

Methods for Preventing Gluconoylation of Proteins

FIELD OF THE INVENTION

This invention is in the field of biochemical engineering. More particularly, this invention relates to fermentation processes for producing polypeptides.

BACKGROUND OF THE INVENTION

Escherichia coli ("*E. coli*") is a commonly used host for expression of proteins for research, diagnostic, therapeutic, and industrial purposes. Modern expression systems are capable of achieving high levels of a wide variety of proteins (Baneyx, *Current Opinion in Biotechnology* 10:411-421(1999)). However, the quality of the expressed protein is often as important or more important than quantity. Proteins expressed in *E. coli* may be formed as insoluble aggregates, or they may have misincorporated amino acids (Bogosian, *et al.*, *Journal of Biological Chemistry* 264:531-539 (1989)) or retain the N-terminal methionine (Chaudhuri, *et al.*, *Journal of Molecular Biology* 285:1179-1194 (1999); Vassileva-Atanassova, *et al.*, *Journal of Biotechnology* 69:63-67 (1999); Yamashita, *et al.*, *Protein Expression & Purification* 16:47-52 (1999)). In addition, undesired post-translational modifications may occur such as oxidation (Berti, *et al.*, *Protein Expression & Purification* 11:111-118 (1997); Konz, *et al.*, *Biotechnology Progress* 14:393-409 (1998)) or α -N-6-phosphogluconoylation (Geoghegan, *et al.*, *Anal. Biochem.* 267:169-184 (1999); Kim *et al.*, *Acta Crystallographica Section D-Biological Crystallography* 57:759-762 (2001); Yan, *et al.* *Biochemical & Biophysical Research Communications* 262:793-800 (1999) "Yan *et al.* I;" Yan, *et al.*, *Biochemical & Biophysical Research Communications* 259:271-282 (1999) "Yan *et al.* II"). These modifications may adversely effect activity, stability, structure, or immunogenicity of the expressed protein, greatly reducing the utility of *E. coli* as a host for polypeptide expression.

Alpha(α)-N-6-phosphogluconoylation of several recombinant proteins fused to hexahistidine affinity tags ("hexa His-tag") has been described

(Geoghegan, *et al.*; Kim, *et al.*; Yan *et al.* I; Yan *et al.* II). In these studies, a gluconic acid derivative was found to attach to the end terminus of the recombinant protein. All of these proteins were expressed in B strains of *E. coli* using pET-based vectors (Novagen). Where reported, LB medium was used.

5 The adduct was detected as an extra mass associated with the polypeptide of either 258 Daltons ("Da"), representing the addition of 6-phosphogluconolactone (6-PGL), or 178 Da, representing the presence of gluconolactone without the phosphate. Phosphogluconoylation was presumed to occur at the N-terminal α -amino group through reaction with endogenous 6-PGL, an intermediate of the pentose phosphate shunt. The +178 Da adduct
10 was proposed to be the result of enzymatic activity acting on the +258 Da adduct to remove the phosphate. Formation of the adduct was shown to be specific to the amino acid sequence at the N-terminus adjacent to the His-tag. Polypeptide sequences of GXXHHHH, where XX is SS, SA, AS, or AA, were
15 the most prone to α -N-6-phosphogluconoylation, whereas SHHHHHH was less prone, and PHHHHHH and PFHHHHHH were not modified at all (Geoghegan, *et al.*). Modifications at other amino groups elsewhere on the protein were not detected *in vivo* or in *in vitro* experiments that used high levels of added gluconolactone. (Geoghegan, *et al.*)

20 N-terminal phosphogluconoylation has been shown to inhibit crystallization of proteins (Kim, *et al.*), but relatively little else is known about its effect on protein function, stability, or immunogenicity. It is expected that 6-PGL, being a potent electrophile, may be involved in glycation reactions *in vivo* (Rakitzis and Papandreou, *Chemico-Biological Interactions* 113:205-216
25 (1998)). Glycation of proteins has been widely studied and is known to play a major role in aging and disease states related to diabetic complications (Baynes and Monnier, *The Maillard Reaction in Aging, Diabetes, and Nutrition*. Alan R. Liss, New York (1989)). Exogenously added delta-gluconolactone has been shown to cause glycation of hemoglobin, which may be a factor in the
30 vascular complications of diabetes (Lindsay, *et al.*, *Clinica Chimica Acta* 263:239-247 (1997)). Furthermore, glycation of alanine aminotransferase at

the epsilon-amino group of Lys313 markedly reduces its catalytic activity (Beranek, *et al.*, *Molecular & Cellular Biochemistry* 218:35-39 (2001)).

6-Phosphogluconolactonase ("pgl") has been shown to be an essential enzyme of the pentose-phosphate pathway, specifically in the hydrolysis of 6-PGL to 6-phosphogluconic acid. (Miclet, *et al.*, *J.Biol.Chem.* 276:34840-34846 (2001)) The gene encoding this enzyme has been identified in human (Collard, *et al.*, *FEBS Letters* 459:223-226 (1999)), *Pseudomonas aeruginosa* (Hager, *et al.*, *Journal of Bacteriology* 182:3934-3941(2000)), and *Trypanosoma brucei* and *Plasmodium falciparum* (Miclet, *et al.*). Although pgl activity has long been observed in *E. coli* (Kupor and Fraenkel, *Journal of Bacteriology* 100:1296-1301 (1969) "Kupor I" and Kupor and Fraenkel, *Journal of Biological Chemistry* 247:1904-1910 (1972) "Kupor II"), no gene sequence responsible for encoding an enzyme with this activity has been identified (Cordwell, S. J. *Arch. Microbiol.* 172:269-279 (1999)). It has been suggested that in addition to enabling metabolic flux through the pentose phosphate shunt, pgl activity inside the cell prevents accumulation of 6-PGL and consequential damaging reactions with intracellular nucleophiles (Miclet, *et al.*). Reported observations of phosphogluconoylation of proteins at the N-terminus supports the hypothesis that the 6-PGL produced in the pathway can modify proteins, but there has been no reported evidence that modulating pgl activity can affect the levels of modified protein.

Furthermore, *Escherichia coli* strain BL21(DE3) is a commonly used host for expression of proteins for research, diagnostic, therapeutic, and industrial purposes Studier, F.W., and Moffatt, B.A., *J. Mol. Biol.* 1986 May 5; 189(1):113-130. This strain is commercially attractive because it achieves very high expression levels of recombinant protein by means of coupling expression of a chromosomal copy of the T7 RNA polymerase and the use of a plasmid based T7 RNA polymerase promoter on the recombinant protein of interest. Accordingly, since the T7 RNA polymerase is an extremely selective and active RNA polymerase, transcription of the recombinant protein accumulate to very high levels, often even to the extent that host cell transcripts are diminished.

Unfortunately, the strain BL21(DE3) releases very low, yet detectable, infectious lambda phage particles on the order of 10-20 plaque forming units /ml (PFU), Stewart Shuman, *Proc. Natl. Acad. Sci. USA* 1989; 89:3489-3493. Apparently, the T7 RNA polymerase gene was introduced into the BL21 host cell chromosome by transduction with the defective lambda phage DE3 carrying the T7 RNA polymerase gene inserted into the lambda *int* gene Studier, F.W., and Moffatt, B.A., *J. Mol. Biol.* 1986; 189(1):113-130. The resulting defective prophage cannot replicate normally due to the *int* gene interruption. Chromosomal excision of the DE3 prophage is a requirement for the replication of the prophage prior to packaging and release of infectious phage particles and is dependant on homologous excisional recombination that is directed by the product of the *int* gene. As described herein very low levels of phage particles released are due to abnormal, *int* independent random prophage excision events. While the release of low levels of infectious phage particles may be acceptable in some research laboratories, any release of infectious phage is totally unacceptable in the biopharmaceuticals manufacturing plant setting both because of considerations for patient safety and because release of infectious agents can put at risk other *E. coli* based manufacturing processes.

A method for expressing or overexpressing polypeptides in a microorganism, such as *E. coli*, with a reduced incidence of phosphogluconoylation during fermentation is greatly needed. In addition, creation of a totally phage free BL21(DE3) host cell would be highly desirable for the manufacture of therapeutic recombinant proteins in the *E. coli* format.

SUMMARY OF THE INVENTION

The present invention provides methods for preventing gluconoylation of polypeptides expressed by microorganisms by growing the microorganism in rich culture medium.

