g/mL G418 and 40 μ g/mL X-Gal. Correctly integration of the expression cassette into the LAC4 locus results in the inability of cells to metabolize X-Gal, yielding white instead of blue colonies.

[0351] After 48h growth on selective medium, white transformant colonies are inoculated into 2 mL YPD with G418 and grown overnight at 30°C with 200 rpm agitation. The following day, the cultures are diluted 100-fold into 2 mL SD medium with 150 μ g/mL G418 (approximately corresponding to a starting optical density of 0.1) and grown at 30°C for 24 h with 200 rpm shaking.

Example 6. “Identification of a functional *Zygosaccharomyces parabailii* uricase”

[0352] A putative *Zygosaccharomyces parabailii* uricase was identified by a BLASTP search of *Zygosaccharomyces* (taxid:4953) proteins through the public online interface available at <https://blast.ncbi.nlm.nih.gov/Blast.cgi> with the default settings with the *Aspergillus flavus* uricase (SEQ ID NO: 2) as the query. One of the search results, accession number AQZ10287.1 was 45.60% identical with an E-value of 5e-85. A search against the conserved domain database through the public online interface available at

<https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi> with the default settings showed this *Zygosaccharomyces parabailii* protein putatively encoded a uricase with extensive similarity to TIGR03383 (E-value of 2.60e-128)

[0353] A synthetic DNA encoding the putative *Zygosaccharomyces parabailii* uricase accession number AQZ10287.1 with codon usage optimized towards *Saccharomyces cerevisiae* through the online codon optimizer available at <https://www.idtdna.com/CodonOpt> with flanking BstBI and NdeI restriction sites (as exemplified in SEQ ID NO:25) was obtained from Integrated DNA Technologies (Coralville, IA). The BstBI / NdeI fragment was excised and subcloned into the BstBI / NdeI sites of the shuttle vector of Example 1 (SEQ ID NO: 19), resulting in the functional replacement of the *Candida utilis* uricase ORF with the putative *Zygosaccharomyces parabailii* uricase ORF.

[0354] The shuttle vector encoding the *Zygosaccharomyces parabailii* uricase ORF was transformed into *S. boulardii* cells as exemplified in Example 1. Cells were selected on YPD plates containing 600 µg / mL G418, a colony was inoculated into YPD medium containing 200 µg / mL G418, and a control culture consisting of *S. boulardii* cells transformed with the vector of Example 1 (SEQ ID NO: 18) was grown in YPD medium without antibiotics.

Example 7. “Identification of a functional *Zygosaccharomyces parabailii* uric acid transporter”

[0355] A putative *Zygosaccharomyces parabailii* uric acid transporter was identified by a BLASTP search of *Zygosaccharomyces* (taxid:4953) proteins through the public online interface available at <https://blast.ncbi.nlm.nih.gov/Blast.cgi> with the default settings with the *Aspergillus nidulus* UapA (SEQ ID NO: 9) as the query. One of the search results, accession number

AQZ18664.1 was 56.28% identical with an E-value of 0. A search against the conserved domain database through the public online interface available at

<https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi> with the default settings showed this *Zygosaccharomyces parabailii* protein putatively encoded a uracil-xanthine permease with extensive similarity to TIGR00801 (E-value of 6.94e-115).

[0356] A synthetic DNA encoding the putative *Zygosaccharomyces parabailii* uricase accession number AYZ18664.1 with codon usage optimized towards *Saccharomyces cerevisiae* through the online codon optimizer available at <https://www.idtdna.com/CodonOpt> with flanking KpnI and NheI restriction sites (as exemplified in SEQ ID NO: 26) was obtained from Integrated DNA Technologies (Coralville, IA). The KpnI / NheI fragment was excised and subcloned into the KpnI / NheI sites of the shuttle vector of Example 1 (SEQ ID NO: 19), resulting in the functional replacement of the *Aspergillus nidulas* UapA uric acid transporter ORF with the putative *Zygosaccharomyces parabailii* uric acid transporter ORF.

[0357] The shuttle vector encoding the *Zygosaccharomyces parabailii* uric acid transporter ORF was transformed into *S. boulardii* cells as exemplified in Example 1. Cells were selected on YPD plates containing 600 µg / mL G418, a colony was inoculated into YPD medium containing 200 µg / mL G418, and a control culture consisting of *S. boulardii* cells transformed with the vector of Example 1 (SEQ ID NO: 18) was grown in YPD medium without antibiotics.

