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Hassan et al.

(54) **OXALOBACTER FORMIGENES (OF)-DERIVED FACTORS FOR THE TREATMENT OF TREATMENT/PREVENTION OF EXCESS OXALATE LEVELS**

(71) Applicant: **The University of Chicago**, Chicago, IL (US)

(72) Inventors: **Hatim A. Hassan**, Chicago Ridge, IL (US); **Donna Arvans**, Chicago, IL (US)

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(57) **ABSTRACT**

Provided herein are compositions comprising *Oxalobacter formigenes* (Of)-derived factors and variants and fragments thereof, and method of use thereof for the treatment/prevention excess oxalate levels and conditions and diseases related thereto.

Specification includes a Sequence Listing.

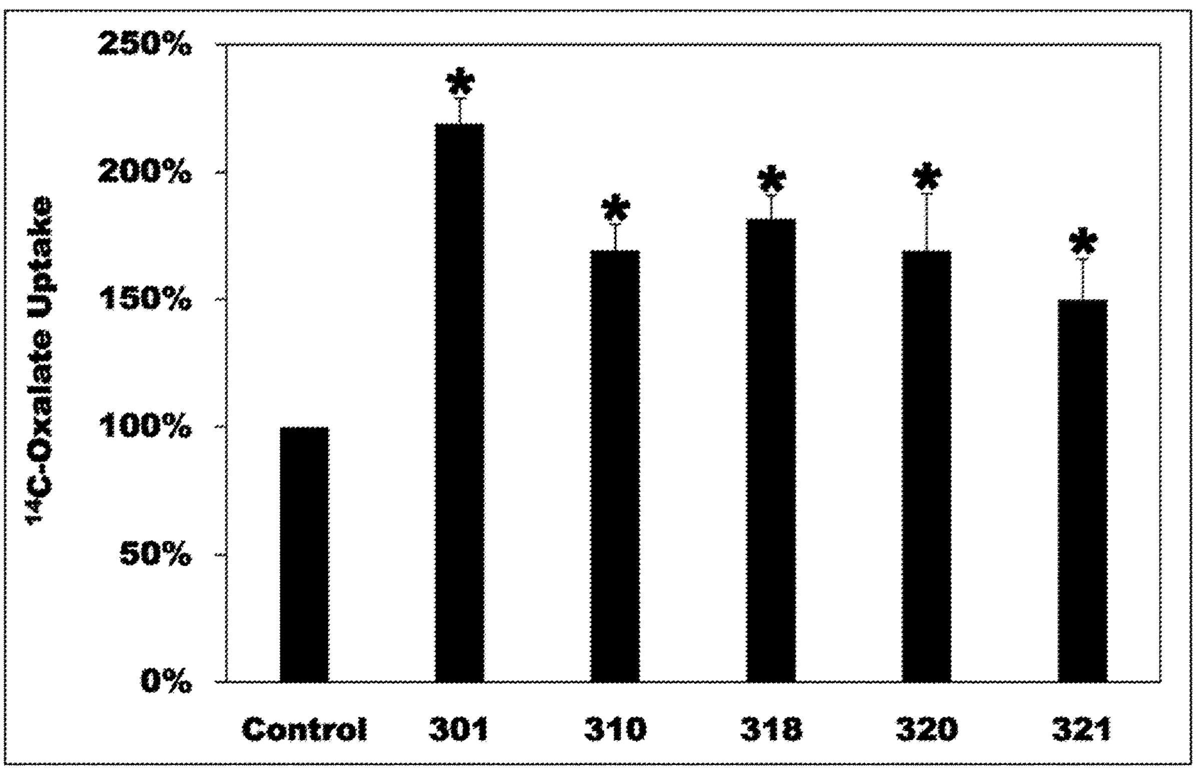


FIG. 1

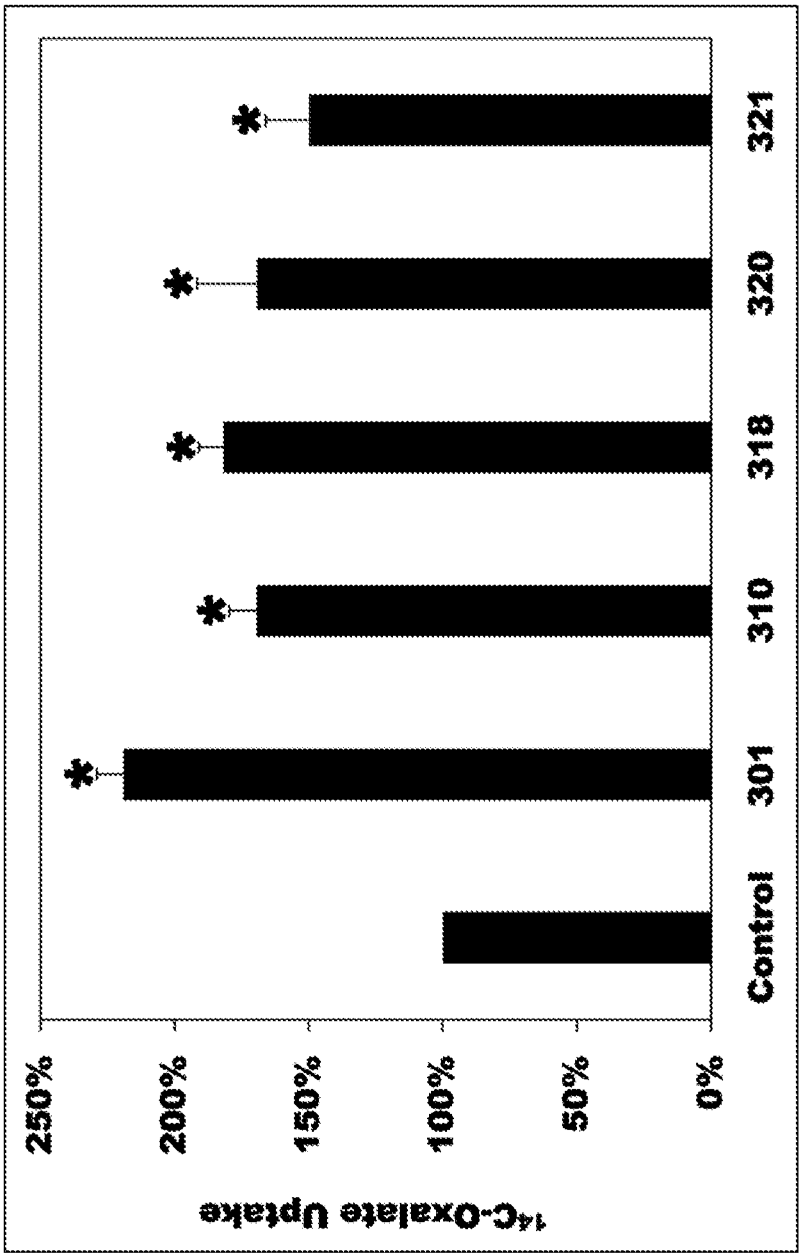

14C-Oxalate Uptake
250%
200%
150%
100%
50%
0%
Control
301
310
318
320
321
*

FIG. 2

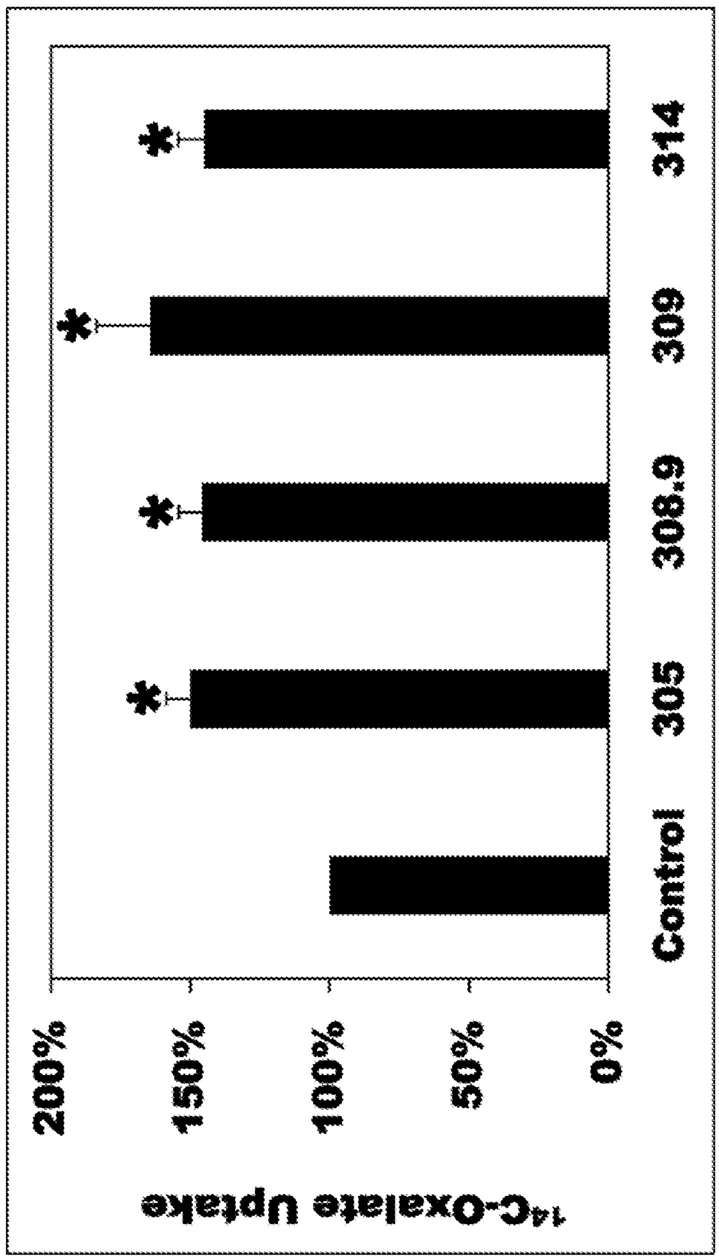
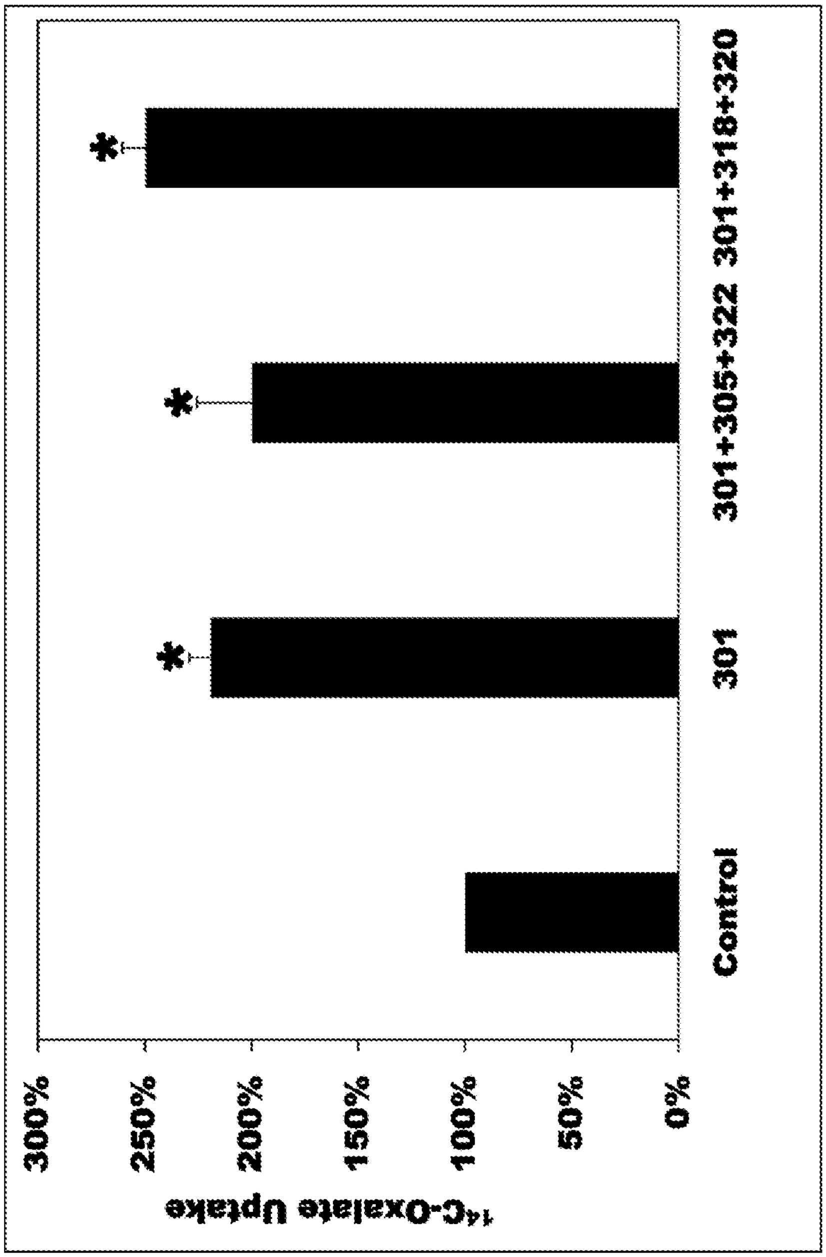


FIG. 3



14C-Oxalate Uptake
300%
250%
200%
150%
100%
50%
0%
Control
301
301+305+322
301+318+320
*
*
*

FIG. 4

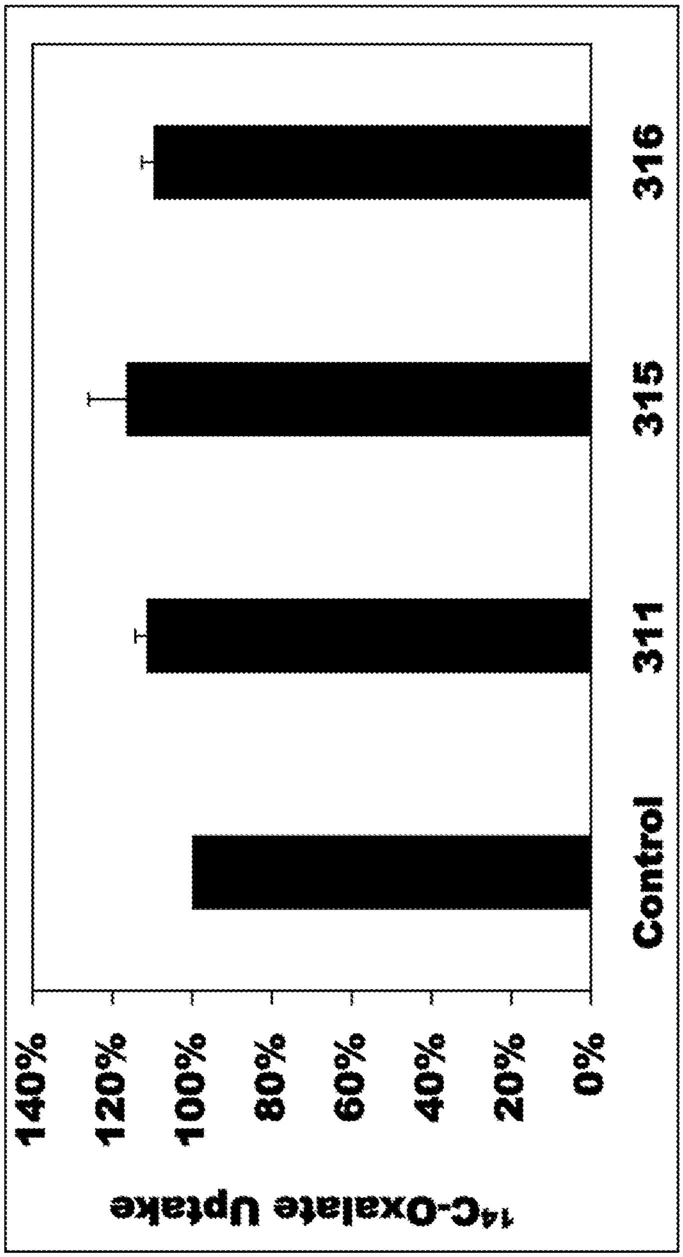

14C-Oxalate Uptake
140%
120%
100%
80%
60%
40%
20%
0%
Control
311
315
316

FIG. 5

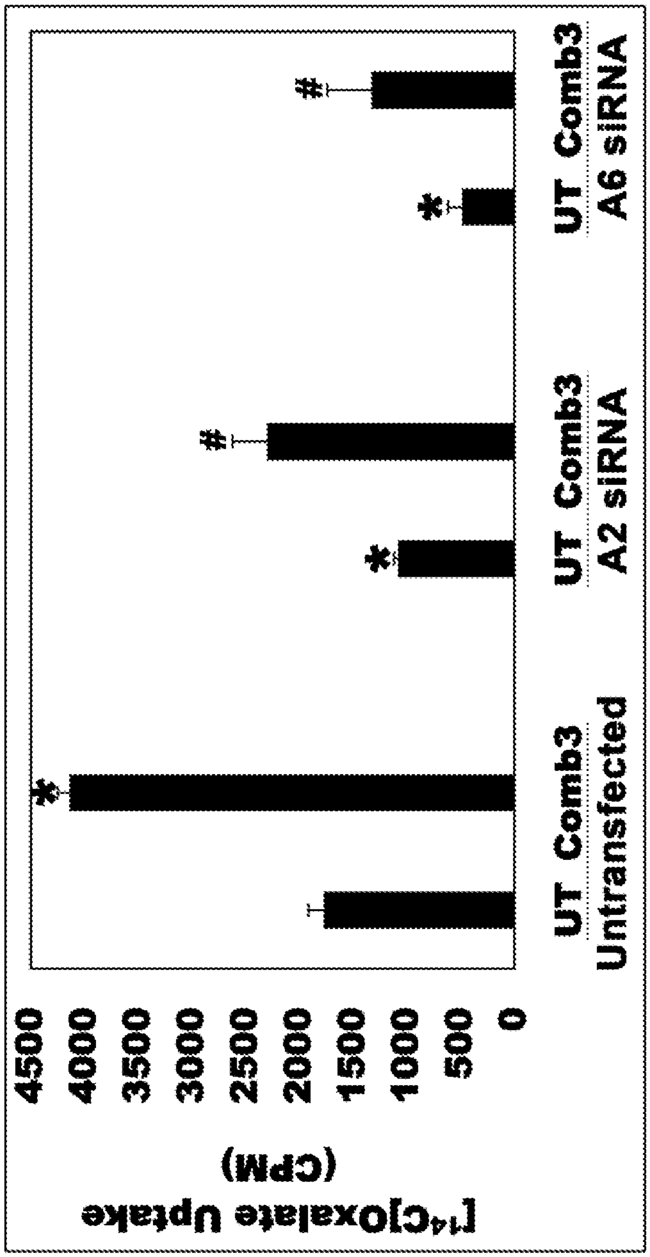
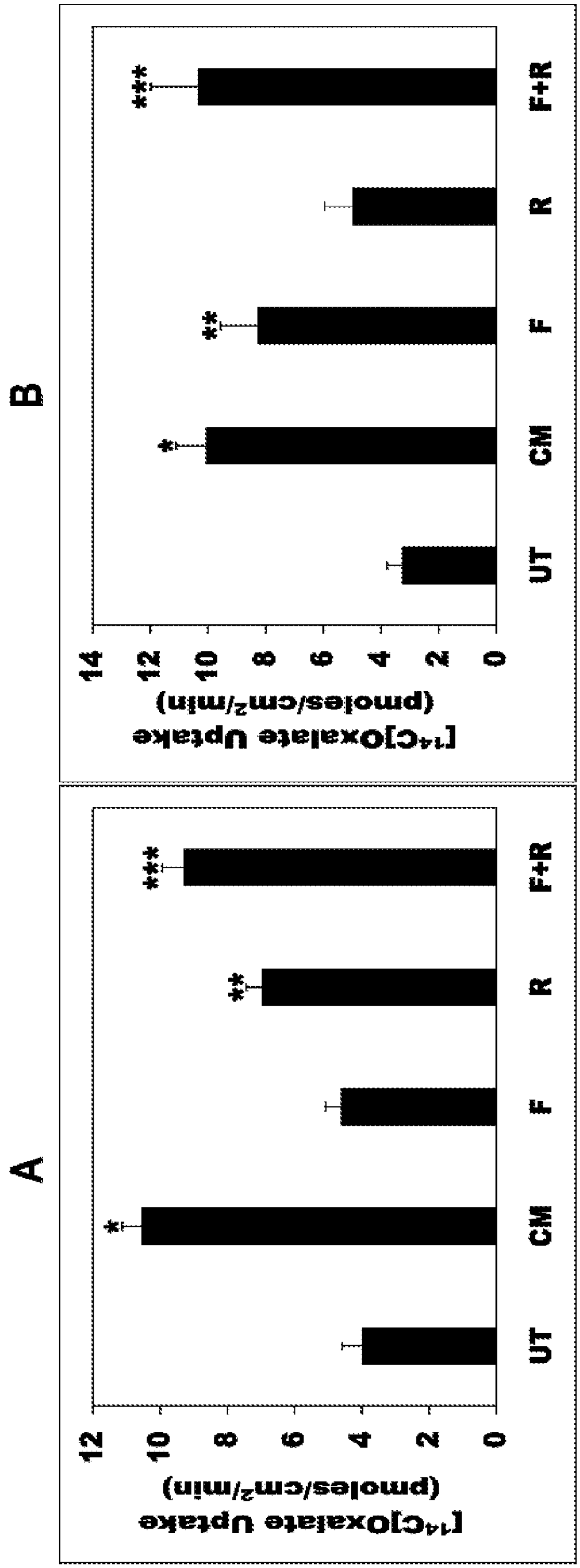

[14C]Oxalate Uptake (CPM)
4500
4000
3500
3000
2500
2000
1500
1000
500
0
*
*
#
*
#
UT Comb3
Untransfected
UT Comb3
A2 siRNA
UT Comb3
A6 siRNA

FIG. 6



OXALOBACTER FORMIGENES (OF)-DERIVED FACTORS FOR THE TREATMENT OF TREATMENT/PREVENTION OF EXCESS OXALATE LEVELS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present invention claims priority to U.S. Provisional Patent Application Ser. No. 62/448,178, filed Jan. 19, 2017, which is incorporated by reference in its entirety.

STATEMENT REGARDING FEDERAL FUNDING

[0002] This invention was made with government support under Grant No. DK067245 and Grant No. DK042086 awarded by the National Institute of Health. The government has certain rights in the invention.

FIELD

[0003] Provided herein are compositions comprising *Oxalobacter formigenes* (O)-derived factors and variants and fragments thereof, and method of use thereof for the treatment/prevention excess oxalate levels and conditions and diseases related thereto.

BACKGROUND

[0004] Nephrolithiasis, or the formation of mineral deposit blockages in the kidney (kidney stones (KS)), is the second most prevalent kidney disease in USA after hypertension, with a rising prevalence and complications including advanced chronic kidney disease (CKD) and end stage renal disease (ESRD). It remains a major source of patient discomfort and disability, lost working days, and health-care expenditure, with an annual economic cost approaching $10 billion. Hyperoxaluria (HO) is a major risk factor for KS, and 70-80% of KS are composed of calcium oxalate. Urinary oxalate is an important determinant of supersaturation, and the risk for stone formation is affected by small increases in urine oxalate. Oxalate is a metabolic end product that cannot be further metabolized and is highly toxic. The mammalian intestine plays a crucial role in oxalate homeostasis, by regulating the amount of absorbed dietary oxalate and providing an avenue for enteric oxalate excretion. Anion exchanger SLC26A6 (A6)-mediated intestinal oxalate secretion plays a critical role in preventing hyperoxaluria and calcium oxalate kidney stones (COKS). Inflammatory bowel disease patients have a significantly increased risk of KS due to the associated enteric hyperoxaluria. Obesity is a risk factor for KS and obese stone formers often have mild to moderate hyperoxaluria. Hyperoxaluria is also emerging as a major complication (developing in >50% of patients) of bariatric surgery for obesity. With the rising prevalence of obesity and increased utilization of bariatric surgery, it is expected that the incidence of hyperoxaluria and related COKS (including the associated cost burden) will continue to increase at a significant rate. Primary hyperoxaluria (PH) is an inherited disease in which there is endogenous oxalate overproduction, which leads to recurrent KS and/or progressive nephrocalcinosis, ESRD, as well as significant hyperoxalemia, systemic oxalosis and premature death. Systemic deposition of calcium oxalate (oxalosis) leads to bone disease, cardiac arrhythmias, cardiomyopathy, skin ulcers, erythropoietin refractory anemia, and digital gangrene. The only treatment known to fully correct the underlying metabolic defect is liver transplantation or combined kidney-liver transplantation once ESRD develops. In addition, significant hyperoxalemia is also seen in ESRD. Cardiovascular diseases are the leading cause of morbidity and mortality in ESRD patients, and a recent report suggest that the ESRD-associated hyperoxalemia may contribute to this increased risk.

[0005] Unfortunately, there is currently no specific therapy that effectively lowers urine and/or plasma oxalate level(s), and the risk of recurrent COKS, nephrocalcinosis, oxalate nephropathy, ESRD, and systemic oxalosis remains substantial in the absence of treatment. *Oxalobacter formigenes* (Of) is an anaerobic bacterium that utilizes oxalate as its exclusive energy source. Of colonization correlates with reduced risk of COKS formation in a number of studies, presumably by reducing intestinal oxalate absorption and urinary oxalate excretion. In addition to degrading intraluminal dietary oxalate, Of also interacts with colonic epithelium by inducing distal colonic oxalate secretion, leading to reduced urinary excretion via a potential unknown secretagogue. Of colonization of PH1 mice (a mouse model of primary hyperoxaluria type 1) significantly reduced serum and urinary oxalate levels due to induction of colonic oxalate secretion. However, all PH1 mice lost colonization within 18 days when switched from a high oxalate/low calcium diet (1.5% oxalate/0.5% calcium; needed to induce and maintain colonization) to regular mouse chow (0.25% oxalate/1% calcium). In addition, colonization cannot be maintained without reducing dietary calcium, which contradicts the current recommendations to increase dietary calcium for preventing recurrent KS. Moreover, it has been suggested from studies in PH patients & PH1 mice that the intraluminal environment in PH is not supportive of sustained Of colonization. Collectively, maintaining Of colonization in the absence of high exogenous oxalate remains problematic (and therefore making use of live Of as a potential therapeutic agent impractical). Treatments and/or therapies for reducing and/or maintaining healthy serum and urinary oxalate levels are needed.

SUMMARY

[0006] Provided herein are compositions comprising *Oxalobacter formigenes* (Of)-derived factors and variants and fragments thereof, and method of use thereof for the treatment/prevention of excess oxalate levels and conditions and diseases related thereto. In some embodiments, the Of-derived factors are derived from the OxB strain and/or OXCC13 strain.

[0007] In some embodiments, provided herein are methods comprising administering to the subject one or more *Oxalobacter formigenes* (Of)-derived factors, and/or bioactive variants and/or fragments thereof, that result in stimulation of oxalate transport. In some embodiments,

conditioned media (CM) (or factors derived therefrom) stimulates oxalate transport by human intestinal Caco2-BBE (C2) cells by activating protein kinase A (PKA) activation and increasing the transport activity of SLC26A6. In some embodiments, Of-derived factors are administered by administering Of CM to the subject. In some embodiments, the Of CM is fractionated, purified, and/or otherwise processed prior to administration. In some embodiments, one or more Of-derived factors are administered by administering peptides and/or polypeptides purified and/or isolated from Of and/or Of CM. In some embodiments, one or more Of-derived factors are administered by administering peptides and/or polypeptides, and/or bioactive variants and/or fragments thereof, produced recombinantly or synthetically. In some embodiments, one or more of the Of-derived factors are Sel1-like repeat (SLR) proteins. In some embodiments, one or more of the Of-derived factors are Sel1 proteins. In some embodiments, one or more of the Of-derived factors are bioactive variants and/or fragments of Of-derived peptidases. In some embodiments, one or more of the Of-derived factors are bioactive variants and/or fragments of SLR proteins (e.g., Sel1 proteins). In some embodiments, one or more of the Of-derived factors comprises 70% or more (e.g., 70%, 75%, 80%, 85%, 90%, 95%, or more, or ranges therebetween) sequence identity to all or a portion of an Of-derived SLR protein (e.g., Sel1 protein). In some embodiments, the SLR protein (e.g., Sel1 protein) or proteins are selected from the group consisting of Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, and MerG. In some embodiments, Of-derived factor is a bioactive peptide fragment of one of Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, and MerG, and/or a bioactive peptide having at least 70% (e.g., 70%, 75%, 80%, 85%, 90%, 95%, or more, or ranges therebetween) sequence identity to a fragment thereof. In some embodiments, the Of-derived factor comprises SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and/or, SEQ ID NO: 102. In some embodiments, the Of-derived factor comprises a bioactive variant having 70% or more (e.g., 70%, 75%, 80%, 85%, 90%, 95%, or more, or ranges therebetween) sequence identity to SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and/or, SEQ ID NO: 102. In some embodiments, the Of-derived factor comprises a bioactive peptide or polypeptide fragment having 70% or more (e.g., 70%, 75%, 80%, 85%, 90%, 95%, or more, or ranges therebetween) sequence identity to a portion of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and/or, SEQ ID NO: 102. In some embodiments, administration comprises rectal administration, oral administration, both rectal and oral, injection, or any other suitable route).

[0008] In some embodiments, methods are provided of treating or preventing hyperoxaluria and/or hyperoxalemia comprising performing the methods described herein. In some embodiments, treating or preventing hyperoxaluria and/or hyperoxalemia lowers a subject's risk of calcium oxalate kidney stones, nephrocalcinosis, oxalate nephropathy, end stage renal disease, and/or systemic oxalosis.

[0009] In some embodiments, provided herein are pharmaceutical compositions comprising one or more *Oxalobacter formigenes* (Of)-derived factors, and/or bioactive variants and/or fragments thereof. In some embodiments, the Of-derived factors are derived from the OxB strain and/or OXCC13 strain. In some embodiments, Of-derived factors (e.g., proteins/fragments/peptides) from other Of human strains (e.g. OXCC13, HOxBLS, HC-1, etc.) corresponding to those identified in the OxB strain are provided and/or find use in embodiments herein. In some embodiments, the pharmaceutical composition comprises Of conditioned media (CM). In some embodiments, the Of CM is fractionated, purified, and/or otherwise processed. In some embodiments, one or more Of-derived factors comprise peptides and/or polypeptides purified and/or isolated from Of and/or Of CM. In some embodiments, one or more Of-derived factors comprise recombinantly or synthetically produced peptides and/or polypeptides. In some embodiments, one or more of the Of-derived factors are selected from polypeptides comprising all or a portion of SEQ ID NOS; 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 101, or 102. In some embodiments, all or a portion of one or more of the Of-derived factors are encoded by all or a portion of a nucleotide of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 96, 100, 101, and 102. In some embodiments, one or more of the Of-derived factors are Sel1-like repeat (SLR) proteins. In some embodiments, one or more of the Of-derived factors are bioactive variants and/or fragments of SLR proteins (e.g., Sel1 protein). In some embodiments, one or more of the Of-derived factors comprises 70% or more (e.g., 70%, 75%, 80%, 85%, 90%, 95%, or more, or ranges therebetween) sequence identity to all or a portion of an Of-derived SLR protein (e.g., Sel1 protein). In some embodiments, the SLR protein (e.g., Sel1 protein) or proteins are selected from the group consisting of Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, and MerG. In some embodiments, the Of-derived factor is a peptide fragment of one of Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, and MerG, and/or a bioactive peptide having at least 70% or more (e.g., 70%, 75%, 80%, 85%, 90%, 95%, or more, or ranges therebetween) sequence identity to a fragment thereof. In some embodiments, the Of-derived factor comprises SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and/or, SEQ ID NO: 102. In some embodiments, the Of-derived factor comprises a bioactive variant having 70% or more (e.g., 70%, 75%, 80%, 85%, 90%, 95%, or more, or ranges therebetween) sequence identity to SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and/or, SEQ ID NO: 102. In some embodiments, the Of-derived factor comprises a bioactive peptide or polypeptide fragment having 70% or more (e.g., 70%, 75%, 80%, 85%, 90%, 95%, or more, or ranges therebetween) sequence identity to a portion of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID

NO: 24, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and/or, SEQ ID NO: 102. In some embodiments, the pharmaceutical composition is formulated for rectal administration, oral administration, and/or injection.

[0010] In some embodiments, provided herein are methods of treating or preventing hyperoxaluria and/or hyperoxalemia comprising administering a pharmaceutical described herein to a subject. In some embodiments, treating or preventing hyperoxaluria and/or hyperoxalemia lowers the subject's risk of the risk of calcium oxalate kidney stones, nephrocalcinosis, oxalate nephropathy, end stage renal disease, and/or systemic oxalosis.

BRIEF DESCRIPTION OF THE DRAWINGS

[0011] FIG. **1**. Sel1 Proteins 301, 310, 318, 320, and 321 significantly stimulate ^{14}C-oxalate influx into Caco2-BBE (C2) cells.

[0012] FIG. **2**. Non-Sel1 proteins 305, 308.9, 309, and 314 significantly stimulate ^{14}C-oxalate influx into Caco2-BBE (C2) cells.

[0013] FIG. **3**. Combination of 301+318+320 stimulate ^{14}C-oxalate influx into Caco2-BBE (C2) cells more than 301 alone.

[0014] FIG. **4**. Non-Sel1 proteins 311, 315, and 316 have no significant effect on ^{14}C-oxalate influx into Caco2-BBE cells.

[0015] FIG. **5**. siRNA knockdown of the oxalate transporters SLC26A6 (A6) and SLC26A2 (A2) greatly reduced the Sel1 (Comb3=301+318+320)-induced stimulation of ^{14}C-oxalate influx into C2 cells, indicating that Sel1 proteins stimulate oxalate transport by C2 cells through mechanisms including enhanced A6 and A2 transport activities.

[0016] FIG. **6**. Effect of selective ultrafiltration using 10 kDa (Panel A) and 30 kDa (Panel B) cutoff spin columns on the CM-induced stimulation of ^{14}C-oxalate uptake by Caco2-BBE (C2) cells. C2 cells were untreated (UT) or were treated with the conditioned medium (CM), the filtrate (F), the retentate (R), or the combined fractions (F+R). The results indicate that the molecular weights s of the factors are largely between 10-30 kDa. Since F+R have a better stimulatory effect than F, while R has no effect, such data suggest the possibility that these factors might exist as a multifunctional complex requiring a bacterial product of >30 kDa for optimal functioning. These results support testing different combinations of Sel1 and other identified proteins to obtain a level of oxalate transport stimulation similar to that observed with the CM.

DEFINITIONS

[0017] Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of embodiments described herein, some preferred methods, compositions, devices, and materials are described herein. However, before the present materials and methods are described, it is to be understood that this invention is not limited to the particular molecules, compositions, methodologies or protocols herein described, as these may vary in accordance with routine experimentation and optimization. It is also to be understood that the terminology used in the description is for the purpose of describing the particular versions or embodiments only, and is not intended to limit the scope of the embodiments described herein.

[0018] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. However, in case of conflict, the present specification, including definitions, will control. Accordingly, in the context of the embodiments described herein, the following definitions apply.

[0019] As used herein and in the appended claims, the singular forms "a", "an" and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to "an Of-derived factor" is a reference to one or more Of-derived factors and equivalents thereof known to those skilled in the art, and so forth.

[0020] As used herein, the term "comprise" and linguistic variations thereof denote the presence of recited feature(s), element(s), method step(s), etc. without the exclusion of the presence of additional feature(s), element(s), method step(s), etc. Conversely, the term "consisting of" and linguistic variations thereof, denotes the presence of recited feature(s), element(s), method step(s), etc. and excludes any unrecited feature(s), element(s), method step(s), etc., except for ordinarily-associated impurities. The phrase "consisting essentially of" denotes the recited feature(s), element(s), method step(s), etc. and any additional feature(s), element(s), method step(s), etc. that do not materially affect the basic nature of the composition, system, or method. Many embodiments herein are described using open "comprising" language. Such embodiments encompass multiple closed "consisting of" and/or "consisting essentially of" embodiments, which may alternatively be claimed or described using such language.

[0021] As used herein, the term "hyperoxaluria" refers to the excessive urinary excretion of oxalate by a subject (e.g., >25 mg/day).

[0022] As used herein, the term "hyperoxalemia" refers to excessive plasma levels of oxalate in a subject. Various studies report a normal range of oxalate in the plasma of 1 to 3 μmol per liter. Subjects with levels exceeding that range are considered to suffer from hyperoxalemia.

[0023] The term "amino acid" refers to natural amino acids, unnatural amino acids, and amino acid analogs, all in their D and L stereoisomers, unless otherwise indicated, if their structures allow such stereoisomeric forms.

[0024] Natural amino acids include alanine (Ala or A), arginine (Arg or R), asparagine (Asn or N), aspartic acid (Asp or D), cysteine (Cys or C), glutamine (Gln or Q), glutamic acid (Glu or E), glycine (Gly or G), histidine (His or H), isoleucine (Ile or I), leucine (Leu or L), Lysine (Lys or K), methionine (Met or M), phenylalanine (Phe or F), proline (Pro or P), serine (Ser or S), threonine (Thr or T), tryptophan (Trp or W), tyrosine (Tyr or Y) and valine (Val or V).

[0025] Unnatural amino acids include, but are not limited to, azetidinecarboxylic acid, 2-aminoadipic acid, 3-aminoadipic acid, beta-alanine, naphthylalanine ("naph"), aminopropionic acid, 2-aminobutyric acid, 4-aminobutyric acid, 6-aminocaproic acid, 2-aminoheptanoic acid, 2-aminoisobutyric acid, 3-aminoisbutyric acid, 2-aminopimelic acid, tertiary-butylglycine ("tBuG"), 2,4-diaminoisobutyric acid, desmosine, 2,2'-diaminopimelic acid, 2,3-diaminopropionic acid, N-ethylglycine, N-ethylasparagine, homoproline ("hPro" or "homoP"), hydroxylysine, allo-hydroxylysine, 3-hydroxyproline ("3Hyp"), 4-hydroxyproline ("4Hyp"), isodesmosine, allo-isoleucine, N-methylalanine ("MeAla" or "Nime"), N-alkylglycine ("NAG") including N-methylglycine, N-methylisoleucine, N-alkylpentylglycine ("NAPG") including N-methylpentylglycine. N-methylvaline, naphthylalanine, norvaline ("Norval"), norleucine ("Norleu"), octylglycine ("OctG"), ornithine ("Orn"), pentylglycine ("pG" or "PGly"), pipecolic acid, thioproline ("ThioP" or "tPro"), homoLysine ("hLys"), and homoArginine ("hArg").

[0026] The term "amino acid analog" refers to a natural or unnatural amino acid where one or more of the C-terminal carboxy group, the N-terminal amino group and side-chain functional group has been chemically blocked, reversibly or irreversibly, or otherwise modified to another functional group. For example, aspartic acid-(beta-methyl ester) is an amino acid analog of aspartic acid; N-ethylglycine is an amino acid analog of glycine; or alanine carboxamide is an amino acid analog of alanine. Other amino acid analogs include methionine sulfoxide, methionine sulfone, S-(carboxymethyl)-cysteine, S-(carboxymethyl)-cysteine sulfoxide and S-(carboxymethyl)-cysteine sulfone.

[0027] As used herein, the term "peptide" refers a short polymer of amino acids linked together by peptide bonds. In contrast to other amino acid polymers (e.g., proteins, polypeptides, etc.), peptides are of about 50 amino acids or less in length. A peptide may comprise natural amino acids, non-natural amino acids, amino acid analogs, and/or modified amino acids. A peptide may be a subsequence of naturally occurring protein or a non-natural (synthetic) sequence.

[0028] As used herein, the term "mutant peptide" or "variant peptide" refers to a peptide having a distinct amino acid sequence from the most common variant occurring in nature, referred to as the "wild-type" sequence. A mutant peptide may be a subsequence of a mutant protein or polypeptide (e.g., a subsequence of a naturally-occurring protein that is not the most common sequence in nature) or may be a peptide that is not a subsequence of a naturally occurring protein or polypeptide. For example, a "mutant SLR peptide" (e.g., a "mutant Sel1 protein") may be a subsequence of a mutant version of SLR protein (e.g., Sel1 protein) or may be distinct sequence not found in naturally-occurring SLR proteins (e.g., Sel1 proteins).

[0029] As used herein, the term "mutant polypeptide" or "variant polypeptide" refers to a polypeptide having a distinct amino acid sequence from the "wild-type" sequence. A mutant polypeptide may be a naturally-occurring protein that is not the most common sequence in nature (or a polypeptide fragment thereof) or may be a polypeptide that is not a subsequence of a naturally occurring protein or polypeptide. For example, a "mutant SLR polypeptide" may be a naturally occurring SLR protein (e.g., Sel1 protein), a polypeptide fragment of a SLR protein (e.g., Sel1 protein), or may be distinct sequence not found in naturally-occurring SLR proteins (e.g., Sel1 proteins).

[0030] As used herein, the term "artificial peptide" or "artificial polypeptide" refers to a peptide or polypeptide having a distinct amino acid sequence from those found in natural peptides and/or proteins. An artificial protein is not a subsequence of a naturally occurring protein, either the wild-type (i.e., most abundant) or mutant versions thereof. For example, an artificial SLR peptide or polypeptide is not a subsequence of naturally occurring SLR protein (e.g., Sel1 protein). An artificial peptide or polypeptide may be produced or synthesized by any suitable method (e.g., recombinant expression, chemical synthesis, enzymatic synthesis, etc.).

[0031] The terms "peptide mimetic" or "peptidomimetic" refer to a peptide-like molecule that emulates a sequence derived from a protein or peptide. A peptide mimetic or peptidomimetic may contain amino acids and/or non-amino acid components. Examples of peptidomimitecs include chemically modified peptides, peptoids (side chains are appended to the nitrogen atom of the peptide backbone, rather than to the α-carbons), β-peptides (amino group bonded to the R carbon rather than the α carbon), etc.

[0032] As used herein, a "conservative" amino acid substitution refers to the substitution of an amino acid in a peptide or polypeptide with another amino acid having similar chemical properties, such as size or charge. For purposes of the present disclosure, each of the following eight groups contains amino acids that are conservative substitutions for one another:

1) Alanine (A) and Glycine (G);

[0033] 2) Aspartic acid (D) and Glutamic acid (E);

3) Asparagine (N) and Glutamine (Q);

4) Arginine (R) and Lysine (K);

5) Isoleucine (I), Leucine (L), Methionine (M), and Valine (V);

6) Phenylalanine (F), Tyrosine (Y), and Tryptophan (W);

7) Serine (S) and Threonine (T); and

8) Cysteine (C) and Methionine (M).

[0034] Naturally occurring residues may be divided into classes based on common side chain properties, for example: polar positive (histidine (H), lysine (K), and arginine (R)); polar negative (aspartic acid (D), glutamic acid (E)); polar neutral (serine (S), threonine (T), asparagine (N), glutamine (Q)); non-polar aliphatic (alanine (A), valine (V), leucine (L), isoleucine (I), methionine (M)); non-polar aromatic (phenylalanine (F), tyrosine (Y), tryptophan (W)); proline and glycine; and cysteine. As used herein, a "semi-conservative" amino acid substitution refers to the substitution of an amino acid in a peptide or polypeptide with another amino acid within the same class.

[0035] In some embodiments, unless otherwise specified, a conservative or semi-conservative amino acid substitution may also encompass non-naturally occurring amino acid residues that have similar chemical properties to the natural residue. These non-natural residues are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems. These include, but are not limited to, peptidomimetics and other reversed or inverted forms of amino acid moieties. Embodiments herein may, in some embodiments, be limited to natural amino acids, non-natural amino acids, and/or amino acid analogs. Non-conservative substitutions may involve the exchange of a member of one class for a member from another class.

[0036] As used herein, the term "sequence identity" refers to the degree to which two polymer sequences (e.g., peptide, polypeptide, nucleic acid, etc.) have the same sequential composition of monomer subunits. The term "sequence similarity" refers to the degree with which two polymer sequences (e.g., peptide, polypeptide, nucleic acid, etc.) differ only by conservative and/or semi-conservative amino acid substitutions. The "percent sequence identity" (or "percent sequence similarity") is calculated by: (1) comparing two optimally aligned sequences over a window of comparison (e.g., the length of the longer sequence, the length of the shorter sequence, a specified window, etc.), (2) determining the number of positions containing identical (or similar) monomers (e.g., same amino acids occurs in both sequences, similar amino acid occurs in both sequences) to yield the number of matched positions, (3) dividing the number of matched positions by the total number of positions in the comparison window (e.g., the length of the longer sequence, the length of the shorter sequence, a specified window), and (4) multiplying the result by 100 to yield the percent sequence identity or percent sequence similarity. For example, if peptides A and B are both 20 amino acids in length and have identical amino acids at all but 1 position, then peptide A and peptide B have 95% sequence identity. If the amino acids at the non-identical position shared the same biophysical characteristics (e.g., both were acidic), then peptide A and peptide B would have 100% sequence similarity. As another example, if peptide C is 20 amino acids in length and peptide D is 15 amino acids in length, and 14 out of 15 amino acids in peptide D are identical to those of a portion of peptide C, then peptides C and D have 70% sequence identity, but peptide D has 93.3% sequence identity to an optimal comparison window of peptide C. For the purpose of calculating "percent sequence identity" (or "percent sequence similarity") herein, any gaps in aligned sequences are treated as mismatches at that position.

[0037] As used herein, the term "subject" broadly refers to any animal, including but not limited to, human and non-human animals (e.g., dogs, cats, cows, horses, sheep, poultry, fish, crustaceans, etc.). As used herein, the term "patient" typically refers to a human subject that is being treated for a disease or condition.

[0038] As used herein, the term "effective amount" refers to the amount of a sufficient to effect beneficial or desired results. An effective amount can be administered in one or more administrations, applications or dosages and is not intended to be limited to a particular formulation or administration route.

[0039] As used herein, the terms "administration" and "administering" refer to the act of giving a drug, prodrug, or other agent, or therapeutic treatment to a subject or in vivo, in vitro, or ex vivo cells, tissues, and organs. Exemplary routes of administration to the human body can be through space under the arachnoid membrane of the brain or spinal cord (intrathecal), the eyes (ophthalmic), mouth (oral), skin (topical or transdermal), nose (nasal), lungs (inhalant), oral mucosa (buccal), ear, rectal, vaginal, by injection (e.g., intravenously, subcutaneously, intratumorally, intraperitoneally, etc.) and the like.

[0040] As used herein, the terms "co-administration" and "co-administering" refer to the administration of at least two agent(s) or therapies to a subject. In some embodiments, the co-administration of two or more agents or therapies is concurrent. In other embodiments, a first agent/therapy is administered prior to a second agent/therapy. Those of skill in the art understand that the formulations and/or routes of administration of the various agents or therapies used may vary. The appropriate dosage for co-administration can be readily determined by one skilled in the art. In some embodiments, when agents or therapies are co-administered, the respective agents or therapies are administered at lower dosages than appropriate for their administration alone. Thus, co-administration is especially desirable in embodiments where the co-administration of the agents or therapies lowers the requisite dosage of a potentially harmful (e.g., toxic) agent(s), and/or when co-administration of two or more agents results in sensitization of a subject to beneficial effects of one of the agents via co-administration of the other agent.

[0041] As used herein, the term "treatment" means an approach to obtaining a beneficial or intended clinical result. The beneficial or intended clinical result may include alleviation of symptoms, a reduction in the severity of the disease, inhibiting a underlying cause of a disease or condition, steadying diseases in a non-advanced state, delaying the progress of a disease, and/or improvement or alleviation of disease conditions.

[0042] As used herein, the term "pharmaceutical composition" refers to the combination of an active agent (e.g., Of-derived factor) with a carrier, inert or active, making the composition especially suitable for diagnostic or therapeutic use in vitro, in vivo or ex vivo. The terms "pharmaceutically acceptable" or "pharmacologically acceptable," as used herein, refer to compositions that do not substantially produce adverse reactions, e.g., toxic, allergic, or immunological reactions, when administered to a subject.

[0043] As used herein, the term "pharmaceutically acceptable carrier" refers to any of the standard pharmaceutical carriers including, but not limited to, phosphate buffered saline solution, water, emulsions (e.g., such as an oil/water or water/oil emulsions), and various types of wetting agents, any and all solvents, dispersion media, coatings, sodium lauryl sulfate, isotonic and absorption delaying agents, disintigrants (e.g., potato starch or sodium starch glycolate), and the like. The compositions also can include stabilizers and preservatives. For examples of carriers, stabilizers and adjuvants, see, e.g., Martin, Remington's Pharmaceutical Sciences, 15th Ed., Mack Publ. Co., Easton, Pa. (1975), incorporated herein by reference in its entirety.

DETAILED DESCRIPTION

[0044] Provided herein are compositions comprising *Oxalobacter formigenes* (Of)-derived factors and variants and fragments thereof, and methods of use thereof for the treatment/prevention excess oxalate levels and conditions and diseases related thereto.