The present invention also provides methods for preventing gluconoylation of polypeptides expressed by microorganisms that include introducing (*e.g.*, transforming, infecting or transfecting) DNA encoding a

polypeptide that demonstrates pgl activity into the microorganism. This polypeptide may be a phosphogluconolactonase enzyme. In another aspect of the invention, the phosphogluconolactonase enzyme may have an amino acid sequence having at least 90% sequence identity to the

5 phosphogluconolactonase enzyme produced by *Pseudomonas*, including but not limited to, *P. aeruginosa*.

The present invention also provides microorganisms capable of preventing gluconoylation of proteins. In one embodiment, a microorganism may contain DNA encoding a polypeptide that demonstrates pgl activity.

10 The present invention also provides an isolated polynucleotide that has at least 90% identity to the polynucleotide set forth in SEQ ID NO:7.

The present invention also provides a microorganism free of detectable infectious lambda phage expression.

15 BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows a restriction enzyme map of vector pECO-1-pgl-2-13..

Figure 2 shows a polynucleotide sequence for vector pECO-1-pgl-2-13. (SEQ ID NO:9)

Figure 3 shows a restriction enzyme map of vector pET28ProIL18Casp5.

20 Figure 4 shows a polynucleotide sequence for vector pET28ProIL18Casp5. (SEQ ID NO:13)

Figure 5 shows a restriction enzyme map of vector pET28proIL18casp5+pgl..

Figure 6 shows a polynucleotide sequence for vector pET28proIL18casp5+pgl (SEQ ID NO:14).

25 Figure 7 shows a polynucleotide sequence, SEQ ID NO:7.

Figure 8 shows a polypeptide sequence, SEQ ID NO:8.

Glossary

"Host cell(s)" is a cell, including but not limited to a bacterial cell or cell

30 of a microorganism, that has been introduced (e.g., transformed, infected or transfected) or is capable of introduction (e.g., transformation, infection or transfection) by an isolated polynucleotide sequence.

"Transformed" as known in the art, is the directed modification of an organism's genome or episome via the introduction of external DNA or RNA, or to any other stable introduction of external DNA or RNA.

"Transfected" as known in the art, is the introduction of external DNA or RNA into a microorganism, including but not limited to recombinant DNA or RNA.

"Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as the case may be, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Methods to determine identity are designed to give the largest match between the sequences tested. Moreover, methods to determine identity are codified in publicly available computer programs. Computer program methods to determine identity between two sequences include, but are not limited to, the GCG program package (Devereux, J., *et al.*, *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Altschul, S.F. *et al.*, *J. Molec. Biol.* 215: 403-410 (1990). The BLAST X program is publicly available from NCBI and other sources (*BLAST Manual*, Altschul, S., *et al.*, NCBI NLM NIH Bethesda, MD 20894; Altschul, S., *et al.*, *J. Mol. Biol.* 215: 403-410 (1990). The well known Smith Waterman algorithm may also be used to determine identity.

Parameters for polypeptide sequence comparison include the following:

Algorithm: Needleman and Wunsch, J. Mol Biol. 48: 443-453 (1970)

Comparison matrix: BLOSSUM62 from Hentikoff and Hentikoff, Proc. Natl. Acad. Sci. USA. 89:10915-10919 (1992)

5 Gap Penalty: 12

Gap Length Penalty: 4

A program useful with these parameters is publicly available as the "gap" program from Genetics Computer Group, Madison WI. The aforementioned parameters are the default parameters for peptide comparisons (along with no
10 penalty for end gaps).

Parameters for polynucleotide comparison include the following:

Algorithm: Needleman and Wunsch, J. Mol Biol. 48: 443-453 (1970)

Comparison matrix: matches = +10, mismatch = 0

Gap Penalty: 50

15 Gap Length Penalty: 3

Available as: The "gap" program from Genetics Computer Group, Madison WI. These are the default parameters for nucleic acid comparisons.

A preferred meaning for "identity" for polynucleotides and polypeptides, as the case may be, are provided in (1) and (2) below.

- 20 (1) Polynucleotide embodiments further include an isolated polynucleotide comprising a polynucleotide sequence having at least a 70, 80, 85, 90, 95, 97 or 100% identity to the reference sequence of SEQ ID NO:7, wherein said polynucleotide sequence may be identical to the reference sequence of SEQ ID NO:7 or may include up to a certain integer number of
25 nucleotide alterations as compared to the reference sequence, wherein said alterations are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions,
30 interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence, and wherein said number of nucleotide alterations is determined by multiplying

the total number of nucleotides in SEQ ID NO:7 by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of nucleotides in SEQ ID NO:7, or:

$$5 \quad n_n \leq x_n - (x_n \bullet y),$$

wherein n_n is the number of nucleotide alterations, x_n is the total number of nucleotides in SEQ ID NO:7, y is 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and $\bullet$ is the symbol for the multiplication operator, and wherein any non-integer product of x_n and y is rounded down to the nearest integer prior to subtracting it from x_n . Alterations of a polynucleotide sequence encoding a polypeptide may create nonsense, missense or frameshift mutations in this coding sequence and thereby alter the polypeptide encoded by the polynucleotide following such alterations.

15 (2) Polypeptide embodiments further include an isolated polypeptide comprising a polypeptide having at least a 70, 80, 85, 90, 95, 97 or 100% identity to a polypeptide reference sequence, wherein said polypeptide sequence may be identical to the reference sequence or may include up to a certain integer number of amino acid alterations as compared to the reference sequence, wherein said alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence, and wherein said number of amino acid alterations is determined by multiplying the total number of amino acids by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of amino acids, or:

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$$n_a \leq x_a - (x_a \bullet y),$$

wherein n_a is the number of amino acid alterations, x_a is the total number of amino acids in the sequence, y is 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and $\bullet$ is the symbol for the multiplication operator, and wherein any non-integer product of x_a and y is rounded down to the nearest integer prior to subtracting it from x_a .

"Isolated" means altered "by the hand of man" from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", including but not limited to when such polynucleotide or polypeptide is introduced back into a cell.

"Polynucleotide(s)" generally refers to any polyribonucleotide or polydeoxyribonucleotide, that may be unmodified RNA or DNA or modified RNA or DNA. "Polynucleotide(s)" include, without limitation, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions or single-, double- and triple-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded regions, or a mixture of single- and double-stranded regions. In addition, "polynucleotide" as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term "polynucleotide(s)" also includes DNAs or RNAs as described above that comprise one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotide(s)" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is

used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term "polynucleotide(s)" as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including, for example, simple and complex cells. "Polynucleotide(s)" also embraces short polynucleotides often referred to as oligonucleotide(s).

"Polypeptide(s)" refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds. "Polypeptide(s)" refers to both short chains, commonly referred to as peptides, oligopeptides and oligomers and to longer chains generally referred to as proteins. Polypeptides may comprise amino acids other than the 20 gene encoded amino acids. "Polypeptide(s)" include those modified either by natural processes, such as processing and other post-translational modifications, but also by chemical modification techniques. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature, and they are well known to those of skill in the art. It will be appreciated that the same type of modification may be present in the same or varying degree at several sites in a given polypeptide. Also, a given polypeptide may comprise many types of modifications. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains, and the amino or carboxyl termini. Modifications include, for example, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, selenoylation, sulfation, transfer-RNA

mediated addition of amino acids to proteins, such as arginylation, and ubiquitination. See, for instance, *PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993) and Wold, F., Posttranslational Protein Modifications: Perspectives and Prospects, pgs. 1-12 in *POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS*, B. C. Johnson, Ed., Academic Press, New York (1983); Seifter *et al.*, *Meth. Enzymol.* 182:626-646 (1990) and Rattan *et al.*, *Protein Synthesis: Posttranslational Modifications and Aging*, Ann. N.Y. Acad. Sci. 663: 48-62 (1992). Polypeptides may be branched or cyclic, with or without branching. Cyclic, branched and branched circular polypeptides may result from post-translational natural processes and may be made by entirely synthetic methods, as well.

"Recombinant expression system(s)" refers to expression systems or portions thereof or polynucleotides of the invention introduced or transformed into a host cell or host cell lysate for the production of the polynucleotides and polypeptides of the invention.

"Variant(s)" as the term is used herein, is a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide respectively, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusion proteins and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. The present invention also includes include

variants of each of the polypeptides of the invention, that is polypeptides that vary from the referents by conservative amino acid substitutions, whereby a residue is substituted by another with like characteristics. Typical such substitutions are among Ala, Val, Leu and Ile; among Ser and Thr; among the acidic residues Asp and Glu; among Asn and Gln; and among the basic residues Lys and Arg; or aromatic residues Phe and Tyr. Particularly preferred are variants in which several, 5-10, 1-5, 1-3, 1-2 or 1 amino acids are substituted, deleted, or added in any combination. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques, by direct synthesis, and by other recombinant methods known to skilled artisans.