Example 8. "Urate consumption assay"

[0358] A urate consumption assay was developed. The assay was performed using an pH 7.0 phosphate buffer (yellow pH 7.0 standard) as the assay buffer (Biopharm UPC 721272377576). The assay solution consisted of assay buffer with 10 mM glucose and uric acid at A293 1.5 – 2.0. A uric acid stock solution was prepared by dissolving a small amount of uric acid (3 mm at tip of small metal spatula) in 20 mL assay buffer in a 50 mL conical tube, and briefly heated up in microwave. Undissolved uric acid was pelleted by centrifuging 5 minutes at 3000xg. The

supernatant was then used for assays. A BioRad SmartSpec™ Plus spectrophotometer was used with a 1 cm quartz glass microcuvette. The spectrophotometer was blanked using buffer only at 293 nm. A dilution was prepared with an A293 of 1.5 - 2.0. Glucose was added to the assay buffer to a final concentration of 10 mM using the 2 M (200X) stock solution prepared in assay buffer.

[0359] Mid-log phase exponentially growing cells were harvested and OD600 (absorbance at 600 nm) of the culture was measured using a BioRad SmartSpec™ Plus spectrophotometer and the spectrophotometer was blanked using water. Cultures were diluted 1:10 in water, and OD600 was measured in the spectrophotometer. The volume of cell culture that is needed was calculated to obtain a final assay solution cell concentration of OD600 = 2. For 4 mL of assay solution at OD600 = 2, an equivalent of 8 OD600 was transferred to a 1.7 mL Eppendorf tube. Cells were pelleted by centrifugation at 20000 x G for 2 minutes. The supernatant was aspirated with a p1000 micro pipette, cells were washed by resuspension in 500 µL H₂O, pelleted again, and the supernatant was carefully aspirated with a p1000 micro pipette. The cell pellet was resuspended in 4 mL assay solution in a round bottom capped falcon tube (BD Falcon #352006). Falcon tubes were then transferred to a shaker incubator set at 37°C and 350 RPM. 500 µL cell suspension aliquots were sampled at intervals, and transferred to a 1.7 mL Eppendorf tube. Cells were pelleted by centrifugation at 20000 x G for 2 minutes. 400 µL of the clarified supernatant was transferred to a 1 cm path length quartz glass cuvette, and A293 was measured. At the end of the assay, OD600 of the cell suspension was measured to confirm suspensions contained equal amounts of cells.

[0360] Cells produced in Example 1, Example 7, and Example 8 were assayed using this urate consumption assay with results shown in FIG. 4. The graph clearly shows that cells produced as

outlined in Example 1 reduced the uric acid concentration in the medium as determined by A293 most rapidly, followed by cells produced as outlined in Example 8, with cells produced as outlined in Example 7 consumed uric acid the slowest.

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US	62959991	2020-01-12

Invention Title

Language	Inventor name
en	Therapeutic Engineered Microbial Cell Systems and Methods for Treating Hyperuricemia and Gout

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Sequences

Sequence 1: "1"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
303	AA	Candida utilis	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..303	MOL_TYPE = protein ORGANISM = Candida utilis

Residues

[illegible]

Sequence 2: "2"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
302	AA	unidentified	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..302	MOL_TYPE = protein ORGANISM = unidentified

Residues

[illegible]

Sequence 3: "3"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
302	AA	<i>Arthrobacter globiformis</i>	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..302	MOL_TYPE = protein; ORGANISM = <i>Arthrobacter globiformis</i>

Residues

[illegible]

Sequence 4: "4"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
304	AA	synthetic construct	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..304	MOL_TYPE = protein ORGANISM = synthetic construct

Residues

```

MRVYKHVKK  MRVYKVRK  YGKMIKVLK  TGDNGKYHSI  EVVATSVOLT  LSPKNGYLEG  1
MRGVLPFTT  LKNVYNVLK  PKGKNGEET  AGTICNFTS  SKKVVTSKY  FVLDVFAKKE  2
ERGVVHVRH  FVIVFSTRE  QEVETKNGE  EVIRSGIKDL  SVLETTDSKY  DDTIKLQITE  3
LPEVKDQTA  TQVYQWRH  QGRQDFEAT  EDTVRSIVLQ  RFAQPTKGE  VAPSVKALN  4
DQVLSLSEV  EETELMEISL  ENRYFNIDM  SPKGLINKES  VLLPLDNFV  KITGIKREKE  5
SSAL