[0045] Most kidney stones (KS) are composed of calcium oxalate, and small increases in urine oxalate affect the stone risk. The mammalian intestine plays a crucial role in oxalate homeostasis. Intestinal oxalate secretion mediated by anion exchanger SLC26A6 (A6) plays a major role in limiting net intestinal absorption of ingested oxalate; thereby preventing hyperoxaluria and calcium oxalate kidney stones (COKS). Hyperoxaluria and a high incidence of KS are commonly seen in IBD patients. Hyperoxaluria is also emerging as a major complication of bariatric surgery for obesity. Primary hyperoxaluria (PH) is an inherited disease in which there is endogenous oxalate overproduction. Enhancing intestinal oxalate secretion is expected to lead to reduced urine and plasma oxalate levels. In addition to degrading intraluminal dietary oxalate, the probiotic bacterium *oxalobacter formigenes* (Of) also interacts with colonic epithelium by inducing colonic oxalate secretion, leading to reduced urinary excretion. Significant difficulties exist in sustaining Of colonization in animals and humans in the absence of high exogenous oxalate.

[0046] Experiments were conducted during development of embodiments herein to determine whether Of CM affects intestinal oxalate transport using the human intestinal Caco2-BBE (C2) cells. DIDS (anion exchange inhibitor)-sensitive apical oxalate influx was measured in the presence of an outward Cl gradient as an assay of Cl-oxalate exchange, ≥50% of which is mediated by A6. Compared with control medium, Of CM significantly stimulated oxalate uptake (>2.4-fold), whereas CM from *Lactobacillus acidophilus* (La) did not. Treating the CM with heat or pepsin completely abolished this bioactivity, and selective ultrafiltration of the CM revealed that the Of-derived factors have molecular masses of 10-30 kDa. Treatment with the PKA inhibitor H89 or DIDS completely blocked the CM-induced oxalate transport. A6 Knockdown also significantly restricted the induction of oxalate transport by CM. In a mouse model of primary hyperoxaluria type 1, rectal administration of Of CM significantly reduced (>32.5%) urinary oxalate excretion and stimulated (>42%) distal colonic oxalate secretion, reflecting the in vivo retention of biologic activity and the therapeutic potential of these factors.

[0047] Experiments conducted during development of embodiments herein to identify the Of-derived bioactive factor(s) inducing colonic oxalate secretion determined that small molecular weight protein(s) and/or peptide(s) secreted by Of in its culture conditioned medium (CM) significantly stimulate(s) oxalate transport (>2.4-fold) by human intestinal Caco2-BBE cells through mechanisms including PKA activation and increased A6 transport activity. Rectal administration of Of CM significantly reduced (>32.5%) urinary oxalate excretion and stimulated (>42%) distal colonic oxalate secretion in PH1 mice. Probiotic bacteria have several health benefits; however, the difficulties in determining intestinal bacterial bioavailability and biosafety concerns when administering live probiotics are problems facing current probiotic clinical applications. These issues are compounded by the difficulties described above in maintaining Of colonization in the absence of high exogenous dietary oxalate.

[0048] Experiments conducted during development of embodiments herein demonstrate that Of-derived factors retain their biological activity when administered in vivo and effectively reduce urinary oxalate excretion in hyperoxaluric mice, thereby demonstrating the utility of the Of-derived factors as therapeutic agents for prevention and/or treatment of hyperoxaluria, hyperoxalemia, COKS, and related diseases/conditions.

[0049] Experiments conducted during development of embodiments herein have identified Sel1 repeat proteins as among the Of-derived factors responsible for stimulation of oxalate transport by C2 cells. Sel1 repeat proteins are involved in signal transduction pathways, and this is very important since we found that Of CM signals through PKA to stimulate oxalate transport by C2 cells. 12 Sel1 repeat proteins were purified and the effects of different concentrations and different incubation periods of the purified proteins on oxalate transport by C2 cells were assessed. Sel1 proteins 301, 310, 318, 320, and 321 significantly stimulate (~1.5-2.2-fold) oxalate transport by C2 cells (FIG. **1**). The combination of 301+318+320 have a better stimulatory effect (2.5-fold) compared to 301 (FIG. **3**). 301+318 also stimulated oxalate transport by ~2.5-fold. Sel1 proteins 304, 317, 319, 322, 323, 324, and 325 also stimulated oxalate transport by C2 cells by ~1.3-1.6-fold. Since all of the 12 tested Sel1 proteins significantly stimulated oxalate transport by C2 cells, it is very likely that the remaining 32 Sel1 proteins (individually or in combination) will also stimulate oxalate and this will be tested. siRNA knockdown of the oxalate transporters SLC26A2 and SLC26A6 greatly reduced Sel1 (Comb3=301+318+320)-induced stimulation of oxalate transport (FIG. **5**) as observed with the CM. In addition, 301-induced stimulation of oxalate transport is completely blocked by the PKA inhibitor H89, indicating that Sel1 proteins act through the PKA signaling pathway to stimulate oxalate transport, which is similar to the CM. Collectively, Sel1 proteins almost fully mimic the effects of the CM. Importantly, 3 non Sel1 proteins (311, 315, and 316) have no significant effects on oxalate transport by C2 cells (FIG. **4**), strongly indicating that the Sel1-induced stimulation of oxalate transport by C2 cells is specific. In addition to Sel1 proteins, 4 other non Sel1 proteins (305, 308.9, 309, and 314) also stimulated oxalate transport (FIG. **2**). In some embodiments, compositions are provided herein that comprise one or more Sel1 proteins or Sel1-derived variants or fragments (e.g., Sel1-derived peptides or polypeptides that stimulate oxalate transport). In some embodiments, methods are provided of treating/preventing excess oxalate levels in the urine and/or plasma by the administration of Sel1 proteins or Sel1-derived variants or fragments (e.g., Sel1-derived peptides or polypeptides that stimulate oxalate transport) to a subject. In some embodiments, compositions are provided herein that comprise one or more Sel1 proteins or Sel1-derived variants or fragments (e.g., Sel1-derived peptides or polypeptides that stimulate oxalate transport). In some embodiments, methods are provided of treating/preventing excess oxalate levels in the urine and/or plasma by the administration of Sel1 proteins or Sel1-derived variants or fragments (e.g., Sel1-derived peptides or polypeptides that stimulate oxalate transport) to a subject.

[0050] Sel1-like repeat (SLR) proteins (e.g. Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, and MerG) are involved in signal transduction pathways. In some embodiments, Of conditioned medium (CM) signals (e.g., through PKA) to stimulate oxalate transport (e.g., by C2 cells) as a result of the signal transduction functions of the SLR proteins (e.g., Sel1 proteins); although embodiments herein are not limited to any particular mechanism of action and an understanding of the mechanism of action is not necessary to practice such embodiments. SLR proteins (e.g., Sel1 proteins) have repeat units (e.g., repeat peptides). Most repeats are 5 to 40 amino acids (e.g., 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, or ranges therebetween), but longer repeat peptides (e.g., 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, or longer or ranges therebetween) are within the scope of the SLR proteins (e.g., Sel1 proteins) herein. In some embodiments, repeat units fold into two to four secondary structural elements. In some embodiments, SLR proteins (e.g., Sel1 proteins) serve as adaptor proteins for the assembly of membrane-bound macromolecular complexes. Several bacterial and eukaryotic SLR proteins (e.g. Sel1 & Hrd3) are activated upon cellular stress. In some embodiments, Of Sel1 proteins are activated when oxalate is low in the culture medium (e.g., as evidenced by the observation of a CM of higher (>2-fold) bioactivity under this condition). Bacterial LpnE, EnhC, HcpA, ExoR, and AlgK proteins mediate the interactions between bacterial and eukaryotic host cells. In some embodiments, the SLR motif establishes a link between signal transduction pathways from eukaryotes and bacteria. In some embodiments, an SLR protein (e.g., Sel1 proteins) comprises leader sequences. In some embodiments, SLR proteins (e.g., Sel1 proteins) without leader sequences, such as PodJ or leaderless analogs of natural SLR proteins (e.g., Sel1 proteins), are active in the periplasmic space. In some embodiments, bacterial SLR proteins (e.g., Sel1 proteins), such as HcpA, ExoR, EnhC and LpnE are responsible for the adaptation of bacteria to different eukaryotic hosts.

[0051] The Of genome has 44 Sel1 proteins and one SelR domain, with many of these proteins having molecular masses between 10-30 kDa (e.g., where most of the CM stimulatory activity lies) (Table 1). In addition, several other Sel1 proteins with molecular masses between 32-139 kDa were also identified (Table 1). Many of the Sel1 proteins are predicted to have signal peptides and therefore are secreted proteins. Moreover, Sel1 proteins with molecular masses of 25 (#1361), 33 (#1414), and 68 (#1362) kDa blast in common with another Sel1 protein having a molecular mass of 59 (#1344) kDa. Five Sel1 proteins (# s 1360-1364) resides in an operon, with carbon starvation protein CstA located immediately upstream of this operon. Sel1 proteins #1343, 1344, and 1356 are also located near this operon. In some embodiments, although most of the CM stimulatory activity is mediated by factors with molecular masses between 10-30 kDa, the results of selective ultrafiltration using 30 kDa cutoff column (FIG. **6**B) indicates that the factors exist as a multifunctional complex requiring a bacterial product of >30 kDa for optimal functioning. The latter result indicates that different combinations of Sel1 and other identified proteins will provide a level of oxalate transport stimulation similar to (or greater than) that observed with the CM.

TABLE 1

Of-derived proteins				
Name	Protien	Description	DNA seq	Protein seq
301	194	Sel1 repeat :: PF08238	SEQ ID NO: 1	SEQ ID NO: 2
317	1343	Sel1 repeat :: PF08238	SEQ ID NO: 15	SEQ ID NO: 16
310	1344	Sel1 repeat :: PF08238	SEQ ID NO: 21	SEQ ID NO: 22
318	1356	Sel1 repeat :: PF08238	SEQ ID NO: 9	SEQ ID NO: 10
319	1360	Sel1 repeat :: PF08238	SEQ ID NO: 11	SEQ ID NO: 12
320	1361	Sel1 repeat :: PF08238	SEQ ID NO: 3	SEQ ID NO: 4
321	1362	Sel1 repeat :: PF08238	SEQ ID NO: 5	SEQ ID NO: 6
304	1363	Sel1 repeat :: PF08238	SEQ ID NO: 7	SEQ ID NO: 8
322	1364	Sel1 repeat :: PF08238	SEQ ID NO: 23	SEQ ID NO: 24
323	1414	Sel1 repeat :: PF08238	SEQ ID NO: 13	SEQ ID NO: 14
324	1548	Sel1 repeat :: PF08238	SEQ ID NO: 17	SEQ ID NO: 18
325	1549	Sel1 repeat :: PF08238	SEQ ID NO: 19	SEQ ID NO: 20
	193	Sel1 repeat :: PF08238	SEQ ID NO: 25	SEQ ID NO: 26
	235	Sel1 repeat :: PF08238	SEQ ID NO: 100	
	238	Sel1 repeat :: PF08238	SEQ ID NO: 27	SEQ ID NO: 28
	240	Sel1 repeat :: PF08238	SEQ ID NO: 29	SEQ ID NO: 30
	275	Sel1 repeat :: PF08238	SEQ ID NO: 31	SEQ ID NO: 32
	841	Sel1 repeat :: PF08238	SEQ ID NO: 33	SEQ ID NO: 34
	1112	Sel1 repeat :: PF08238	SEQ ID NO: 35	SEQ ID NO: 36
	1124	Sel1 repeat :: PF08238	SEQ ID NO: 37	SEQ ID NO: 38
	1143	Sel1 repeat :: PF08238	SEQ ID NO: 39	SEQ ID NO: 40
	1250	Sel1 repeat :: PF08238	SEQ ID NO: 41	SEQ ID NO: 42
	1257	SelR domain :: PF01641	SEQ ID NO: 43	SEQ ID NO: 44
	1412	Sel1 repeat :: PF08238	SEQ ID NO: 45	SEQ ID NO: 46
	1419	Sel1 repeat :: PF08238	SEQ ID NO: 47	SEQ ID NO: 48
	1423	Sel1 repeat :: PF08238	SEQ ID NO: 49	SEQ ID NO: 50
	1551	Sel1 repeat :: PF08238	SEQ ID NO: 51	SEQ ID NO: 52
	1715	Sel1 repeat :: PF08238	SEQ ID NO: 53	SEQ ID NO: 54
	1790	Sel1 repeat :: PF08238	SEQ ID NO: 55	SEQ ID NO: 56
	1942	Sel1 repeat :: PF08238	SEQ ID NO: 57	SEQ ID NO: 58
	1945	Sel1 repeat :: PF08238	SEQ ID NO: 59	SEQ ID NO: 60
	1954	Sel1 repeat :: PF08238	SEQ ID NO: 61	SEQ ID NO: 62
	1955	Sel1 repeat :: PF08238	SEQ ID NO: 63	SEQ ID NO: 64
	1960	Sel1 repeat :: PF08238	SEQ ID NO: 65	SEQ ID NO: 66
	1969	Sel1 repeat :: PF08238	SEQ ID NO: 67	SEQ ID NO: 68
	1970	Sel1 repeat :: PF08238	SEQ ID NO: 69	SEQ ID NO: 70
	2000	Sel1 repeat :: PF08238	SEQ ID NO: 71	SEQ ID NO: 72
	2001	Sel1 repeat :: PF08238	SEQ ID NO: 73	SEQ ID NO: 74
	2022	Sel1 repeat :: PF08238	SEQ ID NO: 75	SEQ ID NO: 76
	2025	Sel1 repeat :: PF08238	SEQ ID NO: 77	SEQ ID NO: 78
	2123	Sel1 repeat :: PF08238	SEQ ID NO: 79	SEQ ID NO: 80
	2176	Sel1 repeat :: PF08238	SEQ ID NO: 81	SEQ ID NO: 82
	2239	Sel1 repeat :: PF08238	SEQ ID NO: 83	SEQ ID NO: 84
	2249	Sel1 repeat :: PF08238	SEQ ID NO: 85	SEQ ID NO: 86
	2270	Sel1 repeat :: PF08238	SEQ ID NO: 87	SEQ ID NO: 88

TABLE 1-continued

Of-derived proteins				
Name	Protien	Description	DNA seq	Protein seq
314	8	LD-carboxypeptidase :: PF02016	SEQ ID NO: 89	SEQ ID NO: 90
309	1525	Peptidase family S49 :: PF01343	SEQ ID NO: 91	SEQ ID NO: 92
305	1524	haloacid dehalogenase-like hydrolase :: PF00702	SEQ ID NO: 98	SEQ ID NO: 101
315	272	Outer membrane efflux protein :: PF02321	SEQ ID NO: 93	SEQ ID NO: 94
316	1285	Outer membrane efflux protein :: PF02321	SEQ ID NO: 95	SEQ ID NO: 96
308	769	EAL domain :: PF00563	SEQ ID NO: 99	SEQ ID NO: 102
311	1847	MotA/TolQ/ExbB proton channel family :: PF01618		

[0052] To evaluate whether one or more of these SLR proteins (e.g., Sel1 proteins) are responsible for mediating the CM-induced stimulation of oxalate transport, a subset of Sel1 proteins were cloned and overexpressed in *E. coli* and the recombinant purified proteins were prepared. 12 Sel1 proteins and 7 additional Of-derived factors were purified (Table 2) and the effects of different concentrations and incubation periods of the purified proteins on oxalate transport by C2 cells were evaluated. Experiments conducted during development of embodiments herein demonstrate that Sel1 proteins (# s 194, 1356, 1361, and 1362), significantly stimulate (up to 2.5-fold) oxalate transport by C2 cells. In addition to the Sel1 proteins, LD-carboxypeptidase (#8), a peptidase (#1525), haloacid dehalogenase-like hydrolase (1524=305), and guanylate cyclase (769=308) also stimulated (~1.4-1.6-fold) oxalate transport by C2 in preliminary studies (FIG. **2**). On the other hand, outer membrane efflux proteins (# s 272 and 1285) and MotA/TolQ/ExbB proton channel family (1847=311) failed to stimulate oxalate transport by C2 cells.

TABLE 2

Purified Of-derived proteins			
Protein name	Protein	DNA seq	Protein seq
301	194|Sel1 repeat :: PF08238	SEQ ID NO: 1	SEQ ID NO: 2
320	1361|Sel1 repeat :: PF08238	SEQ ID NO: 3	SEQ ID NO: 4
321	1362|Sel1 repeat :: PF08238	SEQ ID NO: 5	SEQ ID NO: 6
304	1363|Sel1 repeat :: PF08238	SEQ ID NO: 7	SEQ ID NO: 8
318	1356|Sel1 repeat :: PF08238	SEQ ID NO: 9	SEQ ID NO: 10
319	1360|Sel1 repeat :: PF08238	SEQ ID NO: 11	SEQ ID NO: 12
323	1414|Sel1 repeat :: PF08238	SEQ ID NO: 13	SEQ ID NO: 14
317	1343|Sel1 repeat :: PF08238	SEQ ID NO: 15	SEQ ID NO: 16
324	1548|Sel1 repeat :: PF08238	SEQ ID NO: 17	SEQ ID NO: 18
325	1549|Sel1 repeat :: PF08238	SEQ ID NO: 19	SEQ ID NO: 20
310	1344|Sel1 repeat :: PF08238	SEQ ID NO: 21	SEQ ID NO: 22
309	1525|Peptidase family S49 :: PF01343	SEQ ID NO: 91	SEQ ID NO: 92
315	272|Outer membrane efflux protein :: PF02321	SEQ ID NO: 93	SEQ ID NO: 94
316	1285|Outer membrane efflux protein :: PF02321	SEQ ID NO: 95	SEQ ID NO: 96
314	8|LD-carboxypeptidase :: PF02016	SEQ ID NO: 89	SEQ ID NO: 90
322	1364|Sel1 repeat :: PF08238	SEQ ID NO: 23	SEQ ID NO: 24
305	1524|haloacid dehalogenase-like hydrolase :: PF00702	SEQ ID NO: 98	SEQ ID NO: 101
308	769|EAL domain :: PF00563	SEQ ID NO: 99	SEQ ID NO: 102
311	1847|MotA/TolQ/ExbB proton channel family :: PF01618		

[0053] Experiments conducted during development of embodiments herein demonstrate the capacity for Of conditioned media, Of-derived factors, SLR proteins (e.g., Sel1 proteins), SLR peptides (e.g., Sel1 peptides), SLR variant polypeptides (e.g., Sel1 variant polypeptides), etc. to reduce oxalate concentrations and thereby treat and/or prevent conditions related to excess oxalate in the blood, urine, etc.

[0054] In some embodiments, Of-derived factors that find use in embodiments herein are derived from any suitable species or strain of *Oxalobacter formigenes*, such as, for example, HC-1, Va3, OxK, OxB, OXCC13, BA1, HOxBLS, HOxRW, POxC, etc. In some embodiments, variants, fragments, and/or peptidomimetics of bioactive factors derived from suitable Of strains are provided.

[0055] In some embodiments, media conditioned by the growth of *Oxalobacter formigenes* (CM) is provided. In some embodiments, Of CM is provided in a pharmaceutical composition for the treatment/prevention of conditions related to excess oxalate. In some embodiments, Of CM is processed (e.g., fractionated, purified, concentrated, diluted, filtered, etc.) prior to administration to a subject. In some embodiments, Of CM is formulated for administration by any suitable techniques described herein or known in the field.

[0056] In some embodiments, bioactive Of-derived factors are provided for the treatment/prevention of conditions related to excess oxalate. In some embodiments, such factors are obtained, isolated, and/or purified from Of CM. In some embodiments, such factors are obtained, isolated, and/or purified from Of cultures. In some embodiments, are prepare recombinantly and/or synthetically. In some embodiments, bioactive Of-derived factors are SLR proteins (e.g., Sel1 proteins), such as Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, MerG, and variants, fragment, and peptidomimetics thereof.

[0057] Provided herein are compositions (e.g., Of conditioned media, Of-derived factors, SLR proteins (e.g., Sel1 proteins), SLR peptides (e.g., Sel1 peptides), SLR variant polypeptides (e.g., Sel1 variant polypeptides), etc.) which stimulate the clearance of oxalate (e.g., activate oxalate transport) from a biological environment (e.g., blood, urine, etc.). In some embodiments, compositions significantly reduce oxalate concentrations (e.g., urine oxalate, blood oxalate, etc.) for example, by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or ranges therebetween. In some embodiments, compositions herein stimulate oxalate transport, thereby reducing in vivo oxalate levels in the blood (e.g., plasma oxalate levels), urine, etc., through mechanisms such as, for example, PKA activation and increased activity of SLC26 family members (e.g., SLC26A6) or other transporter(s); although embodiments herein are not limited to any particular mechanism of action and an understanding of the mechanism of action is not necessary to practice such embodiments.

[0058] In some embodiments, provided herein are compositions, kits, systems, and/or methods to treat, prevent, reduce the likelihood, treat/prevent a side effect of one or more of: hyperoxalemia, hyperoxaluria, nephrolithiasis, chronic kidney disease, end stage renal disease, calcium oxalate kidney stones, nephrocalcinosis, oxalate nephropathy, primary hyperoxaluria (PH), enteric hyperoxaluria (seen for example in IBD, following small bowel surgery or bariatric surgery, obesity, and celiac disease) and systemic oxalosis. In some embodiments, the reduction in oxalate levels and/or activation of oxalate transport is activated by compositions and methods described herein. In some embodiments, oxalate transport pathways are activated by the compositions and methods described herein. In some embodiments, compositions and methods are utilized in the treatment and/or prevention of hyperoxalemia, hyperoxaluria, and/or related diseases and conditions. In some embodiments, compositions and methods are utilized in screening for peptides and polypeptides useful in the treatment and/or prevention of hyperoxalemia, hyperoxaluria, and/or related diseases and conditions.

[0059] In some embodiments, provided herein are pharmaceutical compositions, Of CM, Of-derived factors, SLR peptides (e.g., Sel1 peptides), SLR proteins (e.g., Sel1 proteins), SLR polypeptides (e.g., Sel1 polypeptides), nucleic acids encoding peptides, proteins and polypeptides, molecular complexes of the foregoing, etc. for the treatment or prevention of hyperoxalemia, hyperoxaluria, and/or related diseases and conditions. In some embodiments, provided herein are SLR-peptides and SLR-polypeptides (e.g., comprising less than 100% sequence identity with full length native SLR proteins (e.g., SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 90, SEQ ID NO: 92, Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, MerG), or a fragment of full length SLR protein or variant thereof. In some embodiments, a peptide/polypeptide is artificial. In some embodiments, a polypeptide or peptide described herein is prepared by methods known to those of ordinary skill in the art. For example, the peptide or polypeptide can be synthesized using solid phase polypeptide synthesis techniques (e.g. Fmoc or Boc chemistry). Alternatively, the peptide or polypeptide can be produced using recombinant DNA technology (e.g., using bacterial or eukaryotic expression systems). Further, a peptide or polypeptide may be expressed within a subject (e.g., following administration of an appropriate vector). Accordingly, to facilitate such methods, provided herein are genetic vectors (e.g., plasmids, viral vectors (e.g. AAV), etc.) comprising a sequence encoding the polypeptide, as well as host cells comprising such vectors. Furthermore, provided herein are the peptides and polypeptides produced via such methods.

[0060] In some embodiments, the administration of Of-derived factors (e.g., peptides and polypeptides) and compositions related thereto (e.g. variants and mimetics of Of-derived factors, nucleic acids encoding Of-derived factors, etc.) is provided. In some embodiments, provided herein is the administration of bioactive agents which reduce oxalate levels in vivo, or are otherwise described herein. Examples of such peptides and polypeptides include those selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 90, 92, 94, 96, 101, and 102. Other examples include SLR proteins (e.g., Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, MerG) derived from various Of strains, and variants and fragments thereof.

[0061] In some embodiments, a peptide or polypeptide is provided comprising or consisting of all or a portion of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and SEQ ID NO: 102. In some embodiments, a peptide or polypeptide is provided comprising at least 50% sequence identity to one of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and SEQ ID NO: 102 (e.g. at least 60% sequence identity, at least 70% sequence identity, at least 80% sequence identity, at least 90% sequence identity, at least 95% sequence identity, etc.). In some embodiments, peptide and polypeptides comprise at least one mutation from a wild-type sequence (e.g., SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID

NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and SEQ ID NO: 102).

[0062] In some embodiments, a peptide/polypeptide is provided that is a fragment of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and SEQ ID NO: 102. In some embodiments, a peptide/polypeptide is provided that comprises one or more substitutions (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more) compared to a fragment of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and SEQ ID NO: 102.

[0063] In some embodiments, a peptide or polypeptide is provided comprising or consisting of all or a portion of an Of-derived SLR protein (e.g., Sel1 protein) that facilitates reduction of in vivo oxalate levels, such as an SLR protein (e.g., Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, MerG) derived from an Of strains, and variants and fragments thereof. In some embodiments, a peptide or polypeptide is provided comprising at least 50% sequence identity to an SLR protein (e.g., Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, MerG) derived from an Of strains (e.g. at least 60% sequence identity, at least 70% sequence identity, at least 80% sequence identity, at least 90% sequence identity, at least 95% sequence identity, etc.). In some embodiments, peptide and polypeptides comprise at least one mutation from a wild-type sequence (e.g., Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, MerG).

[0064] In some embodiments, a peptide/polypeptide is provided that is a fragment of an SLR protein (e.g., Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, MerG) derived from an Of strain. In some embodiments, a peptide/polypeptide is provided that comprises one or more substitutions (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more) compared to a fragment of an SLR protein (e.g., Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, MerG) derived from an Of strain.

[0065] Embodiments are not limited to the specific sequences listed herein. In some embodiments, peptides/polypeptides meeting limitations described herein (e.g., Of-derived, reduce oxalate in vivo, biostable, bioavailable, biocompatible, etc.), Land having substitutions not explicitly described are within the scope of embodiments here. In some embodiments, the peptides/polypeptides described herein are further modified (e.g., substitution, deletion, or addition of standard amino acids; chemical modification; etc.). Modifications that are understood in the field include N-terminal modification, C-terminal modification (which protects the peptide from proteolytic degradation), alkylation of amide groups, hydrocarbon "stapling" (e.g., to stabilize conformations). In some embodiments, the peptides/polypeptides described herein may be modified by conservative residue substitutions, for example, of the charged residues (K to R, R to K, D to E and E to D). Modifications of the terminal carboxy group include, without limitation, the amide, lower alkyl amide, constrained alkyls (e.g. branched, cyclic, fused, adamantyl) alkyl, dialkyl amide, and lower alkyl ester modifications. Lower alkyl is C1-C4 alkyl. Furthermore, one or more side groups, or terminal groups, may be protected by protective groups known to the ordinarily-skilled peptide chemist. The α-carbon of an amino acid may be mono- or dimethylated.

[0066] In some embodiments, any embodiments described herein may comprise mimetics corresponding to all or a portion of the Of-derived factors and/or SLR proteins (e.g., Sel1 proteins) described herein, with various modifications that are understood in the field. In some embodiments, residues in the peptide sequences described herein may be substituted with amino acids having similar characteristics (e.g., hydrophobic to hydrophobic, neutral to neutral, etc.) or having other desired characteristics (e.g., more acidic, more hydrophobic, less bulky, more bulky, etc.). In some embodiments, non-natural amino acids (or naturally-occurring amino acids other than the standard 20 amino acids) are substituted in order to achieve desired properties.

[0067] In some embodiments, residues having a side chain that is positively charged under physiological conditions, or residues where a positively-charged side chain is desired, are substituted with a residue including, but not limited to: lysine, homolysine, δ-hydroxylysine, homoarginine, 2,4-diaminobutyric acid, 3-homoarginine, D-arginine, arginal (—COOH in arginine is replaced by —CHO), 2-amino-3-guanidinopropionic acid, nitroarginine (N(G)-nitroarginine), nitrosoarginine (N(G)-nitrosoarginine), methylarginine (N-methyl-arginine), ε-N-methyllysine, allo-hydroxylysine, 2,3-diaminopropionic acid, 2,2'-diaminopimelic acid, ornithine, sym-dimethylarginine, asym-dimethyl arginine, 2,6-diaminohexinic acid, p-aminobenzoic acid and 3-aminotyrosine and, histidine, 1-methylhistidine, and 3-methylhistidine.

[0068] A neutral residue is a residue having a side chain that is uncharged under physiological conditions. A polar residue preferably has at least one polar group in the side chain. In some embodiments, polar groups are selected from hydroxyl, sulfhydryl, amine, amide and ester groups or other groups which permit the formation of hydrogen bridges.

[0069] In some embodiments, residues having a side chain that is neutral/polar under physiological conditions, or residues where a neutral side chain is desired, are substituted with a residue including, but not limited to: asparagine, cysteine, glutamine, serine, threonine, tyrosine, citrulline, N-methylserine, homoserine, allo-threonine and 3,5-dinitrotyrosine, and β-homoserine.

[0070] Residues having a non-polar, hydrophobic side chain are residues that are uncharged under physiological conditions, preferably with a hydropathy index above 0, particularly above 3. In some embodiments, non-polar, hydrophobic side chains are selected from alkyl, alkylene, alkoxy, alkenoxy, alkylsulfanyl and alkenylsulfanyl residues having from 1 to 10, preferably from 2 to 6, carbon atoms, or aryl residues having from 5 to 12 carbon atoms. In some embodiments, residues having a non-polar, hydrophobic side chain are, or residues where a non-polar, hydrophobic side chain is desired, are substituted with a residue including, but not limited to: leucine, isoleucine, valine, methionine, alanine, phenylalanine, N-methylleucine, tert-butylglycine, octylglycine, cyclohexylalanine, β-alanine, 1-aminocyclohexylcarboxylic acid, N-methylisoleucine, norleucine, norvaline, and N-methylvaline.

[0071] In some embodiments, peptide and polypeptides are isolated and/or purified (or substantially isolated and/or substantially purified). Accordingly, in such embodiments, peptides and/or polypeptides are provided in substantially isolated form. In some embodiments, peptides and/or polypeptides are isolated from other peptides and/or polypeptides as a result of solid phase peptide synthesis, for example. Alternatively, peptides and/or polypeptides can be substantially isolated from other proteins after cell lysis from recombinant production. Standard methods of protein purification (e.g., HPLC) can be employed to substantially purify peptides and/or polypeptides. In some embodiments, the present invention provides a preparation of peptides and/or polypeptides in a number of formulations, depending on the desired use. For example, where the polypeptide is substantially isolated (or even nearly completely isolated from other proteins), it can be formulated in a suitable medium solution for storage (e.g., under refrigerated conditions or under frozen conditions). Such preparations may contain protective agents, such as buffers, preservatives, cryprotectants (e.g., sugars such as trehalose), etc. The form of such preparations can be solutions, gels, etc. In some embodiments, peptides and/or polypeptides are prepared in lyophilized form. Moreover, such preparations can include other desired agents, such as small molecules or other peptides, polypeptides or proteins. Indeed, such a preparation comprising a mixture of different embodiments of the peptides and/or polypeptides described here may be provided.

[0072] In some embodiments, provided herein are peptidomimetic versions of the peptide sequences described herein or variants thereof. In some embodiments, a peptidomimetic is characterized by an entity that retains the polarity (or non-polarity, hydrophobicity, etc.), three-dimensional size, and functionality (bioactivity) of its peptide equivalent but wherein all or a portion of the peptide bonds have been replaced (e.g., by more stable linkages). In some embodiments, 'stable' refers to being more resistant to chemical degradation or enzymatic degradation by hydrolytic enzymes. In some embodiments, the bond which replaces the amide bond (e.g., amide bond surrogate) conserves some properties of the amide bond (e.g., conformation, steric bulk, electrostatic character, capacity for hydrogen bonding, etc.). Chapter 14 of "Drug Design and Development", Krogsgaard, Larsen, Liljefors and Madsen (Eds) 1996, Horwood Acad. Publishers provides a general discussion of techniques for the design and synthesis of peptidomimetics and is herein incorporated by reference in its entirety. Suitable amide bond surrogates include, but are not limited to: N-alkylation (Schmidt, R. et al., Int. J. Peptide Protein Res., 1995, 46,47; herein incorporated by reference in its entirety), retro-inverse amide (Chorev, M. and Goodman, M., Acc. Chem. Res, 1993, 26, 266; herein incorporated by reference in its entirety), thioamide (Sherman D. B. and Spatola, A. F. J. Am. Chem. Soc., 1990, 112, 433; herein incorporated by reference in its entirety), thioester, phosphonate, ketomethylene (Hoffman, R. V. and Kim, H. O. J. Org. Chem., 1995, 60, 5107; herein incorporated by reference in its entirety), hydroxymethylene, fluorovinyl (Allmendinger, T. et al., Tetrahydron Lett., 1990, 31, 7297; herein incorporated by reference in its entirety), vinyl, methyleneamino (Sasaki, Y and Abe, J. Chem. Pharm. Bull. 1997 45, 13; herein incorporated by reference in its entirety), methylenethio (Spatola, A. F., Methods Neurosci, 1993, 13, 19; herein incorporated by reference in its entirety), alkane (Lavielle, S. et. al., Int. J. Peptide Protein Res., 1993, 42, 270; herein incorporated by reference in its entirety) and sulfonamido (Luisi, G. et al. Tetrahedron Lett. 1993, 34, 2391; herein incorporated by reference in its entirety).

[0073] As well as replacement of amide bonds, peptidomimetics may involve the replacement of larger structural moieties with di- or tripeptidomimetic structures and in this case, mimetic moieties involving the peptide bond, such as azole-derived mimetics may be used as dipeptide replacements. Suitable peptidomimetics include reduced peptides where the amide bond has been reduced to a methylene amine by treatment with a reducing agent (e.g. borane or a hydride reagent such as lithium aluminum-hydride); such a reduction has the added advantage of increasing the overall cationicity of the molecule.

[0074] Other peptidomimetics include peptoids formed, for example, by the stepwise synthesis of amide-functionalised polyglycines. Some peptidomimetic backbones will be readily available from their peptide precursors, such as peptides which have been permethylated, suitable methods are described by Ostresh, J. M. et al. in Proc. Natl. Acad. Sci. USA (1994) 91, 11138-11142; herein incorporated by reference in its entirety.

[0075] In some embodiments, the peptides/polypeptides described herein are provided as fusions with other peptides or polypeptides. Such fusions may be expressed from a recombinant DNA which encodes the SLR and/or Of-derived peptide/polypeptide and the additional peptide/polypeptide or may be formed by chemical synthesis. For instance, the fusion may comprise a SLR and/or Of-derived peptide/polypeptide and an enzyme of interest, a luciferase, RNasin or RNase, and/or a channel protein (e.g., ion channel protein), a receptor, a membrane protein, a cytosolic protein, a nuclear protein, a structural protein, a phosphoprotein, a kinase, a signaling protein, a metabolic protein, a mitochondrial protein, a receptor associated protein, a fluorescent protein, an enzyme substrate, a transcription factor, selectable marker protein, nucleic acid binding protein, extracellular matrix protein, secreted protein, receptor ligand, serum protein, a protein with reactive cysteines, a transporter protein, a targeting sequence (e.g., a myristylation sequence), a mitochondrial localization sequence, or a nuclear localization sequence. The additional peptide/polypeptide may be fused to the N-terminus and/or the C-terminus of the SLR and/or Of-derived peptide/polypeptide. In one embodiment, the fusion protein comprises a first peptide/polypeptide at the N-terminus and another (different) peptide/polypeptide at the C-terminus of the SLR and/or Of-derived peptide/polypeptide. Optionally, the elements in the fusion are separated by a connector sequence, e.g., preferably one having at least 2 amino acid residues, such as one having 13 and up to 40 or 50 amino acid residues. The presence of a connector sequence in a fusion protein of the invention does not substantially alter the function of either element (e.g., the SLR and/or Of-derived peptide/polypeptide) in the fusion relative to the function of each individual element, likely due to the connector sequence providing flexibility (autonomy) for each element in the fusion. In certain embodiment, the connector sequence is a sequence recognized by an enzyme or is photocleavable. For example, the connector sequence may include a protease recognition site.

[0076] In some embodiments, provided herein are pharmaceutical compositions comprising of one or more SLR and/or Of-derived peptide/polypeptide described herein and a pharmaceutically acceptable carrier. Any carrier which can supply an active peptide or polypeptide (e.g., without destroying the peptide or polypeptide within the carrier) is a suitable carrier, and such carriers are well known in the art. In some embodiments, compositions are formulated for administration by any suitable route, including but not limited to, orally (e.g., such as in the form of tablets, capsules, granules or powders), sublingually, bucally, parenterally (such as by subcutaneous, intravenous, intramuscular, intradermal, or intracisternal injection or infusion (e.g., as sterile injectable aqueous or non-aqueous solutions or suspensions, etc.)), nasally (including administration to the nasal membranes, such as by inhalation spray), topically (such as in the form of a cream or ointment), transdermally (such as by transdermal patch), rectally (such as in the form of suppositories), etc.

[0077] In some embodiments, provided herein are methods for treating patients suffering from (or at risk of) hyperoxaluria, hyperoxalemia, and/or in need of treatment (or preventative therapy). In some embodiments, a pharmaceutical composition comprising at least one Of-derived and/or SLR peptide/polypeptide described herein is delivered to such a patient in an amount and at a location sufficient to treat the condition. In some embodiments, peptides and/or polypeptides (or pharmaceutical composition comprising such) can be delivered to the patient systemically or locally, and it will be within the ordinary skill of the medical professional treating such patient to ascertain the most appropriate delivery route, time course, and dosage for treatment. It will be appreciated that application methods of treating a patient most preferably substantially alleviates or even eliminates such symptoms; however, as with many medical treatments, application of the inventive method is deemed successful if, during, following, or otherwise as a result of the inventive method, the symptoms of the disease or disorder in the patient subside to an ascertainable degree.

[0078] A pharmaceutical composition may be administered in the form which is formulated with a pharmaceutically acceptable carrier and optional excipients, adjuvants, etc. in accordance with good pharmaceutical practice. The Of-derived and/or SLR peptide/polypeptide pharmaceutical composition may be in the form of a solid, semi-solid or liquid dosage form: such as powder, solution, elixir, syrup, suspension, cream, drops, paste and spray. As those skilled in the art would recognize, depending on the chosen route of administration (e.g. pill, injection, etc.), the composition form is determined. In general, it is preferred to use a unit dosage form in order to achieve an easy and accurate administration of the active pharmaceutical peptide or polypeptide. In general, the therapeutically effective pharmaceutical compound is present in such a dosage form at a concentration level ranging from about 0.5% to about 99% by weight of the total composition, e.g., in an amount sufficient to provide the desired unit dose. In some embodiments, the pharmaceutical composition may be administered in single or multiple doses. The particular route of administration and the dosage regimen will be determined by one of skill in keeping with the condition of the individual to be treated and said individual's response to the treatment. In some embodiments, an Of-derived and/or SLR peptide/polypeptide pharmaceutical composition is provided in a unit dosage form for administration to a subject, comprising one or more nontoxic pharmaceutically acceptable carriers, adjuvants or vehicles. The amount of the active ingredient that may be combined with such materials to produce a single dosage form will vary depending upon various factors, as indicated above. A variety of materials can be used as carriers, adjuvants and vehicles in the composition of the invention, as available in the pharmaceutical art. Injectable preparations, such as oleaginous solutions, suspensions or emulsions, may be formulated as known in the art, using suitable dispersing or wetting agents and suspending agents, as needed. The sterile injectable preparation may employ a nontoxic parenterally acceptable diluent or solvent such as sterile nonpyrogenic water or 1,3-butanediol. Among the other acceptable vehicles and solvents that may be employed are 5% dextrose injection, Ringer's injection and isotonic sodium chloride injection (as described in the USP/NF). In addition, sterile, fixed oils may be conventionally employed as solvents or suspending media. For this purpose, any bland fixed oil may be used, including synthetic mono-, di- or triglycerides. Fatty acids such as oleic acid can also be used in the preparation of injectable compositions.

[0079] In various embodiments, the peptides and polypeptides disclosed herein are derivatized by conjugation to one or more polymers or small molecule substituents.

[0080] In certain of these embodiments, the peptides and polypeptides described herein are derivatized by coupling to polyethylene glycol (PEG). Coupling may be performed using known processes. See, Int. J. Hematology, 68:1 (1998); Bioconjugate Chem., 6:150 (1995); and Crit. Rev. Therap. Drug Carrier Sys., 9:249 (1992) all of which are incorporated herein by reference in their entirety. Those skilled in the art, therefore, will be able to utilize such well-known techniques for linking one or more polyethylene glycol polymers to the peptides and polypeptides described herein. Suitable polyethylene glycol polymers typically are commercially available or may be made by techniques well known to those skilled in the art. The polyethylene glycol polymers preferably have molecular weights between 500 and 20,000 and may be branched or straight chain polymers.

[0081] The attachment of a PEG to a peptide or polypeptide described herein can be accomplished by coupling to amino, carboxyl or thiol groups. These groups will typically be the N- and C-termini and on the side chains of such naturally occurring amino acids as lysine, aspartic acid, glutamic acid and cysteine. Since the peptides and polypeptides of the present disclosure can be prepared by solid phase peptide chemistry techniques, a variety of moieties containing diamino and dicarboxylic groups with orthogonal protecting groups can be introduced for conjugation to PEG.

[0082] The present disclosure also provides for conjugation of the peptides and polypeptides described herein to one or more polymers other than polyethylene glycol.

[0083] In some embodiments, the peptides and polypeptides described herein are derivatized by conjugation or linkage to, or attachment of, polyamino acids (e.g., poly-his, poly-arg, poly-lys, etc.) and/or fatty acid chains of various lengths to the N- or C-terminus or amino acid residue side chains. In certain embodiments, the peptides and polypeptides described herein are derivatized by the addition of polyamide chains, particularly polyamide chains of precise lengths, as described in U.S. Pat. No. 6,552,167, which is incorporated by reference in its entirety. In yet other embodiments, the peptides and polypeptides are modified by the addition of alkylPEG moieties as described in U.S. Pat. Nos. 5,359,030 and 5,681,811, which are incorporated by reference in their entireties.

[0084] In select embodiments, the peptides and polypeptides disclosed herein are derivatized by conjugation to polymers that include albumin and gelatin. See, Gombotz and Pettit, Bioconjugate Chem., 6:332-351, 1995, which is incorporated herein by reference in its entirety.

[0085] In further embodiments, the peptides and polypeptides disclosed herein are conjugated or fused to immunoglobulins or immunoglobulin fragments, such as antibody Fc regions.

[0086] In some embodiments, the pharmaceutical compositions described herein (e.g., comprising SLR proteins (e.g., Sel1 proteins), Of-derived factors, and/or variants and fragments thereof) find use in the treatment and/or prevention of hyperoxaluria, hyperoxalemia, and related conditions. In some embodiments, the compositions are administered to a subject. In certain embodiments, the patient is an adult. In other embodiments, the patient is a child.

[0087] In various embodiments, the peptide/polypeptide is administered in an amount, on a schedule, and for a duration sufficient to decrease triglyceride levels by at least 5%, 10%, 15%, 20% or 25% or more as compared to levels just prior to initiation of treatment. In some embodiments, the peptide/polypeptide is administered in an amount, on a dosage schedule, and for a duration sufficient to decrease oxalate levels (e.g., in urine, in plasma) by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50%. In particular embodiments, the peptide/polypeptide is administered in an amount, on a schedule, and for a time sufficient to decrease oxalate levels (e.g., in urine, in plasma) by at least 55%, 60%, 65%, even at least about 70% or more.

[0088] In certain embodiments, the peptide/polypeptide is administered in an amount, expressed as a daily equivalent dose regardless of dosing frequency, of 50 micrograms ("mcg") per day, 60 mcg per day, 70 mcg per day, 75 mcg per day, 100 mcg per day, 150 mcg per day, 200 mcg per day, or 250 mcg per day. In some embodiments, the polypeptide is administered in an amount of 500 mcg per day, 750 mcg per day, or 1 milligram ("mg") per day. In yet further embodiments, the polypeptide is administered in an amount, expressed as a daily equivalent dose regardless of dosing frequency, of 1-10 mg per day, including 1 mg per day, 1.5 mg per day, 1.75 mg per day, 2 mg per day, 2.5 mg per day, 3 mg per day, 3.5 mg per day, 4 mg per day, 4.5 mg per day, 5 mg per day, 5.5 mg per day, 6 mg per day, 6.5 mg per day, 7 mg per day, 7.5 mg per day, 8 mg per day, 8.5 mg per day, 9 mg per day, 9.5 mg per day, or 10 mg per day.

[0089] In various embodiments, the peptide/polypeptide is administered on a monthly dosage schedule. In other embodiments, the peptide/polypeptide is administered biweekly. In yet other embodiments, the polypeptide is administered weekly. In certain embodiments, the peptide/polypeptide is administered daily ("QD"). In select embodiments, the polypeptide is administered twice a day ("BID").

[0090] In typical embodiments, the peptide/polypeptide is administered for at least 3 months, at least 6 months, at least 12 months, or more. In some embodiments, the peptide/polypeptide is administered for at least 18 months, 2 years, 3 years, or more.

EXPERIMENTAL

Example 1

[0091] Of interacts with colonic epithelium and induces distal colonic oxalate secretion, leading to reduced urinary excretion (ref. 14; incorporated by reference in its entirety). Of whole cells, cell membranes, and lysates have been tested on oxalate transport across rat distal colonic tissues mounted in Ussing chambers, and were found to have no effect (ref. 14; incorporated by reference in its entirety). Both the whole cells and lysates caused significant degradation of oxalate in the chamber, necessitating heat treatment of samples to eradicate this inherent enzymatic activity. To further understand this phenomenon, Of was obtained from ATCC (strain OxB) and was grown in an anaerobic chamber (ref. 2; incorporated by reference in its entirety). Of cultures were centrifuged (3,000 g at 4° C. for 10 min) and the supernatant (conditioned medium=CM) was filtered through a 0.22 μm filter to sterilize and remove all bacterial cells and stored at −80° C. (ref. 5; incorporated by reference in its entirety). C2 cells were used as a model to evaluate the effects of Of CM on intestinal oxalate transport. Apical ^{14}C-oxalate flux studies in C2 cells were performed. Apical oxalate uptake by C2 cells was assessed by imposing an outward Cl gradient by removing extracellular Cl [Cl_i>Cl_o] and measuring DIDS (anion exchange inhibitor)-sensitive influx of radioactive ^{14}C-oxalate in exchange for intracellular Cl [i.e. apical Cl-oxalate exchange activity, ≥50% of which is mediated by A6 in C2 cells (ref. 12; incorporated by reference in its entirety)]. A6 operates in the direction of exchanging intracellular oxalate for mucosal Cl during the process of transepithelial intestinal oxalate secretion. However, A6 can operate in either direction (ref. 21; incorporated by reference in its entirety), and therefore its activity was measured by the more convenient assay of cellular oxalate uptake. C2 cells grown on TRANSWELLS were treated apically with Of culture medium (OM) or CM (1:50 dilution×24 h) before measuring ^{14}C-oxalate uptake.

[0092] Compared to untreated (UT) and OM, the CM significantly stimulated (>2.4-fold) oxalate transport by C2 cells (ref 4; incorporated by reference in its entirety). Similar effects were also observed with 6- and 16-h incubations, but no effect was seen at 1 h. CM or OM did not affect the medium pH. In addition, OM or CM had no significant effect on the transepithelial resistance, indicating that the OM or the CM does not affect the paracellular permeability. These results indicate that secreted bioactive factors in Of CM are responsible for the observed stimulatory regulation by modulating the activity of the involved anion exchanger(s) (A1, A2, and/or A6). *Lactobacillus acidophilus* (La) degrades intraluminal oxalate (19), but it is unknown whether La similarly interacts with enterocytes and modulates intestinal oxalate transport as Of (ref. 14; incorporated by reference in its entirety). Therefore, to ensure specificity, experiments similarly evaluated the effect of La CM. It was observed that La CM (1:25 dilution×24 h) had no effect on oxalate transport by C2 cells compared to UT cells and cells treated with the control medium (ref. 4; incorporated by reference in its entirety). These results indicate that Of CM-induced stimulation of oxalate transport is specific and is possibly mediated by one or more of Of-derived secreted bioactive factor(s).

[0093] To have an idea about the nature of Of-derived secreted bioactive factor(s), CM was subjected to heat treatment (boiling at 100° C. for 20-30 min). Heat treatment completely abolished the CM-induced stimulation, indicating that the secreted factor(s) are likely to be protein(s) or peptide(s), rather than, for example, small molecules. Pretreatment of the CM with pepsin or trypsin also completely abolished the stimulatory effect, providing further evidence that the secreted factor(s) is/are proteins or peptides. Selective ultrafiltration revealed that the secreted factors have molecular masses (MM) between 10-30 kDa (ref. 4; incorporated by reference in its entirety). Pretreatment with the PKA inhibitor H89 completely blocked the CM-induced stimulation of oxalate transport by C2 cells, indicating that the observed stimulation is mediated by PKA activation. The observed stimulation is also completely blocked by DIDS, indicating that it is due to active anion exchange-mediated transport process. siRNA A6 knockdown greatly reduced the observed stimulation, indicating that a significant component of CM-induced oxalate transport is A6-mediated. The CM significantly increased (>2-fold) the V_{max} (e.g., greater transport capacity) and reduced (>3.4-fold) the K_m (e.g., greater affinity for oxalate) of the involved transporter(s). The CM did not affect A6 mRNA and total/surface protein expression, and in view of the reduced K_m(reflecting greater A6 affinity for oxalate), indicating that the observed stimulation is due to mechanisms including CM-induced enhanced A6 transport activity (e.g., resulting from an increase in the intrinsic activity of the preexisting A6 membrane transporters), although embodiments herein are not limited to any particular mechanism of action and an understanding of the mechanism of action is not necessary to practice such embodiments.