"Microorganism(s)" means a (i) prokaryote, including but not limited to, a member of the genus *Streptococcus*, *Staphylococcus*, *Bordetella*, *Corynebacterium*, *Mycobacterium*, *Neisseria*, *Haemophilus*, *Actinomycetes*, *Streptomyces*, *Nocardia*, *Enterobacter*, *Yersinia*, *Fancisella*, *Pasturella*, *Moraxella*, *Acinetobacter*, *Erysipelothrix*, *Branhamella*, *Actinobacillus*, *Streptobacillus*, *Listeria*, *Calymmatobacterium*, *Brucella*, *Bacillus*, *Clostridium*, *Treponema*, *Escherichia*, *Salmonella*, *Kleibsiella*, *Vibrio*, *Proteus*, *Erwinia*, *Borrelia*, *Leptospira*, *Spirillum*, *Campylobacter*, *Shigella*, *Legionella*, *Pseudomonas*, *Aeromonas*, *Rickettsia*, *Chlamydia*, *Borrelia* and *Mycoplasma*, and further including, but not limited to, a member of the species or group, Group A *Streptococcus*, Group B *Streptococcus*, Group C *Streptococcus*, Group D *Streptococcus*, Group G *Streptococcus*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus agalactiae*, *Streptococcus faecalis*, *Streptococcus faecium*, *Streptococcus durans*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Corynebacterium diphtheriae*, *Gardnerella vaginalis*, *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium ulcerans*, *Mycobacterium leprae*, *Actinomycetes israelii*, *Listeria monocytogenes*, *Bordetella pertussis*, *Bordetella parapertussis*, *Bordetella bronchiseptica*, *Escherichia coli*, *Shigella dysenteriae*, *Haemophilus influenzae*, *Haemophilus aegyptius*, *Haemophilus parainfluenzae*,

Haemophilus ducreyi, *Bordetella*, *Salmonella typhi*, *Citrobacter freundii*, *Proteus mirabilis*, *Proteus vulgaris*, *Yersinia pestis*, *Klebsiella pneumoniae*, *Serratia marcescens*, *Serratia liquefaciens*, *Vibrio cholera*, *Shigella dysenteriae*, *Shigella flexneri*, *Pseudomonas aeruginosa*, *Francisella tularensis*, *Brucella abortus*,
 5 *Bacillus anthracis*, *Bacillus cereus*, *Clostridium perfringens*, *Clostridium tetani*, *Clostridium botulinum*, *Treponema pallidum*, *Rickettsia rickettsii* and *Chlamydia trachomatis*, (ii) an archaeon, including but not limited to *Archaeobacter*, and (iii) a unicellular or filamentous eukaryote, including but not limited to, a protozoan, a fungus, a member of the genus *Saccharomyces*, *Kluyveromyces*, or *Candida*, and
 10 a member of the species *Saccharomyces cerevisiae*, *Kluyveromyces lactis*, or *Candida albicans*.

"Bacteria(um)(l)" means a (i) prokaryote, including but not limited to, a member of the genus *Streptococcus*, *Staphylococcus*, *Bordetella*, *Corynebacterium*, *Mycobacterium*, *Neisseria*, *Haemophilus*, *Actinomycetes*,
 15 *Streptomyces*, *Nocardia*, *Enterobacter*, *Yersinia*, *Francisella*, *Pasteurella*, *Moraxella*, *Acinetobacter*, *Erysipelothrix*, *Branhamella*, *Actinobacillus*, *Streptobacillus*, *Listeria*, *Calymmatobacterium*, *Brucella*, *Bacillus*, *Clostridium*, *Treponema*, *Escherichia*, *Salmonella*, *Klebsiella*, *Vibrio*, *Proteus*, *Erwinia*, *Borrelia*, *Leptospira*, *Spirillum*, *Campylobacter*, *Shigella*, *Legionella*,
 20 *Pseudomonas*, *Aeromonas*, *Rickettsia*, *Chlamydia*, *Borrelia* and *Mycoplasma*, and further including, but not limited to, a member of the species or group, Group A *Streptococcus*, Group B *Streptococcus*, Group C *Streptococcus*, Group D *Streptococcus*, Group G *Streptococcus*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus agalactiae*, *Streptococcus faecalis*,
 25 *Streptococcus faecium*, *Streptococcus durans*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Corynebacterium diphtheriae*, *Gardnerella vaginalis*, *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium ulcerans*, *Mycobacterium leprae*, *Actinomyces israelii*, *Listeria monocytogenes*, *Bordetella pertussis*, *Bordetella parapertussis*, *Bordetella bronchiseptica*, *Escherichia coli*, *Shigella dysenteriae*,
 30 *Haemophilus influenzae*, *Haemophilus aegyptius*, *Haemophilus parainfluenzae*, *Haemophilus ducreyi*, *Bordetella*, *Salmonella typhi*, *Citrobacter freundii*, *Proteus*

mirabilis, *Proteus vulgaris*, *Yersinia pestis*, *Klebsiella pneumoniae*, *Serratia marcescens*, *Serratia liquefaciens*, *Vibrio cholera*, *Shigella dysenterii*, *Shigella flexneri*, *Pseudomonas aeruginosa*, *Francisella tularensis*, *Brucella abortus*, *Bacillus anthracis*, *Bacillus cereus*, *Clostridium perfringens*, *Clostridium tetani*,
5 *Clostridium botulinum*, *Treponema pallidum*, *Rickettsia rickettsii* and *Chlamydia trachomatis*, and (ii) an archaeon, including but not limited to *Archaeobacter*.

As used herein, "heterologous polypeptide(s)" refers to a polypeptide not naturally synthesized by a transformed host cell or microorganism of interest and introduced into the host cell or microorganism by recombinant DNA. For
10 example, *E. coli* may act as a host microorganism for the expression of interleukin, which does not occur in non-transformed *E. coli*. Heterologous polypeptides may include polypeptides that have been modified to facilitate isolation.

As used herein "affinity tag" refers to any moiety associated with a
15 molecule that may give said molecule a selective affinity for another substance or molecule. For instance, an affinity tag may be used to facilitate purification of a molecule by providing the molecule with a selective affinity for a column's packing material. A non-limiting example of an affinity tag is a his-tag.

As used herein, "His-tag" refers to a repeat of histidine amino acids and
20 may include other amino acids encoded into a polypeptide through engineering techniques. Typically, a His-tag contains at least six ("hexa") histidine repeats and is located near the N-terminus of the polypeptide. His-tags can be used to facilitate purification of heterologous polypeptides over Ni-columns.

As used herein, "minimal medium" refers to cell growth medium
25 comprising chemically defined ingredients including, but not limited to, buffers such as phosphate buffer, salts such as magnesium sulfate, calcium chloride, sodium chloride, or manganese sulfate, minerals such as iron, zinc, copper, cobalt, or molybdenum, a carbon source such as glucose or glycerol, and a nitrogen source such as ammonium sulfate or nitrate. An example is M9 media
30 (Kim, YS, JH Seo and HY Cha, *Enzyme and Microbial Technology* 33 (2003):460-465.)

As used herein, "rich medium" refers to cell growth medium comprising undefined ingredients and including, but not limited to, additional components such as buffers (for example phosphate buffer), salts (for example magnesium sulfate, calcium chloride, sodium chloride, or manganese sulfate), and a carbon source which may be glucose or glycerol, for example. The nitrogen source may be comprised of a protein hydrolysate such as yeast extract, meat hydrolysate, or soy hydrolysate. The nitrogen source may be provided at a concentration capable of supporting cell growth at a ratio of complex nitrogen source (in grams per liter) to maximum cell density (in OD units) of 1:1 or greater. Examples of rich medium include, but are not limited to, Superbroth (Atlas RM, Handbook of Microbiological Media; Parks LC Ed.; CRC Press: Boca Raton FL, pp. 281, 523, 529, 859), Terrific Broth (Alpha Biosciences, Baltimore, MD USA), Turbo Broth (Athena Enzyme Systems, Baltimore, MD USA), or Hyper Broth (Athena Enzyme Systems, Baltimore, MD USA).

As used herein, "gluconoylation" refers to the attachment of a gluconic acid derivative to a protein. Gluconoylation may include, but is not limited to, 6-phosphogluconolactone (6-PGL) adduct formation, acetylation, formylation, deformylation, gluconolactonation, or gluconic acid derivatization.