```

Sequence 5: "5"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
296	AA	Schizosaccharomyces pombe	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..296	MOL_TYPE = protein ORGANISM = Schizosaccharomyces pombe

Residues

```

MSETTVVKQC  AYGTILVRFM  KHDIDPKTKT  HTVYEMDVGS  LDTGSELDSEY  TEALNSIVVP  1
TINTQNTIIV  PAKINLVSVF  EVTRAKLAKH  FVKKVXHIAG  APLGIIITPM  TEKEWQGMER  2
SRGPIANQGE  QPKTHVVENQ  GSGFDVVQSL  KDVLVLKSGI  SGPIINFRCE  FTLLPEVTLR  3
IPETSIDQNV  TPKEQDTEED  LAGFDENSEI  ENVKRITLST  FALDDSESVV  RRYVKNADTH  4
INTVPAINEV  GTALPNKHVF  EINLAPPNID  NLGSRGGLKQ  EQATVSSKIK  QIVARK  5

```

Sequence 6: "6"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
494	AA	Bacillus subtilis	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..494	MOL_TYPE = protein ORGANISM = Bacillus subtilis

Residues

```

MPTNDLNM  DTOTLTITL  STEKSSWIA  SKSARLAPFS  SLSELRKMT  QIVKAADREH  1
GLDLINKHES  LGPKVTSMSL  SVREKONAGL  SKLEKQDYDEE  RIMINERYVD  RIGFTSTLLV  2
RGVTRALPK  ALARLESER  RIDESKALLD  AVFLAKHRLA  DITTEKSGTD  RERKINSQKQ  3
NVERVAPLAK  PLGSAVALPS  RLDGPKGNIV  VGVGVVPLAG  GELPGLQPLR  GQNTLVVSTQ  4
SRNMTICQK  ASIGCVHPL  RLVGVKHLH  DTGSGHML  LTGELQVPLR  GQKQDEVS  5
REGLVPAKRI  NERKGVLPK  RLGQVTRHSH  DQVSGHML  LTVKVGQVPLR  GQKQDEVS  6
PGLDNEPLFV  VLNISQVEN  TNLAYATDGA  RIVAAACVQL  ELASTVTRHSH  TQSTQKLLYH  7
IGQRILARFE  QLTQVSPQSQ  NRTWDTVVEE  IPKSRGKVT  EPRPYGPH  FEVTRCALRX  8

```

EQKTRKCR SLRA

494

Sequence 7: "7"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
305	AA	unidentified	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..305	MOL_TYPE = protein ORGANISM = unidentified

Residues

```

MSGLADSTYG  EDNVKPLAVK  EDESNVPECC  MEATVKKVL  KGNPDVSYTE  ADNSPIVPTG  10
EYENTILLIA  EONDTRPTEK  PAAPLALDRA  GHVGHVSGVS  INILCEKNVZ  VVNDGRSSCH  20
GVYHGGPKK  IYELVYKQVN  GETHYKELST  IEDITVLEST  KSNELDINVC  EITTEKPTLG  30
RVLSSTDFAV  WDGESEPLED  LTATAPGASD  LVDFVPVFLA  ADITLDFEAK  ENDSVVCATM  40
YNNGVAILAP  APQVEYVSYE  LNNKHYLFED  LWFPGQLND  NDLPVPEPHQ  NGLIRQVGA  50
RTKRL

```

Sequence 8: "8"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
281	AA	unidentified	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..281	MOL_TYPE = protein ORGANISM = unidentified