[0094] To evaluate the in vivo effects of the CM on overall oxalate homeostasis, CM or OM was given rectally as enemas (100 μl twice daily×21 days) to PH1 mice (a model of PH type 1 due to deficiency in the liver enzyme AGAT and they have significant hyperoxalemia and hyperoxaluria) (ref. 28; incorporated by reference in its entirety). It was confirmed that the PH1 mice have significant hyperoxaluria (>2.7-fold) compared to their controls. The CM significantly reduced urinary oxalate excretion by >32.5%, while the OM had no significant effect (ref. 4; incorporated by reference in its entirety). To determine whether the Of-derived bioactive factor(s) interact(s) with the colonocyte and induce(s) oxalate secretion in vivo, leading to the observed reduction in urinary oxalate excretion in PH1 mice, distal colonic tissues were isolated and mounted in Ussing chambers at the end of the treatment period. While a small net oxalate secretory flux (−4.7±2.4) was observed in distal colonic tissues from OM-treated PH1 mice, a >4.2-fold higher net oxalate secretory flux (−20.0±5.5) was seen in distal colonic tissues from CM-treated PH1 mice (pmol/cm2/h: OM: J_{MS} (absorptive flux)=37.8±5.9, J_{SM} (secretory flux)=42.6±5.5; CM: J_{MS}=40.6±3.7, J_{SM}=60.6±3.1), which is due to significantly increased (>42%) J_{SM} (4). CM or OM had no significant effect on J_{MS}. These results indicate that the Of-derived factors reduce urinary oxalate excretion in PH1 mice through mechanisms including enhanced net distal colonic oxalate secretion, as well as they retain their biological activity in vivo, thus indicating their significant therapeutic value.

[0095] An important factor in purifying the bioactive protein(s) is their presence in a high concentration in the CM. Since Of might secrete these factors as a survival strategy when oxalate is limited (ref. 14; incorporated by reference in its entirety), it was tested whether lower growth medium oxalate concentration lead to more secreted factor (s), and therefore, to a CM with higher bioactivity, by reducing oxalate concentration from 37.5 mM to 18.8 & 9.4 mM. The bioactivity of the CM is significantly higher (>2-fold) with CM9.4 compared to CM37.5 (ref. 4; incorporated by reference in its entirety), demonstrating that the secretion of these factors is inducible, which facilitates their characterization. As a first step in characterizing these factors, secreted proteins in Of CM were purified utilizing column chromatography, using a commercially available kit for rapid screening of a suitable column. 1 ml of the CM was loaded onto different columns (e.g. anion and cation exchange columns) and the flow-through fractions were collected and their effects on oxalate influx into C2 cells were evaluated. The fractions from the weak cationic column (WCC) were found to have no stimulatory effect compared with the parent CM, indicating that this is due to sticking of the potential factor(s) to this column. The factor (s) were then eluted from this column using high salt (0.5-1 M NaCl). Following desalting and concentration of the eluted fraction using a desalting/concentrating column, the eluted fraction is found to have an activity similar to the parent CM (pmoles/cm2/min: UT=1.56±0.30; CM=8.47±0.86; Eluted fraction=7.36±0.69). These findings indicate that the purification process has led to enrichment of the factor(s) in the eluted fraction and the WCC was utilized in subsequent purification studies using FPLC.

[0096] The experiments demonstrate that small molecular weight protein(s) and/or peptide(s) in Of CM significantly stimulate(s) oxalate transport (>2.4-fold) by human intestinal Caco2-BBE cells (FIG. **1**, FIG. **2**, and FIG. **4**). Importantly, Of CM also significantly reduced (>32.5%) urinary oxalate excretion in a mouse model of primary hyperoxaluria (PH1), by stimulating (>42%) distal colonic oxalate secretion, reflecting the in vivo retention of biologic activity and the therapeutic value of these factors.

[0097] The high specific activity elution fraction was run in SDS-PAGE and then stained by Coomassie blue. Several bands in the molecular weight range from 10-30 kDa, as well as bands ~52 and 68 kDa were noted. Tandem mass spectrometry was utilized as a primary strategy to identify candidates for the mediators. The gel sections containing the bands were cut and in-gel trypsin proteolysis was performed. Isolated peptides were subjected to LTQ Orbitrap ESI LC-MS/MS analysis, using standard conditions. The data were analyzed by Mascot and X! Tandem database search against the predicted Of proteome, combined with a reverse decoy database to estimate false discovery rate. The results were then validated and visualized using Scaffold. On the basis of 16S rRNA sequence similarities and lipid content, Of strains are divided into two groups: Group I is represented by strain OxB (the strain used in the above experiments) and human strain OxCC13, while Group II is represented by human strain HOxBLS. OXCC13 and HOxBLS genomes were published. Searching against the OXCC13 genome yielded 52 candidates Of protein CM stimulatory factors. A more stringent search (Maxquant: 20 ppm, with additional filtering at 1% FDR) yielded 6 candidate proteins which are the following: transcriptional regulator, LuxR family (ID # C3X886), Raf-like protein (ID # C3XB51), Tryptophan synthase alpha chain (ID # C3XAU0), Sel1 repeat protein (C3X8T9), Uncharacterized protein (ID C3X964), and Uncharacterized protein (ID #

C3XCY9). CM from OXCC13 is not commercially available to be cultured. Therefore, the OxB whole genome was sequenced and assembled. The data generated by MassSpect was re-analyzed against the OxB genome and the amino acid sequences for the corresponding proteins identified above by searching the OXCC13 genome were obtained.

Example 2

[0098] Several of the identified Of proteins were of interest, especially the Sel1 proteins. Sel1-like repeat (SLR) proteins (e.g. Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, and MerG) are involved in signal transduction pathways (ref 24; incorporated by reference in its entirety). It was found that Of CM signals through PKA to stimulate oxalate transport by C2 cells. SLR proteins have repeat units and most repeats consist of 5 to 40 amino acids (but some could be much larger) that fold into two to four secondary structural elements. All SLR proteins seem to serve as adaptor proteins for the assembly of membrane-bound macromolecular complexes (ref. 24; incorporated by reference in its entirety). Several bacterial and eukaryotic SLR proteins (e.g. Sel1 & Hrd3) are activated upon cellular stress, which is of interest since Of Sel1 proteins might be activated when oxalate is low in the culture medium given the observation of a CM of higher (>2-fold) bioactivity under this condition. Bacterial LpnE, EnhC, HcpA, ExoR, and AlgK proteins mediate the interactions between bacterial and eukaryotic host cells. The SLR motif establishes a link between signal transduction pathways from eukaryotes and bacteria. Many SLR proteins contain leader sequences and even SLR proteins without leader sequences, such as PodJ for example, are active in the periplasmic space. In addition, other bacterial SLR proteins, such as HcpA, ExoR, EnhC and LpnE seem to be responsible for the adaptation of bacteria to different eukaryotic hosts (ref 24; incorporated by reference in its entirety).

[0099] Of has about 44 Sel1 proteins, with many having molecular masses between 10-30 kDa. In addition, several other Sel1 proteins have molecular masses between 32-68 kDa. Most of the Sel1 proteins are predicted to have signal peptides and therefore are secreted proteins. Moreover, Sel1 proteins with molecular masses of 25 (#1361), 33 (#1414), and 68 (#1362) kDa blast in common with another Sel1 protein having a molecular mass of 59 (#1344) kDa. Five Sel1 proteins (# s 1360-1364) resides in an operon, with carbon starvation protein CstA located immediately upstream of this operon. Sel1 proteins #1343, 1344, and 1356 are also located near this operon. Other interesting candidates include diguanylate cyclase, a peptidase, putative outer membrane efflux protein OprC, outer membrane efflux protein OprM, LD-carboxypeptidase, stringent starvation protein B, ribonucleotide reductase, and Hsp20. Although most of the CM stimulatory activity is mediated by factors with masses between 10-30 kDa, the results of selective ultrafiltration using 30 kDa cutoff column indicate that the factors might exist as a multifunctional complex requiring a bacterial product of >30 kDa for optimal functioning. The fact that Sel1 proteins seem to serve as adaptor proteins for the assembly of membrane-bound macromolecular complexes might be of particular interest here. To evaluate whether one or more of these candidate proteins are the Of-derived bioactive factor(s) mediating the CM-induced stimulation of oxalate transport, the proteins (starting with the target Sel1 proteins) were cloned and overexpressed in *E. coli* and the recombinant purified proteins were obtained (Table 2).

[0100] The effects of different concentrations (including different incubation periods) of the purified proteins on oxalate transport by C2 cells is similarly tested, as well as examining the effects of different combinations of the purified proteins. Testing the combined effects of the different proteins is important even if one candidate is found to have a significant stimulatory effect, giving the possibility that this might lead to a much higher stimulation (FIG. **3** and FIG. **5**).

[0101] To evaluate the in vivo effects of the Sel1 proteins, LD-carboxypeptidase, and the peptidase (including any peptidmimetics versions of them or other embodiments), the proteins (individually or in different combinations) are administered (rectally, orally, both oral and rectal, or any other feasible route) to PH1 mice for up to 28 days. The PH1 mice are placed in metabolic cages and urine, plasma, and feces is collected on days 0, 7, 14, 21, and 28. When a factor is found to normalize or significantly reduce serum and urinary oxalate levels in PH1 mice, it is then examined whether the observed changes are due to factor-mediated enhanced net intestinal (small and/or large intestine depending on the route of administration) oxalate secretion. To this end, intestinal tissues (jejunum, ileum, cecum, proximal & distal colon) are isolated and mounted in Ussing chambers at the end of the treatment period found to be associated with the maximum reduction in serum and/or urine oxalate levels. Compared to vehicle-treated PH1 mice, if net basal cecal oxalate flux is converted from absorption to secretion, or significantly higher net basal secretory flux(s) is/re observed in the proximal and/or the distal colon of treated PH1 mice (due to significantly increased secretory flux and/or reduced absorptive flux), then such findings demonstrate that the factor reduces serum and/or urine oxalate levels by enhancing intestinal oxalate secretion. As a result of enhanced intestinal oxalate secretion/excretion, fecal oxalate is higher in the factor-treated mice, which is confirmed. Collectively, such findings provide a molecular basis for therapeutic application of a factor for prevention and/or treatment of hyperoxaluria, hyperoxalemia, and related COKS.

[0102] An alternative approach is to use differential proteomics. As described above, lowering culture medium oxalate from 37.5 mM (5 g/L) to 9.4 mM (1 g/L) led to a CM with >2-fold higher bioactivity, while increasing oxalate to 187.5 (25 g/L) led to a CM with reduced activity by ~50-70%. Further lowering of oxalate (0.5, 0.25, 0. g/L, as well as oxalate free culture medium) may lead to a CM with much higher bioactivity compared with 9.4 mM. If 0.25 g/L is found to be associated with the highest bioactivity, CMs are then prepared from Of cells grown in the low (will designate CM-low and its corresponding control medium will be OM-low) and high (will designate CM-high and its corresponding control medium will be OM-high) oxalate culture media (6 per condition). Label-free differential proteomics is used to analyze the samples. After excluding the proteins showing up in OM-low & high, the abundance of proteins in CM-low & high are compared. Observing proteins with significantly higher abundance in CM-low, while the same proteins are noted to be low or absent in CM-high, indicates that one or more of these proteins is an Of-derived bioactive factor(s). Promising candidate proteins are then be cloned and overexpressed in *E. coli* and the effects of the recombinant protein(s) are tested as above.

[0103] An alternative strategy is to examine the Of transcriptome under low and high oxalate concentrations in the culture medium. To this end, Of cells grown in the low and high oxalate culture media are isolated and RNA for transcriptome analysis is prepared. RNA is extracted from replicate cultures (e.g., 3-5 per condition) grown under the two oxalate concentrations. Ribosomal RNA is subtracted and mRNA is used to generate cDNA libraries for sequencing. Transcript data is mapped to the assembled Of genome sequence using Bowtie (ref. 22; incorporated by reference in its entirety), and data normalization and differential expression analysis is done using the methods implemented in the DESeq2 R package (ref 23; incorporated by reference in its entirety). This approach facilitates the identification of genes (and/or operons) that are differentially regulated under these conditions. If, for example, certain genes are noted to be upregulated under low oxalate, but downregulated under the high oxalate, the protein products of these genes are then overexpressed in *E. coli* and the effects of the recombinant protein(s) are tested.

Example 3

[0104] The CM significantly reduced (>32.5%) urinary oxalate excretion in PH1 mice, indicating that the Of-derived factors retain their biological activity in vivo. To test whether the Of-derived factor(s) also decrease urinary oxalate excretion in enteric hyperoxaluria (EH) (e.g. IBD—and obesity-associated hyperoxaluria), the purified factor(s) are similarly given to SAPM1/YitFc (SAM) and ob/ob (ob) mice. SAM is a mouse model with remarkable similarities to human Crohn's disease developed as an ideal model for the IBD-associated hyperoxaluria (>2-fold hyperoxaluria compared to their controls). ob is an obesity model developed as an ideal model for the obesity associated hyperoxaluria (>3.3-fold hyperoxaluria compared to their controls). SAM and ob mice are treated with the purified factors as described above. SAM and ob mice are placed in metabolic cages and urine & feces are collected (including baseline collection). Observing normalization or significantly reduced urinary oxalate levels in factor-treated SAM and/or ob mice compared with vehicle-treated mice indicates that the factor has therapeutic potential not only for PH but also for EH and related COKS. Experiments then examine whether any observed reduction in urinary oxalate excretion in SAM and/or ob mice is due to factor-mediated enhanced net intestinal oxalate secretion.

[0105] Experiments are also conducted to evaluate the effects of the CM on the hyperoxaluria observed in the SAM and ob mice. Given the unavailability of any specific therapy that effectively reduces urinary oxalate excretion, the CM provides a therapeutic option under conditions in which it significantly reduces urine oxalate levels in these mouse models. Since Of has been given (as a frozen cell paste or a lyophilized Of formulated in enteric coated capsules) to PH patients (ref. 18; incorporated by reference in its entirety), it is reasonable to give a product of this bacterium to PH patients. Of CM or OM will be similarly (as described above with PH1 mice) given to SAM and ob mice and the results will be similarly interpreted.

[0106] Artificial colonization of wild-type mice with the human Of strain HC-1 led to the presence of the bacteria not only in the colon, but unexpectedly also in the small intestine for some time (ref 15; incorporated by reference in its entirety). This was associated with a significant net oxalate secretion in the distal ileum, cecum, and distal colon, as well as significantly reduced urinary oxalate excretion. In view of these findings, it is possible that oral administration of Of CM (or the purified factor(s)) might promote significant stimulation of net oxalate secretion in both small and large intestines, thereby potentially leading to normalization or greater reduction in plasma and urinary oxalate levels in PH1 mice compared to rectal CM. Therefore, gelatin capsules containing freeze-dried Of CM (or the purified factor (s) are prepared for oral administration. To protect the contents of the capsules during passage through the acidic upper gastrointestinal tract, the capsules are coated with Eudragit L 100-55 (ref. 14), which will also protect their contents from protease digestion. Placebo-treated mice will receive Eudragit-coated empty capsules. This approach was used for making encapsulated freeze-dried preparation of Of lysate which was then given orally to hyperoxaluric rats and led to induction of distal colonic oxalate secretion. A 2×2 factorial design is followed with the following 4 groups: placebo-placebo, oral CM, rectal CM, and oral+rectal CM. The PH1, SAM, and ob mice receive the capsules by an intragastric needle twice daily for 5-20 days, and urine, plasma, & feces is collected (including baseline collection), as well as intestinal tissues (jejunum, ileum, cecum, proximal & distal colon) are isolated and mounted in Ussing chambers at the end of the treatment period. The data are analyzed by repeated measures ANOVA with treatment group as the between-subjects factor and time as the within-subjects repeated factor. The treatment group is tested by time interaction to determine whether the change with treatment varies based on treatment received. Observing normalization or a greater reduction in plasma and urinary oxalate levels in PH1 mice with oral CM compared to rectal CM, due to significant stimulation of net oxalate secretion in the small and/or large intestine(s), indicates that the oral route is better. Finding that oral+rectal CM is associated with a much higher reduction in plasma and urinary oxalate levels compared with either oral CM or rectal CM alone, has significant therapeutic implications. Of note is that the CM or OM was given as rectal enemas through special tips that were introduced to ~2 cm from the anus, and the mice were then held from their tails with the heads down and kept in that position for ~one minute.

Example 4

[0107] The nucleotide sequences of the proteins in Table 2 from the OxB *oxalobacter* strain were sequenced compared to the human *oxalobacter* strain OXCC13. The OxB, OXC, or other Of-derived nucleotide sequences, and variants thereof, may find use in embodiments described herein. In some embodiments, nucleic acids and/or polypeptides comprising such sequences find use in the embodiments described herein.

Example 5

[0108] Experiments were conducted during development of embodiments herein to determine the molecular weight(s) (MWs) of the secreted factor(s), the conditioned medium (CM) was subjected to selective ultrafiltration using 10- and 30-kDa cutoff spin columns. C2 cells were untreated (UT) or treated with the CM, filtrate (F), retentate (R), or F+R. Using a 10-kDa column, the R and the F+R significantly stimulated oxalate uptake by C2 cells, while the F has no effect (FIG. 6A). Using a 30-kDa column, the F and the F+R significantly stimulated oxalate uptake by C2 cells, while the R has no effect (FIG. 6B). Collectively, these results indicate that the MWs of the factors are largely between 10-30 kDa. Since F+R have a better stimulatory effect than F, while R has no effect, such data suggest the possibility that these factors might exist as a multifunctional complex requiring a bacterial product of >30 kDa for optimal functioning. Therefore, evaluating the effects of different combinations of the Sel1 proteins and the other proteins (305, 308, 309, & 314) is critical to reach to a level of stimulation similar to the CM-induced stimulation (~3-fold) (FIG. 5 and FIG. 6). Sel1 proteins 304, 317, 319, 322, 323, 324, & 325 stimulate oxalate transport by ~1.2-1.6-fold in preliminary studies.

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[0109] The following references, some of which are cited above, are herein incorporated by reference in their entireties.

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SEQUENCE LISTING

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gcacaagcac agcataatct tggtgttacg tattacgaag gtgagggaat aaaaaaagat    780

tacgccaagg ctgtgtactg gtggaaaaag gcagcagaac aggggattcc ccaatctcag    840

tataaccttg gcattgcata tgaagaaggc tggggcgctg aaaaaaatcc ggagaatgct    900

gtttttggt acagaaaagc ggctgaacag ggacatgctg atgctcaaaa cagacttggc    960

atcgcttaca ggtatggaac cggagtcagg aaaaatcccg cattgtctgt caaatggctg   1020

gaaaaagcgg caaagcaggg gcttgcaaga gcacagttca atttggggaa aaccttctat   1080

atcggagcag gcattaacaa gaatacagac aaagcggttt actggttcat aaaagctgcc   1140

aatcagggtt tcacagaagc acaggcttat attggtatga tttattttaa aggtaaatat   1200

gtcgccaaga acgaaaaaaa aggtttttac tggttaaaaa aagcagcaga aaaagacagt   1260

gctaaagcac aagcatttct tggcgcttta tacattgcag gaaatgaagt gaagccaaat   1320

ataaaggaag gcgttgcctt gacaaaaaaa gcggcattac agggtaatta cgaggcacaa   1380
```

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accctgctcg gtttttgcta cgagaatggc ttggaagtaa aaaaagacct gattgccgca 1440

tatgcgcttt acttgtcggc gtcacctcat ttcgattttg cagaaaaggc gcgtcttgat 1500

cttgaacgga aattaagcga acaggaaata gcaaaggcaa tatccgttaa tacagcaaaa 1560

ttgtttgagt ga 1572

<210> SEQ ID NO 2
<211> LENGTH: 523
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 2

Met Ser Ser Val Ile Ala Asp Ser Gln Gln Pro Ala Val Ser Glu Glu
1 5 10 15

Asn Ala Asn Lys Ile Ile Leu Asp Glu Glu Lys Ala Val Ile Gln Cys
20 25 30

Asn Glu Arg Tyr Lys Thr Glu Asn Asp Glu Lys Gly Asp Glu Glu Thr
35 40 45

Val Ser Trp Cys Arg Lys Ala Ala Lys Ser Gly Asn Ala Glu Ala Gln
50 55 60

Tyr Leu Phe Gly Met Leu Val Tyr Asp Gly Arg Gly Val Gln Gln Asp
65 70 75 80

Asn Cys Val Ala Met Leu Trp Trp Met Lys Ala Ala Glu Gln Asn His
85 90 95

Ala Lys Ala Leu Val Met Leu Gly Asn Leu His Arg Lys Gly Gln Cys
100 105 110

Ile Ala Glu Asn Tyr Pro Lys Ala Ile Ala Tyr Trp Lys Arg Ala Ala
115 120 125

Val Gln Asn Asn Val Trp Ala Tyr His Asn Leu Gly Thr Ala Tyr Tyr
130 135 140

Asp Gly Ile Gly Val Asp Lys Asn Pro His Glu Ala Val Arg Trp Trp
145 150 155 160

Lys Lys Ala Ala Glu Leu Gly Phe Pro Glu Ser Gln Asn Asn Leu Gly
165 170 175

Ala Leu Tyr Asn Asp Gly Asn Gly Val Asp Arg Asp Tyr Gln Glu Ala
180 185 190

Val Phe Trp Tyr Arg Lys Ser Ala Leu Gln Gly Asp Glu Leu Gly Gln
195 200 205

Tyr Asn Leu Gly Val Ala Tyr Tyr Tyr Gly Arg Gly Ile Lys Lys Asp
210 215 220

Phe Ser Glu Ala Val Ser Trp Tyr Lys Lys Ser Ala Glu Gln Asp Tyr
225 230 235 240

Ala Gln Ala Gln His Asn Leu Gly Val Thr Tyr Tyr Glu Gly Glu Gly
245 250 255

Ile Lys Lys Asp Tyr Ala Lys Ala Val Tyr Trp Trp Lys Lys Ala Ala
260 265 270

Glu Gln Gly Ile Pro Gln Ser Gln Tyr Asn Leu Gly Ile Ala Tyr Glu
275 280 285

Glu Gly Trp Gly Ala Glu Lys Asn Pro Glu Asn Ala Val Phe Trp Tyr
290 295 300

Arg Lys Ala Ala Glu Gln Gly His Ala Asp Ala Gln Asn Arg Leu Gly
305 310 315 320

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```
Ile Ala Tyr Arg Tyr Gly Thr Gly Val Arg Lys Asn Pro Ala Leu Ser
                325                 330                 335

Val Lys Trp Leu Glu Lys Ala Ala Lys Gln Gly Leu Ala Arg Ala Gln
            340                 345                 350

Phe Asn Leu Gly Lys Thr Phe Tyr Ile Gly Ala Gly Ile Asn Lys Asn
        355                 360                 365

Thr Asp Lys Ala Val Tyr Trp Phe Ile Lys Ala Ala Asn Gln Gly Phe
    370                 375                 380

Thr Glu Ala Gln Ala Tyr Ile Gly Met Ile Tyr Phe Lys Gly Lys Tyr
385                 390                 395                 400

Val Ala Lys Asn Glu Lys Lys Gly Phe Tyr Trp Leu Lys Lys Ala Ala
                405                 410                 415

Glu Lys Asp Ser Ala Lys Ala Gln Ala Phe Leu Gly Ala Leu Tyr Ile
            420                 425                 430

Ala Gly Asn Glu Val Lys Pro Asn Ile Lys Glu Gly Val Ala Leu Thr
        435                 440                 445

Lys Lys Ala Ala Leu Gln Gly Asn Tyr Glu Ala Gln Thr Leu Leu Gly
    450                 455                 460

Phe Cys Tyr Glu Asn Gly Leu Glu Val Lys Lys Asp Leu Ile Ala Ala
465                 470                 475                 480

Tyr Ala Leu Tyr Leu Ser Ala Ser Pro His Phe Asp Phe Ala Glu Lys
                485                 490                 495

Ala Arg Leu Asp Leu Glu Arg Lys Leu Ser Glu Gln Glu Ile Ala Lys
            500                 505                 510

Ala Ile Ser Val Asn Thr Ala Lys Leu Phe Glu
        515                 520
```

<210> SEQ ID NO 3
<211> LENGTH: 687
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 3

```
atgaaaaatc gtttcgcgaa tgttgtcgat gctgtgatgc tggcctttct ggtttgcggg     60

tttttgtgc ctgtgatggc tgtcgatacc ggttccgttt ccttttcgga tgagcgcaaa    120

aggcgcgatg cacaggaaga gaccatccgt attcaggaat cggttcaatt gctggacatg    180

gcggccagag agggggagcc gcaggccatg gtgttgctgg gcatgatgag cgatgtcggt    240

tttccggtaa agcgcgatct ggatcgtgcg attggctggt acgtcaaggc ggcggacaaa    300

cagtacggga aggcatggtt gccactggcg tttgcgtatg cggagatggg taacgatgtg    360

caggcggggt tctggtttga aaaagcggcc ggattgtatc gggaaacgaa tgcggatgat    420

gttctggtga tggttttcgg ggccgggtat ctggcggact atatcgggaa agaccagttt    480

gcacaaaggc aggaaatcaa caggaaacgc ctgatgtggc ttgaagggct tgccgcgtcg    540

ggtgatccgg tagcctgttc gatgatggcg acggtttatc gcgaggggct cggggtgaaa    600

aaggatgtca gacgcggcga tctctggtgc aaaaaggcag tgacgacaaa tcgggaaggg    660

atggtcgtgg aacggttctg ttattag                                         687
```

<210> SEQ ID NO 4
<211> LENGTH: 228
<212> TYPE: PRT

-continued

<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 4

```
Met Lys Asn Arg Phe Ala Asn Val Val Asp Ala Val Met Leu Ala Phe
1               5                   10                  15

Leu Val Cys Gly Phe Phe Val Pro Val Met Ala Val Asp Thr Gly Ser
            20                  25                  30

Val Ser Phe Ser Asp Glu Arg Lys Arg Arg Asp Ala Gln Glu Glu Thr
        35                  40                  45

Ile Arg Ile Gln Glu Ser Val Gln Leu Leu Asp Met Ala Ala Arg Glu
    50                  55                  60

Gly Glu Pro Gln Ala Met Val Leu Leu Gly Met Met Ser Asp Val Gly
65                  70                  75                  80

Phe Pro Val Lys Arg Asp Leu Asp Arg Ala Ile Gly Trp Tyr Val Lys
                85                  90                  95

Ala Ala Asp Lys Gln Tyr Gly Lys Ala Trp Leu Pro Leu Ala Phe Ala
            100                 105                 110

Tyr Ala Glu Met Gly Asn Asp Val Gln Ala Gly Phe Trp Phe Glu Lys
        115                 120                 125

Ala Ala Gly Leu Tyr Arg Glu Thr Asn Ala Asp Asp Val Leu Val Met
    130                 135                 140

Val Phe Gly Ala Gly Tyr Leu Ala Asp Tyr Ile Gly Lys Asp Gln Phe
145                 150                 155                 160

Ala Gln Arg Gln Glu Ile Asn Arg Lys Arg Leu Met Trp Leu Glu Gly
                165                 170                 175

Leu Ala Ala Ser Gly Asp Pro Val Ala Cys Ser Met Met Ala Thr Val
            180                 185                 190

Tyr Arg Glu Gly Leu Gly Val Lys Lys Asp Val Arg Arg Gly Asp Leu
        195                 200                 205

Trp Cys Lys Lys Ala Val Thr Thr Asn Arg Glu Gly Met Val Val Glu
    210                 215                 220

Arg Phe Cys Tyr
225
```

<210> SEQ ID NO 5
<211> LENGTH: 1920
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 5

```
atgaagtcag tttcgcatat gggtttttat cgtttcaaaa gttttgtttt ttcagttgtc      60

gtttttgcgg cagggtgtgc atgggtaccg tctgtgtcgt ttgccgggca aaaggatgat     120

tgcgcctctg tcgggtgttc cgatacgacg gtacaaaagg acggggatct ggaaaaaatc     180

aggcaaaagg cgcagcaggg cgatgcaaat gcgcagatgg cactgggttt gcgttacctg     240

atggggaacg gccttgccgc agatgaggtt ctcgcgcagg aatggttttt gaagtcggca     300

cagcaaaata atgtggtggc gcaggtggcg ctggcgacga tgctggcttt cgagagtgac     360

aggcaggatc tgcccgcggc ggcgatgtgg ttttcaaagg cggctgatgc cggaaacgtt     420

caggcgatgt cggagctggt acgtctttac gagacgggca gtggtgtgac acgcgatatg     480

gcgaaagccg aagaatggcg agtccgcgca aaaatgcgca gtgatgccgt caagctggag     540

cgggtgtgga aaatcgctct ggccgataag gcgcggtgga tgaggaaaac gtcacgaccg     600
```

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```
gtggagcttg ccgctcagga tggcgttgcc acaacagcgg caaggattga tgtcgttgcg    660

ttgaagaagg cggctgaaaa cggtgacgat catgcccaaa ccttgcttgg tgctttgctg    720

gccactggcg acggggtgaa aaaggatgag aaagccgcga tcggctggtt tgaaaaagcg    780

gcggattcgg gcaatactca ggcgcaggct gttctggggg aactttatgg attgggctgg    840

ggtggcttga agaaggacga ggcgaaggcg gccaaatgga tggagaaggc ggcgctgggc    900

ggtctggttg ctgcaaaggc ggcgtggggc tcgatgctct cgcaaggtaa aggggtggaa    960

aaggacccga aaaaaggtct tgaatggttt gttcaggcgg gccaggacgg tgatggacgt   1020

acccgtctgt tgatggggat gatgttgatc catcagaacc gggatgcggc cgcacaatgg   1080

ttttatggtg cggctgaggt tggcgatgaa gaggtgcttt ccgctttggg aacgttttac   1140

ggctggggaa acggcccggt gctggatgaa agcgagaagc tttccgaggt acgccgttat   1200

gcccagcggg acgagtccga ggcgcagcag atgatgggtt ttctgtatgg cgaaggctgg   1260

ggtgcaaagc gtgatcctgt aaaggcggaa tactggtttg acaaggcagc tgccagcggc   1320

gatgtggaag tgtggttgcc gcttgggctg ttgtatgccg aaacggggcg tgacgatatg   1380

gcagcggccg cttttgccaa ggcggtggct tcgggcggtt tcgggctggc caatgacggg   1440

gagttgcttc agctgatttt cgtcgattcg gagaagatgc cggatgtggg gaatgccctg   1500

aaacgtccgg cttcggcaaa aaaaacggct tccggtgcca aagagccgaa tgggggaaaa   1560

aaggctggcg taaacgacaa ggacggggtt gccagtgatg aacggcttgt ccgcgtggcg   1620

aagaaacggg cttttgttct ggccgaagcg aaaaagggca atccggctgc gcagttgatg   1680

atggcccgta ttctgaaaga aggttggggg gtgaagaagg atgaggaggc agcagcgtct   1740

ttgcgtgctg acggtatcag ggggatgtgt gctgccctga aggacaaggc ggaggaagag   1800

cctttatgtt cgaatgaagg ggacggtgga aacggtggcg ttttgccgga tgccgcttca   1860

gtcgacaagg cggatgtgaa tgattcgacg gtgtttaagg cgagacagga gatgaactga   1920
```

```
<210> SEQ ID NO 6
<211> LENGTH: 639
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 6

Met Lys Ser Val Ser His Met Gly Phe Tyr Arg Phe Lys Ser Phe Val
1               5                   10                  15

Phe Ser Val Val Val Phe Ala Ala Gly Cys Ala Trp Val Pro Ser Val
            20                  25                  30

Ser Phe Ala Gly Gln Lys Asp Asp Cys Ala Ser Val Gly Cys Ser Asp
        35                  40                  45

Thr Thr Val Gln Lys Asp Gly Asp Leu Glu Lys Ile Arg Gln Lys Ala
    50                  55                  60

Gln Gln Gly Asp Ala Asn Ala Gln Met Ala Leu Gly Leu Arg Tyr Leu
65                  70                  75                  80

Met Gly Asn Gly Leu Ala Ala Asp Glu Val Leu Ala Gln Glu Trp Phe
                85                  90                  95

Leu Lys Ser Ala Gln Gln Asn Asn Val Val Ala Gln Val Ala Leu Ala
            100                 105                 110

Thr Met Leu Ala Phe Glu Ser Asp Arg Gln Asp Leu Pro Ala Ala Ala
        115                 120                 125
```

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```
Met Trp Phe Ser Lys Ala Ala Asp Ala Gly Asn Val Gln Ala Met Ser
    130                 135                 140

Glu Leu Val Arg Leu Tyr Glu Thr Gly Ser Gly Val Thr Arg Asp Met
145                 150                 155                 160

Ala Lys Ala Glu Glu Trp Arg Val Arg Ala Lys Met Arg Ser Asp Ala
                165                 170                 175

Val Lys Leu Glu Arg Val Trp Lys Ile Ala Leu Ala Asp Lys Ala Arg
            180                 185                 190

Trp Met Arg Lys Thr Ser Arg Pro Val Glu Leu Ala Ala Gln Asp Gly
        195                 200                 205

Val Ala Thr Thr Ala Ala Arg Ile Asp Val Val Ala Leu Lys Lys Ala
    210                 215                 220

Ala Glu Asn Gly Asp Asp His Ala Gln Thr Leu Leu Gly Ala Leu Leu
225                 230                 235                 240

Ala Thr Gly Asp Gly Val Lys Lys Asp Glu Lys Ala Ala Ile Gly Trp
                245                 250                 255

Phe Glu Lys Ala Ala Asp Ser Gly Asn Thr Gln Ala Gln Ala Val Leu
            260                 265                 270

Gly Glu Leu Tyr Gly Leu Gly Trp Gly Gly Leu Lys Lys Asp Glu Ala
        275                 280                 285

Lys Ala Ala Lys Trp Met Glu Lys Ala Ala Leu Gly Gly Leu Val Ala
    290                 295                 300

Ala Lys Ala Ala Trp Gly Ser Met Leu Ser Gln Gly Lys Gly Val Glu
305                 310                 315                 320

Lys Asp Pro Lys Lys Gly Leu Glu Trp Phe Val Gln Ala Gly Gln Asp
                325                 330                 335

Gly Asp Gly Arg Thr Arg Leu Leu Met Gly Met Met Leu Ile His Gln
            340                 345                 350

Asn Arg Asp Ala Ala Ala Gln Trp Phe Tyr Gly Ala Ala Glu Val Gly
        355                 360                 365

Asp Glu Glu Val Leu Ser Ala Leu Gly Thr Phe Tyr Gly Trp Gly Asn
    370                 375                 380

Gly Pro Val Leu Asp Glu Ser Glu Lys Leu Ser Glu Val Arg Arg Tyr
385                 390                 395                 400

Ala Gln Arg Asp Glu Ser Glu Ala Gln Gln Met Met Gly Phe Leu Tyr
                405                 410                 415

Gly Glu Gly Trp Gly Ala Lys Arg Asp Pro Val Lys Ala Glu Tyr Trp
            420                 425                 430

Phe Asp Lys Ala Ala Ala Ser Gly Asp Val Glu Val Trp Leu Pro Leu
        435                 440                 445

Gly Leu Leu Tyr Ala Glu Thr Gly Arg Asp Asp Met Ala Ala Ala Ala
    450                 455                 460

Phe Ala Lys Ala Val Ala Ser Gly Gly Phe Gly Leu Ala Asn Asp Gly
465                 470                 475                 480

Glu Leu Leu Gln Leu Ile Phe Val Asp Ser Glu Lys Met Pro Asp Val
                485                 490                 495

Gly Asn Ala Leu Lys Arg Pro Ala Ser Ala Lys Lys Thr Ala Ser Gly
            500                 505                 510

Ala Lys Glu Pro Asn Gly Gly Lys Lys Ala Gly Val Asn Asp Lys Asp
        515                 520                 525
```

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```
Gly Val Ala Ser Asp Glu Arg Leu Val Arg Val Ala Lys Lys Arg Ala
    530                 535                 540

Phe Val Leu Ala Glu Ala Lys Lys Gly Asn Pro Ala Ala Gln Leu Met
545                 550                 555                 560

Met Ala Arg Ile Leu Lys Glu Gly Trp Gly Val Lys Lys Asp Glu Glu
                565                 570                 575

Ala Ala Ala Ser Leu Arg Ala Asp Gly Ile Arg Gly Met Cys Ala Ala
            580                 585                 590

Leu Lys Asp Lys Ala Glu Glu Glu Pro Leu Cys Ser Asn Glu Gly Asp
        595                 600                 605

Gly Gly Asn Gly Gly Val Leu Pro Asp Ala Ala Ser Val Asp Lys Ala
    610                 615                 620

Asp Val Asn Asp Ser Thr Val Phe Lys Ala Arg Gln Glu Met Asn
625                 630                 635


<210> SEQ ID NO 7
<211> LENGTH: 456
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 7

atggctttgg cggatggggc ggctgctccg gtggcagtga cgtcttatgc gcagcagccg      60

ttgaagctgg tgcaggaaaa ggcttctgac ggggatgggt ctgccgaact tgaactgggt     120

ttgcggtatg ttttcggctc tgacggggtc aaaaatgtgc cgctcggggt ttcctggatc     180

aataaggcgg ctctaaaggg tattccgcag gcggagcatg agatggggtc gctgtatctg     240

atggggattg gcgttgccca aagcaatgtg atggctgtgg cctggtacag gaaggcggca     300

attcagggtt acgccccgtc gcaaacggcg atggggtatg cgtatgaaga aggggccggg     360

gtgccacagg atgcggatct ggcccgttac tggtttgaca aggcggcggc acagggaaat     420

ggtattgccg tggaaagcct tgaaggaggg atgtag                               456


<210> SEQ ID NO 8
<211> LENGTH: 151
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 8

Met Ala Leu Ala Asp Gly Ala Ala Ala Pro Val Ala Val Thr Ser Tyr
1               5                   10                  15

Ala Gln Gln Pro Leu Lys Leu Val Gln Glu Lys Ala Ser Asp Gly Asp
            20                  25                  30

Gly Ser Ala Glu Leu Glu Leu Gly Leu Arg Tyr Val Phe Gly Ser Asp
        35                  40                  45

Gly Val Lys Asn Val Pro Leu Gly Val Ser Trp Ile Asn Lys Ala Ala
    50                  55                  60

Leu Lys Gly Ile Pro Gln Ala Glu His Glu Met Gly Ser Leu Tyr Leu
65                  70                  75                  80

Met Gly Ile Gly Val Ala Gln Ser Asn Val Met Ala Val Ala Trp Tyr
                85                  90                  95

Arg Lys Ala Ala Ile Gln Gly Tyr Ala Pro Ser Gln Thr Ala Met Gly
            100                 105                 110

Tyr Ala Tyr Glu Glu Gly Ala Gly Val Pro Gln Asp Ala Asp Leu Ala
        115                 120                 125
```

-continued

Arg Tyr Trp Phe Asp Lys Ala Ala Ala Gln Gly Asn Gly Ile Ala Val
    130   135   140

Glu Ser Leu Glu Gly Gly Met
145   150

<210> SEQ ID NO 9
<211> LENGTH: 1470
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 9

atgaaaagac gggttttgta tggtgtgctg tttgcggtgc tggcggggtg ttctgccggt 60

gcgttggcgt ccgtgtccgg cttgtcggat gggctggcgc agcttgaacg gaggcagttc 120

gaatcggctt atgcgacgct catgccggag gcggagaagg ggaatccccg tgcggcgctg 180

gaggtgggga agctgctgtt gacggggcgc ggggtggcaa aggatgaagc ggcggcggtg 240

aagtggcttc tggtggcggc ggatagtggc aaccgggatg cgcagtatat gctgggggcg 300

atgtcggtgg aggggatcgg tctgccgaag gattctcagg tggcgttgac ctggctgtcg 360

aaggcggcgg cgcaggggga tgcgcgtgcg aagacggctt tggggattct gatgcagtcc 420

gccgggccgg gatcgcagca tacggaacag gcagcccggt ggttcgagag ggcggcggcg 480

tcaggggaac cggaggcgca acggcgctgg gcgctgatgc tggcgtctgg ccgggggggtg 540

gccaaaaatg agggtgaggc actgaaatgg tttaagaagg cggctgtcgc gggggatgtg 600

gaagcgcagc gcaatctggg gattatgctc tcgacgggaa agggggtgac gggcggcaag 660

ccggattttg cggaagcggc acgctggtac ggcctggcag cgaagaaggg ggatgcgaag 720

gcgcagtatg ggttgggcat tttgtatgcg aaggggcagg gggtggcgcc cgatcaggaa 780

aaggcgctga ttctgtatcg catggcggcg actcaggggc tggcgacggc ggagtatgcc 840

gtcgggctgg cgtatgcgta tggacggggg acggcacaaa atgatgtgaa ggcggccgac 900

tggttcgagg cggcggcgca gcagggggtg gtgcgtgcgc aatataatct cgctctgatg 960

ctggaggcgg gtcgcggtcg gcctgtggat acggtggcgg cgagcaagtg gtttttgatg 1020

gcggcggaga agggcttgcg ggaggcacaa tacaatatgg ggtatcacta tgccgagggg 1080

aaaggggtgc cacgcgatca gggcaaggcg gtgttctggt atgaaaaggc ggcggctgcc 1140

ggggatgtga aggcccagta caatctgggg atgctgtatc tgaacggggt taatggcaag 1200

gcggatgacg aaaaggcggc ttttttctac cggatggcgg ccggggcggg atatggcccg 1260

gcgatgtacc ggctggcggt gttgtatgag gaaggccgtg gggtaaagca gagttatcag 1320

ctggcagggg aatggtatga gcgggcggat ctggccgcga aagtgaagat tgacgaggcg 1380

atgaaaaaga atccgcatcc gtttgtgcaa cggactctgc aggtgccgga tgatttgaat 1440

caatcttcag ataaattggc gggacattag 1470

<210> SEQ ID NO 10
<211> LENGTH: 489
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 10

Met Lys Arg Arg Val Leu Tyr Gly Val Leu Phe Ala Val Leu Ala Gly
1   5   10   15

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```
Cys Ser Ala Gly Ala Leu Ala Ser Val Ser Gly Leu Ser Asp Gly Leu
            20                  25                  30

Ala Gln Leu Glu Arg Arg Gln Phe Glu Ser Ala Tyr Ala Thr Leu Met
        35                  40                  45

Pro Glu Ala Glu Lys Gly Asn Pro Arg Ala Ala Leu Glu Val Gly Lys
    50                  55                  60

Leu Leu Leu Thr Gly Arg Gly Val Ala Lys Asp Glu Ala Ala Ala Val
65                  70                  75                  80

Lys Trp Leu Leu Val Ala Ala Asp Ser Gly Asn Arg Asp Ala Gln Tyr
                85                  90                  95

Met Leu Gly Ala Met Ser Val Glu Gly Ile Gly Leu Pro Lys Asp Ser
            100                 105                 110

Gln Val Ala Leu Thr Trp Leu Ser Lys Ala Ala Ala Gln Gly Asp Ala
        115                 120                 125

Arg Ala Lys Thr Ala Leu Gly Ile Leu Met Gln Ser Ala Gly Pro Gly
    130                 135                 140

Ser Gln His Thr Glu Gln Ala Ala Arg Trp Phe Glu Arg Ala Ala Ala
145                 150                 155                 160

Ser Gly Glu Pro Glu Ala Gln Arg Arg Trp Ala Leu Met Leu Ala Ser
                165                 170                 175

Gly Arg Gly Val Ala Lys Asn Glu Gly Glu Ala Leu Lys Trp Phe Lys
            180                 185                 190

Lys Ala Ala Val Ala Gly Asp Val Glu Ala Gln Arg Asn Leu Gly Ile
        195                 200                 205

Met Leu Ser Thr Gly Lys Gly Val Thr Gly Gly Lys Pro Asp Phe Ala
    210                 215                 220

Glu Ala Ala Arg Trp Tyr Gly Leu Ala Ala Lys Lys Gly Asp Ala Lys
225                 230                 235                 240

Ala Gln Tyr Gly Leu Gly Ile Leu Tyr Ala Lys Gly Gln Gly Val Ala
                245                 250                 255

Pro Asp Gln Glu Lys Ala Leu Ile Leu Tyr Arg Met Ala Ala Thr Gln
            260                 265                 270

Gly Leu Ala Thr Ala Glu Tyr Ala Val Gly Leu Ala Tyr Ala Tyr Gly
        275                 280                 285

Arg Gly Thr Ala Gln Asn Asp Val Lys Ala Ala Asp Trp Phe Glu Ala
    290                 295                 300

Ala Ala Gln Gln Gly Val Val Arg Ala Gln Tyr Asn Leu Ala Leu Met
305                 310                 315                 320

Leu Glu Ala Gly Arg Gly Arg Pro Val Asp Thr Val Ala Ala Ser Lys
                325                 330                 335

Trp Phe Leu Met Ala Ala Glu Lys Gly Leu Arg Glu Ala Gln Tyr Asn
            340                 345                 350

Met Gly Tyr His Tyr Ala Glu Gly Lys Gly Val Pro Arg Asp Gln Gly
        355                 360                 365

Lys Ala Val Phe Trp Tyr Glu Lys Ala Ala Ala Ala Gly Asp Val Lys
    370                 375                 380

Ala Gln Tyr Asn Leu Gly Met Leu Tyr Leu Asn Gly Val Asn Gly Lys
385                 390                 395                 400

Ala Asp Asp Glu Lys Ala Ala Phe Phe Tyr Arg Met Ala Ala Gly Ala
                405                 410                 415

Gly Tyr Gly Pro Ala Met Tyr Arg Leu Ala Val Leu Tyr Glu Glu Gly
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            420                 425                 430

Arg Gly Val Lys Gln Ser Tyr Gln Leu Ala Gly Glu Trp Tyr Glu Arg
        435                 440                 445

Ala Asp Leu Ala Ala Lys Val Lys Ile Asp Glu Ala Met Lys Lys Asn
    450                 455                 460

Pro His Pro Phe Val Gln Arg Thr Leu Gln Val Pro Asp Asp Leu Asn
465                 470                 475                 480

Gln Ser Ser Asp Lys Leu Ala Gly His
                485


<210> SEQ ID NO 11
<211> LENGTH: 1206
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 11

atgaaaaaag gggttgcgtt cgcgctggtg gctcttggga gcatactggt ttgtacggcc      60

ttggccggaa gcgaaaagaa actggacgcc ttgctggcga tgccggtgaa agagacaaag     120

gtttttgtcg aatcgaatga agagccgttg tttgtgatgt tgaaaagctc gttgtccgaa     180

gagacggatg aaactgtcgg gaagccggtt gtttcggaaa agacggcaga gccgggacaa     240

gacaatgacg gtgaaacagg gggagcctgg atgcagcagc tgcggcatca ggcggatcag     300

ggggatgcga aatccgcttt ctggctgggc cggttcacgg ttgaggacag ccgggacggg     360

aaaacgattg acgagggcat ccgtctgatc cggcgttctg ccgaaggggg attcgtgcgg     420

gcacaattgt atctcggcac gctgtatgcc aatgggactc atgtgaaggc tgacccgcac     480

gaggcggaaa aatggctttc cagggccgca gggcaaggtt ctccgatggt tcagctttat     540

ctcggcctga tgtatggtca tggcaagggt gttccccgtg acttgaacaa gtcgcttttc     600

tgggtggaaa aggcggcgga caggggcttg ccgcatgcgc agctggcgcg tgggcttttt     660

gcgtcgtttt cccattatta tccccgggat gatgaaaagg ccgtgctgta tctgacgaaa     720

gcggcaaagc aggggatgcc gatggcccag ttttatctgg cgctgatgta tcagcgtggc     780

cggggtgtcg aacagagtaa cgagcaggcc ttgcactgga atatgctggc ggcggaacag     840

ggctatccgg atgccgagta tgcgatgtcg cggatggcgg aactcggtat cggggtgacg     900

gccgataagg catggagcat gatgtggctg gatcgtgccg cccatcacgg gatgccgctg     960

gcgcaatatt tgatgggcat ggcctatctg gaaggaaaat cggtcccgca ggacttgcct    1020

gttgcggcgg catggtttta caaggcggcg atgcagggaa atgccgatgc ccagttgcga    1080

ctcggttata tgtatgccag gggaatcggt gttcctgtgg acaagccgaa ggcggttgcc    1140

tggcttgaaa aggccgcttc ggctggcaat acggtggccg ggcagtggct gaaacaactg    1200

gattga                                                               1206


<210> SEQ ID NO 12
<211> LENGTH: 401
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 12

Met Lys Lys Gly Val Ala Phe Ala Leu Val Ala Leu Gly Ser Ile Leu
1               5                   10                  15

Val Cys Thr Ala Leu Ala Gly Ser Glu Lys Lys Leu Asp Ala Leu Leu
```