As used herein, "titer yield" refers to the concentration of a product (e.g., heterologously expressed polypeptide) in solution (e.g., culture broth or cell-lysis mixture or buffer) and it usually expressed as mg/L or g/L. An increase in titer yield may refer to an absolute or relative increase in the concentration of a product produced under two defined set of conditions.

As used herein, "pgl activity" refers to any activity of a 6-Phosphogluconolactonase ("pgl"). Such activity may include hydrolysis of 6-PGL to 6-phosphogluconic acid. Significant pgl activity may be defined as hydrolysis activity of at least 0.2 IU/min/g.

As herein used, the terms "stringent conditions" and a "stringent hybridization conditions" mean hybridization will occur only if there is at least 70% and preferably at least 80%, but especially preferably at least 95% identity between the sequences. An example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5xSSC

(150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in

5 Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein, the disclosure of which is hereby incorporated in its entirety by reference.

DETAILED DESCRIPTION OF THE INVENTION

10 Cellular stresses arising from growth on minimal medium, high cell densities, and high-level heterologous polypeptide expression, among other stresses, may contribute to the gluconoylation of heterologous polypeptide. Alleviating one or more of these stressors may therefore affect the level of gluconoylation of protein expressed in the microorganism, which in turn may

15 effect the purity and titer yield of a desired polypeptide. Some strains of *E. coli* may have higher levels of pgl activity than others (although the gene responsible for this activity has not been identified in *E. coli*. Cordwell, S. J. 1999. *Arch. Microbiol.* 172:269-279. Furthermore, gluconoylation of polypeptides may affect crystallization and structural determination of these

20 polypeptides.

The present invention provides methods for preventing gluconoylation of a polypeptide expressed in a microorganism, comprising growing said microorganism in rich culture medium. In another aspect of the invention, the microorganism does not demonstrate significant 6-phosphogluconolactonase

25 activity when grown in minimal medium. The microorganism may be a strain of *E. coli*. In another aspect of the invention, an *E. coli* is a B strain. In another aspect of the invention, a rich culture medium comprises a complex nitrogen source. A rich culture medium is capable of maintaining cell growth at ratio of 1:1 for concentration of complex nitrogen source to cell density. A complex

30 nitrogen source may comprise tryptone, peptone, or yeast extract. In another aspect of the invention, a culture medium is Superbroth. Superbroth medium may be doubly concentrated. In another aspect of the invention, a

microorganism is transfected with a recombinant DNA molecule encoding a heterologous polypeptide.

In another embodiment of the present invention, methods are provided for preventing gluconoylation of a polypeptide expressed in *E. coli* comprising
5 fermenting a K strain variety of *E. coli* for the expression of the polypeptide. In another aspect of the invention, a K strain demonstrates at least about 100-fold higher phosphogluconolactonase activity compared with B strain grown under substantially the same conditions. In another aspect of the invention, a K strain is K-12.

10 In another embodiment of the present invention, methods are provided for preventing gluconoylation of polypeptides expressed in a microorganism, comprising introducing DNA into the microorganism, wherein the DNA encodes a polypeptide that demonstrates 6-phosphogluconolactonase activity. In another aspect of the invention, a microorganism is *E. coli*. A DNA comprises
15 DNA encoding a 6-phosphogluconolactonase enzyme. In another aspect of the invention, a DNA encoding a 6-phosphogluconolactonase enzyme has at least 70%, 80%, 85%, 90%, 95%, 97%, or 100% sequence identity to a DNA encoding 6-phosphogluconolactonase from a *Pseudomonas*, which may be *P. aeruginosa*. In another aspect of the invention, a DNA encoding a 6-
20 phosphogluconolactonase enzyme has at least 70%, 80%, 85%, 90%, 95%, 97%, or 100% sequence identity to SEQ ID NO:7. In another aspect of the invention, a 6-phosphogluconolactonase enzyme has an amino acid sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, or 100% sequence identity to SEQ ID NO:8. A DNA encoding a 6-phosphogluconolactonase enzyme
25 comprises the sequence set forth in SEQ ID NO:7. DNA may be recombinant DNA, and/or it may be transformed into a genomic DNA of a microorganism.

In another embodiment of the present invention, a microorganism is provided that is capable of preventing gluconoylation of polypeptides. A microorganism comprises DNA that encodes a polypeptide that demonstrates
30 6-phosphogluconolactonase activity. A microorganism comprises DNA that encodes 6-phosphogluconolactonase. In another aspect of the invention, a DNA that encodes 6-phosphogluconolactonase has at least 70%, 80%, 85%,

90%, 95%, 97%, or 100% sequence identity to DNA encoding a 6-phosphogluconolactonase enzyme from a *Pseudomonas* and wherein the microorganism is not *Pseudomonas*. In another aspect of the invention, a DNA that encodes 6-phosphogluconolactonase is from *P. aeruginosa*. In another aspect of the invention, a microorganism is a strain of *E. coli*. In another aspect of the invention, a microorganism is a strain of *E. coli* and the wherein a DNA that encodes 6-phosphogluconolactonase is incorporated into the genome of the microorganism.

In another embodiment of the present invention, an isolated polynucleotide is provided comprising a polynucleotide having at least a 70%, 80%, 85%, 90%, 95%, 97%, or 100% identity to the polynucleotide set forth in SEQ ID NO:7. In another aspect of the invention, an isolated polynucleotide comprises a polynucleotide having at least a 70%, 80%, 85%, 90%, 95%, 97%, or 100% sequence identity to a polynucleotide encoding a polypeptide comprising amino acids having at least 70%, 80%, 85%, 90%, 95%, 97%, or 100% sequence identity to SEQ ID NO:8. In another aspect of the invention, a DNA encodes a protein demonstrating 6-phosphogluconolactonase activity. In another aspect of the invention, a DNA sequence is set forth in SEQ ID NO:7. In another aspect of the invention, a DNA sequence is homologous to a DNA encoding 6-phosphogluconolactonase from *P. aeruginosa*. In another aspect of the invention, an isolated polynucleotide further comprises a polynucleotide that encodes a human interleukin-18, or variant thereof.

In another embodiment of the present invention, methods are provided for improving polypeptide crystal formation comprising expressing said polypeptide by a method of the invention in order to reduce glyconoylation of the polypeptide.

In another embodiment of the present invention, methods are provided for improving growth efficiency and expression of a polypeptide in a microorganism. In one aspect, a polypeptide demonstrates an increased titer yield at fermentation stage compared with gluconoylated polypeptide.

In another embodiment of the present invention, methods are provided for producing a human interleukin comprising co-expressing said human

interleukin in a microorganism with an enzyme having 6-
Phosphogluconolactonase ("pgl") activity. In one aspect, a human interleukin is
an IL-18 protein, or variant thereof. In one aspect, a microorganism is *E. coli*.
In one aspect, the pgl is encoded by a polynucleotide that is transformed or
5 transfected into the *E. coli*, including but not limited to being transformed into
the genome or episome.

In another embodiment of the present invention, methods are provided
producing a human interleukin comprising expressing the human interleukin in
a microorganism that is grown in a rich culture medium. In one aspect, a
10 human interleukin is IL-18 protein, or a variant thereof. In one aspect, the
microorganism is *E. coli*. In one aspect, a rich culture medium comprises
phytone peptone. In one aspect, a rich culture medium comprises bacto yeast
extract.

In another embodiment of the present invention, a microorganism free of
15 detectable infectious lambda phage expression is provided. In one aspect,
lambda phage capsid structural protein, gpE, is deleted or disrupted within a
microorganism. Deletion or disruption of a protein can be achieved in several
non-limiting ways. A gene encoding a protein may be either partially or
completely removed from a microorganism. A gene encoding a protein can be
20 genetically modified by such non-limiting techniques as point mutation or
random mutation. A protein may be cleaved or modified chemically or
enzymatically to disrupt its structure or function. A promoter regulating gene
expression can be disrupted or deleted to eliminate or reduce gene
expression. Solution conditions or temperature can be regulated to effect
25 protein structure or function. In one aspect, a microorganism is an *E. coli*. In
another aspect a microorganism comprises a T7 RNA polymerase gene.

The following examples illustrate various aspects of this invention.
These examples do not limit the scope of this invention which is defined by the
30 appended claims.

EXAMPLES**Example 1**

An improved strain of *E. coli* BL21(DE3) strain was created that is free of detectable infectious lambda phage expression by knocking out a major
 5 lambda phage capsid structural protein gpE. This strain was used in the Examples presented herein.