Residues

```

MYLTLEKNAY  GENAVNLSKI  IIRPNYHEEK  QISVNVSLG  DEETARTLGE  NKKLVSTDTG  10
KIVVVALAKE  HFVDSICNPS  IYLANIFIN  NFOVSGATUH  IIEFPRKMA  PFDGDSHBAK  20
VGGGSEKPTT  TLVYTTETIA  QISSIKDILL  EMTTDSGPEE  NVPLDITTEK  DVADRIHAPK  30
CEANRYTSG  NIDFESIDPK  IASTLLKTEA  HNSLIVKQT  DLANKGSVLE  LNCQVGDPAK  40
IIRPKRKRIY  NLDAPONDW  NEIFLATCEP  YGLTCGVIR  D

```

Sequence 9: "9"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
574	AA	unidentified	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..574	MOL_TYPE = protein ORGANISM = unidentified

Residues

[illegible]

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
588	AA	unidentified	No	No

Feature Key	Feature Location	Qualifiers
SOURCE	1..560	MOL_TYPE = protein ORGANISM = unidentified

[illegible]

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
583	AA	unidentified	No	No

Feature Key	Feature Location	Qualifiers
SOURCE	1..583	MOL_TYPE = protein ORGANISM = unidentified

doi:10.1017/S096382371000060X

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
591	AA	Candida albicans	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..591	MOL_TYPE = protein ORGANISM = <i>Candida albicans</i>

Residues

```

MSRAIKTKLKG  KVRNNTKTKG  LLGDTLVNYL  ETRDIESDTR  ELRTQDLPV  MIDMPHLLGA  1
ILSPAHALAM  LAGIVTVPIM  VASTANLSVD  LEAYLVSTSG  IVRCQSLLE  IIRDPHIEHTG  11
VIGTGLELV  VGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  21
ALDEILLSEM  KPSMLQKIP  PLVTGEVVM  LGVHLVESGF  TIRVGGAGG  DQUTPTTKKH  31
SAPWGDARI  SLGELVYV  ILAREGAS  MKSCAVIFGL  LIGIVVAPL  GQFTSSCNVDG  41
APARCPWV  IIRLVYGV  VLPFLAVIV  LASECTGLV  ATSDVGLV  GQWVSESL  51
GVLGDSIC  IIRLVYGV  MVVDFNAGV  LSTKQK  VLVVAPL  GQWVSESL  61
ATDIEKPOL  GQWVSESL  VAIS  TSTPTKDEM  VLVVAPL  GQWVSESL  71
HYTVGGGK  GQWVSESL  VVV  GQWVSESL  GQWVSESL  GQWVSESL  81
GATSEAD  SERDGVLE  LPSQLSNIK  NGGSPDAITV  LRANDGPE  M  91

```

Sequence 13: "13"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
601	AA	<i>Schizosaccharomyces pombe</i>	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..601	MOL_TYPE = protein ORGANISM = <i>Schizosaccharomyces pombe</i>

Residues

```

MSESIGDACH  EMTIIEKTS  AEVLISPTKD  EWIGDYDYS  LLEAIRFKG  KKKK  1
MAYVPLAL  LLGDTLVNYL  ETRDIESDTR  ELRTQDLPV  MIDMPHLLGA  11
IRVRIPIK  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  21
APLAPACVCS  LLGDTLVNYL  ETRDIESDTR  ELRTQDLPV  MIDMPHLLGA  31
GPTTALAPG  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  41
LVGNTLSAA  TSLGELVYV  ILAREGAS  MKSCAVIFGL  LIGIVVAPL  GQFTSSCNVDG  51
GKSDVSE  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  61
GKSDVSE  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  71
ELTASNLIG  MRLVYGV  MVVDFNAGV  LSTKQK  VLVVAPL  GQWVSESL  81
ILVIEFDL  TNGDGVLE  LPSQLSNIK  NGGSPDAITV  LRANDGPE  M  91

```

Sequence 14: "14"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
439	AA	<i>Bacillus subtilis</i>	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..439	MOL_TYPE = protein ORGANISM = <i>Bacillus subtilis</i>

Residues

```

MKEOHNAQL  MKEOHNAQL  KYAGATVPL  IVGATGLNA  SOLTVELAD  LFMCAATL  1
MKEOHNAQL  MKEOHNAQL  KYAGATVPL  IVGATGLNA  SOLTVELAD  LFMCAATL  11
KPEPPVYNS  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  21
GPRSIATIL  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  31
ALVSVESIS  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  41
GKSDVSE  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  51
GKSDVSE  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  61
GKSDVSE  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  71
GKSDVSE  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  81
GKSDVSE  VVGTSEATIT  VTKAPENNYA  DGTCPMAGDG  VTRLPQDQD  GKILASACCTG  91