-continued

```
            20                  25                  30

Ala Met Pro Val Lys Glu Thr Lys Val Phe Val Glu Ser Asn Glu Glu
        35                  40                  45

Pro Leu Phe Val Met Leu Lys Ser Ser Leu Ser Glu Glu Thr Asp Glu
    50                  55                  60

Thr Val Gly Lys Pro Val Val Ser Glu Lys Thr Ala Glu Pro Gly Gln
65                  70                  75                  80

Asp Asn Asp Gly Glu Thr Gly Gly Ala Trp Met Gln Gln Leu Arg His
                85                  90                  95

Gln Ala Asp Gln Gly Asp Ala Lys Ser Ala Phe Trp Leu Gly Arg Phe
            100                 105                 110

Thr Val Glu Asp Ser Arg Asp Gly Lys Thr Ile Asp Glu Gly Ile Arg
        115                 120                 125

Leu Ile Arg Arg Ser Ala Glu Gly Gly Phe Val Arg Ala Gln Leu Tyr
    130                 135                 140

Leu Gly Thr Leu Tyr Ala Asn Gly Thr His Val Lys Ala Asp Pro His
145                 150                 155                 160

Glu Ala Glu Lys Trp Leu Ser Arg Ala Ala Gly Gln Gly Ser Pro Met
                165                 170                 175

Val Gln Leu Tyr Leu Gly Leu Met Tyr Gly His Gly Lys Gly Val Pro
            180                 185                 190

Arg Asp Leu Asn Lys Ser Leu Phe Trp Val Glu Lys Ala Ala Asp Arg
        195                 200                 205

Gly Leu Pro His Ala Gln Leu Ala Arg Gly Leu Phe Ala Ser Phe Ser
    210                 215                 220

His Tyr Tyr Pro Arg Asp Asp Glu Lys Ala Val Leu Tyr Leu Thr Lys
225                 230                 235                 240

Ala Ala Lys Gln Gly Met Pro Met Ala Gln Phe Tyr Leu Ala Leu Met
                245                 250                 255

Tyr Gln Arg Gly Arg Gly Val Glu Gln Ser Asn Glu Gln Ala Leu His
            260                 265                 270

Trp Asn Met Leu Ala Ala Glu Gln Gly Tyr Pro Asp Ala Glu Tyr Ala
        275                 280                 285

Met Ser Arg Met Ala Glu Leu Gly Ile Gly Val Thr Ala Asp Lys Ala
    290                 295                 300

Trp Ser Met Met Trp Leu Asp Arg Ala Ala His His Gly Met Pro Leu
305                 310                 315                 320

Ala Gln Tyr Leu Met Gly Met Ala Tyr Leu Glu Gly Lys Ser Val Pro
                325                 330                 335

Gln Asp Leu Pro Val Ala Ala Ala Trp Phe Tyr Lys Ala Ala Met Gln
            340                 345                 350

Gly Asn Ala Asp Ala Gln Leu Arg Leu Gly Tyr Met Tyr Ala Arg Gly
        355                 360                 365

Ile Gly Val Pro Val Asp Lys Pro Lys Ala Val Ala Trp Leu Glu Lys
    370                 375                 380

Ala Ala Ser Ala Gly Asn Thr Val Ala Gly Gln Trp Leu Lys Gln Leu
385                 390                 395                 400

Asp
```

<210> SEQ ID NO 13
<211> LENGTH: 900

-continued

<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 13

atgaagaaaa ccatctatca attcgcactt atttttatta ccttaagttt tttaacggcg 60
tgtacaggca atattgattc ggaaagcgaa aataaaggta ttcaacatta taaaaatggg 120
gaatatcaaa aagcaattcc cttattggag aaagctgaag atggcggcag ttccagtgcc 180
gcattctatc ttggagaaat atttcgtaaa ggtgaaggcg ttaatcaaga ttttgggaga 240
tcatgtacgc attatataaa atcagcaaaa ggtggtaata acaatgccta tttactggcc 300
ggttcgtgtt tcgtaatggg aaaaggtgtg aagcaggatt ttgcagaagc attgaaatgg 360
tttaaaaaag cgtccgatga aagtgaaaaa actgatttga ctgaatctga caagaaatat 420
ttaacgcgat cattggccac aatgtactat tccggaaaag gaaccctgca agacttcagc 480
gaagccgcaa agtgggcgga aaaagcggct gaactgggtg atgcgaattc acaggcggtt 540
atggcgttcc tgctttatac ggggcagggc gttctggctg acaggaaggc tgcccggata 600
tgggcgcaaa aatcagcgga tcagggaaac gatctggggg aagtcctgat gggtgtattc 660
aatcaatatg ctgattcccc ggacatgaaa gcggcctttg actggtatga gaaatcggca 720
aaacagggca acccggccgc gcagtatcaa ttgggaacgt tttatgaaga aggcattatt 780
gttcctgaag acattgaaaa agcccacgct tgttataaac aggcggccga tagcaaaaag 840
tcggatactc tggtcaaggc tctgatggat ttcgaggcgc gacagaaaaa acagaaatga 900

<210> SEQ ID NO 14
<211> LENGTH: 299
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 14

Met Lys Lys Thr Ile Tyr Gln Phe Ala Leu Ile Phe Ile Thr Leu Ser
1   5   10   15

Phe Leu Thr Ala Cys Thr Gly Asn Ile Asp Ser Glu Ser Glu Asn Lys
            20   25   30

Gly Ile Gln His Tyr Lys Asn Gly Glu Tyr Gln Lys Ala Ile Pro Leu
        35   40   45

Leu Glu Lys Ala Glu Asp Gly Gly Ser Ser Ser Ala Ala Phe Tyr Leu
    50   55   60

Gly Glu Ile Phe Arg Lys Gly Glu Gly Val Asn Gln Asp Phe Gly Arg
65   70   75   80

Ser Cys Thr His Tyr Ile Lys Ser Ala Lys Gly Gly Asn Asn Asn Ala
                85   90   95

Tyr Leu Leu Ala Gly Ser Cys Phe Val Met Gly Lys Gly Val Lys Gln
            100   105   110

Asp Phe Ala Glu Ala Leu Lys Trp Phe Lys Lys Ala Ser Asp Glu Ser
        115   120   125

Glu Lys Thr Asp Leu Thr Glu Ser Asp Lys Lys Tyr Leu Thr Arg Ser
    130   135   140

Leu Ala Thr Met Tyr Tyr Ser Gly Lys Gly Thr Leu Gln Asp Phe Ser
145   150   155   160

Glu Ala Ala Lys Trp Ala Glu Lys Ala Ala Glu Leu Gly Asp Ala Asn
                165   170   175

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```
Ser Gln Ala Val Met Ala Phe Leu Leu Tyr Thr Gly Gln Gly Val Leu
            180                 185                 190

Ala Asp Arg Lys Ala Ala Arg Ile Trp Ala Gln Lys Ser Ala Asp Gln
        195                 200                 205

Gly Asn Asp Leu Gly Glu Val Leu Met Gly Val Phe Asn Gln Tyr Ala
    210                 215                 220

Asp Ser Pro Asp Met Lys Ala Ala Phe Asp Trp Tyr Glu Lys Ser Ala
225                 230                 235                 240

Lys Gln Gly Asn Pro Ala Ala Gln Tyr Gln Leu Gly Thr Phe Tyr Glu
                245                 250                 255

Glu Gly Ile Ile Val Pro Glu Asp Ile Glu Lys Ala His Ala Cys Tyr
            260                 265                 270

Lys Gln Ala Ala Asp Ser Lys Lys Ser Asp Thr Leu Val Lys Ala Leu
        275                 280                 285

Met Asp Phe Glu Ala Arg Gln Lys Lys Gln Lys
    290                 295


<210> SEQ ID NO 15
<211> LENGTH: 918
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 15

atgtcaaaac agggtgacag gagaaggaca gggatgaaga tgtcgggttt cagatttgcg     60

ttgggggtgt cggtatgtct gttgacggta tgggttccag cgacgtctat ggcaggaaac    120

gtgtcggcgt cggcatatca gatgtctcaa ggcgaagacg aagcatggac gttttatcgt    180

accggacagt acgggaaggc actggccgct ttcagggggc tggagacgaa aggggatgtt    240

gccgccttgt atggactggg tgtgatggcg acgaatggtc tcggtatgcc ccgtaatgat    300

gaaaaggcgc tggtatggtt tagggaaggg gcggcaaaag gctcgcgtga ggcgcaattc    360

gggctggggg cgatgtacga tttgagtcgc ggtgtccggc aggatatgac gctggcgatc    420

gactggtatg aaaagtcggc gagagcggga tatgcgccgg ctctgacgcg gctgggcagg    480

atgaatttgc tggggagggg gatgtcccgc aattatggga aggcgttccg gtttttcaaa    540

cagtcggcac agcgtgggga tagggacggt gagttttatt tcgggatgat gtttatccgt    600

ggctggggga cgaagcggga tgtggaagag gcggctggct ggatcagaaa ggcggcggag    660

aagggacagc cggaagcgat gcgggtgatg tcgaccttgt atgagggtgg ttatggcgtt    720

gcccaaagtg agaaagatgc gctcgtctgg ctggaaaaga gcgttgatgc gggcgacagg    780

gaagcgatga ggcggctggc agcggtgtat gaaaacggca cgttcggtgt gacgccggac    840

aaggagaagg cccgtttgct gaaaaagaag gcagccgagg tgaaaaaggc tgtttttccg    900

gattatgccg tgatgtag                                                  918


<210> SEQ ID NO 16
<211> LENGTH: 305
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 16

Met Ser Lys Gln Gly Asp Arg Arg Arg Thr Gly Met Lys Met Ser Gly
1               5                   10                  15

Phe Arg Phe Ala Leu Gly Val Ser Val Cys Leu Leu Thr Val Trp Val
```

-continued

```
            20                  25                  30

Pro Ala Thr Ser Met Ala Gly Asn Val Ser Ala Ser Ala Tyr Gln Met
        35                  40                  45

Ser Gln Gly Glu Asp Glu Ala Trp Thr Phe Tyr Arg Thr Gly Gln Tyr
    50                  55                  60

Gly Lys Ala Leu Ala Ala Phe Arg Gly Leu Glu Thr Lys Gly Asp Val
65                  70                  75                  80

Ala Ala Leu Tyr Gly Leu Gly Val Met Ala Thr Asn Gly Leu Gly Met
                85                  90                  95

Pro Arg Asn Asp Glu Lys Ala Leu Val Trp Phe Arg Glu Gly Ala Ala
            100                 105                 110

Lys Gly Ser Arg Glu Ala Gln Phe Gly Leu Gly Ala Met Tyr Asp Leu
        115                 120                 125

Ser Arg Gly Val Arg Gln Asp Met Thr Leu Ala Ile Asp Trp Tyr Glu
    130                 135                 140

Lys Ser Ala Arg Ala Gly Tyr Ala Pro Ala Leu Thr Arg Leu Gly Arg
145                 150                 155                 160

Met Asn Leu Leu Gly Arg Gly Met Ser Arg Asn Tyr Gly Lys Ala Phe
                165                 170                 175

Arg Phe Phe Lys Gln Ser Ala Gln Arg Gly Asp Arg Asp Gly Glu Phe
            180                 185                 190

Tyr Phe Gly Met Met Phe Ile Arg Gly Trp Gly Thr Lys Arg Asp Val
        195                 200                 205

Glu Glu Ala Ala Gly Trp Ile Arg Lys Ala Ala Glu Lys Gly Gln Pro
    210                 215                 220

Glu Ala Met Arg Val Met Ser Thr Leu Tyr Glu Gly Gly Tyr Gly Val
225                 230                 235                 240

Ala Gln Ser Glu Lys Asp Ala Leu Val Trp Leu Glu Lys Ser Val Asp
                245                 250                 255

Ala Gly Asp Arg Glu Ala Met Arg Arg Leu Ala Ala Val Tyr Glu Asn
            260                 265                 270

Gly Thr Phe Gly Val Thr Pro Asp Lys Glu Lys Ala Arg Leu Leu Lys
        275                 280                 285

Lys Lys Ala Ala Glu Val Lys Lys Ala Val Phe Pro Asp Tyr Ala Val
    290                 295                 300

Met
305
```

<210> SEQ ID NO 17
<211> LENGTH: 819
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 17

```
atgatgaaaa ccatcctcaa agccctcttc ttcgcattca ttctgattgg ttccactctg      60

gcgttcgccg acaatgttga agaaggcaac catctctata atgctggaaa atatcaggaa     120

gccctgacct tttcatgaa accggatgcg gtcaataacc cagccaccat gaaccggatc      180

gggtatatgt acgacgaagg tcagggagtc aaaaaagatc caaaagaagc cttcaagtgg     240

tacaaaaaag cagctgatgc caatttacca gttgcccagt ttaatctggg gcttatgtat     300

caacatggca ccggcgtctc aaaagatatc aatgaatcca ttaaatggtt tcgtaaagca     360
```

-continued

```
gcagaacaaa atgatcccga cgctgaaatg aaaatgggct atttgaccgc aacaggaaca    420

ggggtcaaaa aagattatca agaagctata caatggtatc aacgcgctgc tgaacatggc    480

gatagtgcag cttatgcaca aattggactt ttctatactc tgggcaatgg tgtcaaaaaa    540

gacgtcaacc gtgctgtcca gtattacatt atgggcgctc aaaagggtga tgccagagca    600

caggcctttt tgggaaaagc atatgccttg ggcagaggta tccaaccgga tagtgaaaaa    660

gccctctact ggtacaaaac agccgccaga aacggcaacg tcaacgccat gaaagaactg    720

ggttccatct atgcaaaagg ccgtctcggt gtcaagccag accagcagga agcacaacga    780

tggaacgaca tggccagaaa agctgaacag aaaaattaa                           819
```

```
<210> SEQ ID NO 18
<211> LENGTH: 272
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 18

Met Met Lys Thr Ile Leu Lys Ala Leu Phe Phe Ala Phe Ile Leu Ile
1               5                   10                  15

Gly Ser Thr Leu Ala Phe Ala Asp Asn Val Glu Glu Gly Asn His Leu
            20                  25                  30

Tyr Asn Ala Gly Lys Tyr Gln Glu Ala Leu Thr Phe Phe Met Lys Pro
        35                  40                  45

Asp Ala Val Asn Asn Pro Ala Thr Met Asn Arg Ile Gly Tyr Met Tyr
    50                  55                  60

Asp Glu Gly Gln Gly Val Lys Lys Asp Pro Lys Glu Ala Phe Lys Trp
65                  70                  75                  80

Tyr Lys Lys Ala Ala Asp Ala Asn Leu Pro Val Ala Gln Phe Asn Leu
                85                  90                  95

Gly Leu Met Tyr Gln His Gly Thr Gly Val Ser Lys Asp Ile Asn Glu
            100                 105                 110

Ser Ile Lys Trp Phe Arg Lys Ala Ala Glu Gln Asn Asp Pro Asp Ala
        115                 120                 125

Glu Met Lys Met Gly Tyr Leu Thr Ala Thr Gly Thr Gly Val Lys Lys
    130                 135                 140

Asp Tyr Gln Glu Ala Ile Gln Trp Tyr Gln Arg Ala Ala Glu His Gly
145                 150                 155                 160

Asp Ser Ala Ala Tyr Ala Gln Ile Gly Leu Phe Tyr Thr Leu Gly Asn
                165                 170                 175

Gly Val Lys Lys Asp Val Asn Arg Ala Val Gln Tyr Tyr Ile Met Gly
            180                 185                 190

Ala Gln Lys Gly Asp Ala Arg Ala Gln Ala Phe Leu Gly Lys Ala Tyr
        195                 200                 205

Ala Leu Gly Arg Gly Ile Gln Pro Asp Ser Glu Lys Ala Leu Tyr Trp
    210                 215                 220

Tyr Lys Thr Ala Ala Arg Asn Gly Asn Val Asn Ala Met Lys Glu Leu
225                 230                 235                 240

Gly Ser Ile Tyr Ala Lys Gly Arg Leu Gly Val Lys Pro Asp Gln Gln
                245                 250                 255

Glu Ala Gln Arg Trp Asn Asp Met Ala Arg Lys Ala Glu Gln Lys Asn
            260                 265                 270
```

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<210> SEQ ID NO 19
<211> LENGTH: 816
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 19

```
atgaaaattt cttacaagct atttctttct ttcattttaa tgctgtgttc ttccgctgtt     60

tttgctgaca atgctcttac agggatcgag ttatacaaag caaaaaaata tgaacaggcc    120

atgacccacc tcatgacgcc tgatgcccag aaaaaccctg cagcacaaaa tcttattgga    180

tatctctatg ataagggctt aggtgtagaa aaaaacgctg aaatagccaa tcaatggtat    240

cttaaagcag ctgaacaggg atttgccaaa gctcaattca accttggact ctcttatgaa    300

aagggtactg gcatttcaaa aaatatggtt gaagctgtca aatggtatcg caaagcagct    360

gaacaaaatc acgccaaagc tgaaatgaaa atggggtatc tcacagtaga aggtatcggt    420

actcaaaaga attacaaaga agccttgcaa tggtatcggc gcgcagcaga acatggtgat    480

aatagggctt atgcagacat tggcctcttc tatgatcagg gaaacggtgt caaaaaagac    540

cccaaccggg ctgtccagta ttacatcatg ggtgcagaaa agggcgatgg cgaagcacag    600

ctttttctcg cggattgcta cgcgaaagca agcgggattc cttatgatgc cgatcgcgcc    660

ttgtattggt acaaggaatc cgccaaaaac ggaaatatca ctgcgatgaa ggtgttgtcc    720

ggcatttaca aacttggcca attgggtata gagaagaatc cggaaaaatc ccgacactgg    780

cttgagatgg ccaaacaaaa agaagctcag ccatga                              816
```

<210> SEQ ID NO 20
<211> LENGTH: 271
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 20

```
Met Lys Ile Ser Tyr Lys Leu Phe Leu Ser Phe Ile Leu Met Leu Cys
1               5                   10                  15

Ser Ser Ala Val Phe Ala Asp Asn Ala Leu Thr Gly Ile Glu Leu Tyr
            20                  25                  30

Lys Ala Lys Lys Tyr Glu Gln Ala Met Thr His Leu Met Thr Pro Asp
        35                  40                  45

Ala Gln Lys Asn Pro Ala Ala Gln Asn Leu Ile Gly Tyr Leu Tyr Asp
    50                  55                  60

Lys Gly Leu Gly Val Glu Lys Asn Ala Glu Ile Ala Asn Gln Trp Tyr
65                  70                  75                  80

Leu Lys Ala Ala Glu Gln Gly Phe Ala Lys Ala Gln Phe Asn Leu Gly
                85                  90                  95

Leu Ser Tyr Glu Lys Gly Thr Gly Ile Ser Lys Asn Met Val Glu Ala
            100                 105                 110

Val Lys Trp Tyr Arg Lys Ala Ala Glu Gln Asn His Ala Lys Ala Glu
        115                 120                 125

Met Lys Met Gly Tyr Leu Thr Val Glu Gly Ile Gly Thr Gln Lys Asn
    130                 135                 140

Tyr Lys Glu Ala Leu Gln Trp Tyr Arg Arg Ala Ala Glu His Gly Asp
145                 150                 155                 160

Asn Arg Ala Tyr Ala Asp Ile Gly Leu Phe Tyr Asp Gln Gly Asn Gly
                165                 170                 175
```

-continued

```
Val Lys Lys Asp Pro Asn Arg Ala Val Gln Tyr Tyr Ile Met Gly Ala
            180                 185                 190

Glu Lys Gly Asp Gly Glu Ala Gln Leu Phe Leu Ala Asp Cys Tyr Ala
        195                 200                 205

Lys Ala Ser Gly Ile Pro Tyr Asp Ala Asp Arg Ala Leu Tyr Trp Tyr
    210                 215                 220

Lys Glu Ser Ala Lys Asn Gly Asn Ile Thr Ala Met Lys Val Leu Ser
225                 230                 235                 240

Gly Ile Tyr Lys Leu Gly Gln Leu Gly Ile Glu Lys Asn Pro Glu Lys
                245                 250                 255

Ser Arg His Trp Leu Glu Met Ala Lys Gln Lys Glu Ala Gln Pro
            260                 265                 270
```

<210> SEQ ID NO 21
<211> LENGTH: 1614
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 21

```
atgtctgaaa caatgttggc tgttctggga tttcctgatc tggatgagct tttgccgatg      60

gcacggctgt ttctggtgtc ttctttgctg gccgggtgtt gtgtggggtc gatgagcttg     120

tttaggggcg gtttcttttc gggcagaggt gcccagggga acgtcgtcat gccgagggat     180

aaaatggatt ggaatttggg tcgtgttcgt caggggacgc tggctgtggt cggttgcctg     240

tttctggcga atgccgcgtg ggcgaacgat tattccgacg gcatgcagtt ctatcaggac     300

aaggattacg agaaagcttt ttcttctttc cagaaggcgg ccgacaaggg caatgcggcg     360

gcgcaatccg cactggctgc cctgtactat aacggggaag ggtggagga agatgaggcc     420

gctgctgcgt tgtggtattc gcgcgctgcc gaacatggcc gaacggatgc gcagtttgcg     480

cttggcgaga tgttcgaagc cggcgaaggg gtcaaacgcg attataaaaa agcggctttc     540

tggtataaaa aggcggcgga caagggccat ttgatggctg ccacgaagct gggcatcctc     600

tatatggaag gtcgcggagt caagcaagat gacgcgaaag cggctgcatt gctttctcat     660

gccgccaaac ggggcattgc gttggcgcag tcgaatctcg gtgttttgta tgcgagcggg     720

cgcggggttg aatccagtcc gaaacgggcg ctggagtggt acaagaaggc ggctgttcag     780

ggaaattcac aagcccagtt ttcgctcggc aatatgtatg aggacggctc tggtgttgaa     840

aagaatctgg cggtagcggc cgcctggtat cagaagtcgg ccgaacaggg gaatgccgag     900

gcccagaata atctgggacg cctttatatg gaaggcggcg agtttgaggg gcgtgaagac     960

gaagcgttta tgtggttctc ccgtgcggcc gatcaggggt atgccgaggc gcaaacgaat    1020

ctgggtgtct tgtattccta tgggcttggt gtggacaagg atttgtccaa ggcgttttac    1080

tggtatcagc aggcggctga aaaggggcag gctgaagggg ctttttttcct ggctgaggcg    1140

tattacaagg gggaaggtgt tcaccgggac gacaaacagg cggttttctg gtatcagaaa    1200

gcggcgaagc tgggtgtccc agaaagtcag gacaggcttg ggttgatgct gacgaacggg    1260

gtcggcgtca aacaggatta caagcaggca tatagctggt tcaggaaggc ggcccgtcag    1320

gggtatgccg aatcccagaa caatctgggg gtcttgtatg cccgtggact cggggtcgaa    1380

aaggattaca aacaggccgt ggcctggtat cgcaaggcgg tgatgcagaa tctgcctcag    1440

gcgcagttca atctgggaac gatgtatttg caggggcatg gtgtcaaaca ggatgtcaaa    1500
```

-continued

caggccagac actggtttac gaaggcggca gcgcaggggt tgccggaagc gcagagaagt 1560

ctggacagga tgccgaaaaa cgggcagacc atcaatacgg atctctcgac ctga 1614

<210> SEQ ID NO 22
<211> LENGTH: 1074
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 22

Met Ser Glu Thr Met Leu Ala Val Leu Gly Phe Pro Asp Leu Asp Glu
1 5 10 15

Leu Leu Pro Met Ala Arg Leu Phe Leu Val Ser Ser Leu Leu Ala Gly
20 25 30

Cys Cys Val Gly Ser Met Ser Leu Phe Arg Gly Gly Phe Phe Ser Gly
35 40 45

Arg Gly Ala Gln Gly Asn Val Val Met Pro Arg Asp Lys Met Asp Trp
50 55 60

Asn Leu Gly Arg Val Arg Gln Gly Thr Leu Ala Val Val Gly Cys Leu
65 70 75 80

Phe Leu Ala Asn Ala Ala Trp Ala Asn Asp Tyr Ser Asp Gly Met Gln
85 90 95

Phe Tyr Gln Asp Lys Asp Tyr Glu Lys Ala Phe Ser Ser Phe Gln Lys
100 105 110

Ala Ala Asp Lys Gly Asn Ala Ala Ala Gln Ser Ala Leu Ala Ala Leu
115 120 125

Tyr Tyr Asn Gly Glu Gly Val Glu Glu Asp Glu Ala Ala Ala Ala Leu
130 135 140

Trp Tyr Ser Arg Ala Ala Glu His Gly Arg Thr Asp Ala Gln Phe Ala
145 150 155 160

Leu Gly Glu Met Phe Glu Ala Gly Glu Gly Val Lys Arg Asp Tyr Lys
165 170 175

Lys Ala Ala Phe Trp Tyr Lys Lys Ala Ala Asp Lys Gly His Leu Met
180 185 190

Ala Ala Thr Lys Leu Gly Ile Leu Tyr Met Glu Gly Arg Gly Val Lys
195 200 205

Gln Asp Asp Ala Lys Ala Ala Ala Leu Leu Ser His Ala Ala Lys Arg
210 215 220

Gly Ile Ala Leu Ala Gln Ser Asn Leu Gly Val Leu Tyr Ala Ser Gly
225 230 235 240

Arg Gly Val Glu Ser Ser Pro Lys Arg Ala Leu Glu Trp Tyr Lys Lys
245 250 255

Ala Ala Val Gln Gly Asn Ser Gln Ala Gln Phe Ser Leu Gly Asn Met
260 265 270

Tyr Glu Asp Gly Ser Gly Val Glu Lys Asn Leu Ala Val Ala Ala Ala
275 280 285

Trp Tyr Gln Lys Ser Ala Glu Gln Gly Asn Ala Glu Ala Gln Asn Asn
290 295 300

Leu Gly Arg Leu Tyr Met Glu Gly Gly Glu Phe Glu Gly Arg Glu Asp
305 310 315 320

Glu Ala Phe Met Trp Phe Ser Arg Ala Ala Asp Gln Gly Tyr Ala Glu
325 330 335

Ala Gln Thr Asn Leu Gly Val Leu Tyr Ser Tyr Gly Leu Gly Val Asp

-continued

```
            340                 345                 350

Lys Asp Leu Ser Lys Ala Phe Tyr Trp Tyr Gln Gln Ala Ala Glu Lys
        355                 360                 365

Gly Gln Ala Glu Gly Ala Phe Phe Leu Ala Glu Ala Tyr Tyr Lys Gly
    370                 375                 380

Glu Gly Val His Arg Asp Asp Lys Gln Ala Val Phe Trp Tyr Gln Lys
385                 390                 395                 400

Ala Ala Lys Leu Gly Val Pro Glu Ser Gln Asp Arg Leu Gly Leu Met
                405                 410                 415

Leu Thr Asn Gly Val Gly Val Lys Gln Asp Tyr Lys Gln Ala Tyr Ser
            420                 425                 430

Trp Phe Arg Lys Ala Ala Arg Gln Gly Tyr Ala Glu Ser Gln Asn Asn
        435                 440                 445

Leu Gly Val Leu Tyr Ala Arg Gly Leu Gly Val Glu Lys Asp Tyr Lys
    450                 455                 460

Gln Ala Val Ala Trp Tyr Arg Lys Ala Val Met Gln Asn Leu Pro Gln
465                 470                 475                 480

Ala Gln Phe Asn Leu Gly Thr Met Tyr Leu Gln Gly His Gly Val Lys
                485                 490                 495

Gln Asp Val Lys Gln Ala Arg His Trp Phe Thr Lys Ala Ala Ala Gln
            500                 505                 510

Gly Leu Pro Glu Ala Gln Arg Ser Leu Asp Arg Met Pro Lys Asn Gly
        515                 520                 525

Gln Thr Ile Asn Thr Asp Leu Ser Thr Met Ser Glu Thr Met Leu Ala
    530                 535                 540

Val Leu Gly Phe Pro Asp Leu Asp Glu Leu Leu Pro Met Ala Arg Leu
545                 550                 555                 560

Phe Leu Val Ser Ser Leu Leu Ala Gly Cys Cys Val Gly Ser Met Ser
                565                 570                 575

Leu Phe Arg Gly Gly Phe Phe Ser Gly Arg Gly Ala Gln Gly Asn Val
            580                 585                 590

Val Met Pro Arg Asp Lys Met Asp Trp Asn Leu Gly Arg Val Arg Gln
        595                 600                 605

Gly Thr Leu Ala Val Val Gly Cys Leu Phe Leu Ala Asn Ala Ala Trp
    610                 615                 620

Ala Asn Asp Tyr Ser Asp Gly Met Gln Phe Tyr Gln Asp Lys Asp Tyr
625                 630                 635                 640

Glu Lys Ala Phe Ser Ser Phe Gln Lys Ala Ala Asp Lys Gly Asn Ala
                645                 650                 655

Ala Ala Gln Ser Ala Leu Ala Ala Leu Tyr Tyr Asn Gly Glu Gly Val
            660                 665                 670

Glu Glu Asp Glu Ala Ala Ala Ala Leu Trp Tyr Ser Arg Ala Ala Glu
        675                 680                 685

His Gly Arg Thr Asp Ala Gln Phe Ala Leu Gly Glu Met Phe Glu Ala
    690                 695                 700

Gly Glu Gly Val Lys Arg Asp Tyr Lys Lys Ala Ala Phe Trp Tyr Lys
705                 710                 715                 720

Lys Ala Ala Asp Lys Gly His Leu Met Ala Ala Thr Lys Leu Gly Ile
                725                 730                 735

Leu Tyr Met Glu Gly Arg Gly Val Lys Gln Asp Asp Ala Lys Ala Ala
            740                 745                 750
```

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Ala Leu Leu Ser His Ala Ala Lys Arg Gly Ile Ala Leu Ala Gln Ser
755 760 765

Asn Leu Gly Val Leu Tyr Ala Ser Gly Arg Gly Val Glu Ser Ser Pro
770 775 780

Lys Arg Ala Leu Glu Trp Tyr Lys Lys Ala Ala Val Gln Gly Asn Ser
785 790 795 800

Gln Ala Gln Phe Ser Leu Gly Asn Met Tyr Glu Asp Gly Ser Gly Val
805 810 815

Glu Lys Asn Leu Ala Val Ala Ala Ala Trp Tyr Gln Lys Ser Ala Glu
820 825 830

Gln Gly Asn Ala Glu Ala Gln Asn Asn Leu Gly Arg Leu Tyr Met Glu
835 840 845

Gly Gly Glu Phe Glu Gly Arg Glu Asp Glu Ala Phe Met Trp Phe Ser
850 855 860

Arg Ala Ala Asp Gln Gly Tyr Ala Glu Ala Gln Thr Asn Leu Gly Val
865 870 875 880

Leu Tyr Ser Tyr Gly Leu Gly Val Asp Lys Asp Leu Ser Lys Ala Phe
885 890 895

Tyr Trp Tyr Gln Gln Ala Ala Glu Lys Gly Gln Ala Glu Gly Ala Phe
900 905 910

Phe Leu Ala Glu Ala Tyr Tyr Lys Gly Glu Gly Val His Arg Asp Asp
915 920 925

Lys Gln Ala Val Phe Trp Tyr Gln Lys Ala Ala Lys Leu Gly Val Pro
930 935 940

Glu Ser Gln Asp Arg Leu Gly Leu Met Leu Thr Asn Gly Val Gly Val
945 950 955 960

Lys Gln Asp Tyr Lys Gln Ala Tyr Ser Trp Phe Arg Lys Ala Ala Arg
965 970 975

Gln Gly Tyr Ala Glu Ser Gln Asn Asn Leu Gly Val Leu Tyr Ala Arg
980 985 990

Gly Leu Gly Val Glu Lys Asp Tyr Lys Gln Ala Val Ala Trp Tyr Arg
995 1000 1005

Lys Ala Val Met Gln Asn Leu Pro Gln Ala Gln Phe Asn Leu Gly
1010 1015 1020

Thr Met Tyr Leu Gln Gly His Gly Val Lys Gln Asp Val Lys Gln
1025 1030 1035

Ala Arg His Trp Phe Thr Lys Ala Ala Ala Gln Gly Leu Pro Glu
1040 1045 1050

Ala Gln Arg Ser Leu Asp Arg Met Pro Lys Asn Gly Gln Thr Ile
1055 1060 1065

Asn Thr Asp Leu Ser Thr
1070

<210> SEQ ID NO 23
<211> LENGTH: 588
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 23

atggttcata caggtttttc cgggcagtcc cgtccgtttt ccggatggat ggggactttt 60

ctgtttctgg tgttttgcca gctggcattg gctgccggtg cgatggcggc ggacccggaa 120

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```
aagaaagcgg tggcttcaaa cgggcagctt tcgaaaaatg tggcatccgg ggatgaggat    180

gtgttgcgcg atctgatgga tttgaagagc aatgcggatt cgggtgatgt gtccgcccag    240

tttgagttga gccgccgtta cttgaacggg gatggccttg agcagaacga tgatgaggca    300

atccgctggc tccgtatggc ggcggaaggt ggtttgccga gggcgcaggc gggtctgggc    360

tggatgtatg cggcgggcag gggggtgaat aaggatgaga cgctgtcttt ttcctggtat    420

gaacgggcgg cggttgccgg ttttcctgtg gcgcagtata tgctgggccg ttattatgaa    480

aagggtatcg gcgtcgccaa agaccgtgtg ctggctaaag agtggtatga aaaggcggca    540

gcgcagggta atgagaaagc gaagaagcgg ttgcaggact ggaaatga                 588
```

```
<210> SEQ ID NO 24
<211> LENGTH: 195
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 24

Met Val His Thr Gly Phe Ser Gly Gln Ser Arg Pro Phe Ser Gly Trp
1               5                   10                  15

Met Gly Thr Phe Leu Phe Leu Val Phe Cys Gln Leu Ala Leu Ala Ala
            20                  25                  30

Gly Ala Met Ala Ala Asp Pro Glu Lys Lys Ala Val Ala Ser Asn Gly
        35                  40                  45

Gln Leu Ser Lys Asn Val Ala Ser Gly Asp Glu Asp Val Leu Arg Asp
    50                  55                  60

Leu Met Asp Leu Lys Ser Asn Ala Asp Ser Gly Asp Val Ser Ala Gln
65                  70                  75                  80

Phe Glu Leu Ser Arg Arg Tyr Leu Asn Gly Asp Gly Leu Glu Gln Asn
                85                  90                  95

Asp Asp Glu Ala Ile Arg Trp Leu Arg Met Ala Ala Glu Gly Gly Leu
            100                 105                 110

Pro Arg Ala Gln Ala Gly Leu Gly Trp Met Tyr Ala Ala Gly Arg Gly
        115                 120                 125

Val Asn Lys Asp Glu Thr Leu Ser Phe Ser Trp Tyr Glu Arg Ala Ala
    130                 135                 140

Val Ala Gly Phe Pro Val Ala Gln Tyr Met Leu Gly Arg Tyr Tyr Glu
145                 150                 155                 160

Lys Gly Ile Gly Val Ala Lys Asp Arg Val Leu Ala Lys Glu Trp Tyr
                165                 170                 175

Glu Lys Ala Ala Ala Gln Gly Asn Glu Lys Ala Lys Lys Arg Leu Gln
            180                 185                 190

Asp Trp Lys
        195
```

```
<210> SEQ ID NO 25
<211> LENGTH: 1200
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 25

atgcgtagaa aactgttctt cttcatttgt ttattttgtt ctattacagc ttcagtctct     60

tttgctgaaa cgaaaatcaa tgaatcgttt ccggaaattg aacggtcggg ggaagaggca    120

aagagagaaa cggctatcaa gctctataat ctgggcgtgg aatatgcaaa aggcagtcgt    180
```

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```
gtcgaaaaag atcgtaaaaa agccaattcc tatttcagac aagctgctga aataggactg    240
cctgaagcgc agtacaatct gggacgagcg tatttcgatg gcgatggtct ggaggtagac    300
aggaaagcag ctattgaatg gtacaaaaag gcagcagaac agggatttgc acaggctcaa    360
tacaacttgg gcgtaatcta ccaaaatggt ttgggcatca aacaggattt tgattcggct    420
gtccagtggt atgagagagc ggcaaatcag ggatttgtat tagcccaata caatcttgga    480
atgttatata taactggagc aggcgttggc aagaatccga aacgagggat tttgtggttg    540
cgcaaggctg ctgaaggggg ttacggtcag gcgcagcata atcttggaac cgtttattac    600
gagggtattg gcgtcagaaa aaattatccg gaagcggtgc aatggttcgc caaagctgct    660
aaacaagagc ttggcatggc gcaatacaat ctggggatgg cttactatca tggagagggc    720
gtcaaaaaaa atcctcagaa agcggtttca tggttgaaaa aagcagcaaa acaaaatctt    780
cttatagctc aggctagtct tggctatata tatgttacgg acaggaattt caaaaataat    840
ctggcagaag gaattttctg gacaaaaaaa gcctccgcat atggtaatgc aagggctcag    900
gcgacacttg gtattgcata tcttattgga aagggtgtag aaaaaaatat tccagaaggc    960
gtttcgtgga taaaaaaagc agcgagacag ggtaattatc cggctcaaag catgcttgct   1020
tcctgttatg aaaatgggat tggcgtaaag caaaacaagg tattggctta tgcactttat   1080
ttacactcat ctccttatac ggaagttgct atggaagaac ggcaaaatct tgaaaaaaag   1140
ctaagcaaag atgaaattgt aaaagcccga tccatcaaca tcgaaaaact tttcgaatga   1200
```

```
<210> SEQ ID NO 26
<211> LENGTH: 399
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 26

Met Arg Arg Lys Leu Phe Phe Phe Ile Cys Leu Phe Cys Ser Ile Thr
1               5                   10                  15

Ala Ser Val Ser Phe Ala Glu Thr Lys Ile Asn Glu Ser Phe Pro Glu
            20                  25                  30

Ile Glu Arg Ser Gly Glu Glu Ala Lys Arg Glu Thr Ala Ile Lys Leu
        35                  40                  45

Tyr Asn Leu Gly Val Glu Tyr Ala Lys Gly Ser Arg Val Glu Lys Asp
    50                  55                  60

Arg Lys Lys Ala Asn Ser Tyr Phe Arg Gln Ala Ala Glu Ile Gly Leu
65                  70                  75                  80

Pro Glu Ala Gln Tyr Asn Leu Gly Arg Ala Tyr Phe Asp Gly Asp Gly
                85                  90                  95

Leu Glu Val Asp Arg Lys Ala Ala Ile Glu Trp Tyr Lys Lys Ala Ala
            100                 105                 110

Glu Gln Gly Phe Ala Gln Ala Gln Tyr Asn Leu Gly Val Ile Tyr Gln
        115                 120                 125

Asn Gly Leu Gly Ile Lys Gln Asp Phe Asp Ser Ala Val Gln Trp Tyr
    130                 135                 140

Glu Arg Ala Ala Asn Gln Gly Phe Val Leu Ala Gln Tyr Asn Leu Gly
145                 150                 155                 160

Met Leu Tyr Ile Thr Gly Ala Gly Val Gly Lys Asn Pro Lys Arg Gly
                165                 170                 175
```

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```
Ile Leu Trp Leu Arg Lys Ala Ala Glu Gly Gly Tyr Gly Gln Ala Gln
            180                 185                 190

His Asn Leu Gly Thr Val Tyr Tyr Glu Gly Ile Gly Val Arg Lys Asn
        195                 200                 205

Tyr Pro Glu Ala Val Gln Trp Phe Ala Lys Ala Ala Lys Gln Glu Leu
    210                 215                 220

Gly Met Ala Gln Tyr Asn Leu Gly Met Ala Tyr Tyr His Gly Glu Gly
225                 230                 235                 240

Val Lys Lys Asn Pro Gln Lys Ala Val Ser Trp Leu Lys Lys Ala Ala
                245                 250                 255

Lys Gln Asn Leu Leu Ile Ala Gln Ala Ser Leu Gly Tyr Ile Tyr Val
            260                 265                 270

Thr Asp Arg Asn Phe Lys Asn Asn Leu Ala Glu Gly Ile Phe Trp Thr
        275                 280                 285

Lys Lys Ala Ser Ala Tyr Gly Asn Ala Arg Ala Gln Ala Thr Leu Gly
    290                 295                 300

Ile Ala Tyr Leu Ile Gly Lys Gly Val Glu Lys Asn Ile Pro Glu Gly
305                 310                 315                 320

Val Ser Trp Ile Lys Lys Ala Ala Arg Gln Gly Asn Tyr Pro Ala Gln
                325                 330                 335

Ser Met Leu Ala Ser Cys Tyr Glu Asn Gly Ile Gly Val Lys Gln Asn
            340                 345                 350

Lys Val Leu Ala Tyr Ala Leu Tyr Leu His Ser Ser Pro Tyr Thr Glu
        355                 360                 365

Val Ala Met Glu Glu Arg Gln Asn Leu Glu Lys Lys Leu Ser Lys Asp
    370                 375                 380

Glu Ile Val Lys Ala Arg Ser Ile Asn Ile Glu Lys Leu Phe Glu
385                 390                 395
```

<210> SEQ ID NO 27
<211> LENGTH: 909
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 27

```
atgaaaaaaa atatttcact catctttttt atatttattt ctttattttc tttgactgga      60

tgtcaaaatg aagataataa agagttaaca gatgaaaaaa caggaattga atactataaa     120

aaaggtgact acgaaaaatc attatccttt ctgaagaaag ccgctgattc cgggagtatc     180

aaagcttccc ggtatttggg aaaaatgtat cagtatggca aaggtgtcga taaagattat     240

ccgctttctt tcaagtggta tttaaacgca gccgaaaaag gagacaaaga atcatccggt     300

atggttggcg ccagttacta tttgggacaa ggcgtaaaac aagactacaa ggaatcgttt     360

agatggttgt taaaggcatc tgaaaaaatt gatgaaaaaa aaccaactga acgggacgga     420

aaactcatgc ttcttttggc taatttatat tttacgggaa aaggtacact tcaggatttc     480

agtgagtcag caaaatgggc gagaagagct gccgaattgg gaaattccga gtcacaagcc     540

atgcttgcat tcttcctcta ttccgggcaa ggcattttac agaacagaac ggaagcgaaa     600

atctgggcag aaaagtctgc cgggcagggg gatagccttg gacaagtcat aatgggaatg     660

ctttatcagt atggcggcgg aacagatgaa ccggatatga agaaagcaat cgactggtac     720

gaaaaatcag ctgaaaaggg aaatccgatt gcacaatatc aactggcaac cctttacgaa     780
```

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```
aatgggaatg gcttgccgaa agatctggaa aaagcaaaat actattatga gcaatcggct    840

aaaagccaat cggaaatacc agtgaaagct ttggcggaat tcaaggccaa acagaaaaga    900

caaaattaa                                                            909


<210> SEQ ID NO 28
<211> LENGTH: 302
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 28

Met Lys Lys Asn Ile Ser Leu Ile Phe Phe Ile Phe Ile Ser Leu Phe
1               5                   10                  15

Ser Leu Thr Gly Cys Gln Asn Glu Asp Asn Lys Glu Leu Thr Asp Glu
            20                  25                  30

Lys Thr Gly Ile Glu Tyr Tyr Lys Lys Gly Asp Tyr Glu Lys Ser Leu
        35                  40                  45

Ser Phe Leu Lys Lys Ala Ala Asp Ser Gly Ser Ile Lys Ala Ser Arg
    50                  55                  60

Tyr Leu Gly Lys Met Tyr Gln Tyr Gly Lys Gly Val Asp Lys Asp Tyr
65                  70                  75                  80

Pro Leu Ser Phe Lys Trp Tyr Leu Asn Ala Ala Glu Lys Gly Asp Lys
                85                  90                  95

Glu Ser Ser Gly Met Val Gly Ala Ser Tyr Tyr Leu Gly Gln Gly Val
            100                 105                 110

Lys Gln Asp Tyr Lys Glu Ser Phe Arg Trp Leu Leu Lys Ala Ser Glu
        115                 120                 125

Lys Ile Asp Glu Lys Lys Pro Thr Glu Arg Asp Gly Lys Leu Met Leu
    130                 135                 140

Leu Leu Ala Asn Leu Tyr Phe Thr Gly Lys Gly Thr Leu Gln Asp Phe
145                 150                 155                 160

Ser Glu Ser Ala Lys Trp Ala Arg Arg Ala Ala Glu Leu Gly Asn Ser
                165                 170                 175

Glu Ser Gln Ala Met Leu Ala Phe Phe Leu Tyr Ser Gly Gln Gly Ile
            180                 185                 190

Leu Gln Asn Arg Thr Glu Ala Lys Ile Trp Ala Glu Lys Ser Ala Gly
        195                 200                 205

Gln Gly Asp Ser Leu Gly Gln Val Ile Met Gly Met Leu Tyr Gln Tyr
    210                 215                 220

Gly Gly Gly Thr Asp Glu Pro Asp Met Lys Lys Ala Ile Asp Trp Tyr
225                 230                 235                 240

Glu Lys Ser Ala Glu Lys Gly Asn Pro Ile Ala Gln Tyr Gln Leu Ala
                245                 250                 255

Thr Leu Tyr Glu Asn Gly Asn Gly Leu Pro Lys Asp Leu Glu Lys Ala
            260                 265                 270

Lys Tyr Tyr Tyr Glu Gln Ser Ala Lys Ser Gln Ser Glu Ile Pro Val
        275                 280                 285

Lys Ala Leu Ala Glu Phe Lys Ala Lys Gln Lys Arg Gln Asn
    290                 295                 300


<210> SEQ ID NO 29
<211> LENGTH: 885
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes
```

-continued

<400> SEQUENCE: 29

```
atgatgaata aaatatttca ggttttttat atcgtaattc tttctttttt tattagttcc     60
tgccacgaat cagacaacag aatatcagaa aataatggtg tcaatctcta caaggcaaag    120
caatatgaaa tggcattgcc tttacttgaa aaggctgcca atgcaggaga tcctcaggcg    180
ccattctatc tcggcataat gttcgatgaa ggatcaggag taatcaaaga tcagaaaaaa    240
tcatttgaat ggtttgaaaa agcggcaaaa aatggtaaca ctgacgcgtt ttttgttatt    300
ggcagcaggt atttatatgg ttctggcgtt gaaaaagatt ataaagaagc cctgaaatgg    360
tataaaagga gtgttgaaga gggcaaaaaa gacgacaaga caatctattt catgatcgga    420
tcgatgtact acaatggttt gggtaccttg aaagatacca gcgaggcagc caaatggtat    480
gaaaaagcgg cagaaaaagg agatgctttt tcacaggcaa tgctcgccat gcaatattac    540
agtggtcagg gtattttgac gaatatggaa aaagccagat actgggccga aaaatccgcg    600
gaacaggatt acgatgccgg acaaatgatg atggggattc tgagccagta tggaacacct    660
gaaccagaca tgaaagccgc aattgactgg tatgaaaaag ccgccagaca gggaaacccg    720
attgcacagt ttctattggc gagaagttat gaaaatggaa acggcgtgcc aaaagatctg    780
gaaaaagccc atgcttatta taaacaggct gccggtggca tgaagtcgga tgacctggcc    840
agggagttta tggaatttga agcaagacag aaaagacaga aataa                    885
```

<210> SEQ ID NO 30
<211> LENGTH: 294
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 30

```
Met Met Asn Lys Ile Phe Gln Val Phe Tyr Ile Val Ile Leu Ser Phe
1               5                   10                  15

Phe Ile Ser Ser Cys His Glu Ser Asp Asn Arg Ile Ser Glu Asn Asn
            20                  25                  30

Gly Val Asn Leu Tyr Lys Ala Lys Gln Tyr Glu Met Ala Leu Pro Leu
        35                  40                  45

Leu Glu Lys Ala Ala Asn Ala Gly Asp Pro Gln Ala Pro Phe Tyr Leu
    50                  55                  60

Gly Ile Met Phe Asp Glu Gly Ser Gly Val Ile Lys Asp Gln Lys Lys
65                  70                  75                  80

Ser Phe Glu Trp Phe Glu Lys Ala Ala Lys Asn Gly Asn Thr Asp Ala
                85                  90                  95

Phe Phe Val Ile Gly Ser Arg Tyr Leu Tyr Gly Ser Gly Val Glu Lys
            100                 105                 110

Asp Tyr Lys Glu Ala Leu Lys Trp Tyr Lys Arg Ser Val Glu Glu Gly
        115                 120                 125

Lys Lys Asp Asp Lys Thr Ile Tyr Phe Met Ile Gly Ser Met Tyr Tyr
    130                 135                 140

Asn Gly Leu Gly Thr Leu Lys Asp Thr Ser Glu Ala Ala Lys Trp Tyr
145                 150                 155                 160