A 413 base pair internal fragment of the gpE coding region was PCR amplified using the primer pair:

10 5' AGCTGGCCATTGCTCAGGTCTGAAG 3' (SEQ ID NO: 1)

 5' GTACTGTCCGGAATACACGACGATG 3' (SEQ ID NO:2)

and BL21(DE3) chromosomal DNA as template. The resulting fragment:

15 AGCTGGCCAT TGCTCAGGTC GAAGAGATGC AGGCAGTTTC TGCCGTGCTT AAGGGCAAAT
 ACACCATGAC CGGTGAAGCC TTCGATCCGG TTGAGGTGGA TATGGGCCGC AGTGAGGAGA
 ATAACATCAC GCAGTCCGGC GGCACGGAGT GGAGCAAGCG TGACAAGTCC ACGTATGACC
 CGACCGACGA **TATC**GAAGCC TACGCGCTGA ACGCCAGCGG TGTGGTGAAT ATCATCGTGT
 TCGATCCGAA AGGCTGGGCG CTGTTCCGTT CCTTCAAAGC CGTCAAGGAG AAGCTGGATA
 20 CCCGTCGTGG CTCTAATTCC GAGCTGGAGA CAGCGGTGAA AGACCTGGGC AAAGCGGTGT
 CCTATAAGGG GATGTATGGC GATGTGGCCA TCGTCGTGTA TTCCGGACAG TAC
 (SEQ ID NO:3)

PCR amplification product was TA cloned and sequence verified using
 25 standard techniques. Next, a functional copy of a chloramphenicol resistance gene was introduced into the EcoRV site centrally located and shown bolded in the cloned gpE sequence. The chloramphenicol interrupted gpE fragment construct was then used as a linear homologous recombination knock-out vector for the genetic knock-out of the lambda (DE3) gpE gene residing in *E.*
 30 *coli* host strain BL21(DE3). This knock-out vector was introduced into the host cell exactly as described by Kirill A. Datsenko and Barry Wanner, *Proc. Natl. Acad. Sci USA* 2000; 97:6640-6645, except the vector described herein was used. Putative gpE knock-outs were preliminarily identified by the ability to grow in the presence of 6 µg/ml chloramphenicol, and were subsequently

confirmed by PCR analysis. One such gpE knock-out of BL21(DE3) was banked and given the GSK designation ECC-023.

ECC-023 was tested for the presence of infectious phage particles in the very sensitive plaque assay. As shown in Table 1, the parental BL21(DE3) expressed barely detectable amounts of phage when not induced to do so, approximately 20 pfu, but nearly three orders of magnitude more when induced by the SOS response to genetic damage (UV irradiation). The gpE knock-out derivative ECC-023 however did not produce any evidence of infectious phage, even when treated to induce the SOS response. The data shows that the BL21(DE3) derivative ECC-023 does not produce any detectable infectious phage particles and accordingly is a suitable host cell strain for biopharmaceutical manufacturing.

Table 1: Production of infectious phage particles from *E. coli*.

	PFU/ml	
	Not Induced	SOS Induced
BL21(DE3)	21	10,000
ECC-023	0	0

Example 2

This example shows that culturing cells in a rich medium can prevent formation of a 6-PGL adduct of His-tagged proteins as compared to minimal medium.

E. coli BL21(DE3) transformed with plasmid pET28FabZSa, which encodes the gene for Hexa-his-FabZ, was grown in MCJK (minimal medium) or MCJKLB (rich medium) at 37°C until an OD₆₀₀ of 1.0 was reached. Medium compositions for MCJK and MCJKLB are described in Table 2.

Table 2: Medium compositions for production of Hexahis-FabZ

Component	MCJK	MCJKLB
K ₂ HPO ₄	56 mM	56 mM
(NH ₄) ₂ SO ₄	38 mM	38 mM
MgSO ₄	5 mM	5 mM
CaCl ₂	1 mM	1 mM
Trace metals*	1 mL/L	1 mL/L

Glucose	10 g/L	10 g/L
Yeast extract	none	5 g/L
Bacto-tryptone	none	10 g/L
*Trace metals: 161 mM FeCl ₂ , 2.7 mM Na ₂ MoO ₄ , 1.4 mM ZnSO ₄ , 2.5 mM MnCl ₂ , 3.2 mM CuSO ₄ , 3.4 mM CoCl ₂ , and 3.2 mM H ₃ BO ₃		

Isopropyl-beta-D-thiogalactopyranoside ("IPTG") was added to a final concentration of 1 mM and the cells were maintained at 37°C for four hours until harvest. Cells were collected by centrifugation at 16,000 x g for 10 min and lysed by gentle agitation in 10 mM Tris, pH 8.0, 1 mM Na₂EDTA, 10 µg/mL lysozyme and 25 U/mL Benzonase (Sigma). Cell debris was removed by centrifugation at 16,000 x g for 10 minutes and the recombinant protein was purified from the soluble extract with Ni-NTA resin in batch mode according to the manufacturer's recommendations (Qiagen Inc., Valencia, CA).

Heterologous proteins were analyzed for the presence of the gluconolactone modification by LC/MS analysis.

MGSSH₄ His-tag heterologous polypeptide is gluconoylated at a level of 34% of total recombinant protein when the culture is performed in minimal medium (MCJK) as shown in Table 3. When the medium is supplemented or made rich with yeast extract and tryptone, gluconoylated protein is not detectable, also shown in Table 3. Thus, the use of a richer medium can prevent formation of the 6-PGL adduct.

Table 3: Effect of minimal vs. rich medium on gluconoylation of a His-tagged protein expressed in *E. coli*

Vector	N-Terminus	Insert	Modified %	Host	Medium	Comments
pET28FabZSa	MGSSH ₆	FabZ	34%	BL21(DE3)	MCJK	minimal medium
pET28FabZSa	MGSSH ₆	FabZ	Not detectable	BL21(DE3)	MCJKLB	rich medium

Example 3

This example demonstrates that an internal lysine residue of a recombinant CXC chemokine (otherwise known as Gro-beta-T) can become gluconoylated when expressed in *E. coli*. The cDNA and amino acid sequences of human Gro-beta-T are provided in International Patent

Application, Publication No. WO 92/00327 (Jan. 9, 1992) as well as U.S. Patent No. 6,042,821 and U.S. Patent No. 6,413,510, incorporated herein by reference in their entirety.

Heterologous protein accumulation during production of a CXC chemokine (Gro-beta-T) was routinely monitored using a quantitative, high throughput reversed phase assay. This separation was interfaced with a high-performance electrospray time-of-flight ("ESI-TOF") mass spectrometer to provide a means of routinely monitoring formation of product related variants.

When expressed in the *E. coli* BL21(DE3) host, two unique product modifications were observed. Deconvolution of the mass spectra characterized the variants as exhibiting mass shifts of +178Da and +258 Da compared to native product at 7,542 Da.

Product derived from these fermentations was passed through a purification procedure. In-process samples were characterized using a high resolution reversed phase assay that is capable of resolving minor product variants. Liquid chromatography mass spectroscopy ("LCMS") analysis confirmed that the new product variants exhibited mass shifts of +258Da (ret. time ~14.8 min) and +178 Da (ret. time ~15.2 Da).

Published literature indicated that these +258 Da and +178 Da mass shifts had previously been observed in proteins expressed with hexa His-tags resulting from the addition of 6-PGL or gluconolactone to the N-terminal residue. The CXC chemokine (Gro-beta-T) was not expressed using a hexa His-tags. Furthermore, the molecule does not exhibit any histidine rich regions. To confirm that the species were product related, each variant was isolated and subjected to N-terminal sequencing. Sequencing confirmed proper product sequence and ensured that no hexa His-tag was present.

Variants were subjected to trypsin digestion and peptide mapping. Comparison with peptide maps generated using product standard revealed two new peaks in the tryptic map with the first peak eluting at 45.8 min (m/z 1094) and the second peak eluting at 46.5 min (m/z 1174). The new peptides were isolated and subjected to N-terminal sequencing which indicated that both had the same sequence (NIQSVKVK (SEQ ID NO:4)). The sequence homology

and presence of a 80 Da mass difference suggested that the species differed only by the presence of phosphorylation.

LCMS mass spectrometry analysis was performed on the peak with m/z 1174. The MS/MS experiment confirmed the peak has a sequence of
5 NIQSVKVK (SEQ ID NO:4). In addition, the y series fragment ions starting from y3 including y3, y4, y5, and y6 shown mass increase of 258 Da. However, the y2 ion did not show mass increase of 258 Da. This data indicated that the modification was on Lysine (no. 23 in the sequence) with mass increase of 258 Da.

10 To confirm that the modification observed was due to product gluconoylation, *in vitro* reactions were developed that employed reactive L-glucono-1,5-lactone or galactonic acid. Previous work had shown that these species were capable of inducing addition of gluconoyl species to the hexa His-tag [Geohegan, *et al.*].