```

Sequence 15: "15"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
450	AA	Bacillus subtilis	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..450	MOL_TYPE = protein ORGANISM = Bacillus subtilis

Residues

```

MKKEDCEKVE  QLGLEKVLAM  VAGAILVELL  VGPALNVYTE  QLSVLELAID  LCCGVATLEQ  60
TGGATVIGIG  LEVNLGSSIV  AVTPHIALSS  NIGIRALTP  ELADGVILPT  PAFATGKATV  120
EPPVVTATIV  QTLIGLILKP  TGVKINAGSS  KIMGGANQSS  QGHEAVLLSG  AVPLILITIN  180
KLVGIVIVIV  ESEVVFALIS  KICGAELEEN  DLVKGIDRAG  TALLIGLLEN  EEPVNTISLQ  240
AGLLQITFVK  TRNIVVTAPQ  ILVGLGILPK  IALASAVEPA  AVLGGATVVM  EKVVIASVVK  300
MLSTADLNK  VHLITACST  ALSGIAGTAP  GITAETPPTI  RILVSDCTIT  GSLTAIFLNL  360
EFLRDKKEL  TAOQTELEVL  EHTALEKEV

```

Sequence 16: "16"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
525	AA	Escherichia coli	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..525	MOL_TYPE = protein ORGANISM = Escherichia coli

Residues

```

MFPQFLSLTP  LPRRNWHTS  NCIDSPFNIN  GCFLLNPANG  EFLMNAIDSG  LPSGGGQDRG  60
TEVDRIILSP  GKLIILGLQ  VLVNVIAGAV  VPEMIGDRIG  LSKETIANLY  ESDLFCGGIV  120
TLLOGLIGDS  ENGILRLVIM  SVTFARVTPS  IALGNNEIDG  LLOIPGATIA  DEPTITILAP  180
LHGLNPLEPE  PLNTGVVITE  IGLEIIVGSI  IMLAGGKGNP  QVGNPVLEAI  SPVILIFLLD  240
ITRIAKGQNS  NVAVLLGIPE  GELLSMRRND  VNLSCGLHDS  WPAIVTMMSS  GNPITPEVSI  300
LNTAVLLIV  FLSGSGPILP  LEEIVGKPLS  SHDITGLIV  DEGTNIGGI  ENEKNTLPTD  360
LVNGVNSYK  VHSRNVCLAS  STILFCMV  ERSAYVAGSI  DPTVLSGGL  VNSQVLTATD  420
FRLSPQNT  NPVNVIVIVE  ISLWGMTET  ESHDPTSEK  RQIQLLHSG  INLATLSAVV  480
LVNTPNGAZH  RADLYPESVS  DEDLKVRIVA  MWLLMSCLAK  NEHSE

```

Sequence 17: "17"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
594	AA	unidentified	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..594	MOL_TYPE = protein ORGANISM = unidentified

Residues

```

MDSVLEQPTN  SESKTIKQVE  SWLSKRFETD  DGLLAGDVN  FLATDQKVD  EPHCLPQV  61
VYVDFEPTG  LNSKVFVLS  NLLGCKHLL  KLAGVETD  MTSKQKVD  KSGVNTLV  62
LITSLILSAV  QITFEETKMT  NLYIDKCLG  IVVQSSAVLG  IVKSGVILM  KSGVNTLV  63
SNEKCLDQAG  ALLOTETPCA  LLEMLLQPTG  RHILQKIPK  VVSGVILM  LKSGCAVIV  64
DWTGQGGV  ALQSSQCGSA  AAFWSSKMT  GGLQVYVIL  LKSGVILM  LKSGCAVIV  65
LVSCVLEAV  GGFSSQIC  AFAITFLWK  TFLQVYVIL  LKSGVILM  LKSGCAVIV  66
ATGVSLELV  TRAFSSRI  QVALLQGG  ALQSSVYV  NGLQKMT  LKSGCAVIV  67
RAYRTCLAV  TRAFSSRI  QVALLQGG  ALQSSVYV  NGLQKMT  LKSGCAVIV  68
VUGALDQV  GCLVLSLW  LVVLMGNH  ALQSTNAIL  LKSGCAVIV  LKSGCAVIV  69
TQGLDQDIL  QDLEVQDNL  SVLSRKQPL  TGVNSKEL  SAELESE  LKSGCAVIV  70