Glu Lys Ala Ala Glu Lys Gly Asp Ala Phe Ser Gln Ala Met Leu Ala
                165                 170                 175

Met Gln Tyr Tyr Ser Gly Gln Gly Ile Leu Thr Asn Met Glu Lys Ala
            180                 185                 190
```

-continued

```
Arg Tyr Trp Ala Glu Lys Ser Ala Glu Gln Asp Tyr Asp Ala Gly Gln
        195                 200                 205

Met Met Met Gly Ile Leu Ser Gln Tyr Gly Thr Pro Glu Pro Asp Met
    210                 215                 220

Lys Ala Ala Ile Asp Trp Tyr Glu Lys Ala Ala Arg Gln Gly Asn Pro
225                 230                 235                 240

Ile Ala Gln Phe Leu Leu Ala Arg Ser Tyr Glu Asn Gly Asn Gly Val
                245                 250                 255

Pro Lys Asp Leu Glu Lys Ala His Ala Tyr Tyr Lys Gln Ala Ala Gly
            260                 265                 270

Gly Met Lys Ser Asp Asp Leu Ala Arg Glu Phe Met Glu Phe Glu Ala
        275                 280                 285

Arg Gln Lys Arg Gln Lys
    290
```

<210> SEQ ID NO 31
<211> LENGTH: 813
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 31

```
atgctgggat atttgtatcg tgaggggtat ggagtcaagc aggattatca aaaggcgttt      60

tttctctatc ttgaaggagc aaaactgggc gacgcaaaaa gccagttcgg tttgggtttt     120

atgtatgagg ggggattatt cgtcaaacag gattatgcca aggcaaaaac atggtatgag     180

tattcatcca atcagggata tctgtctgcg atgaataatc ttggatcgct ttatgacgat     240

gaaaacactg gctttaaaaa cgagaaaatc gcatttgaat ggatattgaa agctgcccaa     300

aaagataacc caactgctca atttaatatc ggtttttttt acgaaaaagg cacaggaacc     360

aaaaaagact atgccgaagc ccgaaagtgg tatgaaaaag cagtcatgca gggatatctt     420

ccggccaaag cgaatctggc aaatctctat cttgatggaa aaggtggccc caaagaccag     480

caaaagggcg ttgccctgat aaaagaagcg gcgaacgagg aatcgaaagc cgcacaatac     540

acactggcaa acctctacgc cgatggcgaa ggcgttccgc aaagcgatga acaggccgtt     600

tactggttcc acaaggccgc tgaaaacgac agcgcgctgg ccatggacat gctcgccaaa     660

gcctacctga acggaaaata cggactgccg aaaagcccga cgaaatggga ctactggcaa     720

aagagggcag ccgaaacgcg cgcccgtaca cacgaagtcg atccttcaag ctggacaata     780

ttcgactgga tcaaatacaa gttaggcaat tga                                  813
```

<210> SEQ ID NO 32
<211> LENGTH: 270
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 32

```
Met Leu Gly Tyr Leu Tyr Arg Glu Gly Tyr Gly Val Lys Gln Asp Tyr
1               5                   10                  15

Gln Lys Ala Phe Phe Leu Tyr Leu Glu Gly Ala Lys Leu Gly Asp Ala
            20                  25                  30

Lys Ser Gln Phe Gly Leu Gly Phe Met Tyr Glu Gly Gly Leu Phe Val
        35                  40                  45

Lys Gln Asp Tyr Ala Lys Ala Lys Thr Trp Tyr Glu Tyr Ser Ser Asn
```

-continued

```
    50                  55                  60

Gln Gly Tyr Leu Ser Ala Met Asn Asn Leu Gly Ser Leu Tyr Asp Asp
65                  70                  75                  80

Glu Asn Thr Gly Phe Lys Asn Glu Lys Ile Ala Phe Glu Trp Ile Leu
                85                  90                  95

Lys Ala Ala Gln Lys Asp Asn Pro Thr Ala Gln Phe Asn Ile Gly Phe
            100                 105                 110

Phe Tyr Glu Lys Gly Thr Gly Thr Lys Lys Asp Tyr Ala Glu Ala Arg
        115                 120                 125

Lys Trp Tyr Glu Lys Ala Val Met Gln Gly Tyr Leu Pro Ala Lys Ala
    130                 135                 140

Asn Leu Ala Asn Leu Tyr Leu Asp Gly Lys Gly Gly Pro Lys Asp Gln
145                 150                 155                 160

Gln Lys Gly Val Ala Leu Ile Lys Glu Ala Ala Asn Glu Glu Ser Lys
                165                 170                 175

Ala Ala Gln Tyr Thr Leu Ala Asn Leu Tyr Ala Asp Gly Glu Gly Val
            180                 185                 190

Pro Gln Ser Asp Glu Gln Ala Val Tyr Trp Phe His Lys Ala Ala Glu
        195                 200                 205

Asn Asp Ser Ala Leu Ala Met Asp Met Leu Ala Lys Ala Tyr Leu Asn
    210                 215                 220

Gly Lys Tyr Gly Leu Pro Lys Ser Pro Thr Lys Trp Asp Tyr Trp Gln
225                 230                 235                 240

Lys Arg Ala Ala Glu Thr Arg Ala Arg Thr His Glu Val Asp Pro Ser
                245                 250                 255

Ser Trp Thr Ile Phe Asp Trp Ile Lys Tyr Lys Leu Gly Asn
            260                 265                 270
```

<210> SEQ ID NO 33
<211> LENGTH: 726
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 33

```
ttgatatttt tcagaaaaaa aagcgacgct ggagaaagtt gcctgagaga tactatgaaa     60

agccgttttt accgcttcaa acatcatttt tcttatatag aaaaatgggt gattttcaat    120

gttgtttttt tgaccatttc tgcttcgtcg tttgcacaaa cgcatccgat aaccggaaca    180

tctgatcccg acagtcaaca tactcaggtt catcaaaaac tcctgtctct cgcagaaaat    240

ggcgatcagg atgcgcagta caatctcgga cgtatatacc tgcaaggaaa aggaacacgt    300

caggattatc aggccgcccg taaatggttc atgcgcgccg ccgaaaaaga ggatgccgga    360

gcccaataca atctgggaaa tatttatcaa aaaggacaag ggattcaaca ggattgcaaa    420

aaagcctttt tctggtacaa aaaggcagct gcaaaattct atgcgccggc tcagtacgct    480

cttggcaagc tttactcaag tggatgtggt gtcaatcaaa attcatataa atcgacagaa    540

tggattctta aggcagccta taatggcatg ccggaagccc aatttcagat aggatatcgg    600

tatctcacag gctatggaat tcaagtcgat aaaaacaagg cctatgaatg gctgttgaag    660

gcggcaaaac aggataaccc agcggcaata aaggttctga aacaaatttt ttccacagaa    720

atatga                                                               726
```

-continued

<210> SEQ ID NO 34
<211> LENGTH: 241
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 34

```
Met Ile Phe Phe Arg Lys Lys Ser Asp Ala Gly Glu Ser Cys Leu Arg
1               5                   10                  15

Asp Thr Met Lys Ser Arg Phe Tyr Arg Phe Lys His His Phe Ser Tyr
            20                  25                  30

Ile Glu Lys Trp Val Ile Phe Asn Val Val Phe Leu Thr Ile Ser Ala
        35                  40                  45

Ser Ser Phe Ala Gln Thr His Pro Ile Thr Gly Thr Ser Asp Pro Asp
    50                  55                  60

Ser Gln His Thr Gln Val His Gln Lys Leu Leu Ser Leu Ala Glu Asn
65                  70                  75                  80

Gly Asp Gln Asp Ala Gln Tyr Asn Leu Gly Arg Ile Tyr Leu Gln Gly
                85                  90                  95

Lys Gly Thr Arg Gln Asp Tyr Gln Ala Ala Arg Lys Trp Phe Met Arg
            100                 105                 110

Ala Ala Glu Lys Glu Asp Ala Gly Ala Gln Tyr Asn Leu Gly Asn Ile
        115                 120                 125

Tyr Gln Lys Gly Gln Gly Ile Gln Gln Asp Cys Lys Lys Ala Phe Phe
    130                 135                 140

Trp Tyr Lys Lys Ala Ala Ala Lys Phe Tyr Ala Pro Ala Gln Tyr Ala
145                 150                 155                 160

Leu Gly Lys Leu Tyr Ser Ser Gly Cys Gly Val Asn Gln Asn Ser Tyr
                165                 170                 175

Lys Ser Thr Glu Trp Ile Leu Lys Ala Ala Tyr Asn Gly Met Pro Glu
            180                 185                 190

Ala Gln Phe Gln Ile Gly Tyr Arg Tyr Leu Thr Gly Tyr Gly Ile Gln
        195                 200                 205

Val Asp Lys Asn Lys Ala Tyr Glu Trp Leu Leu Lys Ala Ala Lys Gln
    210                 215                 220

Asp Asn Pro Ala Ala Ile Lys Val Leu Lys Thr Asn Phe Ser Thr Glu
225                 230                 235                 240

Ile
```

<210> SEQ ID NO 35
<211> LENGTH: 453
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 35

```
atgttttctt ttctgaaaaa agcggttccg gtcagtctcg ttctggtttc tgtcggggtt      60

ttgtctgcct gtactacagg acaggaaatg acggccaagt tgacggcaca ggcggaaaag     120

ggggatgtgg aagcgatggt cgagctggcg gaggtttatt gcggtggcaa aaacatcgaa     180

caggacgacc agatttgcgg catgtggatg aaacgggcag ctgaaaaagg ccatgtccgt     240

gcccagtata tgctcggcag aatgtatgaa ctgggtctgg gtatgagagc cgatccggta     300

caggcataca agtggtatag cttgtctgcc ccccattatc atatgtccca gactggtgca     360

gagactgtat atgccgtcat gacacctgtc cagcagtcag aagccagaaa agtggctgat     420
```

-continued

```
gaggcgaaga aaaccattcc ttcaaaacaa taa                                 453


<210> SEQ ID NO 36
<211> LENGTH: 150
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 36

Met Phe Ser Phe Leu Lys Lys Ala Val Pro Val Ser Leu Val Leu Val
1               5                   10                  15

Ser Val Gly Val Leu Ser Ala Cys Thr Thr Gly Gln Glu Met Thr Ala
            20                  25                  30

Lys Leu Thr Ala Gln Ala Glu Lys Gly Asp Val Glu Ala Met Val Glu
        35                  40                  45

Leu Ala Glu Val Tyr Cys Gly Gly Lys Asn Ile Glu Gln Asp Asp Gln
    50                  55                  60

Ile Cys Gly Met Trp Met Lys Arg Ala Ala Glu Lys Gly His Val Arg
65                  70                  75                  80

Ala Gln Tyr Met Leu Gly Arg Met Tyr Glu Leu Gly Leu Gly Met Arg
                85                  90                  95

Ala Asp Pro Val Gln Ala Tyr Lys Trp Tyr Ser Leu Ser Ala Pro His
            100                 105                 110

Tyr His Met Ser Gln Thr Gly Ala Glu Thr Val Tyr Ala Val Met Thr
        115                 120                 125

Pro Val Gln Gln Ser Glu Ala Arg Lys Val Ala Asp Glu Ala Lys Lys
    130                 135                 140

Thr Ile Pro Ser Lys Gln
145                 150


<210> SEQ ID NO 37
<211> LENGTH: 1536
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 37

atggctaatc gagaagaatt acaactgttg cgtgaagcac gatccaacca tcacgaagcc      60

cagctccagt tgggcaaact gtatttgttc ggaacaaaaa gcctgccgca aagtctgacg     120

accgccctgc actggttaag ccgtgcggcg acacaatcca ataaggaagc gtgccttctg     180

attggcgacc atattcctta tgaaattgcc agaaattttc cggatcaggt ggcgatccag     240

tcctggtaca gaacagccct gacagaaggg cattatgagg ctggtctggt attggcccgg     300

ctgattcttt cagatcccaa tcagatcgat gacaaaaagt atgccgaagc gattcgcatt     360

ctcgaaacaa ttgcagatca tgatattgcc gaagcacaat ggttactggc tgaattggcc     420

aaagatccga atgcccggcc atccattatt aacaatgccc ttaaatggac agcgagagcc     480

gccgatgccg gcattgtcga tgcacagatc gccctgattg aacatgcctg ggaaaacagg     540

gactaccccg tttttctgca gcatgccttg ccgattgccc gatcgattac tcaggcagtc     600

cagcagggtg atgtcattaa tattgacgaa caatcttccc gtttactgtt tcggtgcggg     660

caactgctcc tgaaacagga cggtcatgca tcagaagaga ttcagtccat gtgggaattg     720

gccgccagac agaaaaatgc cgaagccgct ttttcattag gcctgtggta cgcgcgcatg     780

aatgaagacg gtatccgcgt cagtattggc gcggccgcga ccagtttcaa aaaagcgatt     840
```

-continued

```
cgatggctga ctcaggccgg tgaacagggt ctggccaaag catggtacgc actttcactt    900

atttaccaga aggcggaatt ctcacagaga aatatgaatg atgcccaacg ttatctggaa    960

ttggcagcag atcttggaca tgcaacagcc cagtatgaaa gaggcatgca tgcgtggcgg   1020

gcacgccggg atgatgaatc aaatgacatt caggctgttt actggctgca gaaagcaaac   1080

ggaaacggaa aagcggacgc ggcagctgtc cttgataaaa ttgctttcaa ggcgaatcct   1140

gcatcatggg cggtaagcgc acgggaatgc ctgactcacg aaattttcag cagccatcca   1200

tttctggccg cccgtatcga actggctgcc gtattcggac tgacacgtcc ggaagcgctc   1260

ttgctcgata tccacaatgc cgacaaaggc cattgccttc tggtcgatat tcgtgaattt   1320

tacagacgca gcaagcgcaa gctcatcctg attcaaactg gccaggaacg ccagattctc   1380

tcccgaatcg gacgtctttt tgaaaaagtg gattgcggcc tgaatggtcc cgagggtaat   1440

tacagacaac gtcaatatcg cctcaaaacg atgctcccgg ccgcttatca ggaaaattca   1500

gatgatgaag aatatcggga aacagccgaa gcctag                             1536
```

```
<210> SEQ ID NO 38
<211> LENGTH: 511
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 38

Met Ala Asn Arg Glu Glu Leu Gln Leu Leu Arg Glu Ala Arg Ser Asn
1               5                   10                  15

His His Glu Ala Gln Leu Gln Leu Gly Lys Leu Tyr Leu Phe Gly Thr
            20                  25                  30

Lys Ser Leu Pro Gln Ser Leu Thr Thr Ala Leu His Trp Leu Ser Arg
        35                  40                  45

Ala Ala Thr Gln Ser Asn Lys Glu Ala Cys Leu Leu Ile Gly Asp His
    50                  55                  60

Ile Pro Tyr Glu Ile Ala Arg Asn Phe Pro Asp Gln Val Ala Ile Gln
65                  70                  75                  80

Ser Trp Tyr Arg Thr Ala Leu Thr Glu Gly His Tyr Glu Ala Gly Leu
                85                  90                  95

Val Leu Ala Arg Leu Ile Leu Ser Asp Pro Asn Gln Ile Asp Asp Lys
            100                 105                 110

Lys Tyr Ala Glu Ala Ile Arg Ile Leu Glu Thr Ile Ala Asp His Asp
        115                 120                 125

Ile Ala Glu Ala Gln Trp Leu Leu Ala Glu Leu Ala Lys Asp Pro Asn
    130                 135                 140

Ala Arg Pro Ser Ile Ile Asn Asn Ala Leu Lys Trp Thr Ala Arg Ala
145                 150                 155                 160

Ala Asp Ala Gly Ile Val Asp Ala Gln Ile Ala Leu Ile Glu His Ala
                165                 170                 175

Trp Glu Asn Arg Asp Tyr Pro Val Phe Leu Gln His Ala Leu Pro Ile
            180                 185                 190

Ala Arg Ser Ile Thr Gln Ala Val Gln Gln Gly Asp Val Ile Asn Ile
        195                 200                 205

Asp Glu Gln Ser Ser Arg Leu Leu Phe Arg Cys Gly Gln Leu Leu Leu
    210                 215                 220

Lys Gln Asp Gly His Ala Ser Glu Glu Ile Gln Ser Met Trp Glu Leu
225                 230                 235                 240
```

-continued

```
Ala Ala Arg Gln Lys Asn Ala Glu Ala Ala Phe Ser Leu Gly Leu Trp
            245                 250                 255

Tyr Ala Arg Met Asn Glu Asp Gly Ile Arg Val Ser Ile Gly Ala Ala
        260                 265                 270

Ala Thr Ser Phe Lys Lys Ala Ile Arg Trp Leu Thr Gln Ala Gly Glu
    275                 280                 285

Gln Gly Leu Ala Lys Ala Trp Tyr Ala Leu Ser Leu Ile Tyr Gln Lys
    290                 295                 300

Ala Glu Phe Ser Gln Arg Asn Met Asn Asp Ala Gln Arg Tyr Leu Glu
305                 310                 315                 320

Leu Ala Ala Asp Leu Gly His Ala Thr Ala Gln Tyr Glu Arg Gly Met
            325                 330                 335

His Ala Trp Arg Ala Arg Arg Asp Asp Glu Ser Asn Asp Ile Gln Ala
        340                 345                 350

Val Tyr Trp Leu Gln Lys Ala Asn Gly Asn Gly Lys Ala Asp Ala Ala
    355                 360                 365

Ala Val Leu Asp Lys Ile Ala Phe Lys Ala Asn Pro Ala Ser Trp Ala
    370                 375                 380

Val Ser Ala Arg Glu Cys Leu Thr His Glu Ile Phe Ser Ser His Pro
385                 390                 395                 400

Phe Leu Ala Ala Arg Ile Glu Leu Ala Ala Val Phe Gly Leu Thr Arg
            405                 410                 415

Pro Glu Ala Leu Leu Leu Asp Ile His Asn Ala Asp Lys Gly His Cys
        420                 425                 430

Leu Leu Val Asp Ile Arg Glu Phe Tyr Arg Arg Ser Lys Arg Lys Leu
    435                 440                 445

Ile Leu Ile Gln Thr Gly Gln Glu Arg Gln Ile Leu Ser Arg Ile Gly
    450                 455                 460

Arg Leu Phe Glu Lys Val Asp Cys Gly Leu Asn Gly Pro Glu Gly Asn
465                 470                 475                 480

Tyr Arg Gln Arg Gln Tyr Arg Leu Lys Thr Met Leu Pro Ala Ala Tyr
            485                 490                 495

Gln Glu Asn Ser Asp Asp Glu Glu Tyr Arg Glu Thr Ala Glu Ala
        500                 505                 510


<210> SEQ ID NO 39
<211> LENGTH: 798
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 39

ttggaaaaac ttaatttctt taagaagcaa cctgaactct ctatcaatga attagctttc      60

aaagcaaggc aaggcgatct cgatgcttta aaacgattgc aagaagcagc cgagcaaaat     120

gatgcgaatg cccagaatag acttggggtt atatatgccg atggcaaagg catcccgaga     180

aacgagaact tggctgctga caggttccaa aaagcagctg aattagaaaa cgctgaagca     240

caggctaacc tagccgccct atatagaaat tcattagttg tcccacgtga taatgcgaag     300

gttatttact gggctcagaa ggctgctgaa catggaaatc ctagaggaca gaatattcta     360

gggtttatgt atatgatcgg agaaggtgta cagcaagatg acgccaaagc agcttcttgg     420

tatcaaaaag ccgctgagca gggattcgca ggagggcaga ggaatttagc gtttatgtat     480
```

-continued

```
ctcaatggaa agggtgttcc gcaagatgac gctacagcaa cttattggta tcaaaaagcg    540

gcaaatcaag gtgacataca agcgcaaaaa agtttaaaga tgattcaaga aaaaagtaaa    600

gaaatgagta actataattt aaatacggta caacaatcac ctccccaggc atcatctcat    660

cagccacttc ccaaagcatc accttcaaat gaaagaaatt tatcaccttt aaaaaatatc    720

tttgacaaac tgaagcagaa ttctgcaaag atgaaatctg ctcctcccgg caacgaagaa    780

caggattacc tgaaatag                                                   798
```

```
<210> SEQ ID NO 40
<211> LENGTH: 265
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 40

Met Glu Lys Leu Asn Phe Phe Lys Lys Gln Pro Glu Leu Ser Ile Asn
1               5                   10                  15

Glu Leu Ala Phe Lys Ala Arg Gln Gly Asp Leu Asp Ala Leu Lys Arg
            20                  25                  30

Leu Gln Glu Ala Ala Glu Gln Asn Asp Ala Asn Ala Gln Asn Arg Leu
        35                  40                  45

Gly Val Ile Tyr Ala Asp Gly Lys Gly Ile Pro Arg Asn Glu Asn Leu
    50                  55                  60

Ala Ala Asp Arg Phe Gln Lys Ala Ala Glu Leu Glu Asn Ala Glu Ala
65                  70                  75                  80

Gln Ala Asn Leu Ala Ala Leu Tyr Arg Asn Ser Leu Val Val Pro Arg
                85                  90                  95

Asp Asn Ala Lys Val Ile Tyr Trp Ala Gln Lys Ala Ala Glu His Gly
            100                 105                 110

Asn Pro Arg Gly Gln Asn Ile Leu Gly Phe Met Tyr Met Ile Gly Glu
        115                 120                 125

Gly Val Gln Gln Asp Asp Ala Lys Ala Ala Ser Trp Tyr Gln Lys Ala
    130                 135                 140

Ala Glu Gln Gly Phe Ala Gly Gly Gln Arg Asn Leu Ala Phe Met Tyr
145                 150                 155                 160

Leu Asn Gly Lys Gly Val Pro Gln Asp Asp Ala Thr Ala Thr Tyr Trp
                165                 170                 175

Tyr Gln Lys Ala Ala Asn Gln Gly Asp Ile Gln Ala Gln Lys Ser Leu
            180                 185                 190

Lys Met Ile Gln Glu Lys Ser Lys Glu Met Ser Asn Tyr Asn Leu Asn
        195                 200                 205

Thr Val Gln Gln Ser Pro Pro Gln Ala Ser Ser His Gln Pro Leu Pro
    210                 215                 220

Lys Ala Ser Pro Ser Asn Glu Arg Asn Leu Ser Pro Leu Lys Asn Ile
225                 230                 235                 240

Phe Asp Lys Leu Lys Gln Asn Ser Ala Lys Met Lys Ser Ala Pro Pro
                245                 250                 255

Gly Asn Glu Glu Gln Asp Tyr Leu Lys
            260                 265


<210> SEQ ID NO 41
<211> LENGTH: 888
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes
```

-continued

<400> SEQUENCE: 41

atgaacagcc agactgccag aaaaatgttt tctttcgata tcagggcaaa ccattttttt 60
cgagcttttt tgctgcttgc catgtcactt cttgccggtg ttgcctttgc tgacgatttc 120
aacgatggtg tcagcgccta caaaagcggg aactaccagc aggcactgtc gctatttgag 180
gcgggcgcga aaaaggacga cccgaaatcg acgtatgccc tcggccttct gtataaaaac 240
ggcgtgatcg tcagaaaaga tatcggacgt ggcctgaatc tgatcatgaa atctgccaat 300
cagggattcg cgagagccca gaattatctc ggagtcacct actacgatgg caatgaggtc 360
gaacaggact acaaggaagc gttcgactgg tatggcaagg cagccgttca gggttatcct 420
gatgcggaat acaatctggc cgtcatgtat ggtcttggga agggaacccg gcaggatttt 480
tccgaaacca tcaaatggct gcgcaaggcc gccatgcacc agcttcctga agcccagtac 540
ggtcttggcg taatgtattc ccgaggactt ggtgtcgtga aaaacgatga acagtccgct 600
tactggtttt caaaggcagc gcgggccggt tacctgaaag cgcaaaacaa actgggtatt 660
ttatattccg aaggaaaagg tctggaaaag gacgagaaaa aagcgttcca ctggttcgag 720
gccgctgccg aaaaaggcta tgcaaaagcc caattcaatc tggcggtcat gtacgacaag 780
ggaattggcg ttgcaaagga tgtgtccaaa gccattatgt ggtaccgcaa agcggctaca 840
caaggcaatg tggctgcaca gaaacggttg aaacaactgc attcctaa 888

<210> SEQ ID NO 42
<211> LENGTH: 295
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 42

Met Asn Ser Gln Thr Ala Arg Lys Met Phe Ser Phe Asp Ile Arg Ala
1   5   10   15

Asn His Phe Phe Arg Ala Phe Leu Leu Leu Ala Met Ser Leu Leu Ala
            20   25   30

Gly Val Ala Phe Ala Asp Asp Phe Asn Asp Gly Val Ser Ala Tyr Lys
        35   40   45

Ser Gly Asn Tyr Gln Gln Ala Leu Ser Leu Phe Glu Ala Gly Ala Lys
    50   55   60

Lys Asp Asp Pro Lys Ser Thr Tyr Ala Leu Gly Leu Leu Tyr Lys Asn
65   70   75   80

Gly Val Ile Val Arg Lys Asp Ile Gly Arg Gly Leu Asn Leu Ile Met
                85   90   95

Lys Ser Ala Asn Gln Gly Phe Ala Arg Ala Gln Asn Tyr Leu Gly Val
            100   105   110

Thr Tyr Tyr Asp Gly Asn Glu Val Glu Gln Asp Tyr Lys Glu Ala Phe
        115   120   125

Asp Trp Tyr Gly Lys Ala Ala Val Gln Gly Tyr Pro Asp Ala Glu Tyr
    130   135   140

Asn Leu Ala Val Met Tyr Gly Leu Gly Lys Gly Thr Arg Gln Asp Phe
145   150   155   160

Ser Glu Thr Ile Lys Trp Leu Arg Lys Ala Ala Met His Gln Leu Pro
                165   170   175

Glu Ala Gln Tyr Gly Leu Gly Val Met Tyr Ser Arg Gly Leu Gly Val
            180   185   190

-continued

Val Lys Asn Asp Glu Gln Ser Ala Tyr Trp Phe Ser Lys Ala Ala Arg
195 200 205

Ala Gly Tyr Leu Lys Ala Gln Asn Lys Leu Gly Ile Leu Tyr Ser Glu
210 215 220

Gly Lys Gly Leu Glu Lys Asp Glu Lys Lys Ala Phe His Trp Phe Glu
225 230 235 240

Ala Ala Ala Glu Lys Gly Tyr Ala Lys Ala Gln Phe Asn Leu Ala Val
245 250 255

Met Tyr Asp Lys Gly Ile Gly Val Ala Lys Asp Val Ser Lys Ala Ile
260 265 270

Met Trp Tyr Arg Lys Ala Ala Thr Gln Gly Asn Val Ala Ala Gln Lys
275 280 285

Arg Leu Lys Gln Leu His Ser
290 295

<210> SEQ ID NO 43
<211> LENGTH: 459
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 43

ttgaaagagt tcaatatcct gcaaggagcg attatgagca aacccagagt tcaaaagacg 60

gatgccgaat ggagagcgca gctttcccct gtggcgtatg ccgtgacccg acaggcagcg 120

acggaaccgc cctttaccgg cgagtactgg aaccatgacg agaccggtgt ttatacgtgc 180

gtcaattgtg gaacgcccct gttcatttcc gatacgaaat tcgacgccgg ttgtggctgg 240

ccaagttttt ttgcaccgat cgaccctgaa aatgtaaggg aaaaggtcga tgtctcgctg 300

ggcatggtgc gtaccgaaat tatctgtgcc atttgtgatg cccatctggg ccatgtgttt 360

gacgacggcc cacccccaac ggggctgcgt tattgtatta attctgccgc tttgcggttc 420

gacccgctac cgaagaaggc agaatcttct gacaagtga 459

<210> SEQ ID NO 44
<211> LENGTH: 152
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 44

Met Lys Glu Phe Asn Ile Leu Gln Gly Ala Ile Met Ser Lys Pro Arg
1 5 10 15

Val Gln Lys Thr Asp Ala Glu Trp Arg Ala Gln Leu Ser Pro Val Ala
20 25 30

Tyr Ala Val Thr Arg Gln Ala Ala Thr Glu Pro Pro Phe Thr Gly Glu
35 40 45

Tyr Trp Asn His Asp Glu Thr Gly Val Tyr Thr Cys Val Asn Cys Gly
50 55 60

Thr Pro Leu Phe Ile Ser Asp Thr Lys Phe Asp Ala Gly Cys Gly Trp
65 70 75 80

Pro Ser Phe Phe Ala Pro Ile Asp Pro Glu Asn Val Arg Glu Lys Val
85 90 95

Asp Val Ser Leu Gly Met Val Arg Thr Glu Ile Ile Cys Ala Ile Cys
100 105 110

Asp Ala His Leu Gly His Val Phe Asp Asp Gly Pro Pro Pro Thr Gly

-continued

```
        115                 120                 125

Leu Arg Tyr Cys Ile Asn Ser Ala Ala Leu Arg Phe Asp Pro Leu Pro
    130                 135                 140

Lys Lys Ala Glu Ser Ser Asp Lys
145                 150
```

<210> SEQ ID NO 45
<211> LENGTH: 900
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 45

```
atgcaagaaa aaaaacagac gcaaagctgg ttcagcaaat acgccaccct gctgattctg     60

gtcatcctga tcgcacctgc cggactggtt ttcgcaagtc cgcaagacgc cgccaaaggc    120

atggcgctct atgaaacgaa acactatcag gatgctttcc cgctcctgaa aaaagccgct    180

gaagaaggcg acgtgaccgc ccagctctac gttggcaaca tgtaccgtga aggcctcggc    240

gtcaaaaaag attacgcaaa aaccattcca tggtttgaaa aagccgccaa tgccggcaat    300

gccaaagcgc aaacctacct cggcatcgcc tacagcgaag gccttggcgt cgctcccgac    360

tacaccaaag ccgcccagtg gtttgaaaaa gccgccaacc agaactacgg cccggcccag    420

actttggttg gcgttatgta ttacaaggga atgggcgttg aacaaaactt cggaaccgcc    480

aaaatgtggc ttgaaaaagc atctgcacag ggcgaaaaag acgcacagtc cttcctcggc    540

ctcatgtacc ttgaaggcga cgacaacaac aagaacccga aaaaggccgt tgaactcctg    600

acaaaggcag ccgatcagaa cgaaccgctg gcccagaccg tactcggcat catgtacatc    660

cagggcaaat tcgtcaaaca ggactacaaa aaagcggaag aactgctgac caaaggcgcc    720

gaagccggca ataccgacgc agcgaccttc ctcggcaaca tgtactaccg tggccagggc    780

gttgacaagg acaaggccaa agccgtcaaa tggctggaaa aagccgccat ccgtggcgac    840

gtcgatgcac aggaactgct ccaccgcatc cactacggca cccccggcgc accgaaataa    900
```

<210> SEQ ID NO 46
<211> LENGTH: 299
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 46

```
Met Gln Glu Lys Lys Gln Thr Gln Ser Trp Phe Ser Lys Tyr Ala Thr
1               5                   10                  15

Leu Leu Ile Leu Val Ile Leu Ile Ala Pro Ala Gly Leu Val Phe Ala
            20                  25                  30

Ser Pro Gln Asp Ala Ala Lys Gly Met Ala Leu Tyr Glu Thr Lys His
        35                  40                  45

Tyr Gln Asp Ala Phe Pro Leu Leu Lys Lys Ala Ala Glu Glu Gly Asp
    50                  55                  60

Val Thr Ala Gln Leu Tyr Val Gly Asn Met Tyr Arg Glu Gly Leu Gly
65                  70                  75                  80

Val Lys Lys Asp Tyr Ala Lys Thr Ile Pro Trp Phe Glu Lys Ala Ala
                85                  90                  95

Asn Ala Gly Asn Ala Lys Ala Gln Thr Tyr Leu Gly Ile Ala Tyr Ser
            100                 105                 110

Glu Gly Leu Gly Val Ala Pro Asp Tyr Thr Lys Ala Ala Gln Trp Phe
```

-continued

```
        115                 120                 125

Glu Lys Ala Ala Asn Gln Asn Tyr Gly Pro Ala Gln Thr Leu Val Gly
    130                 135                 140

Val Met Tyr Tyr Lys Gly Met Gly Val Glu Gln Asn Phe Gly Thr Ala
145                 150                 155                 160

Lys Met Trp Leu Glu Lys Ala Ser Ala Gln Gly Glu Lys Asp Ala Gln
                165                 170                 175

Ser Phe Leu Gly Leu Met Tyr Leu Glu Gly Asp Asp Asn Asn Lys Asn
            180                 185                 190

Pro Lys Lys Ala Val Glu Leu Leu Thr Lys Ala Ala Asp Gln Asn Glu
        195                 200                 205

Pro Leu Ala Gln Thr Val Leu Gly Ile Met Tyr Ile Gln Gly Lys Phe
    210                 215                 220

Val Lys Gln Asp Tyr Lys Lys Ala Glu Glu Leu Leu Thr Lys Gly Ala
225                 230                 235                 240

Glu Ala Gly Asn Thr Asp Ala Ala Thr Phe Leu Gly Asn Met Tyr Tyr
                245                 250                 255

Arg Gly Gln Gly Val Asp Lys Asp Lys Ala Lys Ala Val Lys Trp Leu
            260                 265                 270

Glu Lys Ala Ala Ile Arg Gly Asp Val Asp Ala Gln Glu Leu Leu His
        275                 280                 285

Arg Ile His Tyr Gly Thr Pro Gly Ala Pro Lys
    290                 295
```

<210> SEQ ID NO 47
<211> LENGTH: 669
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 47

```
atggcaaaca aaacttttca gaaaaccctg ctgggttgct ccatcgccct gatgtccgct      60

ttcgtcgccg gcaatgccag cgcggccaaa aaagtcgacg acacctactc cagactgaac     120

cagtgtatcg gctactacaa ccagagccag tacacccagg caatcccctg ctttactcca     180

ctggcaaaag ccggtaacga tcaggcacag acctatctgg gcatcatgta ccagcacggt     240

ttcggtaccc aaaaagacat ggcaaccgct gccatgtggt ataacagggc cgcccgtcag     300

ggagacaaat gggcctacga caacctcaaa gccatgggta atccgaaact ggcaaccggc     360

aaaacctggg cggattacag aaacaccgtc gaacagaaag ccgctgcggg tgaagcctcg     420

gcccagaccg ctctgggcag cctgtactac ttcggtgtcg gtggcgtcaa acaggactac     480

aacaccgcca aaaactggta tgccaaagcc gccgtcaatg gcgatgcagc cgccatgaac     540

tacctcggtc gcatgtatta ctacgcactg ggcgtcgaac agaattccat gatggccaaa     600

caatacctga acgcagccgc caaagccggt aacgttcagg caaaaaacct gctgaaaaaa     660

atcaaataa                                                             669
```

<210> SEQ ID NO 48
<211> LENGTH: 222
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 48

```
Met Ala Asn Lys Thr Phe Gln Lys Thr Leu Leu Gly Cys Ser Ile Ala
```

-continued

```
1               5                   10                  15

Leu Met Ser Ala Phe Val Ala Gly Asn Ala Ser Ala Ala Lys Lys Val
            20                  25                  30

Asp Asp Thr Tyr Ser Arg Leu Asn Gln Cys Ile Gly Tyr Tyr Asn Gln
        35                  40                  45

Ser Gln Tyr Thr Gln Ala Ile Pro Cys Phe Thr Pro Leu Ala Lys Ala
    50                  55                  60

Gly Asn Asp Gln Ala Gln Thr Tyr Leu Gly Ile Met Tyr Gln His Gly
65                  70                  75                  80

Phe Gly Thr Gln Lys Asp Met Ala Thr Ala Ala Met Trp Tyr Asn Arg
                85                  90                  95

Ala Ala Arg Gln Gly Asp Lys Trp Ala Tyr Asp Asn Leu Lys Ala Met
            100                 105                 110

Gly Asn Pro Lys Leu Ala Thr Gly Lys Thr Trp Ala Asp Tyr Arg Asn
        115                 120                 125

Thr Val Glu Gln Lys Ala Ala Ala Gly Glu Ala Ser Ala Gln Thr Ala
    130                 135                 140

Leu Gly Ser Leu Tyr Tyr Phe Gly Val Gly Gly Val Lys Gln Asp Tyr
145                 150                 155                 160

Asn Thr Ala Lys Asn Trp Tyr Ala Lys Ala Ala Val Asn Gly Asp Ala
                165                 170                 175

Ala Ala Met Asn Tyr Leu Gly Arg Met Tyr Tyr Tyr Ala Leu Gly Val
            180                 185                 190

Glu Gln Asn Ser Met Met Ala Lys Gln Tyr Leu Asn Ala Ala Ala Lys
        195                 200                 205

Ala Gly Asn Val Gln Ala Lys Asn Leu Leu Lys Lys Ile Lys
    210                 215                 220
```

<210> SEQ ID NO 49
<211> LENGTH: 942
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 49

```
atgttgctga tggatattcg aatagaaaaa ctgaagataa aaaacgatct caaagataat     60

aatttcttga ccgaacttag caatgctgat gataatgaat cagcattgct tctttattat    120

gaaatgatga aaactatctt aaaagcttta tttgtttgtc ttttttttctt cctcggcaat    180

catgcaattg ccgataatct catggaagga aataggctat tcgatgctgg acaatataag    240

gaagccatga cctttcttat gcaacccgat gtacatgatg atccagaagc attaaatctt    300

gtcgcttata tgtataacca tggccttggc gtcagcaaaa atgctgaaaa agcatttatg    360

tgctatatga aatcggcaga atccggatta gctattgctc aatttaacgt gggactggcg    420

tatgaacagg gtaacggtat cctgaaaaat cttccagaag cagtcaagtg gtatagaaaa    480

gctgctgaac aagaagatgc tgatgctgaa gcaaaaatgg gttatttgac tgtaaacggc    540

ataggtatcg gaaagaatta taaagaagcc atgaaatggt atcaaagggc ggccgaacat    600

ggagattatg attcgtatgc cgatatcggt atgatgtatt ccaggggaga tggtgtcaaa    660

aggaatttga accatgcagt tcagtattac atttttgggg ctcaaaaagg cagtacatat    720

tcacaggctt tattgggaaa tgcatatgca tacggaaaag gtatccaaaa ggacatagaa    780

caagcactct actggtacaa gcaggctgcc agaaacggaa acgtcaatgc catgaaagaa    840
```

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```
ctcggctaca tatacgagac cggtcgactt ggtgtgaaaa aagacccaaa agaagcacaa    900

tactggaaag acatggctga aagagcgggc aaaaaacagt aa                       942


<210> SEQ ID NO 50
<211> LENGTH: 313
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 50

Met Leu Leu Met Asp Ile Arg Ile Glu Lys Leu Lys Ile Lys Asn Asp
1               5                   10                  15

Leu Lys Asp Asn Asn Phe Leu Thr Glu Leu Ser Asn Ala Asp Asp Asn
            20                  25                  30

Glu Ser Ala Leu Leu Leu Tyr Tyr Glu Met Met Lys Thr Ile Leu Lys
        35                  40                  45

Ala Leu Phe Val Cys Leu Phe Phe Phe Leu Gly Asn His Ala Ile Ala
    50                  55                  60

Asp Asn Leu Met Glu Gly Asn Arg Leu Phe Asp Ala Gly Gln Tyr Lys
65                  70                  75                  80

Glu Ala Met Thr Phe Leu Met Gln Pro Asp Val His Asp Asp Pro Glu
                85                  90                  95

Ala Leu Asn Leu Val Ala Tyr Met Tyr Asn His Gly Leu Gly Val Ser
            100                 105                 110

Lys Asn Ala Glu Lys Ala Phe Met Cys Tyr Met Lys Ser Ala Glu Ser
        115                 120                 125

Gly Leu Ala Ile Ala Gln Phe Asn Val Gly Leu Ala Tyr Glu Gln Gly
    130                 135                 140

Asn Gly Ile Leu Lys Asn Leu Pro Glu Ala Val Lys Trp Tyr Arg Lys
145                 150                 155                 160

Ala Ala Glu Gln Glu Asp Ala Asp Ala Glu Ala Lys Met Gly Tyr Leu
                165                 170                 175

Thr Val Asn Gly Ile Gly Ile Gly Lys Asn Tyr Lys Glu Ala Met Lys
            180                 185                 190

Trp Tyr Gln Arg Ala Ala Glu His Gly Asp Tyr Asp Ser Tyr Ala Asp
        195                 200                 205

Ile Gly Met Met Tyr Ser Arg Gly Asp Gly Val Lys Arg Asn Leu Asn
    210                 215                 220

His Ala Val Gln Tyr Tyr Ile Phe Gly Ala Gln Lys Gly Ser Thr Tyr
225                 230                 235                 240

Ser Gln Ala Leu Leu Gly Asn Ala Tyr Ala Tyr Gly Lys Gly Ile Gln
                245                 250                 255

Lys Asp Ile Glu Gln Ala Leu Tyr Trp Tyr Lys Gln Ala Ala Arg Asn
            260                 265                 270

Gly Asn Val Asn Ala Met Lys Glu Leu Gly Tyr Ile Tyr Glu Thr Gly
        275                 280                 285

Arg Leu Gly Val Lys Lys Asp Pro Lys Glu Ala Gln Tyr Trp Lys Asp
    290                 295                 300

Met Ala Glu Arg Ala Gly Lys Lys Gln
305                 310


<210> SEQ ID NO 51
<211> LENGTH: 195
```

-continued

<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 51

```
atgcctatgg aaaaggaatt tccaaagata ccaaaagccc tctactggta caaaaccgca     60

gccaaaaacg gaaacgtcaa tgccatgaaa gaactgggtt ccatttatgc agaaggtgat    120

ctcggagtcc aaaaggacat acaagaagcg aaacgatgga acgacatggc cagaaaagcg    180

gaacaaaaga aataa                                                     195
```

<210> SEQ ID NO 52
<211> LENGTH: 64
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 52

```
Met Pro Met Glu Lys Glu Phe Pro Lys Ile Pro Lys Ala Leu Tyr Trp
1               5                   10                  15

Tyr Lys Thr Ala Ala Lys Asn Gly Asn Val Asn Ala Met Lys Glu Leu
            20                  25                  30

Gly Ser Ile Tyr Ala Glu Gly Asp Leu Gly Val Gln Lys Asp Ile Gln
        35                  40                  45

Glu Ala Lys Arg Trp Asn Asp Met Ala Arg Lys Ala Glu Gln Lys Lys
    50                  55                  60
```

<210> SEQ ID NO 53
<211> LENGTH: 948
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 53

```
atggttacgc ccgaatcgga taatgaaatc gacgacatca tctggtcaga aattgaatcc     60

agtgattcgc acggtgattt cgtctgctat gccgttcacg ctccatataa ggcaaaatat    120

ctggagaatg ccaaagctcg tatcgaatcc ggaaaatatc tggacaacct cgctcctgtc    180

cgctatctga aggctgttga acgtattgaa aaactggccg gaacgggcga cccggcggca    240

acattccaca tgggaaaaat atatgccatt ggcattgccg ttccgcaaaa tgtacccaaa    300

gccgttgaat ggtatgaaaa ggccatcgca ctcggagaac ccagagctta cgccaatctc    360

ggctggtttt atcaatcggg ttacggtgtt ccgactgaca aatcgaaagc tttcgaattg    420

ctgtcgttcg gtgctgaaaa cggagttttg tctgcaaagg ctgccatcgg catgatgctt    480

ttgaacgggg aaggatgtac cctgaatccg gaactcgggt ttcagaaact tgaggaatcg    540

ttcaacagcg gttatctgaa tgcgggcaac cacatttctg atgtgtattt tgaaggcaaa    600

ctggttccag gggatatcga gcttgcccat gaatggctac agaaagtggc ggatagcggc    660

gatgaaagat caatggcgat ccttggccac tatcttgtga caggaagtca tggaaagaca    720

gacacggcaa aagggcttga tttgcttgag caggcaaccc gactgcaata tctgcctgcc    780

tatttatggc tgggtacctt gtacaaaaaa gggcttggcg ttgagctgga tgccgaaaaa    840

gccattgaat ggttcaaaaa gggcatcaag gcgggctgtc gcgactgcca gatagcactt    900

acgatgatgt ccatgcctga aacggacaat ccgaagtcgt atcattaa                948
```

<210> SEQ ID NO 54
<211> LENGTH: 315

-continued

<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 54

```
Met Val Thr Pro Glu Ser Asp Asn Glu Ile Asp Asp Ile Ile Trp Ser
1               5                   10                  15

Glu Ile Glu Ser Ser Asp Ser His Gly Asp Phe Val Cys Tyr Ala Val
            20                  25                  30

His Ala Pro Tyr Lys Ala Lys Tyr Leu Glu Asn Ala Lys Ala Arg Ile
        35                  40                  45

Glu Ser Gly Lys Tyr Leu Asp Asn Leu Ala Pro Val Arg Tyr Leu Lys
    50                  55                  60

Ala Val Glu Arg Ile Glu Lys Leu Ala Gly Thr Gly Asp Pro Ala Ala
65                  70                  75                  80

Thr Phe His Met Gly Lys Ile Tyr Ala Ile Gly Ile Ala Val Pro Gln
                85                  90                  95

Asn Val Pro Lys Ala Val Glu Trp Tyr Glu Lys Ala Ile Ala Leu Gly
            100                 105                 110

Glu Pro Arg Ala Tyr Ala Asn Leu Gly Trp Phe Tyr Gln Ser Gly Tyr
        115                 120                 125

Gly Val Pro Thr Asp Lys Ser Lys Ala Phe Glu Leu Leu Ser Phe Gly
    130                 135                 140

Ala Glu Asn Gly Val Leu Ser Ala Lys Ala Ala Ile Gly Met Met Leu
145                 150                 155                 160

Leu Asn Gly Glu Gly Cys Thr Leu Asn Pro Glu Leu Gly Phe Gln Lys
                165                 170                 175

Leu Glu Glu Ser Phe Asn Ser Gly Tyr Leu Asn Ala Gly Asn His Ile
            180                 185                 190

Ser Asp Val Tyr Phe Glu Gly Lys Leu Val Pro Gly Asp Ile Glu Leu
        195                 200                 205

Ala His Glu Trp Leu Gln Lys Val Ala Asp Ser Gly Asp Glu Arg Ser
    210                 215                 220

Met Ala Ile Leu Gly His Tyr Leu Val Thr Gly Ser His Gly Lys Thr
225                 230                 235                 240

Asp Thr Ala Lys Gly Leu Asp Leu Leu Glu Gln Ala Thr Arg Leu Gln
                245                 250                 255

Tyr Leu Pro Ala Tyr Leu Trp Leu Gly Thr Leu Tyr Lys Lys Gly Leu
            260                 265                 270

Gly Val Glu Leu Asp Ala Glu Lys Ala Ile Glu Trp Phe Lys Lys Gly
        275                 280                 285

Ile Lys Ala Gly Cys Arg Asp Cys Gln Ile Ala Leu Thr Met Met Ser
    290                 295                 300

Met Pro Glu Thr Asp Asn Pro Lys Ser Tyr His
305                 310                 315
```

<210> SEQ ID NO 55
<211> LENGTH: 912
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 55

```
atgaacaagc cttatccaaa cctgtcattt caaatgaaat cttttttcaa gatcttctgt      60

atagtctgtc tgtttctttt cagtgttcct tcttttgccg acaacgccaa ggaaggcatg     120
```

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```
cgtctgttcc aggctggaaa atatcagcag gccatgacat atttcatgaa gccggatgcc    180

caaaagaatc cggatgtatt aaaccgcata gcttatatgt atgacaaagg ctttggtgtt    240

gaaaagaatc tgcaaacaag tgtcaagtgg tataaaaaag cagctgaaat gggattcaaa    300

gtagcacagt tcaatctcgg attaagttat caaaaaggct tgggagttcc aaaagatatc    360

aatgaagcca tcaaatggta ccgtaaatca gcagaacagg gatatcccag cgccgaatcc    420

aaaatgggtt atttcactgt caagggaaaa ggaataaaac aggattttgc acaagccttg    480

aaatggtatc gtctcgctgc tgaacatggc gatgaccgtt cttatgccga tatcggcatt    540

ttttatgccg aaggttatgg cgtcaaaaaa gacaggaacc gtgccgtgca gtattacatc    600

atgggtgctg aaaaaggcga cgcttatgcc cagtatcttt taggccgcgc ctatgagcag    660

gggcggggca ttcaatactc tcccgaacgt tcactttact ggctcaaaaa agctgccgac    720

aatggaagtt tccttgccat gaaagaactc gggatcgttt atgccaatgg acttctggac    780

cagaaaatgg atacggatgc tgccgcaaaa tggggtgaaa aagcctggga aacccgcaag    840

aagaacgggg aatccgatcc ggaggtcgac cgcagactgc gctttttcgg catagacccg    900

gatgacttat ag                                                        912
```

<210> SEQ ID NO 56
<211> LENGTH: 303
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 56

```
Met Asn Lys Pro Tyr Pro Asn Leu Ser Phe Gln Met Lys Ser Phe Phe
1               5                   10                  15