15 Purified CXC chemokine (Gro-beta-T) was buffer exchanged into a TRIS buffer at pH 8.0. L-glucono-1,5-lactone or galactonic acid were added to a concentration of 450 mM and samples were incubated at room temperature for twenty minutes. Both lactones induced the same +178 Da modification of the CXC chemokine observed during expression in *E. coli*.

20

Example 4

This example illustrates the gluconoylation of internal lysine residues of a recombinant human interleukin (human IL-18) expressed in *E. coli*.

High resolution reversed phase HPLC coupled with ESI-TOF mass
25 spectrometry was employed to screen an interleukin product for 6-PGL adducts. Analysis of B-strain expressed interleukin yielded a product related species exhibiting a mass difference of +178 Da. Since the protein was expressed without a hexa His-tag, the modification was likely occurring at an internal lysine residue as had been observed with the CXC chemokine (see
30 Example 3).

High resolution reverse phase HPLC analysis of the interleukin molecule enabled identification of multiple product species exhibiting +178 Da mass

shifts at RT 21.0, 22.0, 23.0 minutes and an additional minor species exhibiting a +258 Da shift (RT ~27.5 minutes).

In vitro modification of the interleukin was also evaluated with L-glucono-1,5-lactone at pH 8.0, as described in the previous example. This reaction again yielded the same +178 Da modifications observed when the interleukin was expressed in B strain of *E. coli*.

Example 5

This example shows that culturing cells in rich medium prevents gluconoylation or PGL adduct formation of internal lysine residues of a recombinant protein. Three fed-batch fermentation processes were compared in this study. The difference between the fermentation runs was the batch medium and feed compositions used during the production phase. A rich medium was used in the Process I fermentation, while the second and third batches (Processes II and III) were performed with a minimal medium. Glycerol was used as feed medium in Process I and II, while glucose was used in Process III.

The fermentation process to produce a recombinant interleukin in *E. coli* was carried out in a fed-batch mode in a 15-liter fermenter. The fermentation was started as a batch process. The inoculum was prepared by aseptically transferring 0.5 mL of a glycerol stock culture into 1000 ml of PYE medium in a 2.8-L flask, as shown in Table 4.

Table 4. Seed medium composition for expansion of inoculum into fermenters.

Item	Batch Medium concentration
Yeast Extract	5 g/L
Phytone peptone	10 g/L
Sodium chloride	10 g/L
Dextrose	10 g/L
Kanamycin sulfate	50 mg/L

The culture was grown overnight at 27.5°C on a rotary shaker. The shake flask culture was then transferred into a fermenter containing 5 L of batch medium. The production medium consists of salts, amino acids, and kanamycin sulfate. Additionally, the rich medium is supplemented with high concentrations of yeast extract and phytone peptone, as shown in Table 5.

Table 5. Production stage medium composition for comparison of rich vs. minimal medium.

Item	Batch Medium Concentration		
	Process I	Process II	Process III
Yeast Extract	48 g/L	5.8 g/L	5.8 g/L
Phytone peptone	24 g/L	1.6 g/L	1.6 g/L
(NH ₄) ₂ SO ₄	none	5 g/L	5 g/L
NaCl	none	1.3 g/L	1.3 g/L
Dextrose	none	none	33.5 g/L
Glycerol	26 g/L	26 g/L	none
K ₂ HPO ₄	15.3 g/L	6 g/L	6 g/L
KH ₂ PO ₄	1.7 g/L	3 g/L	3 g/L
Trace metals*	1 mL/L	1 mL/L	1 mL/L
MgSO ₄	5 mM	5 mM	5 mM
CaCl ₂	1 mM	1 mM	1 mM
Kanamycin sulfate	30 mg/L	30 mg/L	30 mg/L
* Trace Metals solution: FeCl ₂ ·6H ₂ O, 37.8 g/L; Na ₂ MoO ₄ ·H ₂ O, 0.7 g/L; ZnSO ₄ ·7H ₂ O, 0.4 g/L; MnCl ₂ ·4H ₂ O, 0.5 g/L; CuSO ₄ ·5H ₂ O, 0.8 g/L; CoCl ₂ ·6H ₂ O, 0.8 g/L; H ₃ BO ₃ , 0.2 g/L.			

The pH of each medium was maintained at approximately 7.3 using ammonium hydroxide. Temperature was controlled at about 27.5°C. Feed medium, glycerol or dextrose was sterilized separately and aseptically connected to a fermenter using silicone rubber tubing.

Supply of feed medium was initiated when the initial batch amount in culture was depleted. A polarographic oxygen electrode monitored dissolved oxygen tension in the fermenter. Carbon feed rate was controlled in a cascade mode to keep constant dissolved oxygen tension above 20%. Aeration was maintained at 10 slpm and pressure at 7.0 psig over pressure. Agitation speed of 800 rpm was used from beginning to the end of the fermentation run. At an OD₅₅₀ of approximately 40 units, 100 mL of 1 mM IPTG was injected into culture to induce recombinant gene expression.

Reverse-phase HPLC analysis of the samples collected 24 hours post IPTG addition indicated reduction in the level of gluconolactone in the product. The absence of 6-PGL adduct in Process I, and its presence in Process II and III, indicates that the use of rich medium, and not glycerol carbon source, was responsible for elimination of the 6-PGL adduct. Table 6 summarizes the results of the analysis.

Table 6. Analysis of phosphogluconolactone adduct in three fermentation processes to produce a recombinant interleukin.

Process No.	phosphogluconolactone adduct on human interleukin (IL-18)
Process I	Absent
Process II	Present
Process III	Present

Example 6

This example shows that the K-12 strain of *E. coli* has 100-fold higher pgl activity than B strain.

6-Phosphogluconolactonase activity was measured in extracts of two different strains with BL12(DE3) as the parental one, ECC005 and ECO680, and two other strains originated from a K-12 genotype, ECO706 and ATG3995.

To culture the strains, 2-L shake flasks containing 1 L of PYE medium + 1% glucose and 50 µg/ml kanamycin were inoculated with 0.4 mL of cell suspension from frozen vials. Incubation was at 30°C, with an agitation of 220 rpm for 6 or 7.5 hours. Samples were taken at the indicated time points to measure the optical density at 550 nm and collect pellets to measure the pgl activity. Details of *in vitro* assay to measure the pgl activity is presented below.

The pgl activity was assayed fluorimetrically, at 340 nm and 25°C, in cell-free extracts. The cell-free extracts were prepared as previously described (Maitra and Lobo, *Journal of Biological Chemistry* 246: 475-488(1971)); with essentially the same resuspension buffers, 50 mM-HEPES pH 7.3 containing 5 mM-EDTA and 5 mM-β-mercaptoethanol, but cells were broken by sonication (5 cycles of 20 sec.).

The pgl was assayed using a previously published method (Sinha and Maitra *Journal of General Microbiology*, 1992; 138: 1865-1873) with some modifications. The assay consisted of a pre-incubation of 1 mL-mixture containing 50 μ M-glucose-6-phosphate, 0.5 mM-NADP⁺, and 1 unit of glucose-6-phosphate dehydrogenase in 100 mM-MES buffer, pH 6.5, containing 25 mM-KCl and 10 mM-MgCl₂. Once the reaction reached the plateau, it was followed by the addition of 2 units of 6-phosphogluconate dehydrogenase resulting in a slow increase in the absorbance due to the spontaneous hydrolysis of the 6-PGL formed during the pre-incubation step. At the addition of cell-free extracts, any significant increment in the fluorescence is because of the phosphoglunolactonase activity. All pgl activities were estimated in the linear range of the absorbance increase following addition of the cell-free extract.

The enzyme activity was estimated by subtracting the rate of spontaneous hydrolysis of 6-PGL. The enzyme activities were expressed in mmol NADPH per minute and per mg of total protein. Total protein was determined by the Bicinchoninic acid (BCA) Protein Assay (Pierce, Illinois, USA).

In the strains based parentally in a K-12 genotype, we have detected upwards of 100-fold more activity than in B strains.

Table 7 summarizes the results of the enzyme assays on the two strain backgrounds.