```

Sequence 18: "18"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
451	AA	unidentified	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..451	MOL_TYPE = protein ORGANISM = unidentified

Residues

```

MGEFVNRDST  PLVYGLERDV  PLVPALLVSL  QVGMNVVCT  ITFALLLSGI  INTDQDQAY  61
LVSNALVKA  DGELEQKPL  QITSSGLSL  KATSSKEL  LKAGVYVIL  PLVYGLERDV  62
TEVOLALPT  DENLKSVP  IVSGIVVILL  GUSLIPKMP  STALPESG  PLVYGLERDV  63
IVINVMILAO  SIGVANARMA  AVLVSVVTC  TITGLMGRLO  SPSLNGSWL  TLEVEEFG  64
AFKNELLFSE  AFILVGVLE  AMGLITAT  LSGLPTDGL  HWRIPGSH  DGLACIGST  65
LIGGFFSAT  AQNGVITAM  GVAAPRIOW  NAVILLCEL  RPEVGNIT  MDSVLEQV  66
TMLPGLVNS  GILNVSSGL  SQDALIAL  SLOVGLGVE  QEWLNTLP  VVQFLESQ  67
SAGGLAELL  NLELRASR  KMSPEADM  L  68

```

Sequence 19: "19"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
9930	DNA	synthetic construct	No	No

Features

Feature Key	Feature Location	Qualifiers
SOURCE	1..9930	mol_type = other DNA organism = synthetic construct

Residues

```

ccgacccccc  ccgacccccc  ccttattccac  ccttattccac  ccttattccac  ccttattccac  61
ccgacccccc  ccttattccac  ccttattccac  ccttattccac  ccttattccac  ccttattccac  62
ccgacccccc  ccttattccac  ccttattccac  ccttattccac  ccttattccac  ccttattccac  63
ccgacccccc  ccttattccac  ccttattccac  ccttattccac  ccttattccac  ccttattccac  64
ccgacccccc  ccttattccac  ccttattccac  ccttattccac  ccttattccac  ccttattccac  65
ccgacccccc  ccttattccac  ccttattccac  ccttattccac  ccttattccac  ccttattccac  66
ccgacccccc  ccttattccac  ccttattccac  ccttattccac  ccttattccac  ccttattccac  67
ccgacccccc  ccttattccac  ccttattccac  ccttattccac  ccttattccac  ccttattccac  68
ccgacccccc  ccttattccac  ccttattccac  ccttattccac  ccttattccac  ccttattccac  69
ccgacccccc  ccttattccac  ccttattccac  ccttattccac  ccttattccac  ccttattccac  70

```

The residues listing has been truncated as it exceeds the configured limit: (1200 max residues to print)

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
1272	DNA	synthetic construct	No	No

Feature Key	Feature Location	Qualifiers
source	1..1272	mol_type = other DNA organism = synthetic construct

[illegible]

The residues listing has been truncated as it exceeds the configured limit: (1200 max residues to print)

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
1950	DNA	synthetic construct	No	No

Feature Key	Feature Location	Qualifiers
source	1..1960	mol_type = other DNA organism = synthetic construct

[illegible]

The residues listing has been truncated as it exceeds the configured limit: (1200 max residues to print)

117

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
11378	DNA	synthetic construct	No	No

Features

Feature Key	Feature Location	Qualifiers
source	1..11378	mol_type = other DNA organism = synthetic construct

Residues

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 104

The residues listing has been truncated as it exceeds the configured limit: (1200 max residues to print)

Sequence 23: "23"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
6047	DNA	synthetic construct	No	No

Features

Feature Key	Feature Location	Qualifiers
source	1..6047	mol_type = other DNA organism = synthetic construct

Residues

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Sequence 24: "24"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
8126	DNA	synthetic construct	No	No

Features

Feature Key	Feature Location	Qualifiers
source	1..8128	mol_type = other DNA organism = synthetic construct

Residues

[illegible]

The residues listing has been truncated as it exceeds the configured limit (1200 max residues to print)