Lys Ile Phe Cys Ile Val Cys Leu Phe Leu Phe Ser Val Pro Ser Phe
            20                  25                  30

Ala Asp Asn Ala Lys Glu Gly Met Arg Leu Phe Gln Ala Gly Lys Tyr
        35                  40                  45

Gln Gln Ala Met Thr Tyr Phe Met Lys Pro Asp Ala Gln Lys Asn Pro
    50                  55                  60

Asp Val Leu Asn Arg Ile Ala Tyr Met Tyr Asp Lys Gly Phe Gly Val
65                  70                  75                  80

Glu Lys Asn Leu Gln Thr Ser Val Lys Trp Tyr Lys Lys Ala Ala Glu
                85                  90                  95

Met Gly Phe Lys Val Ala Gln Phe Asn Leu Gly Leu Ser Tyr Gln Lys
            100                 105                 110

Gly Leu Gly Val Pro Lys Asp Ile Asn Glu Ala Ile Lys Trp Tyr Arg
        115                 120                 125

Lys Ser Ala Glu Gln Gly Tyr Pro Ser Ala Glu Ser Lys Met Gly Tyr
    130                 135                 140

Phe Thr Val Lys Gly Lys Gly Ile Lys Gln Asp Phe Ala Gln Ala Leu
145                 150                 155                 160

Lys Trp Tyr Arg Leu Ala Ala Glu His Gly Asp Asp Arg Ser Tyr Ala
                165                 170                 175

Asp Ile Gly Ile Phe Tyr Ala Glu Gly Tyr Gly Val Lys Lys Asp Arg
            180                 185                 190

Asn Arg Ala Val Gln Tyr Tyr Ile Met Gly Ala Glu Lys Gly Asp Ala
        195                 200                 205
```

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```
Tyr Ala Gln Tyr Leu Leu Gly Arg Ala Tyr Glu Gln Gly Arg Gly Ile
    210                 215                 220

Gln Tyr Ser Pro Glu Arg Ser Leu Tyr Trp Leu Lys Lys Ala Ala Asp
225                 230                 235                 240

Asn Gly Ser Phe Leu Ala Met Lys Glu Leu Gly Ile Val Tyr Ala Asn
                245                 250                 255

Gly Leu Leu Asp Gln Lys Met Asp Thr Asp Ala Ala Ala Lys Trp Gly
            260                 265                 270

Glu Lys Ala Trp Glu Thr Arg Lys Lys Asn Gly Glu Ser Asp Pro Glu
        275                 280                 285

Val Asp Arg Arg Leu Arg Phe Phe Gly Ile Asp Pro Asp Asp Leu
    290                 295                 300


<210> SEQ ID NO 57
<211> LENGTH: 936
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 57

atggcactcc cttctttccc gtcatcccca ttcatcaagt ggctctcccg tctggcgctg     60

gtctgtttca tcctgcccgc gatgccgatc gaagccgttg caaaagaccg gagcgaaggt    120

gtgaagcttt actataacca gcaatacaaa aaggccgccc ctttcctgat gaaagaagcc    180

aaaaaaggca atgccaaggc acaggtctgc ctcgggatga tgtatcagga gggtcttggc    240

ctgaaacaga actacatgct ggccagacgc tggtatgaaa aatcggcgaa gaaaaaccgg    300

gctgacgcac aaactttcct cggcatgctc tacagtcagg ggcttggtgt ggcgaaagat    360

ttcgaaaaag ccaaatattg gttcgacaag gccgccggac agggctttgc ccctgcccag    420

acactcgtcg gcctgatgta cgccaaaggc gtcggcaccg caaaaagcat gtcgcaagcg    480

gaaaaatggc tgcggctggc cgccaaacag ggtgaaccgg acgcccagac ctatctgggc    540

cttttgtacc ttgacggcac tgaactgccg caggacgtag gtgaagccgc gcgacttttg    600

aaagaagcgg ccgtaaaagg cgacccgaac gcccagtctg cactgggcat gatgtatttt    660

tccggcaagg gggtcgatca ggacatgaac gagtcggaaa aatggcttga aaaggcggcc    720

attgccggta acgtcgatgc acagactttc ctcggcaacc tctattacaa gggtatcggc    780

gtcgcgaaag acgatacccg cgcacgctac tggcttcaga aagcggcgat tgccggtgat    840

ccggacgcac aggccacatt aaatgatatg ttgaaagacg atgcagcgcc cgttttgccc    900

ttcgaggaca agaagcccct ttccggttcc ctgtaa                              936


<210> SEQ ID NO 58
<211> LENGTH: 311
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 58

Met Ala Leu Pro Ser Phe Pro Ser Ser Pro Phe Ile Lys Trp Leu Ser
1               5                   10                  15

Arg Leu Ala Leu Val Cys Phe Ile Leu Pro Ala Met Pro Ile Glu Ala
            20                  25                  30

Val Ala Lys Asp Arg Ser Glu Gly Val Lys Leu Tyr Tyr Asn Gln Gln
        35                  40                  45

Tyr Lys Lys Ala Ala Pro Phe Leu Met Lys Glu Ala Lys Lys Gly Asn
```

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```
    50                  55                  60

Ala Lys Ala Gln Val Cys Leu Gly Met Met Tyr Gln Glu Gly Leu Gly
65                  70                  75                  80

Leu Lys Gln Asn Tyr Met Leu Ala Arg Arg Trp Tyr Glu Lys Ser Ala
                85                  90                  95

Lys Lys Asn Arg Ala Asp Ala Gln Thr Phe Leu Gly Met Leu Tyr Ser
            100                 105                 110

Gln Gly Leu Gly Val Ala Lys Asp Phe Glu Lys Ala Lys Tyr Trp Phe
        115                 120                 125

Asp Lys Ala Ala Gly Gln Gly Phe Ala Pro Ala Gln Thr Leu Val Gly
    130                 135                 140

Leu Met Tyr Ala Lys Gly Val Gly Thr Ala Lys Ser Met Ser Gln Ala
145                 150                 155                 160

Glu Lys Trp Leu Arg Leu Ala Ala Lys Gln Gly Glu Pro Asp Ala Gln
                165                 170                 175

Thr Tyr Leu Gly Leu Leu Tyr Leu Asp Gly Thr Glu Leu Pro Gln Asp
            180                 185                 190

Val Gly Glu Ala Ala Arg Leu Leu Lys Glu Ala Ala Val Lys Gly Asp
        195                 200                 205

Pro Asn Ala Gln Ser Ala Leu Gly Met Met Tyr Phe Ser Gly Lys Gly
    210                 215                 220

Val Asp Gln Asp Met Asn Glu Ser Glu Lys Trp Leu Glu Lys Ala Ala
225                 230                 235                 240

Ile Ala Gly Asn Val Asp Ala Gln Thr Phe Leu Gly Asn Leu Tyr Tyr
                245                 250                 255

Lys Gly Ile Gly Val Ala Lys Asp Asp Thr Arg Ala Arg Tyr Trp Leu
            260                 265                 270

Gln Lys Ala Ala Ile Ala Gly Asp Pro Asp Ala Gln Ala Thr Leu Asn
        275                 280                 285

Asp Met Leu Lys Asp Asp Ala Ala Pro Val Leu Pro Phe Glu Asp Lys
    290                 295                 300

Lys Pro Leu Ser Gly Ser Leu
305                 310


<210> SEQ ID NO 59
<211> LENGTH: 660
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 59

atgtccaggg gttccaaaaa caaaaagctt tttttatggc tcattctcgc cgccacgatc      60

atcctgatca tcatcagcca gactgctttc gcagtcggtg agcgcgacct tgaacaggcg     120

atgcagtcct attccgccgg acaatacaaa gaggctgttc cccaattcga aaaagcggca     180

acgctgggca acaacaaggc acaaaccatg ctgggtgtcc tgtattttca gggcaaggga     240

tgcgaaaagg actacgtgaa ggccgccgaa tggttcgacc gtgcggccaa tggcggcaat     300

atcgaagcgc aaaccttcat gggcatcatc aatcttgaag gcctcggtac tcccaaaaac     360

gaaaaaacgg cctattactg gttcgaaaaa gccgcccgtg gcggtgaaac cagcgcacag     420

aattatctcg gcaccctgct catgaatgga cagggcacga aaagagactc tgcaaaagcg     480

gctgaatggt ttaccaaagc cgccgaaaag ggtgacctga acgcccggaa aatccttggc     540
```

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gcgatgtact ttcagggcac aggcgttgcc aaagacatgg taaaagcccg gtactggctg 600

caaaaagcgg ctgatgacgg tgacatggac gcaaaaaaca tgctctccga actcaaataa 660

<210> SEQ ID NO 60
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 60

Met Ser Arg Gly Ser Lys Asn Lys Lys Leu Phe Leu Trp Leu Ile Leu
1 5 10 15

Ala Ala Thr Ile Ile Leu Ile Ile Ile Ser Gln Thr Ala Phe Ala Val
20 25 30

Gly Glu Arg Asp Leu Glu Gln Ala Met Gln Ser Tyr Ser Ala Gly Gln
35 40 45

Tyr Lys Glu Ala Val Pro Gln Phe Glu Lys Ala Ala Thr Leu Gly Asn
50 55 60

Asn Lys Ala Gln Thr Met Leu Gly Val Leu Tyr Phe Gln Gly Lys Gly
65 70 75 80

Cys Glu Lys Asp Tyr Val Lys Ala Ala Glu Trp Phe Asp Arg Ala Ala
85 90 95

Asn Gly Gly Asn Ile Glu Ala Gln Thr Phe Met Gly Ile Ile Asn Leu
100 105 110

Glu Gly Leu Gly Thr Pro Lys Asn Glu Lys Thr Ala Tyr Tyr Trp Phe
115 120 125

Glu Lys Ala Ala Arg Gly Gly Glu Thr Ser Ala Gln Asn Tyr Leu Gly
130 135 140

Thr Leu Leu Met Asn Gly Gln Gly Thr Lys Arg Asp Ser Ala Lys Ala
145 150 155 160

Ala Glu Trp Phe Thr Lys Ala Ala Glu Lys Gly Asp Leu Asn Ala Arg
165 170 175

Lys Ile Leu Gly Ala Met Tyr Phe Gln Gly Thr Gly Val Ala Lys Asp
180 185 190

Met Val Lys Ala Arg Tyr Trp Leu Gln Lys Ala Ala Asp Asp Gly Asp
195 200 205

Met Asp Ala Lys Asn Met Leu Ser Glu Leu Lys
210 215

<210> SEQ ID NO 61
<211> LENGTH: 3546
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 61

atgaattctt ttcaatggca cattgtcaaa ctcaaacacc gcgcacttct gtccagcctg 60

atcgtcgcgg cggctttcat tcccttttca tcgacaacag cagggacagc aaacccgccc 120

accattcaga aaactcccga acttgcccgt caggtcaatg aaacgcttaa cttcgatcac 180

aaaacagaag acatcctgaa aacactgacg gaatcaaaaa acccgtccga taaaaccctg 240

atgggagcgt tttacggttc cggtgcaggt ggaaaacagg actggggaaa agcccggatg 300

tggtttgaaa aagcggccag tgaaggcgat gcgcacgctg aatattttct gggtcttctt 360

tacatggggg gtctgggcac ccccaaagat tatgacaagg cgtttcattg gctattgttg 420

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```
gccgcccgta aggacattcc cgacgcacag taccagttga gttggttcta tgccaacgga    480
aaaggtacga gccaaagtct gcgtgaaacg gtttactgga tacaaaaggc agcccacaag    540
gggcatgtag tagccatgcg aagcatggga atgctcagtt actcgggatt aggcatgccc    600
gaaaacaagg tcgacgcttt caaatggttt gaaaaagcgg cgagtgcagg cgatgccgaa    660
gcccaatatc accttggcat gtcctatatg gcaggcaagg gaacggaaaa agacggaaaa    720
aagggagaag aatggcttta tcgtgccgcg ctgcaaaatc agacgaaagc ccaggattat    780
ctttccgtcc tttatgtgca gcgattgctt gataaaaaaa acaggccggg cgaaatcgaa    840
caggcaagac agtggctgga aaacgccgcc cgacgaaacg ataaaaatgc gatatacatg    900
ctgaacgtca ttgagcagta ttctcgcaaa acatcgaaaa atcaggccga aaccctcgac    960
acccttcgtc gtcgcgccga acagggcaat gccgattccc aattcatgct gggagaggcc   1020
ctgcttgccg gaacgggaat gaagaaaaat ccggaagaag ctgtccgctg gtttgaaaaa   1080
gcggcaaaac agggcaacat tgatgcacag tccgccctgg gatatatgca ttatttcggc   1140
gtccatgtcc ctgtcgatta cgcaaaagcc attcccctgt taaaacaggg tgccgataag   1200
gggaacagcc aggcacaaac cgctatggga ttcgcctatg ccagtggaac aggaattgcc   1260
aaaaacgagc aaaaagcatt tgaactgttt gaaaaagcgg cccggaacaa tgtccgaagt   1320
gcccagtttt acctcggtga aatgcttgaa aatggcattg gaacccaacg aaacgtccca   1380
gagggattgg catggatcga aaaatcggcg aaggcaggat acgaccaggc ccagtttacg   1440
atgggaataa acgctctccg tggcaaggac aagatgcaaa atattgacga agcgcgcaaa   1500
tggatgcgtc tggccgccaa acagaatcat gcagaagccc agtacatgct cggcatgtca   1560
tattttctgg gagaactgac accggaaaat caaaaggaag gtattttctg gtgggacaag   1620
gccgccgccc aaaatcacgt cgaagcccgg ctcatgctgt tcaagtatca ctgcgatccc   1680
aaaatgcatt atgcggatcg taaacgatgt tcctcgatct ctgaacaaat gcacgatatc   1740
cgtgaccctg acgcgcttta ttcccttgga gaattatttt ttttcggtaa tgacaaccat   1800
aaaaaaaacg tcccgaaagc tgtcgatttt ttcagcaagg cggctgatct gaaccataca   1860
gaaagccagt acatgctggg gctgattctc tattccaaaa cggatgtcgg acaaaacaaa   1920
aaacaagcct gccagtggtt tgaaaaagcg gcaagtcaca atcacccgga aagccaatat   1980
atgctcggaa tctgtgttct cgaggggaac cacacttccg ccgacaaaaa aaaggcgctt   2040
gaactgatca gactggcagc cgacaaaaac gtcagcatcg cccagaacaa aatggggtat   2100
ctgtatgaaa caggccatat cgttccgaaa gacatgaaaa aagccatcga atggtacaca   2160
cttgccgaac agaatggatt tacggatgcg gcttaccatc tggccctgtt gtaccttgcc   2220
agttccccac ccctgcaaaa cgatccgctg gctctgcgtt atcttgaaaa agcggctagc   2280
gcaaacaata caaatgctct ttataaactg ggaacgtttt atttccacgg tcaatactcg   2340
gccacaaaag atcggaaaaa agcggcggag tatttccgcc gtgccgccaa actcggccat   2400
aaaaacagcc aaatagccta tgccgacatc ctccaaaaag gtaagggagt tgaaaaaaac   2460
gaaaaactgg cttgcgaaat ctatgaaaaa acagccaaag aaggtagccc ttacggacaa   2520
ttccgctcag gactgtgcta tcagacaggt cttggaaata gacccaaaaa tcctgccaaa   2580
gcggtcagtc tttttgaaca ggcagccaga caaaacctgc cggatggcca gattgccctg   2640
gcatactgtt atgaaaccgg acagggcgtt gcccaaaatc ttgcgctggc gttcaaatgg   2700
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tacaaaatgg cagctgaaaa gggagatgtc ggcagcatga tcacaaccgg aaagatgctg   2760

gacaagggag aaggaacagc acgcgacagc aaacaggctt tttactggtt ttcaaaagcg   2820

gctgagaaag gatcacccga agcagaagtt cagttgggcc aactgtatta tgccggacgt   2880

ggcatttccg ctgacatgaa aaaagcggtt tccctcttcg accattcggc cagacaaggc   2940

aacgctttgg ctcaatactg gatgggttat ctctgtcttc acggaaaagg ggtcgaaaaa   3000

aatgagccac tggctcgtga ctggctcgaa aaagccgccg tccagaatca gacaggcgcc   3060

gcttttgaac tggcaaaaca gtattggaat ggcaacggca tcccgtccga tccggaacag   3120

gctattgtct ggttcaccaa agccgcacaa aataacgatg ttcaggcaca aagagcactg   3180

gcgttcattt atagcgtcca tggcgcgaaa aaagggataa agccggatga ccaaaaagcc   3240

ttttactggg caaacaaagc cgccagatat aacgatgatc cctcgaccag actgttgctg   3300

ggaacgtttt atatctcggg aaaagggacc gctgtagatg aaaaaaaagg ccttctcctt   3360

ctgaaagaag ccgcagagaa aaactatccc caggcaatgg cgatgctggg tgagttctat   3420

cttgagaaaa aagacaggaa agaagcacaa atgtggttca agcgtgctgc cgcctccggt   3480

gatcagaagg tcatcgaaat aatgaagaaa aaaggcgttt atccgcaaaa ccccgtccat   3540

ccctga                                                              3546
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<210> SEQ ID NO 62
<211> LENGTH: 1181
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 62

Met Asn Ser Phe Gln Trp His Ile Val Lys Leu Lys His Arg Ala Leu
1               5                   10                  15

Leu Ser Ser Leu Ile Val Ala Ala Ala Phe Ile Pro Phe Ser Ser Thr
            20                  25                  30

Thr Ala Gly Thr Ala Asn Pro Pro Thr Ile Gln Lys Thr Pro Glu Leu
        35                  40                  45

Ala Arg Gln Val Asn Glu Thr Leu Asn Phe Asp His Lys Thr Glu Asp
    50                  55                  60

Ile Leu Lys Thr Leu Thr Glu Ser Lys Asn Pro Ser Asp Lys Thr Leu
65                  70                  75                  80

Met Gly Ala Phe Tyr Gly Ser Gly Ala Gly Gly Lys Gln Asp Trp Gly
                85                  90                  95

Lys Ala Arg Met Trp Phe Glu Lys Ala Ala Ser Glu Gly Asp Ala His
            100                 105                 110

Ala Glu Tyr Phe Leu Gly Leu Leu Tyr Met Gly Gly Leu Gly Thr Pro
        115                 120                 125

Lys Asp Tyr Asp Lys Ala Phe His Trp Leu Leu Leu Ala Ala Arg Lys
    130                 135                 140

Asp Ile Pro Asp Ala Gln Tyr Gln Leu Ser Trp Phe Tyr Ala Asn Gly
145                 150                 155                 160

Lys Gly Thr Ser Gln Ser Leu Arg Glu Thr Val Tyr Trp Ile Gln Lys
                165                 170                 175

Ala Ala His Lys Gly His Val Val Ala Met Arg Ser Met Gly Met Leu
            180                 185                 190

Ser Tyr Ser Gly Leu Gly Met Pro Glu Asn Lys Val Asp Ala Phe Lys
        195                 200                 205
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Trp Phe Glu Lys Ala Ala Ser Ala Gly Asp Ala Glu Ala Gln Tyr His
    210                 215                 220

Leu Gly Met Ser Tyr Met Ala Gly Lys Gly Thr Glu Lys Asp Gly Lys
225                 230                 235                 240

Lys Gly Glu Glu Trp Leu Tyr Arg Ala Ala Leu Gln Asn Gln Thr Lys
                245                 250                 255

Ala Gln Asp Tyr Leu Ser Val Leu Tyr Val Gln Arg Leu Leu Asp Lys
            260                 265                 270

Lys Asn Arg Pro Gly Glu Ile Glu Gln Ala Arg Gln Trp Leu Glu Asn
        275                 280                 285

Ala Ala Arg Arg Asn Asp Lys Asn Ala Ile Tyr Met Leu Asn Val Ile
    290                 295                 300

Glu Gln Tyr Ser Arg Lys Thr Ser Lys Asn Gln Ala Glu Thr Leu Asp
305                 310                 315                 320

Thr Leu Arg Arg Arg Ala Glu Gln Gly Asn Ala Asp Ser Gln Phe Met
                325                 330                 335

Leu Gly Glu Ala Leu Leu Ala Gly Thr Gly Met Lys Lys Asn Pro Glu
            340                 345                 350

Glu Ala Val Arg Trp Phe Glu Lys Ala Ala Lys Gln Gly Asn Ile Asp
        355                 360                 365

Ala Gln Ser Ala Leu Gly Tyr Met His Tyr Phe Gly Val His Val Pro
    370                 375                 380

Val Asp Tyr Ala Lys Ala Ile Pro Leu Leu Lys Gln Gly Ala Asp Lys
385                 390                 395                 400

Gly Asn Ser Gln Ala Gln Thr Ala Met Gly Phe Ala Tyr Ala Ser Gly
                405                 410                 415

Thr Gly Ile Ala Lys Asn Glu Gln Lys Ala Phe Glu Leu Phe Glu Lys
            420                 425                 430

Ala Ala Arg Asn Asn Val Arg Ser Ala Gln Phe Tyr Leu Gly Glu Met
        435                 440                 445

Leu Glu Asn Gly Ile Gly Thr Gln Arg Asn Val Pro Glu Gly Leu Ala
    450                 455                 460

Trp Ile Glu Lys Ser Ala Lys Ala Gly Tyr Asp Gln Ala Gln Phe Thr
465                 470                 475                 480

Met Gly Ile Asn Ala Leu Arg Gly Lys Asp Lys Met Gln Asn Ile Asp
                485                 490                 495

Glu Ala Arg Lys Trp Met Arg Leu Ala Ala Lys Gln Asn His Ala Glu
            500                 505                 510

Ala Gln Tyr Met Leu Gly Met Ser Tyr Phe Leu Gly Glu Leu Thr Pro
        515                 520                 525

Glu Asn Gln Lys Glu Gly Ile Phe Trp Trp Asp Lys Ala Ala Ala Gln
    530                 535                 540

Asn His Val Glu Ala Arg Leu Met Leu Phe Lys Tyr His Cys Asp Pro
545                 550                 555                 560

Lys Met His Tyr Ala Asp Arg Lys Arg Cys Ser Ser Ile Ser Glu Gln
                565                 570                 575

Met His Asp Ile Arg Asp Pro Asp Ala Leu Tyr Ser Leu Gly Glu Leu
            580                 585                 590

Phe Phe Phe Gly Asn Asp Asn His Lys Lys Asn Val Pro Lys Ala Val
        595                 600                 605
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```
Asp Phe Phe Ser Lys Ala Ala Asp Leu Asn His Thr Glu Ser Gln Tyr
    610                 615                 620

Met Leu Gly Leu Ile Leu Tyr Ser Lys Thr Asp Val Gly Gln Asn Lys
625                 630                 635                 640

Lys Gln Ala Cys Gln Trp Phe Glu Lys Ala Ala Ser His Asn His Pro
                645                 650                 655

Glu Ser Gln Tyr Met Leu Gly Ile Cys Val Leu Glu Gly Asn His Thr
            660                 665                 670

Ser Ala Asp Lys Lys Lys Ala Leu Glu Leu Ile Arg Leu Ala Ala Asp
        675                 680                 685

Lys Asn Val Ser Ile Ala Gln Asn Lys Met Gly Tyr Leu Tyr Glu Thr
    690                 695                 700

Gly His Ile Val Pro Lys Asp Met Lys Lys Ala Ile Glu Trp Tyr Thr
705                 710                 715                 720

Leu Ala Glu Gln Asn Gly Phe Thr Asp Ala Ala Tyr His Leu Ala Leu
                725                 730                 735

Leu Tyr Leu Ala Ser Ser Pro Pro Leu Gln Asn Asp Pro Leu Ala Leu
            740                 745                 750

Arg Tyr Leu Glu Lys Ala Ala Ser Ala Asn Asn Thr Asn Ala Leu Tyr
        755                 760                 765

Lys Leu Gly Thr Phe Tyr Phe His Gly Gln Tyr Ser Ala Thr Lys Asp
    770                 775                 780

Arg Lys Lys Ala Ala Glu Tyr Phe Arg Arg Ala Ala Lys Leu Gly His
785                 790                 795                 800

Lys Asn Ser Gln Ile Ala Tyr Ala Asp Ile Leu Gln Lys Gly Lys Gly
                805                 810                 815

Val Glu Lys Asn Glu Lys Leu Ala Cys Glu Ile Tyr Glu Lys Thr Ala
            820                 825                 830

Lys Glu Gly Ser Pro Tyr Gly Gln Phe Arg Ser Gly Leu Cys Tyr Gln
        835                 840                 845

Thr Gly Leu Gly Asn Arg Pro Lys Asn Pro Ala Lys Ala Val Ser Leu
    850                 855                 860

Phe Glu Gln Ala Ala Arg Gln Asn Leu Pro Asp Gly Gln Ile Ala Leu
865                 870                 875                 880

Ala Tyr Cys Tyr Glu Thr Gly Gln Gly Val Ala Gln Asn Leu Ala Leu
                885                 890                 895

Ala Phe Lys Trp Tyr Lys Met Ala Ala Glu Lys Gly Asp Val Gly Ser
            900                 905                 910

Met Ile Thr Thr Gly Lys Met Leu Asp Lys Gly Glu Gly Thr Ala Arg
        915                 920                 925

Asp Ser Lys Gln Ala Phe Tyr Trp Phe Ser Lys Ala Ala Glu Lys Gly
    930                 935                 940

Ser Pro Glu Ala Glu Val Gln Leu Gly Gln Leu Tyr Tyr Ala Gly Arg
945                 950                 955                 960

Gly Ile Ser Ala Asp Met Lys Lys Ala Val Ser Leu Phe Asp His Ser
                965                 970                 975

Ala Arg Gln Gly Asn Ala Leu Ala Gln Tyr Trp Met Gly Tyr Leu Cys
            980                 985                 990

Leu His Gly Lys Gly Val Glu Lys  Asn Glu Pro Leu Ala  Arg Asp Trp
        995                 1000                 1005

Leu Glu  Lys Ala Ala Val Gln  Asn Gln Thr Gly Ala  Ala Phe Glu
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    1010                1015                1020

Leu Ala  Lys Gln Tyr Trp Asn  Gly Asn Gly Ile Pro  Ser Asp Pro
    1025                1030                1035

Glu Gln  Ala Ile Val Trp Phe  Thr Lys Ala Ala Gln  Asn Asn Asp
    1040                1045                1050

Val Gln  Ala Gln Arg Ala Leu  Ala Phe Ile Tyr Ser  Val His Gly
    1055                1060                1065

Ala Lys  Lys Gly Ile Lys Pro  Asp Asp Gln Lys Ala  Phe Tyr Trp
    1070                1075                1080

Ala Asn  Lys Ala Ala Arg Tyr  Asn Asp Asp Pro Ser  Thr Arg Leu
    1085                1090                1095

Leu Leu  Gly Thr Phe Tyr Ile  Ser Gly Lys Gly Thr  Ala Val Asp
    1100                1105                1110

Glu Lys  Lys Gly Leu Leu Leu  Leu Lys Glu Ala Ala  Glu Lys Asn
    1115                1120                1125

Tyr Pro  Gln Ala Met Ala Met  Leu Gly Glu Phe Tyr  Leu Glu Lys
    1130                1135                1140

Lys Asp  Arg Lys Glu Ala Gln  Met Trp Phe Lys Arg  Ala Ala Ala
    1145                1150                1155

Ser Gly  Asp Gln Lys Val Ile  Glu Ile Met Lys Lys  Lys Gly Val
    1160                1165                1170

Tyr Pro  Gln Asn Pro Val His  Pro
    1175                1180


<210> SEQ ID NO 63
<211> LENGTH: 3852
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 63

atgaaccctt tgccatcaga cagccatttt ttcaaacgtt ttgtacgggg atatatcctg     60

ccttgccttt tcttccccat cacggtagcc acagcctctc cggctcagca ccttgtttat    120

ccggagatca tggaaatgcc acaggagata gaccaaaccc tgctggtcga tcatgacagt    180

gaaaaaatac tgaacaaact ggcggactca aacgcccccg ccatgaaaac actcatggga    240

gcctggtacg ctatcggagc cggaggcaaa agggactgga tcaaagcccg catctggttt    300

gaaaaagccg ccactgaagg cgacacaaga gccgcatatc cctcggtctt tttatactcg    360

gccggtctgg gcacccccat cgattacgac aaggcctttt actggctgtc aatcgcggca    420

cgccagaata ttccggatgc ccagtaccgg ctggcaggac tttatcagga aggaaaagga    480

accgccaaaa gcgaacgtga attcgcttac tgggtaaaaa aagccgctgg aaacggacac    540

attgacgccc agagagccat gggaatgatc cttcattatg gtctcggagt tcacaaaaac    600

cttcctgaat cggtcaaatg gtttgaaaaa gcagccaatg ccggaaacgc aaccgcacaa    660

tattatctcg gcatggatta tatgaatggt aatggcctcg ccaaaaatga aagggaagga    720

gaaaagtggc tttatcgcgc cgccatgcaa gaccatcttg aagctcaaac atatctcggc    780

accatttatc tgaaacgcaa gcttcaaaat gaaggtcagc caccggaaac cgcccttgcc    840

atccagtgga tggaaaatgc cgctacgcga aatgacccgt acgctatccg gcttctatcc    900

atggtgtaca ggcatattcc cgaactgcaa aacaacgcca aaggcatgct tcatcttcgc    960

cgcagtgccg agatggggaa tgcatcagcc caattcgatc tcggaagaac cctgtttcag   1020
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gataaaaact cacctgcaaa acgcaaggaa gctgtcgtct ggcttgaaaa agccgcgcaa 1080
caggacgaac gtagggcaca ggcttttctt ggtaacatgt attactatgg cgagttcgtt 1140
cctgtcgatt atgtcaaggc gctccctctt ttgatgaggg ctgccgacaa gggagacagc 1200
tttgcacaat acacgcttgg tttggcttat atcgatggga atggcattgc caaagatgaa 1260
cgaaaggctt tttcatggtt ggaaaaatca gccagtcaaa acagggcaag tgcccagtat 1320
tttttaggac ttatgtacct tgatggaaca gggacacctg tcaatgagga aaaaggcatc 1380
cgtttgctca aagaattagc aaagacaggg tatgtctatg cccaatataa gcttggtacc 1440
tacgcccata gcgggcttca tatggccaaa gatctggcag aagcgagaaa atggtaccag 1500
ttggcggcca gtcaggatca tatcaaggcg aaatactggc tcggcatgtc cctctttcag 1560
ggcccggaca gtgaacagga caggaaaaaa ggcgtttact ggttcaccga agcagcaaaa 1620
caggatgacc cggatgcgca gcttgaactg ggaaaatccc tgctctacgg cgatggtatc 1680
gacaaaaacg aaaagcaggc gtgcacgtgg ttcaaaaaag ccgccaataa ccaacagcac 1740
accggccagt attacgcagg aatgtgcctt atgcggggca tcaatgggcc ggtcgatatt 1800
ccgaaaggaa tgtcactcat tgaaatgtct gcgaataata aggtctcaat ggcccagttc 1860
cagcttggga aactgtatga atatggtttg aaagagttgc cgaaagacat ctcgaaagcc 1920
attggctggt acacacgtgc cgcagaaaat ggacatgcaa ctgcccaata ccggctggga 1980
aagctttatc tcaaagctga tactccactc aaaaatattc cgctcggcct cgaattcctt 2040
gaaaaatccg cttcacaaaa tataaccagt gccatttttg atctgggtaa catttactat 2100
gacggaaaaa ttgtcaaaca ggatatggca aaagcgttga attactttca gaagggaacc 2160
ggactgggcc atctcccgag ccagaatttt gtcggattca tgatcgagaa tggaagcgga 2220
gttaaaaagg ataaagaaaa agcatgcaaa atctatgatg aaaccggtcg acgcggaagt 2280
gcatatggac tttaccgcta tggcttgtgc cagctttccg atcccgatcc atccccggaa 2340
aaccagaaaa aagcgtttat tcttttcgaa caggctgccc gaaaaaatct ggcagacgcc 2400
caatactttt tagccctgtg ttacgaatat ggcaaaggga ctcccaaaaa ccctggcgaa 2460
gctattgaat ggtacaggcg tgcctcggaa aacgacaaac cggaagcact gtaccagttg 2520
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ctggagaaag cagccgcccg ggatctgtcg tccgcattca acgaactggg ccgaatttat 2640
tatgacggga aaatcgtcag gcaggatctc aaaaaatccg tcttctggta tcgcaaggga 2700
gcacaatcgg gagatacaag aagccagaat gatctggctt atatgatgga atacggtaaa 2760
ggtcttgaaa aagacgaaaa ggcggcctgc acgatgtatg aaaaaacggc aggggaaaaa 2820
aacgcttatg gccagttccg tctggggctc tgctatctga atggaaaagg cggtaaagcg 2880
aaggatcaac gggaagcagt ccggctcttc gaatctgccg ccggacaaaa tctggcgtct 2940
gcccaatatt ttctgggaat ttaccataaa gaaggtaaag gtgtcgtcaa aaacatgaat 3000
gaggctttca aatggtacct gacggcagcc gataacggtc acgtcagttc catgtttgaa 3060
gtcggtaaaa tgttcgctaa tggcagaggt acggaacgcg acgacaaaaa ggcatttcac 3120
tggtttgaga aagcagctga aaacgggtct gattccgctt tgacccagct gggcattatg 3180
tattataaag gcttgggcat ttcagccgac aaaagcaaag ccgcctcctt ttttttgaaa 3240
gctgccgaaa aaaacaattc atacgcccaa cactggctcg gctatatgta cctgtacggt 3300

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aaggggctgg aaaaaaacgg ggagctggca aatcagtggt tatcaaaagc ggctgaccag 3360

aatgaaacgg gcgcgatttt tgaactggga aaacaatact ggtatggcat gggcgtcccg 3420

gtcaatcctg aaaaggcaat cgtcctgctt caaaaagcag ggaacgatgg ccatgttatt 3480

gcacaaagga tactgggcta tatttatgct gatggcggcc cggaaaaagg gattcccctt 3540

gatttcgaaa aggccgtcca atggtttgaa aaagcggccc gacaagacga cgccgccggg 3600

aaaatggggt tggcattgct cactctgacc ggaaaaggaa ctccaaaaaa tgaggagaaa 3660

ggtatccggc ttttgacgca gtctgcaaac atgaattatc catccgcgat ggaactgctc 3720

ggggattttt atcgtgaaga aaaaggtgat aaaaaagaag cggaaaaatg gtatcgtcgt 3780

gccgccgaaa ccggcgacaa aaccgttatc gaatccatga agaaaaaagg cgtttatccg 3840

gcaaacccgt aa 3852

<210> SEQ ID NO 64
<211> LENGTH: 1283
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 64

Met Asn Pro Leu Pro Ser Asp Ser His Phe Phe Lys Arg Phe Val Arg
1 5 10 15

Gly Tyr Ile Leu Pro Cys Leu Phe Phe Pro Ile Thr Val Ala Thr Ala
20 25 30

Ser Pro Ala Gln His Leu Val Tyr Pro Glu Ile Met Glu Met Pro Gln
35 40 45

Glu Ile Asp Gln Thr Leu Leu Val Asp His Asp Ser Glu Lys Ile Leu
50 55 60

Asn Lys Leu Ala Asp Ser Asn Ala Pro Ala Met Lys Thr Leu Met Gly
65 70 75 80

Ala Trp Tyr Ala Ile Gly Ala Gly Gly Lys Arg Asp Trp Ile Lys Ala
85 90 95

Arg Ile Trp Phe Glu Lys Ala Ala Thr Glu Gly Asp Thr Arg Ala Ala
100 105 110

Tyr Pro Leu Gly Leu Leu Tyr Ser Ala Gly Leu Gly Thr Pro Ile Asp
115 120 125

Tyr Asp Lys Ala Phe Tyr Trp Leu Ser Ile Ala Ala Arg Gln Asn Ile
130 135 140

Pro Asp Ala Gln Tyr Arg Leu Ala Gly Leu Tyr Gln Glu Gly Lys Gly
145 150 155 160

Thr Ala Lys Ser Glu Arg Glu Phe Ala Tyr Trp Val Lys Lys Ala Ala
165 170 175

Gly Asn Gly His Ile Asp Ala Gln Arg Ala Met Gly Met Ile Leu His
180 185 190

Tyr Gly Leu Gly Val His Lys Asn Leu Pro Glu Ser Val Lys Trp Phe
195 200 205

Glu Lys Ala Ala Asn Ala Gly Asn Ala Thr Ala Gln Tyr Tyr Leu Gly
210 215 220

Met Asp Tyr Met Asn Gly Asn Gly Leu Ala Lys Asn Glu Arg Glu Gly
225 230 235 240

Glu Lys Trp Leu Tyr Arg Ala Ala Met Gln Asp His Leu Glu Ala Gln
245 250 255

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Thr Tyr Leu Gly Thr Ile Tyr Leu Lys Arg Lys Leu Gln Asn Glu Gly
            260                 265                 270

Gln Pro Pro Glu Thr Ala Leu Ala Ile Gln Trp Met Glu Asn Ala Ala
        275                 280                 285

Thr Arg Asn Asp Pro Tyr Ala Ile Arg Leu Leu Ser Met Val Tyr Arg
    290                 295                 300

His Ile Pro Glu Leu Gln Asn Asn Ala Lys Gly Met Leu His Leu Arg
305                 310                 315                 320

Arg Ser Ala Glu Met Gly Asn Ala Ser Ala Gln Phe Asp Leu Gly Arg
                325                 330                 335

Thr Leu Phe Gln Asp Lys Asn Ser Pro Ala Lys Arg Lys Glu Ala Val
            340                 345                 350

Val Trp Leu Glu Lys Ala Ala Gln Gln Asp Glu Arg Arg Ala Gln Ala
        355                 360                 365

Phe Leu Gly Asn Met Tyr Tyr Tyr Gly Glu Phe Val Pro Val Asp Tyr
    370                 375                 380

Val Lys Ala Leu Pro Leu Leu Met Arg Ala Ala Asp Lys Gly Asp Ser
385                 390                 395                 400

Phe Ala Gln Tyr Thr Leu Gly Leu Ala Tyr Ile Asp Gly Asn Gly Ile
                405                 410                 415

Ala Lys Asp Glu Arg Lys Ala Phe Ser Trp Leu Glu Lys Ser Ala Ser
            420                 425                 430

Gln Asn Arg Ala Ser Ala Gln Tyr Phe Leu Gly Leu Met Tyr Leu Asp
        435                 440                 445

Gly Thr Gly Thr Pro Val Asn Glu Glu Lys Gly Ile Arg Leu Leu Lys
    450                 455                 460

Glu Leu Ala Lys Thr Gly Tyr Val Tyr Ala Gln Tyr Lys Leu Gly Thr
465                 470                 475                 480

Tyr Ala His Ser Gly Leu His Met Ala Lys Asp Leu Ala Glu Ala Arg
                485                 490                 495

Lys Trp Tyr Gln Leu Ala Ala Ser Gln Asp His Ile Lys Ala Lys Tyr
            500                 505                 510

Trp Leu Gly Met Ser Leu Phe Gln Gly Pro Asp Ser Glu Gln Asp Arg
        515                 520                 525

Lys Lys Gly Val Tyr Trp Phe Thr Glu Ala Ala Lys Gln Asp Asp Pro
    530                 535                 540

Asp Ala Gln Leu Glu Leu Gly Lys Ser Leu Leu Tyr Gly Asp Gly Ile
545                 550                 555                 560

Asp Lys Asn Glu Lys Gln Ala Cys Thr Trp Phe Lys Lys Ala Ala Asn
                565                 570                 575

Asn Gln Gln His Thr Gly Gln Tyr Tyr Ala Gly Met Cys Leu Met Arg
            580                 585                 590

Gly Ile Asn Gly Pro Val Asp Ile Pro Lys Gly Met Ser Leu Ile Glu
        595                 600                 605

Met Ser Ala Asn Asn Lys Val Ser Met Ala Gln Phe Gln Leu Gly Lys
    610                 615                 620

Leu Tyr Glu Tyr Gly Leu Lys Glu Leu Pro Lys Asp Ile Ser Lys Ala
625                 630                 635                 640

Ile Gly Trp Tyr Thr Arg Ala Ala Glu Asn Gly His Ala Thr Ala Gln
                645                 650                 655
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Tyr Arg Leu Gly Lys Leu Tyr Leu Lys Ala Asp Thr Pro Leu Lys Asn
            660                 665                 670

Ile Pro Leu Gly Leu Glu Phe Leu Glu Lys Ser Ala Ser Gln Asn Ile
        675                 680                 685

Thr Ser Ala Ile Phe Asp Leu Gly Asn Ile Tyr Tyr Asp Gly Lys Ile
    690                 695                 700

Val Lys Gln Asp Met Ala Lys Ala Leu Asn Tyr Phe Gln Lys Gly Thr
705                 710                 715                 720

Gly Leu Gly His Leu Pro Ser Gln Asn Phe Val Gly Phe Met Ile Glu
                725                 730                 735

Asn Gly Ser Gly Val Lys Lys Asp Lys Glu Lys Ala Cys Lys Ile Tyr
            740                 745                 750

Asp Glu Thr Gly Arg Arg Gly Ser Ala Tyr Gly Leu Tyr Arg Tyr Gly
        755                 760                 765

Leu Cys Gln Leu Ser Asp Pro Asp Pro Ser Pro Glu Asn Gln Lys Lys
    770                 775                 780

Ala Phe Ile Leu Phe Glu Gln Ala Ala Arg Lys Asn Leu Ala Asp Ala
785                 790                 795                 800

Gln Tyr Phe Leu Ala Leu Cys Tyr Glu Tyr Gly Lys Gly Thr Pro Lys
                805                 810                 815

Asn Pro Gly Glu Ala Ile Glu Trp Tyr Arg Arg Ala Ser Glu Asn Asp
            820                 825                 830

Lys Pro Glu Ala Leu Tyr Gln Leu Gly Met Leu Tyr Ile Thr Ser Pro
        835                 840                 845

Ser Pro Arg Gln Asn Ile Pro Leu Gly Leu Asp Tyr Leu Glu Lys Ala
    850                 855                 860

Ala Ala Arg Asp Leu Ser Ser Ala Phe Asn Glu Leu Gly Arg Ile Tyr
865                 870                 875                 880

Tyr Asp Gly Lys Ile Val Arg Gln Asp Leu Lys Lys Ser Val Phe Trp
                885                 890                 895

Tyr Arg Lys Gly Ala Gln Ser Gly Asp Thr Arg Ser Gln Asn Asp Leu
            900                 905                 910

Ala Tyr Met Met Glu Tyr Gly Lys Gly Leu Glu Lys Asp Glu Lys Ala
        915                 920                 925

Ala Cys Thr Met Tyr Glu Lys Thr Ala Gly Glu Lys Asn Ala Tyr Gly
    930                 935                 940

Gln Phe Arg Leu Gly Leu Cys Tyr Leu Asn Gly Lys Gly Gly Lys Ala
945                 950                 955                 960

Lys Asp Gln Arg Glu Ala Val Arg Leu Phe Glu Ser Ala Ala Gly Gln
                965                 970                 975

Asn Leu Ala Ser Ala Gln Tyr Phe Leu Gly Ile Tyr His Lys Glu Gly
            980                 985                 990

Lys Gly Val Val Lys Asn Met Asn  Glu Ala Phe Lys Trp  Tyr Leu Thr
        995                 1000                 1005

Ala Ala  Asp Asn Gly His Val  Ser Ser Met Phe Glu  Val Gly Lys
    1010                 1015                 1020

Met Phe  Ala Asn Gly Arg Gly  Thr Glu Arg Asp Asp  Lys Lys Ala
    1025                 1030                 1035

Phe His  Trp Phe Glu Lys Ala  Ala Glu Asn Gly Ser  Asp Ser Ala
    1040                 1045                 1050

Leu Thr  Gln Leu Gly Ile Met  Tyr Tyr Lys Gly Leu  Gly Ile Ser
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    1055                1060                1065

Ala Asp  Lys Ser Lys Ala Ala  Ser Phe Phe Leu Lys  Ala Ala Glu
    1070                1075                1080

Lys Asn  Asn Ser Tyr Ala Gln  His Trp Leu Gly Tyr  Met Tyr Leu
    1085                1090                1095

Tyr Gly  Lys Gly Leu Glu Lys  Asn Gly Glu Leu Ala  Asn Gln Trp
    1100                1105                1110

Leu Ser  Lys Ala Ala Asp Gln  Asn Glu Thr Gly Ala  Ile Phe Glu
    1115                1120                1125

Leu Gly  Lys Gln Tyr Trp Tyr  Gly Met Gly Val Pro  Val Asn Pro
    1130                1135                1140

Glu Lys  Ala Ile Val Leu Leu  Gln Lys Ala Gly Asn  Asp Gly His
    1145                1150                1155

Val Ile  Ala Gln Arg Ile Leu  Gly Tyr Ile Tyr Ala  Asp Gly Gly
    1160                1165                1170

Pro Glu  Lys Gly Ile Pro Leu  Asp Phe Glu Lys Ala  Val Gln Trp
    1175                1180                1185

Phe Glu  Lys Ala Ala Arg Gln  Asp Asp Ala Ala Gly  Lys Met Gly
    1190                1195                1200

Leu Ala  Leu Leu Thr Leu Thr  Gly Lys Gly Thr Pro  Lys Asn Glu
    1205                1210                1215

Glu Lys  Gly Ile Arg Leu Leu  Thr Gln Ser Ala Asn  Met Asn Tyr
    1220                1225                1230

Pro Ser  Ala Met Glu Leu Leu  Gly Asp Phe Tyr Arg  Glu Glu Lys
    1235                1240                1245

Gly Asp  Lys Lys Glu Ala Glu  Lys Trp Tyr Arg Arg  Ala Ala Glu
    1250                1255                1260

Thr Gly  Asp Lys Thr Val Ile  Glu Ser Met Lys Lys  Lys Gly Val
    1265                1270                1275

Tyr Pro  Ala Asn Pro
    1280
```

<210> SEQ ID NO 65
<211> LENGTH: 1245
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 65

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atgactctat ccctgttccg aaaaattcat atgaaagctg cctttgcctg ctgcgctttc    120

ctgatagcct tgccttttc cgcaagccat gcaggaaata tcgtccattc cgggttgccc    180

ggagcgcccg ttattgtcgg gacggaaaac cggaaacctc cggaaaccgt ctctgaaaac    240

aatgttcccg aagcagcccg ttcaccagtc gatcagaacg acgcaaaaac acagtttcat    300

cttgggctga tgtcgaaaaa cggctatgga gtccctgtcg acccggtaaa agcccgcgaa    360

tggtttgcga aagcggccgg acaaaattac cagcccgccc aataccagct tgccctcatg    420

caattttcag gcacaggcgg cacagaaaac aaaagtgccg cgatcgaaca attcaaaaaa    480

ctggcttctg aaggatatgc tcccgcccaa tacacgctcg gatatctgaa cctgaaaggc    540

gatggcatcc cgcaaaattc cggagaagcc cgcttctggt tcgaaaaggc cgccgcaaaa    600

aacgatgtgc gcgcaaccgc tgcactggca tggctttatc tgaaaggcgt cggcgctccc    660
```

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```
atcgatgaga aaaaagccgc cgtcctgttt gaaaaagctg ccaatatggg tgacgcatac    720

agccaggatc aattcggcat gatgctcggt cagggaactg gcatgaatgc cgaacccgaa    780

aaagcgtttt tatggattga aaaagcggca aaccagcaat atccggttgc cgaataccat    840

atggccatga tgtacctgac aggttcggga acggaaaaaa atccggagct agccgtcaaa    900

tggcttgaaa aagccgcttt ccacgggaac gtcgatgccc agaatttcta tgccagcctg    960

ctttatctcg gttatggaat caaacaggac attcccaggg ccatcgggta ttttaccgaa   1020

gcggccgagg gcggacacgc cgaatcccag ttcttgctgg gaaccatcta cgtcaaggga   1080

aatggcgttt taacgaacct gaaaactgcc cgaaactggt ttgaaaaagc ggaaaagaac   1140

ggacaccccg atgcaaaagc cgcactggaa aaactggatg aaatggaagg caaaggccgt   1200

gcaacacctg aaaagaccga taccggcaat cactatccat cttga                   1245
```