Table 7: Phosphogluconolactonase activity measured in K-12 and B strains of *E. coli*

"K" STRAINS			
	Cultivation	Activity	Sp. Hydrolysis
Strain	Time (h)	(mmol NADH/min/mg protein)	(mmol/min/mg protein)
ATCC 10798	5.5	1.061	0.0011
	6.5	2.899	0.0012
	7.5	2.584	0.0012
K-12 expressing a human interleukin (IL-18)	7.5	3.539	0.0011
"B" STRAINS			
	Cultivation	Activity	Sp. Hydrolysis
Strain	Time (h)	(mmol NADH/min/mg protein)	(mmol/min/mg protein)
ATCC 47092	5.5	0.028	0.0012
BL21(DE3) expressing a human interleukin (IL-18)	5.5	0.032	0.0012
	6.5	0.019	0.0011
	7.5	0.032	0.0012

5 Example 7

This example shows that expressing a heterologous polypeptide, a CXC chemokine (otherwise known as Gro-beta-T), in *E. coli* BL21 strain results in 6-PGL adduct, whereas expressing the same polypeptide in a K-12 strain prevents gluconoylation of internal lysines.

10 Ten fermentation runs were carried out using four different strains of *E. coli* constructed to recombinantly express a CXC chemokine. This example demonstrates the effect of host background versus promoter system on the presence of 6-PGL adduct formation of the recombinant protein by using two expression systems with each host cell background. Table 8 describes the

15 strains that were used.

Table 8: Host background and promoter systems used to express a CXC chemokine in *E. coli*.

Strain No.	Host Background	Promoter system
1	BL21 (DE3)	T7 polymerase
2	K-12 (DE3)	T7 polymerase
3	BL21 (DE3)	Lambda pL
4	K-12	Lambda pL

Fermentation to produce the CXC chemokine (Gro-beta-T) in *E. coli* was carried out in a fed-batch mode in a 15-liter fermenter. Fermentation was started as a batch process. Inoculum was prepared by aseptically transferring 0.75 mL of a glycerol stock culture into 100 mL of PYE medium in a 500 mL baffled flask. Culture was grown for 7 hours at 32.0°C on a rotary shaker. Shaken flask culture was then mixed with 1.0 L of PYE medium and transferred into a fermenter containing 8.0 L of batch medium. Production medium consisted of salts and either carbenicillin or kanamycin sulfate depending on the promoter. Media formulations for seed expansion are provided in Table 9, and medium formulation for production of CXC chemokine in *E. coli* are provided in Table 10.

Table 9: Medium formulation for seed expansion.

Component	Concentration
Yeast Extract	5 g/L
Phytone peptone	10 g/L
Sodium chloride	10 g/L
Dextrose	10 g/L
Kanamycin sulfate	50 mg/L

Table 10: Medium formulation for production of CXC chemokine in *E. coli*

Component	Concentration
Ammonium Sulfate	5 g/L
Potassium phosphate, Dibasic	6 g/L
Potassium phosphate, Monobasic	3 g/L
Sodium chloride	1.3 g/L
Dextrose	18 g/L
Magnesium sulfate	4.8 g/L
Biotin	1 mg/L
Trace Metals *	10 mL/L
Kanamycin sulfate	50 mg/L
	-or-
Carbenicillin	25 mg/L
* Trace Metals solution: FeCl ₂ ·6H ₂ O, 3.78 g/L; Na ₂ MoO ₄ ·H ₂ O, 0.7 g/L; ZnSO ₄ ·7H ₂ O, 0.4 g/L; MnCl ₂ ·4H ₂ O, 0.5 g/L; CuSO ₄ ·5H ₂ O, 0.8 g/L; CoCl ₂ ·6H ₂ O, 0.8 g/L; H ₃ BO ₃ , 0.2 g/L.	

pH of each medium was maintained at about 7.0 using ammonium hydroxide. Temperature was controlled at about 32.0°C and increased to about 37.5°C at induction. Feed medium and dextrose were sterilized separately and aseptically connected to a fermenter using silicone rubber
5 tubing.

Supply of feed medium was initiated when the initial batch amount in the culture was depleted. A polarographic oxygen electrode monitored dissolved oxygen tension in the fermenter. Carbon feed rate was controlled in a cascade mode to keep constant dissolved oxygen tension above about 25%. Aeration
10 was maintained at about 10 slpm and the pressure at about 7.0 psig over pressure. Agitation speed of about 400 rpm was used at the beginning and increased as required to maintain about 25% dissolved oxygen tension. At an OD₅₅₀ of approximately 14 units, 100 mL of 1.0 mM IPTG was injected into the culture, or the temperature was increased to 37.5°C to induce recombinant
15 gene expression.

None of the fermentation runs using a K-12 host background had detectable 6-PGL adduct formation on recombinantly expressed polypeptide, whereas runs using B strain in concert with T7 promoter all exhibited the presence of detectable 6-PGL adduct formation on recombinantly expressed
20 polypeptide. The three runs using B strain and the pL promoter did not have detectable adduct formation. These data demonstrate that expressing a recombinant protein in a host strain having pgl activity, e.g. K-12, may prevent 6-PGL adduct formation in recombinant proteins that are susceptible to this modification, see Example 3. The presence of 6-PGL adduct formation in CXC
25 chemokine expressed in *E. coli* B and K-12 strains is presented for each fermentation in Table 11.

Table 11: Presence of 6-PGL adduct on CXC chemokine expressed by T7 or pL promoter in *E. coli* B and K-12 strains.

Strain genotype	Promoter	Run No.	Gluconolactone adduct 5 hr post induction [% of product peak]
B	T7	1	21.7
		2	5.8
		3	4.2
		Average	10.6
K-12	T7	1	0
		2	0
		Average	0
B	pL	1	0
		2	0
		3	0
		Average	0
K12	pL	1	0
		2	0
		Average	0

Example 8

5 This example shows that expressing a heterologous polypeptide, human interleukin (human IL-18), in *E. coli* BL21 strain results in 6-PGL adduct formation, whereas expressing the same polypeptide in a K-12 strain will prevent 6-phosphogluconoylation of internal lysines.

10 *E. coli* BL21 (DE3) and K-12 strains were constructed to express a human interleukin (IL-18). Cultures were grown in minimal medium as described in Example . Monitoring for product modification with 6-PGL was conducted at various time points throughout the culture, using methods described in Example .

15 Results are expressed as peak area ratios of unmodified product to modified product. Higher numbers indicate a lesser proportion of gluconoylated product. It is evident that the extent of gluconoylation in BL21(DE3) strain is significantly greater than in K-12 strain. Phosphogluconoylation of a human

interleukin (IL-18) expressed in B and K-12 strains of *E. coli* is summarized in Table 12.

5 **Table 12: Phosphogluconoylation of a human interleukin expressed in B and K-12 strains of *E. coli***

<i>E. coli</i> strain	Time post induction (h)	Area ratio of unmodified product to modified product
K-12	16	58.4
	18	44.5
	20	N/d
	22	29.3
	24	30.0
BL21(DE3)	22	8.3
	24	7.7
N/d = modified product not detectable		

Example 9

This example illustrates that overexpression of heterologous *pgl* in *E. coli* host cells leads to increased metabolic conversion of 6-PGL to its product 6-phosphogluconate thereby reducing the pool of 6-PGL available for adduct formation. A *P. aeruginosa pgl* gene was cloned and engineered into a plasmid based inducible expression vector system that is compatible with *colE1* origin of replication based plasmids, such that two different plasmids may be maintained in the same host cell. The inducible expression level of *P. aeruginosa pgl* can be regulated at will, in a fashion independent of endogenous *E. coli* metabolic pathways and independent of the inducible expression of the recombinant protein of interest. Accordingly, recombinant *pgl* expression can be regulated such that the pool of 6-PGL was diminished below the level required for adduct formation, but not to the extent that host cell resources were substantially affected. Therefore, the level of the desired recombinant protein can be separately regulated to give very high expression levels.

Cloning of *P. aeruginosa* pgl.

P. aeruginosa pgl was cloned as follows. *P. aeruginosa* was obtained from the American Type Culture Collection (American Type Culture Collection, 12301 Parklawn Drive, Rockville MD 20852-1776): *Pseudomonas aeruginosa*, strain ATCC 27853. 5' and 3' PCR amplification primers were designed and synthesized to direct the PCR amplification of the entire pgl gene, including the region just upstream of the initiation codon ATG. The sequence of the sense and anti-sense amplification primers are:

10 5' **GGCCTCGAG**CTCGGTGGCCCTGGTGGCCC 3' (SEQ ID NO:4)
and
 5' **GCCCTCGAG**TCCGCCACTCAGGGGTACCAAT 3' (SEQ ID NO:5)

respectively. Bolded sequences indicate XhoI sites introduced into the gene to enable subsequent cloning steps.