Sequence 25: "25"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
976	DNA	synthetic construct	No	No

Features

Feature Key	Feature Location	Qualifiers
source	1..976	mol_type = other DNA organism = synthetic construct

Residues

[illegible]

Sequence 26: "26"

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
--------	---------------	----------	--------------------------------	------------------

Length	Molecule Type	Organism	Contains DNA and RNA fragments	Skipped Sequence
2410	DNA	synthetic construct	No	No

Features

Feature Key	Feature Location	Qualifiers
source	1..2410	mol_type = other DNA organism = synthetic construct

Residues

The residues listing has been truncated as it exceeds the configured limit: (1200 max residues to print)

The residues listing has been truncated as it exceeds the configured limit: (1200 max residues to print)

CLAIMS

What is claimed is:

1. An engineered microbial cell comprising:
 - a plurality of microbial cells;
 - the microbial cells expressing at least two exogenous polypeptides, including a first exogenous polypeptide and a second exogenous polypeptide;
 - the first exogenous polypeptide is a uric acid degrading polypeptide; and
 - the second exogenous polypeptide is a uric acid transporter that brings in uric acid from outside of the microbial cells.
2. The engineered microbial cell of claim 1, further comprising:
 - the uric acid transporter is at least 60% homologous to a uric acid transporter selected from a group, or a combination selected from the group, consisting of: *Aspergillus nidulans* UapA [SEQ ID NO: 9], *Aspergillus nidulans* UapC [SEQ ID NO: 10], *Aspergillus fumigatus* UapC [SEQ ID NO: 11], *Candida albicans* Xut1 [SEQ ID NO: 12], *Schizosaccharomyces pombe* Q9HE12 [SEQ ID NO: 13], *Bacillus subtilis* PucK [SEQ ID NO: 14], *Bacillus subtilis* PucJ [SEQ ID NO: 15], *Escherichia coli* YgfU [SEQ ID NO: 16], *Zygosaccharomyces parabailii* AQZ18664 [SEQ ID NO: 17], or *Spirosoma sp.* KCTC 42546 WP_142773020 [SEQ ID NO: 18].
3. The engineered microbial cell of claim 2, further comprising:
 - the microbial cells are fungal cells.

4. The engineered microbial cell of claim 3, further comprising:
the uric acid degrading polypeptide is a uricase.
5. The engineered microbial cell of claim 4, further comprising:
the uricase is a fungal uricase.
6. The engineered microbial cell of claim 5, further comprising:
the fungal uricase is selected from a group, or a combination selected from the group,
consisting of: *Candida utilis* [SEQ ID NO: 1], *Aspergillus flavus* [SEQ ID NO: 2],
Schizosaccharomyces pombe [SEQ ID NO: 5], or *Zygosaccharomyces parabailii*
[SEQ ID NO: 7].
7. The engineered microbial cell of claim 4, further comprising:
the uricase is a bacterial uricase.
8. The engineered microbial cell of claim 7, further comprising:
The bacterial uricase is selected from a group, or a combination selected from the
group, consisting of: *Arthrobacter globiformis* [SEQ ID NO: 2], *Bacillus subtilis*
[SEQ ID NO: 6], or *Spirosoma sp.* [SEQ ID NO: 8].
9. The engineered microbial cell of claim 4, further comprising:
the uricase is a mutant uricase, including chimera and/or overexpression variants of
the uricase.

10. The engineered microbial cell of claim 9, further comprising:
the mutant uricase is a porcine-baboon chimera uricase [SEQ ID NO: 4].
11. The engineered microbial cell of claim 2, further comprising:
the microbial cells are bacterial cells.
12. The engineered microbial cell of claim 11, further comprising:
the uric acid degrading polypeptide is a uricase.
13. The engineered microbial cell of claim 12, further comprising:
the uricase is a fungal uricase.
14. The engineered microbial cell of claim 13, further comprising:
the fungal uricase is selected from a group, or a combination selected from the group,
consisting of: *Candida utilis* [SEQ ID NO:1], *Aspergillus flavus* [SEQ ID NO: 2],
Arthrobacter globiformis [SEQ ID NO: 3], Chimeric porcine baboon [SEQ ID
NO: 4], *Schizosaccharomyces pombe* [SEQ ID NO: 5], or *Zygosaccharomyces
parabailii* [SEQ ID NO: 7].
15. The engineered microbial cell of claim 12, further comprising:
the uricase is a bacterial uricase.