<210> SEQ ID NO 66
<211> LENGTH: 414
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 66

```
Met Pro Tyr Trp Ser Gly Ala His Leu Arg Tyr Asn Asp Ser Lys Ile
1               5                   10                  15

Lys Phe Pro Val Met Thr Leu Ser Leu Phe Arg Lys Ile His Met Lys
            20                  25                  30

Ala Ala Phe Ala Cys Cys Ala Phe Leu Ile Ala Leu Pro Phe Ser Ala
        35                  40                  45

Ser His Ala Gly Asn Ile Val His Ser Gly Leu Pro Gly Ala Pro Val
    50                  55                  60

Ile Val Gly Thr Glu Asn Arg Lys Pro Pro Glu Thr Val Ser Glu Asn
65                  70                  75                  80

Asn Val Pro Glu Ala Ala Arg Ser Pro Val Asp Gln Asn Asp Ala Lys
                85                  90                  95

Thr Gln Phe His Leu Gly Leu Met Ser Lys Asn Gly Tyr Gly Val Pro
            100                 105                 110

Val Asp Pro Val Lys Ala Arg Glu Trp Phe Ala Lys Ala Ala Gly Gln
        115                 120                 125

Asn Tyr Gln Pro Ala Gln Tyr Gln Leu Ala Leu Met Gln Phe Ser Gly
    130                 135                 140

Thr Gly Gly Thr Glu Asn Lys Ser Ala Ala Ile Glu Gln Phe Lys Lys
145                 150                 155                 160

Leu Ala Ser Glu Gly Tyr Ala Pro Ala Gln Tyr Thr Leu Gly Tyr Leu
                165                 170                 175

Asn Leu Lys Gly Asp Gly Ile Pro Gln Asn Ser Gly Glu Ala Arg Phe
            180                 185                 190

Trp Phe Glu Lys Ala Ala Ala Lys Asn Asp Val Arg Ala Thr Ala Ala
        195                 200                 205

Leu Ala Trp Leu Tyr Leu Lys Gly Val Gly Ala Pro Ile Asp Glu Lys
    210                 215                 220

Lys Ala Ala Val Leu Phe Glu Lys Ala Ala Asn Met Gly Asp Ala Tyr
225                 230                 235                 240

Ser Gln Asp Gln Phe Gly Met Met Leu Gly Gln Gly Thr Gly Met Asn
                245                 250                 255
```

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Ala Glu Pro Glu Lys Ala Phe Leu Trp Ile Glu Lys Ala Ala Asn Gln
260 265 270

Gln Tyr Pro Val Ala Glu Tyr His Met Ala Met Met Tyr Leu Thr Gly
275 280 285

Ser Gly Thr Glu Lys Asn Pro Glu Leu Ala Val Lys Trp Leu Glu Lys
290 295 300

Ala Ala Phe His Gly Asn Val Asp Ala Gln Asn Phe Tyr Ala Ser Leu
305 310 315 320

Leu Tyr Leu Gly Tyr Gly Ile Lys Gln Asp Ile Pro Arg Ala Ile Gly
325 330 335

Tyr Phe Thr Glu Ala Ala Glu Gly Gly His Ala Glu Ser Gln Phe Leu
340 345 350

Leu Gly Thr Ile Tyr Val Lys Gly Asn Gly Val Leu Thr Asn Leu Lys
355 360 365

Thr Ala Arg Asn Trp Phe Glu Lys Ala Glu Lys Asn Gly His Pro Asp
370 375 380

Ala Lys Ala Ala Leu Glu Lys Leu Asp Glu Met Glu Gly Lys Gly Arg
385 390 395 400

Ala Thr Pro Glu Lys Thr Asp Thr Gly Asn His Tyr Pro Ser
405 410

<210> SEQ ID NO 67
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 67

atggagtgct tgagcctgaa aaaaacaggc tgttccctga tggcaatgac cctttgtttc 60

attttccttt cggcgtgcaa accaaaaacc attttggaca ccactccgct gaaagcggaa 120

atcgcgcagg aatttgccaa agccgataaa ggcgacgcgg ctgcccggtt caatatcggc 180

ctcatgtact tcaggggaga aggtgtccct caggattacc ggcaggcgcg cgtctggttt 240

gaaaaagcgg ccatgcaagg gctcggcgaa gcccaataca atatgggagc catgctggag 300

cagggactcg gcacagaaaa gaatgccgcc acagccagaa cctggtatga aaaagcggca 360

gcacagggca acgctcacgc ccagtacaac cttgccaggc tttacctgac aggcaaaggc 420

acgtcacaaa acatcggcaa ggcaggtgaa tggatgcaaa aagcggcagc acagggaatg 480

acagaagcaa aagaacgctt ttccattcta ttcgacagtc aatccggctc atttaaaccg 540

gcaaaaatcc agtcatggat tgaacaatcg gtccagaccg gtggggaaaa agcgaaaatc 600

ctgcaggaaa aaataagaag ccatagctga 630

<210> SEQ ID NO 68
<211> LENGTH: 209
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 68

Met Glu Cys Leu Ser Leu Lys Lys Thr Gly Cys Ser Leu Met Ala Met
1 5 10 15

Thr Leu Cys Phe Ile Phe Leu Ser Ala Cys Lys Pro Lys Thr Ile Leu
20 25 30

Asp Thr Thr Pro Leu Lys Ala Glu Ile Ala Gln Glu Phe Ala Lys Ala

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```
        35                  40                  45

Asp Lys Gly Asp Ala Ala Ala Arg Phe Asn Ile Gly Leu Met Tyr Phe
    50                  55                  60

Arg Gly Glu Gly Val Pro Gln Asp Tyr Arg Gln Ala Arg Val Trp Phe
65                  70                  75                  80

Glu Lys Ala Ala Met Gln Gly Leu Gly Glu Ala Gln Tyr Asn Met Gly
                85                  90                  95

Ala Met Leu Glu Gln Gly Leu Gly Thr Glu Lys Asn Ala Ala Thr Ala
            100                 105                 110

Arg Thr Trp Tyr Glu Lys Ala Ala Ala Gln Gly Asn Ala His Ala Gln
        115                 120                 125

Tyr Asn Leu Ala Arg Leu Tyr Leu Thr Gly Lys Gly Thr Ser Gln Asn
    130                 135                 140

Ile Gly Lys Ala Gly Glu Trp Met Gln Lys Ala Ala Ala Gln Gly Met
145                 150                 155                 160

Thr Glu Ala Lys Glu Arg Phe Ser Ile Leu Phe Asp Ser Gln Ser Gly
                165                 170                 175

Ser Phe Lys Pro Ala Lys Ile Gln Ser Trp Ile Glu Gln Ser Val Gln
            180                 185                 190

Thr Gly Gly Glu Lys Ala Lys Ile Leu Gln Glu Lys Ile Arg Ser His
        195                 200                 205

Ser
```

<210> SEQ ID NO 69
<211> LENGTH: 1461
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 69

```
atgaatgaat cgacgtcttt tcaaacagtg aaatcccatt tcatgaaaac cggctttatt     60

tcaatctgca aacgggcgat tcccgtcctg ctcttctcat tcatggcttc cctgtcgaat    120

ccggcagcgg gacaaaccga cgccgatgcg aaaaccgaag gcatcaggct gtatcaggaa    180

aaaaaataca tcgaagccct tccctacctc aatgcgcccg atgcccaaaa agacccgctt    240

gtccagagcg cgctcggcaa tatgttttca atggggctgg gcgtcgacgt caatcaggaa    300

aaagccttcg actggtacct gaaagccgcc aaacagaata acgcgatggc ccagctctac    360

gtcgcctata tgcttgaaaa aggacttggc gtccgcaaaa acgacaggga agccttcaac    420

tggtacaaaa aagcagccga acagaacgta ccgaacgcac aatacaaact cggcactctt    480

tacgaaaaag gcatcggcac ccgaatcaat ctgaaagaag ccctgaactg gtaccggaaa    540

gccgccgaag gaggcctgtc gggagcgcaa gtcaaactgg gccgcctgta cagcgaaggc    600

atcggcgtca aacgcgacta taccgaagcc gcccgctggt tctaccctgc agccgaaaaa    660

ggggacgtca tggcacagac tgcccttgcc ttcctctttg aaaacgggct tggcgtccag    720

caggatgacg ccttcgctat cagctggtac tccaaagcgg ccgaaaaggg tttcgctcct    780

gcccagaaca atctgggtta cctgtacgac aacggcatcg gcgtcctgcg tgactacacc    840

accgccagaa aatggtacga agccgccgca aaacagggga atgtggaagc ccagttcaac    900

ctcggccagc tctacaccct tggccacggc accgttcagg actacggcaa ggccgccgaa    960

tggctcgaaa aagccgctgc caaaggccac ccgaaagccc tgaacaatct cggcatggcc   1020
```

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```
agtcttgacg gcatgggcgt tccgatggat cgcgtcaagg ccggagaata cttccggaaa   1080

gccgccctgc tcggcaacgc ccatgcccag tacaatctgg ctaccctgta cgtccagcat   1140

ccagacgcac tgacaaaaga caagcgaagc aaaaccgacg ctttggccct gcaatggttc   1200

aaaaaaagcg cggctgccgg tcaccctgcc gcgatggcct atctggctga cgtctatacc   1260

tacggcaaac tgggacagag acccaaccgg aaactggccg ccagctggaa acagaaagcc   1320

gatgccgccg aagaaaaacg caaaagagca cagaccatca ctccgctgcc cagaaccgaa   1380

gcggccagac ccgccaaaac cgaaccggtc aagcccgtca caaaggattt caatcccaac   1440

gaccgcgact ggctggaata g                                              1461
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<210> SEQ ID NO 70
<211> LENGTH: 486
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 70

Met Asn Glu Ser Thr Ser Phe Gln Thr Val Lys Ser His Phe Met Lys
1               5                   10                  15

Thr Gly Phe Ile Ser Ile Cys Lys Arg Ala Ile Pro Val Leu Leu Phe
            20                  25                  30

Ser Phe Met Ala Ser Leu Ser Asn Pro Ala Ala Gly Gln Thr Asp Ala
        35                  40                  45

Asp Ala Lys Thr Glu Gly Ile Arg Leu Tyr Gln Glu Lys Lys Tyr Ile
    50                  55                  60

Glu Ala Leu Pro Tyr Leu Asn Ala Pro Asp Ala Gln Lys Asp Pro Leu
65                  70                  75                  80

Val Gln Ser Ala Leu Gly Asn Met Phe Ser Met Gly Leu Gly Val Asp
                85                  90                  95

Val Asn Gln Glu Lys Ala Phe Asp Trp Tyr Leu Lys Ala Ala Lys Gln
            100                 105                 110

Asn Asn Ala Met Ala Gln Leu Tyr Val Ala Tyr Met Leu Glu Lys Gly
        115                 120                 125

Leu Gly Val Arg Lys Asn Asp Arg Glu Ala Phe Asn Trp Tyr Lys Lys
    130                 135                 140

Ala Ala Glu Gln Asn Val Pro Asn Ala Gln Tyr Lys Leu Gly Thr Leu
145                 150                 155                 160

Tyr Glu Lys Gly Ile Gly Thr Arg Ile Asn Leu Lys Glu Ala Leu Asn
                165                 170                 175

Trp Tyr Arg Lys Ala Ala Glu Gly Gly Leu Ser Gly Ala Gln Val Lys
            180                 185                 190

Leu Gly Arg Leu Tyr Ser Glu Gly Ile Gly Val Lys Arg Asp Tyr Thr
        195                 200                 205

Glu Ala Ala Arg Trp Phe Tyr Pro Ala Ala Glu Lys Gly Asp Val Met
    210                 215                 220

Ala Gln Thr Ala Leu Ala Phe Leu Phe Glu Asn Gly Leu Gly Val Gln
225                 230                 235                 240

Gln Asp Asp Ala Phe Ala Ile Ser Trp Tyr Ser Lys Ala Ala Glu Lys
                245                 250                 255

Gly Phe Ala Pro Ala Gln Asn Asn Leu Gly Tyr Leu Tyr Asp Asn Gly
            260                 265                 270

Ile Gly Val Leu Arg Asp Tyr Thr Thr Ala Arg Lys Trp Tyr Glu Ala
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        275                 280                 285

Ala Ala Lys Gln Gly Asn Val Glu Ala Gln Phe Asn Leu Gly Gln Leu
    290                 295                 300

Tyr Thr Leu Gly His Gly Thr Val Gln Asp Tyr Gly Lys Ala Ala Glu
305                 310                 315                 320

Trp Leu Glu Lys Ala Ala Ala Lys Gly His Pro Lys Ala Leu Asn Asn
                325                 330                 335

Leu Gly Met Ala Ser Leu Asp Gly Met Gly Val Pro Met Asp Arg Val
            340                 345                 350

Lys Ala Gly Glu Tyr Phe Arg Lys Ala Ala Leu Leu Gly Asn Ala His
        355                 360                 365

Ala Gln Tyr Asn Leu Ala Thr Leu Tyr Val Gln His Pro Asp Ala Leu
    370                 375                 380

Thr Lys Asp Lys Arg Ser Lys Thr Asp Ala Leu Ala Leu Gln Trp Phe
385                 390                 395                 400

Lys Lys Ser Ala Ala Ala Gly His Pro Ala Ala Met Ala Tyr Leu Ala
                405                 410                 415

Asp Val Tyr Thr Tyr Gly Lys Leu Gly Gln Arg Pro Asn Arg Lys Leu
            420                 425                 430

Ala Ala Ser Trp Lys Gln Lys Ala Asp Ala Ala Glu Glu Lys Arg Lys
        435                 440                 445

Arg Ala Gln Thr Ile Thr Pro Leu Pro Arg Thr Glu Ala Ala Arg Pro
    450                 455                 460

Ala Lys Thr Glu Pro Val Lys Pro Val Thr Lys Asp Phe Asn Pro Asn
465                 470                 475                 480

Asp Arg Asp Trp Leu Glu
                485
```

<210> SEQ ID NO 71
<211> LENGTH: 885
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 71

```
atgatcaatc gttctttcaa gaatgcaaaa attatattta tcctttttct tttatcattt      60

tgtataaatg tgtttgccgg tgatatagaa aaaggattaa agctgttcaa aaaacaggaa     120

tatgaaaagg cattgcctta ttttcagaaa ccggttgcgc aaaaaaatcc ggacgttcag     180

gctgcattgg gatacatgta tcgtgaaggt ttagccgttc cgaaagacat tcaaaaggca     240

tttgatttat ttctggagtc agccagacaa aacaatccga gaggacagta tggaatggga     300

accatgtatg accttggact gattgtcaaa caggataaag aaaaagcgtt caaatggtat     360

atgtatgcag ctgaaaatgg atacaagaat gcccaatata atattgggat tatgtatgcc     420

agaggaagag gaacaaaacg ggattacaaa aaagccaggg aatggtatga aaaagccgtt     480

ttgcagggac acaagggtgc tatgacgaat ttgggacttc tttattatcg gggatggggc     540

ggcccgaaag attatgctaa atcagcagaa ctgaatacac gggcggctaa attaggtgat     600

gatatagccc aatataatct ggcacgtgat tatgaaaatg gtaccggcgt tccaaaagat     660

tacaagcagg ctgtttactg gtatttcaag gggctgaaa atggaaatgc aatggcgatg     720

gaacgattgt atgaagccta tcacctcaac cgattgggtt tgccgagaga cgatgaaaaa     780

gcgcattact gggctgaaaa agcccgggaa acccgccgta aaacaggaga actggctccc     840
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gagtcaatga gcattatcga aaaaatagag cgaatctggt tctga                  885


<210> SEQ ID NO 72
<211> LENGTH: 294
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 72

Met Ile Asn Arg Ser Phe Lys Asn Ala Lys Ile Ile Phe Ile Leu Phe
1               5                   10                  15

Leu Leu Ser Phe Cys Ile Asn Val Phe Ala Gly Asp Ile Glu Lys Gly
            20                  25                  30

Leu Lys Leu Phe Lys Lys Gln Glu Tyr Glu Lys Ala Leu Pro Tyr Phe
        35                  40                  45

Gln Lys Pro Val Ala Gln Lys Asn Pro Asp Val Gln Ala Ala Leu Gly
    50                  55                  60

Tyr Met Tyr Arg Glu Gly Leu Ala Val Pro Lys Asp Ile Gln Lys Ala
65                  70                  75                  80

Phe Asp Leu Phe Leu Glu Ser Ala Arg Gln Asn Asn Pro Arg Gly Gln
                85                  90                  95

Tyr Gly Met Gly Thr Met Tyr Asp Leu Gly Leu Ile Val Lys Gln Asp
            100                 105                 110

Lys Glu Lys Ala Phe Lys Trp Tyr Met Tyr Ala Ala Glu Asn Gly Tyr
        115                 120                 125

Lys Asn Ala Gln Tyr Asn Ile Gly Ile Met Tyr Ala Arg Gly Arg Gly
    130                 135                 140

Thr Lys Arg Asp Tyr Lys Lys Ala Arg Glu Trp Tyr Glu Lys Ala Val
145                 150                 155                 160

Leu Gln Gly His Lys Gly Ala Met Thr Asn Leu Gly Leu Leu Tyr Tyr
                165                 170                 175

Arg Gly Trp Gly Gly Pro Lys Asp Tyr Ala Lys Ser Ala Glu Leu Asn
            180                 185                 190

Thr Arg Ala Ala Lys Leu Gly Asp Asp Ile Ala Gln Tyr Asn Leu Ala
        195                 200                 205

Arg Asp Tyr Glu Asn Gly Thr Gly Val Pro Lys Asp Tyr Lys Gln Ala
    210                 215                 220

Val Tyr Trp Tyr Phe Lys Gly Ala Glu Asn Gly Asn Ala Met Ala Met
225                 230                 235                 240

Glu Arg Leu Tyr Glu Ala Tyr His Leu Asn Arg Leu Gly Leu Pro Arg
                245                 250                 255

Asp Asp Glu Lys Ala His Tyr Trp Ala Glu Lys Ala Arg Glu Thr Arg
            260                 265                 270

Arg Lys Thr Gly Glu Leu Ala Pro Glu Ser Met Ser Ile Ile Glu Lys
        275                 280                 285

Ile Glu Arg Ile Trp Phe
    290


<210> SEQ ID NO 73
<211> LENGTH: 888
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 73
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```
atggttgatt ttttatttaa aaatatcaga attatattta tcctctcttt ggtttcattc     60
agcctgaacc ttgaagccgc cgataccata aaccaaggac tggatttatt tcaaaaaaaa    120
caattcgaaa aagcgttacc ctatctggaa gcatcacatt ccaaaaacga tcctcgagta    180
caagcggcat taggatatat gtatcgggat gggctgggag tcgaaaaaga ttatcagaaa    240
gcgtttatgt tatttctgga gtctgccaaa caatccaatc ccaagggaca gttcggcgta    300
ggaagtatgt atgatcgtgg atttttttgtt aaacgtaata aggaaaaagc gtttaaatgg    360
tatctatacg cagctgagaa tggttatagt tctgctcaaa ataatgtagc ctggtcttat    420
gtacatggag agggaattcc taaagattac aaaaaagcca gagaatggta tgaaaaagca    480
atgattcaag gacattcgaa tgccatggtt ggtttatcct ttatgtatta ttggggaaaa    540
ggcgtaaaaa aagatcgtaa taaagcagcg gaactggaca aacgggcggc agcgttggga    600
aacagaaaag gacagttcaa tctgggccgg gattacgaag atggaacagg tgttcccaaa    660
gactacaagc aagccgttta ctggtacttt aaagccgctg aaaacggtga tcccatggct    720
atggaacgtc tttatgaagc ctatcacctc aaccgattgg gtctgaagag agacgatgaa    780
aaagcccatt actgggctga gaaagcccgg gaaacccgtc gaaaaacggg agaagtcgat    840
ccgcgttcat tgtctgtcat tgaaaaagtc agaatgatct ggttctga                 888
```

```
<210> SEQ ID NO 74
<211> LENGTH: 295
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 74

Met Val Asp Phe Leu Phe Lys Asn Ile Arg Ile Ile Phe Ile Leu Ser
1               5                   10                  15

Leu Val Ser Phe Ser Leu Asn Leu Glu Ala Ala Asp Thr Ile Asn Gln
            20                  25                  30

Gly Leu Asp Leu Phe Gln Lys Lys Gln Phe Glu Lys Ala Leu Pro Tyr
        35                  40                  45

Leu Glu Ala Ser His Ser Lys Asn Asp Pro Arg Val Gln Ala Ala Leu
    50                  55                  60

Gly Tyr Met Tyr Arg Asp Gly Leu Gly Val Glu Lys Asp Tyr Gln Lys
65                  70                  75                  80

Ala Phe Met Leu Phe Leu Glu Ser Ala Lys Gln Ser Asn Pro Lys Gly
                85                  90                  95

Gln Phe Gly Val Gly Ser Met Tyr Asp Arg Gly Phe Phe Val Lys Arg
            100                 105                 110

Asn Lys Glu Lys Ala Phe Lys Trp Tyr Leu Tyr Ala Ala Glu Asn Gly
        115                 120                 125

Tyr Ser Ser Ala Gln Asn Asn Val Ala Trp Ser Tyr Val His Gly Glu
    130                 135                 140

Gly Ile Pro Lys Asp Tyr Lys Lys Ala Arg Glu Trp Tyr Glu Lys Ala
145                 150                 155                 160

Met Ile Gln Gly His Ser Asn Ala Met Val Gly Leu Ser Phe Met Tyr
                165                 170                 175

Tyr Trp Gly Lys Gly Val Lys Lys Asp Arg Asn Lys Ala Ala Glu Leu
            180                 185                 190

Asp Lys Arg Ala Ala Ala Leu Gly Asn Arg Lys Gly Gln Phe Asn Leu
        195                 200                 205
```

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Gly Arg Asp Tyr Glu Asp Gly Thr Gly Val Pro Lys Asp Tyr Lys Gln
    210   215   220

Ala Val Tyr Trp Tyr Phe Lys Ala Ala Glu Asn Gly Asp Pro Met Ala
225   230   235   240

Met Glu Arg Leu Tyr Glu Ala Tyr His Leu Asn Arg Leu Gly Leu Lys
                245   250   255

Arg Asp Asp Glu Lys Ala His Tyr Trp Ala Glu Lys Ala Arg Glu Thr
            260   265   270

Arg Arg Lys Thr Gly Glu Val Asp Pro Arg Ser Leu Ser Val Ile Glu
        275   280   285

Lys Val Arg Met Ile Trp Phe
    290   295

<210> SEQ ID NO 75
<211> LENGTH: 954
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 75

atggaaagcc ataaagaaat caagtcaatt ttaaaagaac ttagccagat gaaaaaacaa 60

tctttatttc tcatcataat tgcaatgatt ctgacaatat ccgcttgtac agaaaaagag 120

tataaatacc tcgcagatga aaaagcagga atcgaatact atcaaaacgg atcatatgat 180

aaagcgttgg catcactaaa aaaaacatat ggttccggaa gtatggaagc cgcttattat 240

cttggcgaaa tgtatcgtca gggtaatggg gttgaaaaag atagaatcgt ttcttgcaat 300

tactatcaaa aatcagcaga agggggaaac aggaaagcct tttgagagc aggaacctgt 360

catataccgg ataccagaga tggagaagga ttcaaagaaa cattcaaatg gtttaaaaaa 420

gcgtctgaag aattaaaaga aaccgatttg aatgaagcag aaaaaaaaga catgtatatc 480

aggcttggaa ttatgtatta cgctggaaaa ggtacactac aggattggag tgaagccgcg 540

aagtggtttg aaaaagctgc cgaaatgggg gatgcctact cacagggagg tctggcgtta 600

ttatattatt ccggcgatgg tgttttaact gacaggaaaa aagcgcgtta ttgggcagaa 660

aaagcagcgg cacaaggtaa tagtacagga gaaggtattc ttggaatgtt ataccaatat 720

agtcttccgc cggataaaga tatgagaaaa gctgtctatt ggtacaagaa atcagccgat 780

cagggaaatc caatatccca gtatcaattg gctgttatct atgaaaatgg tgatggtgtt 840

ccaaaaaacc tcgaaaaagc gcgctattac tatgaacagg catcgaaaag caaatatgat 900

ctgacaaaaa acagtttaaa ggaatttgaa tcgcgaaaca aaagtttgca gtga 954

<210> SEQ ID NO 76
<211> LENGTH: 317
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 76

Met Glu Ser His Lys Glu Ile Lys Ser Ile Leu Lys Glu Leu Ser Gln
1   5   10   15

Met Lys Lys Gln Ser Leu Phe Leu Ile Ile Ile Ala Met Ile Leu Thr
            20   25   30

Ile Ser Ala Cys Thr Glu Lys Glu Tyr Lys Tyr Leu Ala Asp Glu Lys
        35   40   45

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Ala Gly Ile Glu Tyr Tyr Gln Asn Gly Ser Tyr Asp Lys Ala Leu Ala
    50                  55                  60

Ser Leu Lys Lys Thr Tyr Gly Ser Gly Ser Met Glu Ala Ala Tyr Tyr
65                  70                  75                  80

Leu Gly Glu Met Tyr Arg Gln Gly Asn Gly Val Glu Lys Asp Arg Ile
                85                  90                  95

Val Ser Cys Asn Tyr Tyr Gln Lys Ser Ala Glu Gly Gly Asn Arg Lys
            100                 105                 110

Ala Phe Leu Arg Ala Gly Thr Cys His Ile Pro Asp Thr Arg Asp Gly
        115                 120                 125

Glu Gly Phe Lys Glu Thr Phe Lys Trp Phe Lys Lys Ala Ser Glu Glu
    130                 135                 140

Leu Lys Glu Thr Asp Leu Asn Glu Ala Glu Lys Lys Asp Met Tyr Ile
145                 150                 155                 160

Arg Leu Gly Ile Met Tyr Tyr Ala Gly Lys Gly Thr Leu Gln Asp Trp
                165                 170                 175

Ser Glu Ala Ala Lys Trp Phe Glu Lys Ala Ala Glu Met Gly Asp Ala
            180                 185                 190

Tyr Ser Gln Gly Gly Leu Ala Leu Leu Tyr Tyr Ser Gly Asp Gly Val
        195                 200                 205

Leu Thr Asp Arg Lys Lys Ala Arg Tyr Trp Ala Glu Lys Ala Ala Ala
    210                 215                 220

Gln Gly Asn Ser Thr Gly Glu Gly Ile Leu Gly Met Leu Tyr Gln Tyr
225                 230                 235                 240

Ser Leu Pro Pro Asp Lys Asp Met Arg Lys Ala Val Tyr Trp Tyr Lys
                245                 250                 255

Lys Ser Ala Asp Gln Gly Asn Pro Ile Ser Gln Tyr Gln Leu Ala Val
            260                 265                 270

Ile Tyr Glu Asn Gly Asp Gly Val Pro Lys Asn Leu Glu Lys Ala Arg
        275                 280                 285

Tyr Tyr Tyr Glu Gln Ala Ser Lys Ser Lys Tyr Asp Leu Thr Lys Asn
    290                 295                 300

Ser Leu Lys Glu Phe Glu Ser Arg Asn Lys Ser Leu Gln
305                 310                 315
```

```
<210> SEQ ID NO 77
<211> LENGTH: 1083
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 77

atgctgaaaa aatcattatc tctttcgatt atcctttttc tcttgttttc cttatcgggc      60

tgtgagaaga acggtgagga aaacaagagc aagggggatg ttttttattc cagaggggat     120

tatgaaaatg ccctgtctgt ttacaaacag gaggcaaaac ggggcgattc gcatgccttg     180

ctcggtttgt gcaagatgta tgaggatgga aagggggtca aggaaaacga tcggctggct     240

ttccagtatt gcatgcaggc ggccaaacgg ggtgaggtga aggcacagaa gcgtctgggg     300

atgatgtatt acaagggtac cggggtggcg aggaatgtgc atgaagcgcg tttctggttc     360

aatcaggcgg ccttgtcgga cgatccggag gcgctttatt atctcgggat cgcttatttg     420

aaagggatcg gcggggagaa agactttcat caggcgcatg acctttttga aagggcggcc     480

gatgagggac atgtgaatgc catgtggaag ctgtatgaga tgttcaatga aggaaccggt     540
```

-continued

```
gtcaggcagg acaggcagga ggcgttcaaa tggctgatga agctggcggc cgatggcgac    600

atacgcgcgc agttccttgc cggttcgtcg tatctgaccg gcaatggggt gaaggctgat    660

cctgccgagg cggtcaggtg gtttgaaaag gcggcgcagc agggcagtgt tgatgcccag    720

acttcactgg ttttatatta tctgggcaac gagccagtcc gtctggatga agcgcgaagc    780

tgggcggcga aactggaaaa ccagacgggt tcgcgcggtg tcggggcggt gttcaggcgt    840

tttttcactg agatgggaga gtggcctgag ccggaacgca cgcatgaacg gataaaagac    900

tggttcgatt ctctttttc gacgaaagac ccggatctgc tttatggtct cggcttttg     960

tacgagctgg gttatcaggg gcagcgcgat atggacaagg cgctcgccct ctataaaagg   1020

gcggcggctc tggggaacgt gaatgcgatt aaaaaactga aagaactcca gtccgttttt   1080

taa                                                                 1083
```

```
<210> SEQ ID NO 78
<211> LENGTH: 360
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 78

Met Leu Lys Lys Ser Leu Ser Leu Ser Ile Ile Leu Phe Leu Leu Phe
1               5                   10                  15

Ser Leu Ser Gly Cys Glu Lys Asn Gly Glu Glu Asn Lys Ser Lys Gly
            20                  25                  30

Asp Val Phe Tyr Ser Arg Gly Asp Tyr Glu Asn Ala Leu Ser Val Tyr
        35                  40                  45

Lys Gln Glu Ala Lys Arg Gly Asp Ser His Ala Leu Leu Gly Leu Cys
    50                  55                  60

Lys Met Tyr Glu Asp Gly Lys Gly Val Lys Glu Asn Asp Arg Leu Ala
65                  70                  75                  80

Phe Gln Tyr Cys Met Gln Ala Ala Lys Arg Gly Glu Val Lys Ala Gln
                85                  90                  95

Lys Arg Leu Gly Met Met Tyr Tyr Lys Gly Thr Gly Val Ala Arg Asn
            100                 105                 110

Val His Glu Ala Arg Phe Trp Phe Asn Gln Ala Ala Leu Ser Asp Asp
        115                 120                 125

Pro Glu Ala Leu Tyr Tyr Leu Gly Ile Ala Tyr Leu Lys Gly Ile Gly
    130                 135                 140

Gly Glu Lys Asp Phe His Gln Ala His Asp Leu Phe Glu Arg Ala Ala
145                 150                 155                 160

Asp Glu Gly His Val Asn Ala Met Trp Lys Leu Tyr Glu Met Phe Asn
                165                 170                 175

Glu Gly Thr Gly Val Arg Gln Asp Arg Gln Glu Ala Phe Lys Trp Leu
            180                 185                 190

Met Lys Leu Ala Ala Asp Gly Asp Ile Arg Ala Gln Phe Leu Ala Gly
        195                 200                 205

Ser Ser Tyr Leu Thr Gly Asn Gly Val Lys Ala Asp Pro Ala Glu Ala
    210                 215                 220

Val Arg Trp Phe Glu Lys Ala Ala Gln Gln Gly Ser Val Asp Ala Gln
225                 230                 235                 240

Thr Ser Leu Val Leu Tyr Tyr Leu Gly Asn Glu Pro Val Arg Leu Asp
                245                 250                 255
```

-continued

```
Glu Ala Arg Ser Trp Ala Ala Lys Leu Glu Asn Gln Thr Gly Ser Arg
            260                 265                 270

Gly Val Gly Ala Val Phe Arg Arg Phe Phe Thr Glu Met Gly Glu Trp
        275                 280                 285

Pro Glu Pro Glu Arg Thr His Glu Arg Ile Lys Asp Trp Phe Asp Ser
    290                 295                 300

Leu Phe Ser Thr Lys Asp Pro Asp Leu Leu Tyr Gly Leu Gly Phe Leu
305                 310                 315                 320

Tyr Glu Leu Gly Tyr Gln Gly Gln Arg Asp Met Asp Lys Ala Leu Ala
                325                 330                 335

Leu Tyr Lys Arg Ala Ala Ala Leu Gly Asn Val Asn Ala Ile Lys Lys
            340                 345                 350

Leu Lys Glu Leu Gln Ser Val Phe
        355                 360
```

<210> SEQ ID NO 79
<211> LENGTH: 876
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 79

```
atgaaacgat tttgtaaagc acttttcctc tcactcctga tgcttgtagg tatacatgct      60

ctggctgata acgttactga aggtaaccgg ctttataggg caaaacaata tgaagaggcg     120

atgagctttt tcatgaagct ggatgcgcag aaaagtccgg aaatcatgaa tcgtatcggt     180

ttcatgtatg acgctggtcg gggggtggaa agaaacggga atattgcttt tcaatggtat     240

cgcaaggcag ctgaaacagg attggcaaaa gctcaataca atctgggatt atgctttcaa     300

aatggaattg gtgttaaaaa agatatcaac gaagccataa aatggtatct caaggccgca     360

gaacagggat atcccgatgc ggaatccaaa atgggttatc tgaccgtaac cgggaaaggc     420

gtcaaacagg atttcaaaca ggccatgcaa tggtaccggc gtgctgtaga gcatggcaac     480

atacatgcca tcccggagct cggtatcatg tatgaggaag gtcttggcgt caaaaaggac     540

aagacccatg ctgtccagta ttacattatg gggcggaaa aggaaacgt ccgggcacag      600

tttttgctgg cggaagccta ccgttacggc cggggcatca aaaacgacga tgagcgttcg     660

ctctactggt acaagaaggc ggcggaaaac ggcagtgccg atgcctacga tgcgttaggc     720

agcgtgtatg ccaacgaaca gctggggcag aaaaaggaca ggaaaaaagc cggggaaatg     780

gtggaaaaag ccattgaaat ccgcaagcag aatggagagg gcgatcccga tgccagacgc     840

cgcctgaagt tttcggggt gaagctggat gattag                              876
```

<210> SEQ ID NO 80
<211> LENGTH: 291
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 80

```
Met Lys Arg Phe Cys Lys Ala Leu Phe Leu Ser Leu Leu Met Leu Val
1               5                   10                  15

Gly Ile His Ala Leu Ala Asp Asn Val Thr Glu Gly Asn Arg Leu Tyr
            20                  25                  30

Arg Ala Lys Gln Tyr Glu Glu Ala Met Ser Phe Phe Met Lys Leu Asp
        35                  40                  45
```

-continued

```
Ala Gln Lys Ser Pro Glu Ile Met Asn Arg Ile Gly Phe Met Tyr Asp
    50                  55                  60

Ala Gly Arg Gly Val Glu Arg Asn Gly Asn Ile Ala Phe Gln Trp Tyr
65                  70                  75                  80

Arg Lys Ala Ala Glu Thr Gly Leu Ala Lys Ala Gln Tyr Asn Leu Gly
                85                  90                  95

Leu Cys Phe Gln Asn Gly Ile Gly Val Lys Lys Asp Ile Asn Glu Ala
            100                 105                 110

Ile Lys Trp Tyr Leu Lys Ala Ala Glu Gln Gly Tyr Pro Asp Ala Glu
        115                 120                 125

Ser Lys Met Gly Tyr Leu Thr Val Thr Gly Lys Gly Val Lys Gln Asp
    130                 135                 140

Phe Lys Gln Ala Met Gln Trp Tyr Arg Arg Ala Val Glu His Gly Asn
145                 150                 155                 160

Ile His Ala Ile Pro Glu Leu Gly Ile Met Tyr Glu Glu Gly Leu Gly
                165                 170                 175

Val Lys Lys Asp Lys Thr His Ala Val Gln Tyr Tyr Ile Met Gly Ala
            180                 185                 190

Glu Lys Gly Asn Val Arg Ala Gln Phe Leu Leu Ala Glu Ala Tyr Arg
        195                 200                 205

Tyr Gly Arg Gly Ile Lys Asn Asp Asp Glu Arg Ser Leu Tyr Trp Tyr
    210                 215                 220

Lys Lys Ala Ala Glu Asn Gly Ser Ala Asp Ala Tyr Asp Ala Leu Gly
225                 230                 235                 240

Ser Val Tyr Ala Asn Glu Gln Leu Gly Gln Lys Lys Asp Arg Lys Lys
                245                 250                 255

Ala Gly Glu Met Val Glu Lys Ala Ile Glu Ile Arg Lys Gln Asn Gly
            260                 265                 270

Glu Gly Asp Pro Asp Ala Arg Arg Arg Leu Lys Phe Phe Gly Val Lys
        275                 280                 285

Leu Asp Asp
    290
```

<210> SEQ ID NO 81
<211> LENGTH: 852
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 81

```
atgtgtaaaa actattcaat tgattacaga atatattttc gcgttttaat tcttttttta      60

ttggcttgtt ttcttttaac gcctgcatac gccaatgaca ttactcaggg attgaaatac     120

tataaaaaag aagaatatca aaaagcatat cgttattttt ccacaccggc tgctcaaaag     180

aatccccggg ttcaacgtat attgggatat atgtatttaa agggtcttgc cgtcaagcag     240

gattatcaaa aggcgatgtt ctggtatggc aaatcagctg atcagggtaa tcctcaagcc     300

atgtacgata ttggcgttat gtacgatttt ggacagggtg tgaaacagga tcatgaaaaa     360

gcgattcaat ggtatcagcg ctccgcttta aaaggatatg ctgacgcaca atataacctt     420

ggtatcgctt atgaaaaggg agaaggtact cagcaaaatt acgctaaagc gcgtgaatgg     480

tatcaaaaag cagtcacaca gggtaatgtc agtgctatgg tcaatttagg caatctttat     540

ggggaaggtc tcggcggtga aaaaaacgac tcaaaagcct ttgatcttta caaaaaagct     600
```

-continued

```
gccgaaaaag gtgattcggc cgcccaatat aatctcgccg aatactaccg tgccggctta    660

gctaccccac gagacctcga caaagccatc tactggtacg aaaagagcgc tgcagagggc    720

accatcaagg caatggacaa actggccaga atctatcggg tcggctacaa acacatccct    780

gccaatcagg ccttgtccga tgaatgggcc gacaaggctg caaaggcacg tgcaagggaa    840

gccgtcaggt aa                                                        852
```

```
<210> SEQ ID NO 82
<211> LENGTH: 283
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 82

Met Cys Lys Asn Tyr Ser Ile Asp Tyr Arg Ile Tyr Phe Arg Val Leu
1               5                   10                  15

Ile Leu Phe Leu Leu Ala Cys Phe Leu Leu Thr Pro Ala Tyr Ala Asn
            20                  25                  30

Asp Ile Thr Gln Gly Leu Lys Tyr Tyr Lys Lys Glu Glu Tyr Gln Lys
        35                  40                  45

Ala Tyr Arg Tyr Phe Ser Thr Pro Ala Ala Gln Lys Asn Pro Arg Val
    50                  55                  60

Gln Arg Ile Leu Gly Tyr Met Tyr Leu Lys Gly Leu Ala Val Lys Gln
65                  70                  75                  80

Asp Tyr Gln Lys Ala Met Phe Trp Tyr Gly Lys Ser Ala Asp Gln Gly
                85                  90                  95

Asn Pro Gln Ala Met Tyr Asp Ile Gly Val Met Tyr Asp Phe Gly Gln
            100                 105                 110

Gly Val Lys Gln Asp His Glu Lys Ala Ile Gln Trp Tyr Gln Arg Ser
        115                 120                 125

Ala Leu Lys Gly Tyr Ala Asp Ala Gln Tyr Asn Leu Gly Ile Ala Tyr
    130                 135                 140

Glu Lys Gly Glu Gly Thr Gln Gln Asn Tyr Ala Lys Ala Arg Glu Trp
145                 150                 155                 160

Tyr Gln Lys Ala Val Thr Gln Gly Asn Val Ser Ala Met Val Asn Leu
                165                 170                 175

Gly Asn Leu Tyr Gly Glu Gly Leu Gly Gly Glu Lys Asn Asp Ser Lys
            180                 185                 190

Ala Phe Asp Leu Tyr Lys Lys Ala Ala Glu Lys Gly Asp Ser Ala Ala
        195                 200                 205

Gln Tyr Asn Leu Ala Glu Tyr Tyr Arg Ala Gly Leu Ala Thr Pro Arg
    210                 215                 220

Asp Leu Asp Lys Ala Ile Tyr Trp Tyr Glu Lys Ser Ala Ala Glu Gly
225                 230                 235                 240

Thr Ile Lys Ala Met Asp Lys Leu Ala Arg Ile Tyr Arg Val Gly Tyr
                245                 250                 255

Lys His Ile Pro Ala Asn Gln Ala Leu Ser Asp Glu Trp Ala Asp Lys
            260                 265                 270

Ala Ala Lys Ala Arg Ala Arg Glu Ala Val Arg
        275                 280


<210> SEQ ID NO 83
<211> LENGTH: 909
```

-continued

<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 83

atgaaacagc cttatccata tttgttcttc aaaatgaaat ttctttcaaa aatattcttt 60
ttttattttt ttttaggtat aagcagcagt gtttttgcag ataatgcaaa aacagggatg 120
agtttgttcg agtcagcgaa atatgagcaa gcgatgactt atttcctgaa accggatgct 180
cagagaaatg cagaagtact taatcatatt ggttatatgt atgacaatgg attaggtgtt 240
aggcaaaatc caaaactggc taatcaatgg tatagaaaag catcagaaaa aggatttcct 300
gctgctgatt tcaatattgg attaagtttt gaatcaggat ctggtgttaa aaaagatatc 360
aacgaagcca taaaatggta tctcaaggct gcagaacagg gatatcccga tgcagaatcc 420
aaaatgggtt atctgaccgt aaccggaaaa ggcgtcaaac aggatttcaa acaggccatg 480
caatggtacc ggcgtgccgt tgaacatggc agtgttcatg ccatttcaga gctcggtatc 540
ctgtatgagg aaggtcttgg cgtcaaaaag gacaagaccc atgccgtcca gtattacatc 600
atgggtgccg aaaagggaaa cgtcagggca cagttcctgt tggcggaagc ctaccgttac 660
ggcctgggca tcaaaaacga cgatgagcgt tcgctctact ggtacaacaa ggcagcggaa 720
aacgggagtg ccgatgccta cgatgcgtta ggcagcgtgt atgccaacga acagctgggc 780
cagaaaaaag acaggaaaaa agcaggcgaa atggtggaaa aagccattga aatccgcaag 840
cagaatggag agggcgatcc cgatgccaga cgccgcctga ggtttttcgg ggtgaagctg 900
gatgactga 909

<210> SEQ ID NO 84
<211> LENGTH: 302
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 84

Met Lys Gln Pro Tyr Pro Tyr Leu Phe Phe Lys Met Lys Phe Leu Ser
1 5 10 15

Lys Ile Phe Phe Phe Tyr Phe Phe Leu Gly Ile Ser Ser Ser Val Phe
20 25 30

Ala Asp Asn Ala Lys Thr Gly Met Ser Leu Phe Glu Ser Ala Lys Tyr
35 40 45

Glu Gln Ala Met Thr Tyr Phe Leu Lys Pro Asp Ala Gln Arg Asn Ala
50 55 60

Glu Val Leu Asn His Ile Gly Tyr Met Tyr Asp Asn Gly Leu Gly Val
65 70 75 80

Arg Gln Asn Pro Lys Leu Ala Asn Gln Trp Tyr Arg Lys Ala Ser Glu
85 90 95

Lys Gly Phe Pro Ala Ala Asp Phe Asn Ile Gly Leu Ser Phe Glu Ser
100 105 110

Gly Ser Gly Val Lys Lys Asp Ile Asn Glu Ala Ile Lys Trp Tyr Leu
115 120 125

Lys Ala Ala Glu Gln Gly Tyr Pro Asp Ala Glu Ser Lys Met Gly Tyr
130 135 140

Leu Thr Val Thr Gly Lys Gly Val Lys Gln Asp Phe Lys Gln Ala Met
145 150 155 160

Gln Trp Tyr Arg Arg Ala Val Glu His Gly Ser Val His Ala Ile Ser

-continued

```
                165                 170                 175

Glu Leu Gly Ile Leu Tyr Glu Glu Gly Leu Gly Val Lys Lys Asp Lys
            180                 185                 190

Thr His Ala Val Gln Tyr Tyr Ile Met Gly Ala Glu Lys Gly Asn Val
        195                 200                 205

Arg Ala Gln Phe Leu Leu Ala Glu Ala Tyr Arg Tyr Gly Leu Gly Ile
    210                 215                 220

Lys Asn Asp Asp Glu Arg Ser Leu Tyr Trp Tyr Asn Lys Ala Ala Glu
225                 230                 235                 240

Asn Gly Ser Ala Asp Ala Tyr Asp Ala Leu Gly Ser Val Tyr Ala Asn
                245                 250                 255

Glu Gln Leu Gly Gln Lys Lys Asp Arg Lys Lys Ala Gly Glu Met Val
            260                 265                 270

Glu Lys Ala Ile Glu Ile Arg Lys Gln Asn Gly Glu Gly Asp Pro Asp
        275                 280                 285

Ala Arg Arg Arg Leu Arg Phe Phe Gly Val Lys Leu Asp Asp
    290                 295                 300


<210> SEQ ID NO 85
<211> LENGTH: 789
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 85

atgcggctgt ttgaagctgg aaaataccag caggccatga cgtatttcat gaaggaggat      60

gcccagaaga atccggccgt gatcaatcgt attggctata tgtatgatta cgggctcggc     120

gttgaaaaaa acaggcaaat cagttttcag tggtataaaa aagcaggaga aatgggggag     180

gccgctgcgc agtttaatgt cggactattc tatgagaaag gttatggcgt tcctcaagat     240

ataaatatgg ctatcgaatg gtttcgtaaa tctgcaaaac aacaatatcc gaatgctgaa     300

gcgaaaatgg gttatctgac ggcgacagga aaaggaacca aacaaagttt tgtggaagct     360

atgaagtggt atcggtcagc tgctgagcat ggcaatatta atgttttctc agaaatagga     420

attatgtatg aggaggggta tggcgtcaaa aaaaacaaga accgtgctgt ccagtattac     480

attatgggag ctgataaagg aaatgccaaa gcgcagtatc ttttaggtca tgcctaccaa     540

tatggtcgtg gcatcaaaga tgatcctgaa cgggcgctgc actggtatcg taaagcggcg     600

gaacagggaa atgccgatgc cttgcaggca ctgggggggta tttatgtaca tggcctgttg     660

aaccagaagg aagacaggga aaaaggtgaa aaatatattg aagaggcgat tagaatccgc     720

aagcaaacgg gtcagctaga tccggctgcg atgaggcggt tgcggctttt gggcatcgat     780

atagagtga                                                             789


<210> SEQ ID NO 86
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 86

Met Arg Leu Phe Glu Ala Gly Lys Tyr Gln Gln Ala Met Thr Tyr Phe
1               5                   10                  15

Met Lys Glu Asp Ala Gln Lys Asn Pro Ala Val Ile Asn Arg Ile Gly
            20                  25                  30
```

-continued

```
Tyr Met Tyr Asp Tyr Gly Leu Gly Val Glu Lys Asn Arg Gln Ile Ser
        35                  40                  45

Phe Gln Trp Tyr Lys Lys Ala Gly Glu Met Gly Glu Ala Ala Ala Gln
    50                  55                  60

Phe Asn Val Gly Leu Phe Tyr Glu Lys Gly Tyr Gly Val Pro Gln Asp
65                  70                  75                  80

Ile Asn Met Ala Ile Glu Trp Phe Arg Lys Ser Ala Lys Gln Gln Tyr
                85                  90                  95

Pro Asn Ala Glu Ala Lys Met Gly Tyr Leu Thr Ala Thr Gly Lys Gly
            100                 105                 110

Thr Lys Gln Ser Phe Val Glu Ala Met Lys Trp Tyr Arg Ser Ala Ala
        115                 120                 125

Glu His Gly Asn Ile Asn Val Phe Ser Glu Ile Gly Ile Met Tyr Glu
    130                 135                 140

Glu Gly Tyr Gly Val Lys Lys Asn Lys Asn Arg Ala Val Gln Tyr Tyr
145                 150                 155                 160

Ile Met Gly Ala Asp Lys Gly Asn Ala Lys Ala Gln Tyr Leu Leu Gly
                165                 170                 175

His Ala Tyr Gln Tyr Gly Arg Gly Ile Lys Asp Asp Pro Glu Arg Ala
            180                 185                 190

Leu His Trp Tyr Arg Lys Ala Ala Glu Gln Gly Asn Ala Asp Ala Leu
        195                 200                 205

Gln Ala Leu Gly Gly Ile Tyr Val His Gly Leu Leu Asn Gln Lys Glu
    210                 215                 220

Asp Arg Glu Lys Gly Glu Lys Tyr Ile Glu Glu Ala Ile Arg Ile Arg
225                 230                 235                 240

Lys Gln Thr Gly Gln Leu Asp Pro Ala Ala Met Arg Arg Leu Arg Leu
                245                 250                 255

Leu Gly Ile Asp Ile Glu
            260
```

<210> SEQ ID NO 87
<211> LENGTH: 939
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 87

```
atgttaaaat acatcctgtt aattcagata gtatcaatta tgaaaaaatt tttattttat     60

tttttgtttt tatcaatttc attactgata atgtcaggat gtgacgataa aaatatactt    120

gatgaaaaag aaggtgttga atattataaa cagaaacaat atgaaaaagc gttacctcta    180

ttggaaaagt cggcttcatc aggtaattcc atcgcatctt attatttagg agagatgttt    240

tataaaggtg aaggagttga aaagaatgaa aataccggtt gtcaacgata tctggaatct    300

tcaaaagggg gcaataaaaa cgcttatttg gtgacggcca tctgttttta tacaggtagg    360

ggattggaaa agaatgatgc cgaagcattc aaatgggcga aaaaagttga aaatgaaata    420

aatgaaacag gtcttggtga gtatgaccgg aaacattttt attttctaat gcagaatatc    480

tatttgtcag gaagaggtac tttgcaggat ttgagcgagg cagccaaatg gacagagaaa    540

atcgccaatt tgggtgatcc tgtctcacag ggtggtttag cggttttgta ctataatggc    600

aatggagttt tgaccgacag gaaaaaagcg cgttactggg cagaaaaagc ggccgcgcaa    660

ggcaatgata caggagaagt ggttcttggt atgttgaacc agtatagttt gcctcctgaa    720
```

-continued

```
caaaatttgg aaaaagcagc agaatggtat ttgaaatcag cagctcaggg aaataccgca    780

gcacaacatc agttggcggt tatgtatgaa aagggagaag gggttccgca agatttgaaa    840

aaagcccgtt attattatga agaagcggca aagagtaagt atgaagaacc caaaaaagcc    900

cttgaggaat tcaatgccac gtatcaaagt aaaaactaa                           939


<210> SEQ ID NO 88
<211> LENGTH: 312
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 88

Met Leu Lys Tyr Ile Leu Leu Ile Gln Ile Val Ser Ile Met Lys Lys
1               5                   10                  15

Phe Leu Phe Tyr Phe Leu Phe Leu Ser Ile Ser Leu Leu Ile Met Ser
            20                  25                  30

Gly Cys Asp Asp Lys Asn Ile Leu Asp Glu Lys Glu Gly Val Glu Tyr
        35                  40                  45

Tyr Lys Gln Lys Gln Tyr Glu Lys Ala Leu Pro Leu Leu Glu Lys Ser
    50                  55                  60

Ala Ser Ser Gly Asn Ser Ile Ala Ser Tyr Tyr Leu Gly Glu Met Phe
65                  70                  75                  80

Tyr Lys Gly Glu Gly Val Glu Lys Asn Glu Asn Thr Gly Cys Gln Arg
                85                  90                  95

Tyr Leu Glu Ser Ser Lys Gly Gly Asn Lys Asn Ala Tyr Leu Val Thr
            100                 105                 110

Ala Ile Cys Phe Tyr Thr Gly Arg Gly Leu Glu Lys Asn Asp Ala Glu
        115                 120                 125

Ala Phe Lys Trp Ala Lys Lys Val Glu Asn Glu Ile Asn Glu Thr Gly
    130                 135                 140

Leu Gly Glu Tyr Asp Arg Lys His Phe Tyr Phe Leu Met Gln Asn Ile
145                 150                 155                 160

Tyr Leu Ser Gly Arg Gly Thr Leu Gln Asp Leu Ser Glu Ala Ala Lys
                165                 170                 175

Trp Thr Glu Lys Ile Ala Asn Leu Gly Asp Pro Val Ser Gln Gly Gly
            180                 185                 190

Leu Ala Val Leu Tyr Tyr Asn Gly Asn Gly Val Leu Thr Asp Arg Lys
        195                 200                 205

Lys Ala Arg Tyr Trp Ala Glu Lys Ala Ala Ala Gln Gly Asn Asp Thr
    210                 215                 220

Gly Glu Val Val Leu Gly Met Leu Asn Gln Tyr Ser Leu Pro Pro Glu
225                 230                 235                 240

Gln Asn Leu Glu Lys Ala Ala Glu Trp Tyr Leu Lys Ser Ala Ala Gln
                245                 250                 255

Gly Asn Thr Ala Ala Gln His Gln Leu Ala Val Met Tyr Glu Lys Gly
            260                 265                 270

Glu Gly Val Pro Gln Asp Leu Lys Lys Ala Arg Tyr Tyr Tyr Glu Glu
        275                 280                 285

Ala Ala Lys Ser Lys Tyr Glu Glu Pro Lys Lys Ala Leu Glu Glu Phe
    290                 295                 300

Asn Ala Thr Tyr Gln Ser Lys Asn
305                 310
```

-continued

<210> SEQ ID NO 89
<211> LENGTH: 1104
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 89

```
atgaaaaagt ttattgtttc agtgttttta ttgggatggc ttccgttata tgctgccggt     60

tcttctttgc aggaaacaga agaagtcgct gtggcaaatg aaatgagtga agccggttcg    120

gtcgatacag atcgtttcaa tgttccattg caaaaagaaa agaagcgcca gtcacctcgt    180

gaaaaacaaa aaagagtgat gaatacagag aaaacaggta ttgcgatcat cgcacccggc    240

ggttatgttc cggattcgga ccttcagcgg gcaatcggtg tgctgaagtc caggggatat    300

gaggttttca attatgttga tccccaaaaa cgtcatgaac gttttgcggc aaatgatgaa    360

gagcgaagcc gtcagattat ggaagcggca acgaatccgg atgtgaagat tgtgattgca    420

ttgcggggtg gctacgggac gacgcggctt ttgcacgatc ttgattttgc caaactggcc    480

aaaagcggaa aactctttgt cggtcacagc gatttcacgg ttttcgaaat ggcattgtta    540

aagcatggag ccgtcagttt ttccggcccg atgattcaaa gcgattttac gcgaggtgat    600

ctgagcgctt ttaccttgaa tcatttcgat gaaaccatga catcgccgga aacatcggtc    660

aagtgggttt ccaaagacaa tcccgatgtc gatgtcgagg gaacgctgtg gggcggcaac    720

ctgacaatgc tggctcatat ggccgggact ccctggatgc cggacatttc cggtggcatt    780

ctgtttgtgg aagacattca cgaacatccc tatcgcgtcg agcgtatgct gctccagctg    840

gatgaatcag gtatcctcaa gaaacagaaa gctctcgtgt tgggacattt ttccgaattc    900

aaactttccg actacgataa tggctacgat ttcaacgcca tgctttcctg gctccgttcg    960

cgtctgtcga tacccgttgt gaccggtttg cctttcgggc atacgaaaga caaagtcact   1020

ttgcctgtcg gggcagagc gcatttgatg tccaaggcag gcaagattca actcgatatt   1080

ggggattatc caacggtaag gtaa                                          1104
```

<210> SEQ ID NO 90
<211> LENGTH: 367
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 90

```
Met Lys Lys Phe Ile Val Ser Val Phe Leu Leu Gly Trp Leu Pro Leu
1               5                   10                  15

Tyr Ala Ala Gly Ser Ser Leu Gln Glu Thr Glu Glu Val Ala Val Ala
            20                  25                  30

Asn Glu Met Ser Glu Ala Gly Ser Val Asp Thr Asp Arg Phe Asn Val
        35                  40                  45

Pro Leu Gln Lys Glu Lys Lys Arg Gln Ser Pro Arg Glu Lys Gln Lys
    50                  55                  60

Arg Val Met Asn Thr Glu Lys Thr Gly Ile Ala Ile Ile Ala Pro Gly
65                  70                  75                  80

Gly Tyr Val Pro Asp Ser Asp Leu Gln Arg Ala Ile Gly Val Leu Lys
                85                  90                  95

Ser Arg Gly Tyr Glu Val Phe Asn Tyr Val Asp Pro Gln Lys Arg His
            100                 105                 110
```

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```
Glu Arg Phe Ala Ala Asn Asp Glu Glu Arg Ser Arg Gln Ile Met Glu
        115                 120                 125

Ala Ala Thr Asn Pro Asp Val Lys Ile Val Ile Ala Leu Arg Gly Gly
    130                 135                 140

Tyr Gly Thr Thr Arg Leu Leu His Asp Leu Asp Phe Ala Lys Leu Ala
145                 150                 155                 160

Lys Ser Gly Lys Leu Phe Val Gly His Ser Asp Phe Thr Val Phe Glu
                165                 170                 175

Met Ala Leu Leu Lys His Gly Ala Val Ser Phe Ser Gly Pro Met Ile
            180                 185                 190

Gln Ser Asp Phe Thr Arg Gly Asp Leu Ser Ala Phe Thr Leu Asn His
        195                 200                 205

Phe Asp Glu Thr Met Thr Ser Pro Glu Thr Ser Val Lys Trp Val Ser
    210                 215                 220

Lys Asp Asn Pro Asp Val Asp Val Glu Gly Thr Leu Trp Gly Gly Asn
225                 230                 235                 240

Leu Thr Met Leu Ala His Met Ala Gly Thr Pro Trp Met Pro Asp Ile
                245                 250                 255

Ser Gly Gly Ile Leu Phe Val Glu Asp Ile His Glu His Pro Tyr Arg
            260                 265                 270

Val Glu Arg Met Leu Leu Gln Leu Asp Glu Ser Gly Ile Leu Lys Lys
        275                 280                 285

Gln Lys Ala Leu Val Leu Gly His Phe Ser Glu Phe Lys Leu Ser Asp
    290                 295                 300

Tyr Asp Asn Gly Tyr Asp Phe Asn Ala Met Leu Ser Trp Leu Arg Ser
305                 310                 315                 320

Arg Leu Ser Ile Pro Val Val Thr Gly Leu Pro Phe Gly His Thr Lys
                325                 330                 335

Asp Lys Val Thr Leu Pro Val Gly Gly Arg Ala His Leu Met Ser Lys
            340                 345                 350

Ala Gly Lys Ile Gln Leu Asp Ile Gly Asp Tyr Pro Thr Val Arg
        355                 360                 365
```

<210> SEQ ID NO 91
<211> LENGTH: 948
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 91

```
atgagtgaaa acggctggga acgtgaagtt ctcgaaaaac tgatgctgca aaccctgaaa      60

gagcaacggg cacgccgccg gtggggtatc tttttcaagc tgacgacgat cattctggtt     120

atttttgtca ttttctcgat caagagcctt tctttttcca gcaaggaaac cgttcccgtc     180

cagaaacata cggcgatggt cgaaatccgc gggacgatcg attcctccgg caattcgtcg     240

gcagccaata tcatcaaggc gctggacaag gcctatgacg agccactggc aacaggcgtt     300

atcctgaaaa tcaacagccc gggcggaagc cctgttcagg caggcatgat ttatgatgaa     360

atccggcgtt tgcgtgaggt tcatcccgac aagcctcttt acgtcgtcgt tgaagaatta     420

tgcgcttccg gcggttatta tgttgccgca gcggcagaca agatctttgt cgacaaggcc     480

agtctggtcg gttccatcgg tgtcatgatc aacggtttcg gagtcaccgg cctgatgcag     540

aaactcggcg tcgagcgccg cctgttgacg gccggggaat acaagggttt tctcgacccg     600
```

-continued

```
ttttctcccc aaacgccaca gcaggtccag tatgcccaat ccatgctgaa ccagattcac    660

cagcaattca tcgaagttgt ccgtcagggc aggggcgaca ggctgaaaga aaacagggaa    720

atctatagcg gtctggtttt tctcggtcct gaagcgatca aaatggggct ggctgacgaa    780

ctgggtacgg tcgaaagtgt tgcccgtgac gtgatcgggg aacctgtcat cgtcgattac    840

accgaacagg aaagactgtc tgaccgtttc ctgaagaaat tcggtgcctc cgtcggttat    900

ggagcggttc aggccggtct ggatatcaat cccgttccct tgcattga                 948
```

<210> SEQ ID NO 92
<211> LENGTH: 315
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 92

```
Met Ser Glu Asn Gly Trp Glu Arg Glu Val Leu Glu Lys Leu Met Leu
1               5                   10                  15

Gln Thr Leu Lys Glu Gln Arg Ala Arg Arg Arg Trp Gly Ile Phe Phe
            20                  25                  30

Lys Leu Thr Thr Ile Ile Leu Val Ile Phe Val Ile Phe Ser Ile Lys
        35                  40                  45

Ser Leu Ser Phe Ser Ser Lys Glu Thr Val Pro Val Gln Lys His Thr
    50                  55                  60

Ala Met Val Glu Ile Arg Gly Thr Ile Asp Ser Ser Gly Asn Ser Ser
65                  70                  75                  80

Ala Ala Asn Ile Ile Lys Ala Leu Asp Lys Ala Tyr Asp Glu Pro Leu
                85                  90                  95

Ala Thr Gly Val Ile Leu Lys Ile Asn Ser Pro Gly Gly Ser Pro Val
            100                 105                 110

Gln Ala Gly Met Ile Tyr Asp Glu Ile Arg Arg Leu Arg Glu Val His
        115                 120                 125

Pro Asp Lys Pro Leu Tyr Val Val Val Glu Glu Leu Cys Ala Ser Gly
    130                 135                 140

Gly Tyr Tyr Val Ala Ala Ala Ala Asp Lys Ile Phe Val Asp Lys Ala
145                 150                 155                 160

Ser Leu Val Gly Ser Ile Gly Val Met Ile Asn Gly Phe Gly Val Thr
                165                 170                 175

Gly Leu Met Gln Lys Leu Gly Val Glu Arg Arg Leu Leu Thr Ala Gly
            180                 185                 190

Glu Tyr Lys Gly Phe Leu Asp Pro Phe Ser Pro Gln Thr Pro Gln Gln
        195                 200                 205

Val Gln Tyr Ala Gln Ser Met Leu Asn Gln Ile His Gln Gln Phe Ile
    210                 215                 220

Glu Val Val Arg Gln Gly Arg Gly Asp Arg Leu Lys Glu Asn Arg Glu
225                 230                 235                 240

Ile Tyr Ser Gly Leu Val Phe Leu Gly Pro Glu Ala Ile Lys Met Gly
                245                 250                 255

Leu Ala Asp Glu Leu Gly Thr Val Glu Ser Val Ala Arg Asp Val Ile
            260                 265                 270

Gly Glu Pro Val Ile Val Asp Tyr Thr Glu Gln Glu Arg Leu Ser Asp
        275                 280                 285

Arg Phe Leu Lys Lys Phe Gly Ala Ser Val Gly Tyr Gly Ala Val Gln
    290                 295                 300
```

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```
Ala Gly Leu Asp Ile Asn Pro Val Pro Leu His
305                 310                 315
```

<210> SEQ ID NO 93
<211> LENGTH: 1638
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 93

```
atgaaaaccg atttgccagg caaaaacgcc ataccgaaga acagaatgac catcaaccgg     60
ctgtttgcct acacccggat tccccgcatc cggccagccc tgaccatggc cctgtgtgcc    120
gccaccctgg ccggttgcgc cgtcggcccc gattacgtcc agccgccaat cgacgtacct    180
gccacctaca aggaagacag cctctggaaa accgccaaac cctcggacga atacccgcgc    240
ggcgcatggt ggagcgtttt caaagaccct gaactcgacc gactgatggt tctcttaaac    300
aagcagaacc tgaccatcgc gcaggcagaa gcccagtacc ggcaggcgca ggccctgttg    360
cgacaggcac agtccagcct cttcccgagc ctgtcgctgg acgcctccag aacacgcggt    420
ttccagtcca ataccagcac ctcggccagt acgcaaaacg ccttcgtcgg caacctgtca    480
tgggaagtgg acatctgggg tggcgtccgc cgcaacgtcg aagcgggcga agccggacgg    540
caagccagtg ctgcccagct ggaagccatc aaactgtcgt cacaggcgca aatggccacg    600
gcctacctgc aactggtcat cactgaccgt caggtcaaac aactggaaga aagcgaaacc    660
ctgctggccg aatcgctccg gctgacgaaa aaccagtttg ccgtcggtat cgtctccgac    720
gccgatgtgg cgcaggcgga aagccagctg aaaacggcac aggccgccac cgtcgacatg    780
aaactggcgc gcagccagct cgaacactca atcgccgtct ctatcggaca agccccgtcc    840
accttgacca tcgacatggc gaaagccgac ccctacctgc cgcaaatccc ggccgggctg    900
ccttcggccc tgctccagcg ccgtcctgac gtcgcttccg ccgaacgcaa ggtcgcgcag    960
gccaacgccc tgatcggcgt cgcgaaatcc gccttcttcc cggccctgtc catctcggcc   1020
tccggcggct tccgcaattc ctccttcgcc gacctgttca ccgtaccgaa ccgcatctgg   1080
tcgatcggcc cgcaaatcgc cctgtccatc ttcgatgcag gcctgcgcag cgcccagacc   1140
gatcaggcaa tcgccgtcta tgatgaaacc gtcgccgcct accgccagaa agtgctgatc   1200
gccttccagg aagtcgagga caacctcgcg gcacaagcca tgctcggcga cgcatccgac   1260
atgcaaacag ctgccctgaa tgcggcgaaa cgggccgaga ccatcaccat gaaccagtac   1320
aaggccggcg tcgtcagtta catcaacgtg ctgatcgccc agaacacccg catcgcagca   1380
gaaaacaccc tgtacaacgt caaaaaacgc cagttcacca gcagcgtcgc cttaatcgcc   1440
gccattggcg ggcaatggga gacgccaaag caaacagcaa aataccggca cggcatcacc   1500
ggaaaaaatg gagcagaaaa cggaaatgaa aagttaggga cgttttgtta ccggatcaat   1560
gattcctcat tcgggactga ttcggtaact tatcgacaaa tattcaaatc tgacaaaaga   1620
gaaaatacat ggatatag                                                  1638
```

<210> SEQ ID NO 94
<211> LENGTH: 545
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 94

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```
Met Lys Thr Asp Leu Pro Gly Lys Asn Ala Ile Pro Lys Asn Arg Met
1               5                   10                  15

Thr Ile Asn Arg Leu Phe Ala Tyr Thr Arg Ile Pro Arg Ile Arg Pro
            20                  25                  30

Ala Leu Thr Met Ala Leu Cys Ala Ala Thr Leu Ala Gly Cys Ala Val
        35                  40                  45

Gly Pro Asp Tyr Val Gln Pro Pro Ile Asp Val Pro Ala Thr Tyr Lys
    50                  55                  60

Glu Asp Ser Leu Trp Lys Thr Ala Lys Pro Ser Asp Glu Tyr Pro Arg
65                  70                  75                  80

Gly Ala Trp Trp Ser Val Phe Lys Asp Pro Glu Leu Asp Arg Leu Met
                85                  90                  95

Val Leu Leu Asn Lys Gln Asn Leu Thr Ile Ala Gln Ala Glu Ala Gln
            100                 105                 110

Tyr Arg Gln Ala Gln Ala Leu Leu Arg Gln Ala Gln Ser Ser Leu Phe
        115                 120                 125

Pro Ser Leu Ser Leu Asp Ala Ser Arg Thr Arg Gly Phe Gln Ser Asn
    130                 135                 140

Thr Ser Thr Ser Ala Ser Thr Gln Asn Ala Phe Val Gly Asn Leu Ser
145                 150                 155                 160

Trp Glu Val Asp Ile Trp Gly Gly Val Arg Arg Asn Val Glu Ala Gly
                165                 170                 175

Glu Ala Gly Arg Gln Ala Ser Ala Ala Gln Leu Glu Ala Ile Lys Leu
            180                 185                 190

Ser Ser Gln Ala Gln Met Ala Thr Ala Tyr Leu Gln Leu Val Ile Thr
        195                 200                 205

Asp Arg Gln Val Lys Gln Leu Glu Glu Ser Glu Thr Leu Leu Ala Glu
    210                 215                 220

Ser Leu Arg Leu Thr Lys Asn Gln Phe Ala Val Gly Ile Val Ser Asp
225                 230                 235                 240

Ala Asp Val Ala Gln Ala Glu Ser Gln Leu Lys Thr Ala Gln Ala Ala
                245                 250                 255

Thr Val Asp Met Lys Leu Ala Arg Ser Gln Leu Glu His Ser Ile Ala
            260                 265                 270

Val Ser Ile Gly Gln Ala Pro Ser Thr Leu Thr Ile Asp Met Ala Lys
        275                 280                 285

Ala Asp Pro Tyr Leu Pro Gln Ile Pro Ala Gly Leu Pro Ser Ala Leu
    290                 295                 300

Leu Gln Arg Arg Pro Asp Val Ala Ser Ala Glu Arg Lys Val Ala Gln
305                 310                 315                 320

Ala Asn Ala Leu Ile Gly Val Ala Lys Ser Ala Phe Phe Pro Ala Leu
                325                 330                 335

Ser Ile Ser Ala Ser Gly Gly Phe Arg Asn Ser Ser Phe Ala Asp Leu
            340                 345                 350

Phe Thr Val Pro Asn Arg Ile Trp Ser Ile Gly Pro Gln Ile Ala Leu
        355                 360                 365

Ser Ile Phe Asp Ala Gly Leu Arg Ser Ala Gln Thr Asp Gln Ala Ile
    370                 375                 380

Ala Val Tyr Asp Glu Thr Val Ala Ala Tyr Arg Gln Lys Val Leu Ile
385                 390                 395                 400

Ala Phe Gln Glu Val Glu Asp Asn Leu Ala Ala Gln Ala Met Leu Gly
```

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```
                405                 410                 415

Asp Ala Ser Asp Met Gln Thr Ala Ala Leu Asn Ala Ala Lys Arg Ala
            420                 425                 430

Glu Thr Ile Thr Met Asn Gln Tyr Lys Ala Gly Val Val Ser Tyr Ile
        435                 440                 445

Asn Val Leu Ile Ala Gln Asn Thr Arg Ile Ala Ala Glu Asn Thr Leu
    450                 455                 460

Tyr Asn Val Lys Lys Arg Gln Phe Thr Ser Ser Val Ala Leu Ile Ala
465                 470                 475                 480

Ala Ile Gly Gly Gln Trp Glu Thr Pro Lys Gln Thr Ala Lys Tyr Arg
                485                 490                 495

His Gly Ile Thr Gly Lys Asn Gly Ala Glu Asn Gly Asn Glu Lys Leu
            500                 505                 510

Gly Thr Phe Cys Tyr Arg Ile Asn Asp Ser Ser Phe Gly Thr Asp Ser
        515                 520                 525

Val Thr Tyr Arg Gln Ile Phe Lys Ser Asp Lys Arg Glu Asn Thr Trp
    530                 535                 540

Ile
545
```

<210> SEQ ID NO 95
<211> LENGTH: 1476
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 95

```
atgaaagtca gaaggacaaa gaagatgatt aagaaattaa ccctcgtttt actggctgcc     60

ggtgtcttga gcagttgcag tatggcgccc aattacgtgc gaccggatgc cccgattgaa    120

agccagttcc cgggcaacgc ggatgacgct tctgcaaaaa cgcccgtgac gcaaatcgga    180

tggaatgaat tttccatgga accgcgattg aaagcgctga tcgctgccgc aattgaaaac    240

aatcgtgatt tgagagtagc agccttgcga attgaggaag cgcgtgccct gtatggcatc    300

cagtgggctg accgtctccc gaatttcgaa gctcagggag ccggaacccg tcaaagaacg    360

gtcggcacaa ccggcggcat ggtaacacag ggcaattaca ctgttggcct gggtctggct    420

gccttcgagc tggacttctt cggaagggtg aaaagcctgt cggacgctgc actggcagaa    480

tatctggcca cggaagaagc ccaacgtgcc gcctatatca gccttgtttc ggaagtggcc    540

aaaacctatc tgaccgaacg tgcacaagcg cgacagattg agttggcaaa agaatcctac    600

gagtcttaca aacgcagcta tgagctgatg caaaagcgtt atgaagtcgg tgcatcttcc    660

gcactggaat tgcgtcagta tgaaacgctg atgcaatcgg cactggtttc gctctccacc    720

ctgcaaagac aacgcgccca gacagaaaac gcacttgtcg tactgattgg tggaaagcag    780

atcaaggatc ttcctgcggc gcacgacttg tcggaagacg acatcatgca ggacattccc    840

gccggattgc cgtccgatct gatcaacaac cggccggaca ttcgccagta tgaacaattg    900

ctcaagtcag cgaacgccaa tatcggcgca gccagagcag ccttttttccc gcgtattacc    960

ctgacaggtt ttgccggaac agcaagcccg actttatccg gccttttcga tgccgggtcc   1020

ggtgcatgga catttatgcc gcaactgaca ctgccgattt tcgatgcagg ccgcaatatc   1080

agcaatctgg atctggcaga ggctcgcaag aatatcgcgg tggcccaata tgaaaaaacc   1140

gttcaggtcg ctttccgtga agtcgctgac gccctgatgg cacgcgactg gttgaatgaa   1200
```

-continued

caggtcaagg ctcaggctgc tgttctgaaa tcagagacgg aacgcctgaa actgtccgaa 1260

gcgcggtaca acaacggtat tgccagttcg ctggaagtat tcgattcaca acgccagcaa 1320

tttgcggcac agcagtcgct ggttgacgca cgtctgttac gcctgatcaa tacagtggaa 1380

ctgtatcgtt cactgggtgg cggcatcgtc gatgccaatg cgccgaaaac agccaaaaca 1440

actgctgaac cggtagcgca aaatactgaa ggctga 1476

<210> SEQ ID NO 96
<211> LENGTH: 491
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 96

Met Lys Val Arg Arg Thr Lys Lys Met Ile Lys Lys Leu Thr Leu Val
1 5 10 15

Leu Leu Ala Ala Gly Val Leu Ser Ser Cys Ser Met Ala Pro Asn Tyr
20 25 30

Val Arg Pro Asp Ala Pro Ile Glu Ser Gln Phe Pro Gly Asn Ala Asp
35 40 45

Asp Ala Ser Ala Lys Thr Pro Val Thr Gln Ile Gly Trp Asn Glu Phe
50 55 60

Phe His Glu Pro Arg Leu Lys Ala Leu Ile Ala Ala Ala Ile Glu Asn
65 70 75 80

Asn Arg Asp Leu Arg Val Ala Ala Leu Arg Ile Glu Glu Ala Arg Ala
85 90 95

Leu Tyr Gly Ile Gln Trp Ala Asp Arg Leu Pro Asn Phe Glu Ala Gln
100 105 110

Gly Ala Gly Thr Arg Gln Arg Thr Val Gly Thr Thr Gly Gly Met Val
115 120 125

Thr Gln Gly Asn Tyr Thr Val Gly Leu Gly Leu Ala Ala Phe Glu Leu
130 135 140

Asp Phe Phe Gly Arg Val Lys Ser Leu Ser Asp Ala Ala Leu Ala Glu
145 150 155 160

Tyr Leu Ala Thr Glu Glu Ala Gln Arg Ala Ala Tyr Ile Ser Leu Val
165 170 175

Ser Glu Val Ala Lys Thr Tyr Leu Thr Glu Arg Ala Gln Ala Arg Gln
180 185 190

Ile Glu Leu Ala Lys Glu Ser Tyr Glu Ser Tyr Lys Arg Ser Tyr Glu
195 200 205

Leu Met Gln Lys Arg Tyr Glu Val Gly Ala Ser Ser Ala Leu Glu Leu
210 215 220

Arg Gln Tyr Glu Thr Leu Met Gln Ser Ala Leu Val Ser Leu Ser Thr
225 230 235 240

Leu Gln Arg Gln Arg Ala Gln Thr Glu Asn Ala Leu Val Val Leu Ile
245 250 255

Gly Gly Lys Gln Ile Lys Asp Leu Pro Ala Ala His Asp Leu Ser Glu
260 265 270

Asp Asp Ile Met Gln Asp Ile Pro Ala Gly Leu Pro Ser Asp Leu Ile
275 280 285

Asn Asn Arg Pro Asp Ile Arg Gln Tyr Glu Gln Leu Leu Lys Ser Ala
290 295 300

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```
Asn Ala Asn Ile Gly Ala Ala Arg Ala Ala Phe Phe Pro Arg Ile Thr
305                 310                 315                 320

Leu Thr Gly Phe Ala Gly Thr Ala Ser Pro Thr Leu Ser Gly Leu Phe
                325                 330                 335

Asp Ala Gly Ser Gly Ala Trp Thr Phe Met Pro Gln Leu Thr Leu Pro
            340                 345                 350

Ile Phe Asp Ala Gly Arg Asn Ile Ser Asn Leu Asp Leu Ala Glu Ala
        355                 360                 365

Arg Lys Asn Ile Ala Val Ala Gln Tyr Glu Lys Thr Val Gln Val Ala
    370                 375                 380

Phe Arg Glu Val Ala Asp Ala Leu Met Ala Arg Asp Trp Leu Asn Glu
385                 390                 395                 400

Gln Val Lys Ala Gln Ala Ala Val Leu Lys Ser Glu Thr Glu Arg Leu
                405                 410                 415

Lys Leu Ser Glu Ala Arg Tyr Asn Asn Gly Ile Ala Ser Ser Leu Glu
            420                 425                 430

Val Phe Asp Ser Gln Arg Gln Gln Phe Ala Ala Gln Gln Ser Leu Val
        435                 440                 445

Asp Ala Arg Leu Leu Arg Leu Ile Asn Thr Val Glu Leu Tyr Arg Ser
    450                 455                 460

Leu Gly Gly Gly Ile Val Asp Ala Asn Ala Pro Lys Thr Ala Lys Thr
465                 470                 475                 480

Thr Ala Glu Pro Val Ala Gln Asn Thr Glu Gly
                485                 490


<210> SEQ ID NO 97
<211> LENGTH: 602
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 97

taacgtgagg aacagatcac atcgacaagc cttgccgatt gtctttccat ctcgatcaga      60

aaactgtcga caagcgcccg gaaatgacga taaaaaacga gagtcggcat ggcaatcagc     120

aaaccgaagc cggtattgta aagcgccaca gaaatcccgt gagccagttc cgcaggattg     180

gcccctccgg cattttgtga accgaaaatc tcgatcatcc cgacaaccgt accgaacagg     240

cccatcaggg gagccagcgt ggcaatcgtc ccgatcgtcg tcagaaagcg ttccatctgg     300

agagcgacac tgcggccggt ttcttccatc gcttccttca tattgtcgcg ggaaacatcg     360

gaatgctgca atccggtcgc cagcactgtc cccaaaggcg aaccctttc cagtttgtcg     420

attgtcgccg catccacacg accttcacga tactcacgta tgacctgatc cagaagatgt     480

ggcggcaaaa tctttcggcg tctcagataa atgagacgtt cgataatcag ggccaatgca     540

ataacagagg cgatcagcaa aaaccagatc ggccatcctg ccgcttgaat gattgaaaac     600

ac                                                                    602


<210> SEQ ID NO 98
<211> LENGTH: 659
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 98

tgtccaaaca acaatttaac ctgatcgttt tcgattggga cggcaccctg atggacagta      60
```

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```
cgtccgccat cgtcaagagc cttcaggatt cggcagccga tctgggcttg cccacaccag    120
acaaaaagaa agcggcgcat gtgatcggcc tcggccttcg agaagcgctg gaaaccgtcc    180
tgccggacgt cagcccggaa tactatccga aactcatcga gcgctatcgt acccatttcc    240
tgaaaaacag cgtatcgctt tccctgttcg acggtgtcag ggaaatgctc gacgacctga    300
agaatcagga ttattttctg gcagtggcca ccggaaaaag ccgggccggt ctgaaccgcg    360
ccatcgacga ggtgggcttg cagggatatt tcgatgccag ccgcacggct gatgaaacgc    420
attccaaacc tcatccggcc atgttgctgg aactgaccga acagttgggc gaaccgatga    480
aacgcacggt catgatcggt gataccaccc atgatttgct gatggcaaac aatgccggtg    540
cctcgggcat cgctgtacaa tacggtgcac attcacccaa agaactgcaa ttgatgcatc    600
cgatgtattc agccgatacg gtcgaagaac tgcatcgctg gctgaatgaa aatgcctga     659
```

<210> SEQ ID NO 99
<211> LENGTH: 2747
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 99

```
tatcgttcaa gccggttcga ttcaagcagt ttttcaaatt ccgccgctgt caggggttca     60
gagaaaagat atccctgacc ataattgcat ccggcaccgg ccaacaacaa tctctgtcca    120
tcgtcctgga caccttcggc aatcactttc atgtccagtt tgtgcgccat aacgataatc    180
gcctcacaca aggccatatc cttgggttca ttttcgatat ggcgaacgaa agcctgatcg    240
attttcagat agtcgatcgg aaattttttc agataagaca atgaagaata tcccgtcccg    300
aaatcgtcca gtgccacttc cattccatat tgatgaaatt ccgccagccg atcaagcacc    360
tgggtattcg aaacaatcaa aacaccttct gttatttcca tcacgatgct gctgccaggt    420
acattcagtt tttctagcac ttcgaaccag tcgctgtaat cattcttgtt ctggaacacg    480
ataggcgaga tattgaaact gatttgcaag tcagggaaga gatgttctct ccatcggctg    540
agctccctgg caacctcccc gaaagcccag tccgagatcg tcaaaatctg accggtttct    600
tccgcaatga aaatgaattc tgtgggactg ataatgccac gaaccggatg gtgccagcgg    660
atcagtgctt cggctttctg gatgcggcca gtctcaatct cgacaatcgg ctgatacagc    720
atttcaaatt gatgttcatt tatagctata cgcatgtcat tggccagcct tatccggttt    780
tgcgcagccg cctgcatgga tgccgtaaag taactcatcc ggttacgtcc ggccagtttg    840
gcggcataca aggcctgatc ggcatttctc atgagtgtat cgatatccgt gccgtcatcc    900
ggataaaccg taatgccgat acttcctgtc acatacgcaa tttcgctacc caactggtaa    960
ggctgggcca gggaacgcag gatgctgtgc gcaatttttt ccattgtcgg caaatcggac   1020
aactctgtca gaataatggc aaactcatcg ccacccagac gtgacacggt atcgaattca   1080
cggacgcaat ccttcagacg tttcgcgacg tccagtaaca ggtgatcgcc cgcatcgtgc   1140
ccaagggtat cgttgatatc cttgaaatta tccagatcga gaaacagcag cgccagtttt   1200
tttccggact ggttgacctt gactagttcc tgtttcatcc tgtccatcag catgcgacga   1260
ttcggcaaat tcgtcaggaa atcgaaattc gcctgacgcc atatcatgtc ttccgcttct   1320
tttttctccg tgaaatcatt ggagagttca acgtaataac gaacggatct gtcttcgttg   1380
taaaccacat tgattgtcag ccatgatgca tacgattcgc cattcttgcg ccggttccag   1440
```

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agttccccac gccagtaccc tttctcatcc aatgcatccc acatcgcctt gtaaaatgcc 1500

ttgtcctggc gtcccgaact caacagtttc ggatccctgc cgatcacttc ggcagcggta 1560

tagcctgtaa tttttcaaa ggccggattg actgcaagaa tatgattgtc ggcattactg 1620

atcaaaatcg cttcactgga gttacggtac accagtgctg ccagttccag tttttcctcg 1680

tcttcctttc ttcgcgtaat atcccgtccg attcccagaa cacccaccag ttcgccgtcc 1740

ggcgttctga caggtgcctt gatcacatcg aaaaacaccc tgttgccaga caatgcataa 1800

gtgccccact gcttgatcac cagtggtttg ccttccttca gaatacgttt gtcctgttct 1860

tcaaaaagct cggcttcgtc atggctgaat atatcgaaat cggttttacc gataatatgc 1920

tcgtcagaaa gcccgacata atccttgtaa gcctgattac aggccagata aacgcccgca 1980

gaatttttca tccataccag atcgggaata ttttcaaaaa cgcttttcag tcgcgcctcg 2040

ctttgggtca gaacgacatt gaccttgttc agatcgtccg ttctgatctc aaccagtttc 2100

tccagattga caagcaactg gttccggatt tcctgcaagc ggaccataaa tagaatggcc 2160

aaaaagaaca gcgccatgag ggcgattgaa atcccgatga ctttggtgcc ccaataaaaa 2220

aggtctgcat tatatgcgcc cagcggcaaa agcgtgatga ctttccattt ataggcactg 2280

acatcacggg gaccctgtcc tccggaaaaa atttcgctac tgcctttact ggttttggta 2340

tcggccgaga gaggtgaaag cgttttgaac gtccataggc cttcccgggt aatgaactgg 2400

ccttcttcct gatttttcat ccgctcccag gcagcaggat atcgatgagc catactcaag 2460

tcatttttat tgaacatgaa tccgaattca tcgttggaaa ccggtccttt cagccagaat 2520

ccgttctgat tgacgagcca ggcagaattg ccacgcatgc tcgtcaactg ctggaaccgg 2580

ccgatcattg aagtggcata gtagttcaac agaagaatgc ccttttttctc ccctttttg 2640

ttgaagagag gcatcccgaa acggatcgtc gggacataag gctcctggat atggtcatct 2700

tcaatattca ggtcaagagg tgaaacatag acttcccctt ctttcaa 2747

<210> SEQ ID NO 100
<211> LENGTH: 659
<212> TYPE: DNA
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 100

tgtccaaaca acaatttaac ctgatcgttt tcgattggga cggcaccctg atggacagta 60

cgtccgccat cgtcaagagc cttcaggatt cggcagccga tctgggcttg cccacaccag 120

acaaaaagaa agcggcgcat gtgatcggcc tcggccttcg agaagcgctg gaaaccgtcc 180

tgccggacgt cagcccggaa tactatccga aactcatcga gcgctatcgt acccatttcc 240

tgaaaaacag cgtatcgctt tccctgttcg acggtgtcag ggaaatgctc gacgacctga 300

agaatcagga ttattttctg gcagtggcca ccggaaaaag ccgggccggt ctgaaccgcg 360

ccatcgacga ggtgggcttg cagggatatt tcgatgccag ccgcacggct gatgaaacgc 420

attccaaacc tcatccggcc atgttgctgg aactgaccga acagttgggc gaaccgatga 480

aacgcacggt catgatcggt gataccaccc atgatttgct gatggcaaac aatgccggtg 540

cctcgggcat cgctgtacaa tacggtgcac attcacccaa agaactgcaa ttgatgcatc 600

cgatgtattc agccgatacg gtcgaagaac tgcatcgctg gctgaatgaa aatgcctga 659

<210> SEQ ID NO 101

-continued

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<211> LENGTH: 190
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 101

Leu Ile Val Phe Asp Trp Asp Gly Thr Leu Met Asp Ser Thr Ser Ala
1               5                   10                  15

Ile Val Lys Ser Leu Gln Asp Ser Ala Ala Asp Leu Gly Leu Pro Thr
            20                  25                  30

Pro Asp Lys Lys Lys Ala Ala His Val Ile Gly Leu Gly Leu Arg Glu
        35                  40                  45

Ala Leu Glu Thr Val Leu Pro Asp Val Ser Pro Glu Tyr Tyr Pro Lys
    50                  55                  60

Leu Ile Glu Arg Tyr Arg Thr His Phe Leu Lys Asn Ser Val Ser Leu
65                  70                  75                  80

Ser Leu Phe Asp Gly Val Arg Glu Met Leu Asp Asp Leu Lys Asn Gln
                85                  90                  95

Asp Tyr Phe Leu Ala Val Ala Thr Gly Lys Ser Arg Ala Gly Leu Asn
            100                 105                 110

Arg Ala Ile Asp Glu Val Gly Leu Gln Gly Tyr Phe Asp Ala Ser Arg
        115                 120                 125

Thr Ala Asp Glu Thr His Ser Lys Pro His Pro Ala Met Leu Leu Glu
    130                 135                 140

Leu Thr Glu Gln Leu Gly Glu Pro Met Lys Arg Thr Val Met Ile Gly
145                 150                 155                 160

Asp Thr Thr His Asp Leu Leu Met Ala Asn Asn Ala Gly Ala Ser Gly
                165                 170                 175

Ile Ala Val Gln Tyr Gly Ala His Ser Pro Lys Glu Leu Gln
            180                 185                 190


<210> SEQ ID NO 102
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 102

Phe Glu Asn Ile Pro Asp Leu Val Trp Met Lys Asn Ser Ala Gly Val
1               5                   10                  15

Tyr Leu Ala Cys Asn Gln Ala Tyr Lys Asp Tyr Val Gly Leu Ser Asp
            20                  25                  30

Glu His Ile Ile Gly Lys Thr Asp Phe Asp Ile Phe Ser His Asp Glu
        35                  40                  45

Ala Glu Leu Phe Glu Glu Gln Asp Lys Arg Ile Leu Lys Glu Gly Lys
    50                  55                  60

Pro Leu Val Ile Lys Gln Trp Gly Thr Tyr Ala Leu Ser Gly Asn Arg
65                  70                  75                  80

Val Phe Phe Asp Val Ile Lys Ala Pro Val Arg Thr Pro Asp Gly Glu
                85                  90                  95

Leu Val Gly Val Leu Gly Ile Gly Arg Asp Ile Thr Arg Arg Lys Glu
            100                 105                 110


<210> SEQ ID NO 103
<211> LENGTH: 190
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes
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<400> SEQUENCE: 103

Lys Ala Ala Lys Ser Gly Asn Ala Glu Ala Gln Tyr Leu Phe Gly Met
1 5 10 15

Leu Val Tyr Asp Gly Arg Gly Val Gln Gln Asp Asn Cys Val Ala Met
20 25 30

Leu Trp Trp Met Lys Ala Ala Glu Gln Asn His Ala Lys Ala Leu Val
35 40 45

Met Leu Gly Asn Leu His Arg Lys Gly Gln Cys Ile Ala Glu Asn Tyr
50 55 60

Pro Lys Ala Ile Ala Tyr Trp Lys Arg Ala Ala Val Gln Asn Asn Val
65 70 75 80

Trp Ala Tyr His Asn Leu Gly Thr Ala Tyr Tyr Asp Gly Ile Gly Val
85 90 95

Asp Lys Asn Pro His Glu Ala Val Arg Trp Trp Lys Lys Ala Ala Glu
100 105 110

Leu Gly Phe Pro Glu Ser Gln Asn Asn Leu Gly Ala Leu Tyr Asn Asp
115 120 125

Gly Asn Gly Val Asp Arg Asp Tyr Gln Glu Ala Val Phe Trp Tyr Arg
130 135 140

Lys Ser Ala Leu Gln Gly Asp Glu Leu Gly Gln Tyr Asn Leu Gly Val
145 150 155 160

Ala Tyr Tyr Tyr Gly Arg Gly Ile Lys Lys Asp Phe Ser Glu Ala Val
165 170 175

Ser Trp Tyr Lys Lys Ser Ala Glu Gln Asp Tyr Ala Gln Ala
180 185 190

<210> SEQ ID NO 104
<211> LENGTH: 249
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 104

Leu Gly Thr Ala Tyr Tyr Asp Gly Ile Gly Val Asp Lys Asn Pro His
1 5 10 15

Glu Ala Val Arg Trp Trp Lys Lys Ala Ala Glu Leu Gly Phe Pro Glu
20 25 30

Ser Gln Asn Asn Leu Gly Ala Leu Tyr Asn Asp Gly Asn Gly Val Asp
35 40 45

Arg Asp Tyr Gln Glu Ala Val Phe Trp Tyr Arg Lys Ser Ala Leu Gln
50 55 60

Gly Asp Glu Leu Gly Gln Tyr Asn Leu Gly Val Ala Tyr Tyr Tyr Gly
65 70 75 80

Arg Gly Ile Lys Lys Asp Phe Ser Glu Ala Val Ser Trp Tyr Lys Lys
85 90 95

Ser Ala Glu Gln Asp Tyr Ala Gln Ala Gln His Asn Leu Gly Val Thr
100 105 110

Tyr Tyr Glu Gly Glu Gly Ile Lys Lys Asp Tyr Ala Lys Ala Val Tyr
115 120 125

Trp Trp Lys Lys Ala Ala Glu Gln Gly Ile Pro Gln Ser Gln Tyr Asn
130 135 140

Leu Gly Ile Ala Tyr Glu Glu Gly Trp Gly Ala Glu Lys Asn Pro Glu
145 150 155 160

-continued

Asn Ala Val Phe Trp Tyr Arg Lys Ala Ala Glu Gln Gly His Ala Asp
165 170 175

Ala Gln Asn Arg Leu Gly Ile Ala Tyr Arg Tyr Gly Thr Gly Val Arg
180 185 190

Lys Asn Pro Ala Leu Ser Val Lys Trp Leu Glu Lys Ala Ala Lys Gln
195 200 205

Gly Leu Ala Arg Ala Gln Phe Asn Leu Gly Lys Thr Phe Tyr Ile Gly
210 215 220

Ala Gly Ile Asn Lys Asn Thr Asp Lys Ala Val Tyr Trp Phe Ile Lys
225 230 235 240

Ala Ala Asn Gln Gly Phe Thr Glu Ala
245

<210> SEQ ID NO 105
<211> LENGTH: 172
<212> TYPE: PRT
<213> ORGANISM: Oxalobacter formigenes

<400> SEQUENCE: 105

Tyr Arg Lys Ala Ala Glu Gln Gly His Ala Asp Ala Gln Asn Arg Leu
1 5 10 15

Gly Ile Ala Tyr Arg Tyr Gly Thr Gly Val Arg Lys Asn Pro Ala Leu
20 25 30

Ser Val Lys Trp Leu Glu Lys Ala Ala Lys Gln Gly Leu Ala Arg Ala
35 40 45

Gln Phe Asn Leu Gly Lys Thr Phe Tyr Ile Gly Ala Gly Ile Asn Lys
50 55 60

Asn Thr Asp Lys Ala Val Tyr Trp Phe Ile Lys Ala Ala Asn Gln Gly
65 70 75 80

Phe Thr Glu Ala Gln Ala Tyr Ile Gly Met Ile Tyr Phe Lys Gly Lys
85 90 95

Tyr Val Ala Lys Asn Glu Lys Lys Gly Phe Tyr Trp Leu Lys Lys Ala
100 105 110

Ala Glu Lys Asp Ser Ala Lys Ala Gln Ala Phe Leu Gly Ala Leu Tyr
115 120 125

Ile Ala Gly Asn Glu Val Lys Pro Asn Ile Lys Glu Gly Val Ala Leu
130 135 140

Thr Lys Lys Ala Ala Leu Gln Gly Asn Tyr Glu Ala Gln Thr Leu Leu
145 150 155 160

Gly Phe Cys Tyr Glu Asn Gly Leu Glu Val Lys Lys
165 170

1. A method comprising administering to the subject one or more *Oxalobacter formigenes* (Of)-derived factors, and/or bioactive variants and/or fragments thereof, that result in stimulation of oxalate transport.

2. (canceled)

3. The method of claim **1**, wherein the one or more Of-derived factors are administered by administering Of conditioned media (CM) to the subject.

4. The method of claim **3**, wherein the Of CM is fractionated, purified, and/or otherwise processed prior to administration.

5.-**6**. (canceled)

7. The method of claim **1**, wherein one or more of the Of-derived factors are Sel1-like repeat (SLR) proteins or bioactive variants and/or fragments of Sel1 proteins.

8. (canceled)

9. The method of claim **7**, wherein one or more of the Of-derived factors comprises 70% or greater sequence identity to all or a portion of an Of-derived Sel1 protein.

10. The method of claim **7**, wherein the Sel1 protein or proteins are selected from the group consisting of Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, and MerG.

11. The method of claim **10**, wherein the Of-derived factor is a peptide fragment of one of Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, and MerG, and/or a bioactive peptide having at least 70% sequence identity to a fragment thereof.

12. The method of claim **7**, wherein the Of-derived factor comprises SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and SEQ ID NO: 102.

13. The method of claim **7**, wherein the Of-derived factor comprises a bioactive variant having 70% sequence identity to SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, and SEQ ID NO: 102.

14. (canceled)

15. The method of claim **1**, wherein administration comprises rectal administration, oral administration, and/or injection.

16.-**17**. (canceled)

18. A pharmaceutical composition comprising one or more *Oxalobacter formigenes* (O)-derived factors, and/or bioactive variants and/or fragments thereof.

19. The pharmaceutical composition of claim **1**, comprising Of conditioned media (CM).

20. The pharmaceutical composition of claim **3**, wherein the Of CM is fractionated, purified, and/or otherwise processed.

21.-**22**. (canceled)

23. The pharmaceutical composition of claim **20**, wherein one or more of the Of-derived factors are selected from polypeptides comprising all or a portion of SEQ ID NOS; 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 101, or 102.

24. The pharmaceutical composition of claim **20**, wherein one or more of the Of-derived factors are Sel1-like repeat (SLR) proteins or bioactive variants and/or fragments of Sel1 proteins.

25. (canceled)

26. The pharmaceutical composition of claim **24**, wherein one or more of the Of-derived factors comprises 70% or greater sequence identity to all or a portion of an Of-derived Sel1 protein.

27. The pharmaceutical composition of claim **24**, wherein the Sel1 protein or proteins are selected from the group consisting of Sel1, Hrd3, Chs4, Nif1, PodJ, ExoR, AlgK, HcpA, Hsp12, EnhC, LpnE, MotX, and MerG.

28. (canceled)

29. The pharmaceutical composition of claim **24**, wherein the Of-derived factor comprises SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, or SEQ ID NO: 102.

30. The pharmaceutical composition of claim **24**, wherein the Of-derived factor comprises a bioactive variant having 70% or more sequence identity to SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 101, or SEQ ID NO: 102.

31. (canceled)

32. The pharmaceutical composition of claim **18**, wherein the pharmaceutical composition is formulated for rectal administration, oral administration, and/or injection.

33.-**34**. (canceled)

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