16. The engineered microbial cell of claim 15, further comprising:

The bacterial uricase is selected from a group, or a combination selected from the group, consisting of: *Arthrobacter globiformis* [SEQ ID NO: 2], *Bacillus subtilis* [SEQ ID NO: 6], or *Spirosoma sp.* [SEQ ID NO: 8].

17. The engineered microbial cell of claim 12, further comprising:

the uricase is a mutant uricase, including chimera and/or overexpression variants of the uricase.

18. The engineered microbial cell of claim 17, further comprising:

the mutant uricase is porcine-baboon chimera uricase [SEQ ID NO: 4].

19. A method of lowering uric acid in the gastrointestinal tract of a recipient, comprising the steps of:

preparing a therapeutically effective dose of the engineered microbial cell selected from a group, or a combination selected from the group, consisting of: claims 1-18;

orally administering the therapeutically effective dose; and

allowing time for the selected engineered microbial cell to transport and degrade uric acid.

20. A method for treating a patient suffering from a condition selected from a group, or a combination selected from the group, consisting of: gout, rheumatoid arthritis, cerebral stroke, heart disease, arrhythmia, chronic renal disease, and chronic refractory gout; the method comprising the steps of:
- determining whether the patient has a serum uric acid level of ≥ 6.8 mg/dl prior to initiating urate lowering therapy; and
 - if the patient has a serum uric acid level of ≥ 6.8 mg/dl prior to initiating urate lowering therapy, then orally administering the engineered microbial cell selected from a group, or a combination selected from the group, consisting of: claims 1-18, in an amount of 10^6 to 10^{12} microbial cells.
21. The method for treating a patient of claim 20, further comprising:
- the amount of microbial cells orally administered is approximately 10^9 cells.
22. The method for treating a patient of claim 20, further comprising:
- the condition selected from a group, or a combination selected from the group, is chronic refractory gout.
23. The method for treating a patient of claim 20, further comprising:
- the engineered microbial cell selected from a group, or a combination selected from the group, is administered with a pharmaceutically acceptable carrier.
24. A method for determining uric acid degradation, comprising the steps of:
- creating an assay solution including an assay buffer and a uric acid solution;
 - selecting a cell;
 - washing and suspending the cell in the assay solution;

incubating the cell in the assay solution at conditions acceptable for uric acid degradation;
sampling aliquots of the assay solution at intervals; and
measuring absorbance of the aliquots in a spectrophotometer at substantially a wavelength of 293nm.

25. A method of identifying uric acid degrading polypeptides, comprising the steps of:

selecting a cell that expresses a uric acid transporter polypeptide;
operatively linking a promoter that is functional in the cell to a nucleotide sequence encoding a putative uric acid degrading polypeptide;
introducing the promoter linked to the nucleotide sequence encoding the putative uric acid degrading polypeptide into the cell;
performing the method of claim 24; and
identifying and quantifying whether uric acid degrading increased.

26. The method of identifying uric acid degrading polypeptides of claim 25, further comprising the steps of:

the uric acid transporter polypeptide of the cell is selected from a group, or a combination selected from the group, consisting of: SEQ ID NO: 9-18.

27. A method of identifying uric acid transporters, comprising the steps of:
- selecting a cell that expresses a uric acid degrading polypeptide;
 - operatively linking a promoter that is functional in the cell to a nucleotide sequence encoding a putative uric acid transporter polypeptide;
 - introducing the promoter linked to the nucleotide sequence encoding the putative uric acid transporter polypeptide into the cell;
 - performing the method of claim 24; and
 - identifying and quantifying whether uric acid degrading increased.
28. The method of identifying uric acid transporter of claim 27, further comprising the steps of:
- the uric acid degrading polypeptide of the cell is selected from a group, or a combination selected from the group, consisting of: SEQ ID NO: 1-8.
29. An engineered microbial cell, comprising:
- a cell expressing the uric acid degrading polypeptide identified by the methods of either claim 25 or claim 26; and
 - the cell expressing the uric acid transporter polypeptide identified by the methods of either claim 27 or claim 28.