It was additionally found that the *P. aeruginosa* gene is very GC-rich and will not PCR amplify under normal amplification conditions. It was found that PCR amplification requires the use of PCR amplification conditions that are optimized for GC-rich templates, specifically Advantage-GC cDNA Polymerase Mix (cat. 8419-1; BD Biosciences Clontech: Palo Alto, CA; USA). The corresponding pgl DNA sequence (SEQ ID NO:7) encoding the polypeptide SEQ ID NO:8 was PCR amplified from whole *P. aeruginosa* cells after 25 cycles of 94°C for 30 seconds followed by 68°C for 1.5 minutes. The amplification was then completed by a single incubation at 68°C for 3 minutes. The PCR product was isolated by agarose gel electrophoresis and column chromatography over a QIAquick Gel Extraction Kit (cat. 28704, Qiagen: Valencia, CA; USA). The amplified, gel purified pgl DNA was eluted in water and immediately cloned into the cloning vector pCR2.1 using a TOPO TA Cloning® kit (cat. K4550-40, Invitrogen: Carlsbad, CA; USA) and transformed into One Shot® TOP10 Chemically Competent *E. coli* (cat. C4040-06, Invitrogen: Carlsbad, CA; USA). Resulting amp^r colonies were screened for inserts by EcoRI digestion and electrophoresis of the products. Sequence

verified inserts were released from the cloning vector by XhoI digestion and purified using the QIAquick Gel Extraction Kit. pECO-1 expression vector DNA (BioCat 73552, GlaxoSmithKline: King of Prussia, PA;USA) was cut with Sall and treated with Calf Intestinal Alkaline Phosphatase (CIP) (cat M0290S, New England Biolabs:Beverly, MA; USA), and then purified using the QIAquick Gel Extraction Kit. The XhoI digested inserts and the Sall treated pECO-1 were ligated using T4 DNA ligase essentially as described by the manufacturer (cat. M0202S; New England Biolabs: Beverly, MA; USA). Two microliters (2 µl) of the ligation reaction was transformed into One Shot® TOP10 chemically Competent *E. coli* cells as described by the manufacturer (cat. C4040-06; Invitrogen: Carlsbad, CA; USA). Colonies were screened for the presence pgl inserts in the correct orientation by PCR. Clone pECO-1pglcl2-13 was selected for further study as set forth below.

The resulting construct is based on the pACYC184 plasmid backbone, and comprises the following genetic functional elements: (1) p15A ori, which allows plasmid episomal maintenance in the same host cell as heterologous plasmids with the colE1-type ori element; (2) chloramphenical^r selectable marker; (3) a tetracycline inducible promoter upstream of a multiple cloning site; (4) the full length *P. aeruginosa* pgl gene.

The final construct, pECO-1pglcl2-13, was transformed as described above into BL21 (DE3) cells expressing a human interleukin for further study. The DNA sequence of pECO-1pglcl2-13 sequence is presented as SEQ ID NO:9 and the restriction map of pECO-1pglcl2-13 is presented in Figure 1.

Cultures were performed as described in Example 3. Analysis for 6-PGL adduct was performed as described in Example 4. Phosphogluconolactonase activity was measured as described in Example 6. Additional strains expressing the human interleukin (IL-18) that were examined in the study include BL21 (DE3) without pECO-1pglcl2-13 and K-12. The strains with the pgl plasmid were examined with and without the addition of anhydrotetracycline at 20 ng/mL. A summary of the presence of absence of 6-PGL adduct formation in cells expressing pgl is summarized in Table 13 as shown below.

Table 13: Impact of pgl expression on phosphogluconoylation of a human interleukin

Strain	Maximum pgl activity IU/min/g DCW	6-PGL adduct formation on human interleukin (IL-18)
BL21 (DE3)	0.002	Present
BL21 (DE3) pECO-1pglcl2-13, no tet	0.56 ± 0.13	Absent
BL21 (DE3) pECO-1pglcl2-13, tet induced	0.64 ± 0.11	Absent
K-12	0.96 ± 0.14	Absent
DCW=dry cell weight		

This example has demonstrated that co-expression of *Pseudomonas* phosphogluconolactonase with the human interleukin (IL-18) successfully prevents formation of the 6-PGL adduct in the B strain of *E. coli*.

Example 10

Human interleukin-18 (IL-18) is an immunomodulatory cytokine that is being developed as an anti-cancer agent for the treatment of renal cell carcinoma and malignant melanoma. Descriptions of human and murine IL-18 are presented in the following U.S. patents: U.S. Pat. No. 6,582,689, U.S. Pat. No. 5,914,253, U.S. Pat. No. 5,879,942, U.S. Pat. No. 5,912,324, U.S. Pat. No. 5,914,253, U.S. Pat. No. 6,060,283, U.S. Pat. No. 6,087,116, and U.S. Pat. No. 6,214,584, which are incorporated herein by reference in their entirety. IL-18 is believed to stimulate the immune system, promote Fas-induced tumor cell death and cell mediated immunity. The polypeptide sequence of IL-18 (SEQ ID NO:10) may be produced in *E. coli* BL21(DE3). It may be expressed from the polynucleotide sequence for pro-IL18 (SEQ ID NO:11), which is further processed to mature IL-18 by a processing enzyme, Caspase 5, co-expressed in the same cell.

6-Phosphogluconolactonase from Gram-negative bacterium, *Pseudomonas aeruginosa*, was cloned into a BL21(DE3) strain. Production of IL-18 in this strain produces IL-18 with no detectable adduct formation resulting in a direct increase in the yield of the desired product. Furthermore, the

correction of the pgl deficiency has also resulted in >10% increase in specific productivity. Thus, the combined effect of product quality and specific productivity improvements by the use of this modified production strain has translated into a >25% increase in titer yield at the fermentation stage. It is anticipated that the elimination of adduct formation will have a direct, positive impact on the purification process and further increase the overall process yield.

Example 11

Gluconoylation of IL-18 was monitored by HPLC analyses on IL-18 produced in BL21(DE3) cells with and without co-expression of pgl. Adduct formation was detected as a shoulder peak eluting approximately two minutes after purified IL-18. When IL-18 was expressed in and purified from *E. coli* strain BL21DE3 (pgl minus), the main peak area (i.e., area of the peak for IL-18 having no detectable gluconoyl adduct formation) for IL-18 was approximately 56%. While expression and purification of IL-18 in BL21(DE3) (pgl plus) cells produced a main peak area of about 88% and showed no adduct formation based on the High Resolution HPLC assay."

Example 12

Two vectors were created comprising polynucleotides that encode pro-IL-18 (SEQ ID NO: 11), Caspase 5 (SEQ ID NO:12). Both were pET vectors wherein polypeptide production was induced using aT7 promoter. One vector also comprised a polynucleotide encoding pgl from *P. aeruginosa* (SEQ ID NO:7) that was induced by the same promoter as pro-IL-18. The entire sequence of the pET vector comprising pro-IL-18 and Caspase 5 is presented in SEQ ID NO:13. A restriction map of this vector is presented in Figure 2. The entire sequence of the pET vector comprising pro-IL-18, Caspase 5 and pgl is presented in SEQ ID NO:14. A restriction map of this vector is presented in 3. When IL-18 was expressed in *E. coli* BL21(DE3) cells using these vectors, the amount of recoverable IL-18 was greatly improved when the polypeptide was co-expressed with pgl compared with the expression of IL-18 without pgl. The

amount of recovered IL-18 obtained from each expression vector in *E. coli* BL21(DE3) cells is presented in Table 14.

Table 14: IL-18 Maximum Titer Produced in "B" Strain *E. coli* with and without Co-expression of pgl

Strain*	pgl gene	Maximum Titer (g/L)
RBB057	No	4.32 (+/- 0.4)
RBB059	Yes	6.78 (+/- 0.1)
*Both strains are <i>E. coli</i> B strain		

5

All publications and references, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference in their entirety as if each individual publication or reference were specifically and individually indicated to be incorporated by reference herein as being fully set forth. Any patent application to which this application claims
10 priority is also incorporated by reference herein in its entirety in the manner described above for publications and references.

Claims

1. A method for preventing gluconoylation of a polypeptide expressed in a microorganism, comprising growing said microorganism in rich culture medium.
- 5 2. The method of claim 1, wherein the microorganism does not demonstrate significant 6-phosphogluconolactonase activity when grown in minimal medium.
3. The method of claim 1, wherein the microorganism is *E. coli*.
4. The method of claim 3, wherein the *E. coli* is B strain.
- 10 5. The method of claim 1, wherein the rich culture medium comprises a complex nitrogen source.
6. The method of claim 5, wherein the rich culture medium is capable of maintaining cell growth at ratio of 1:1 for concentration of complex nitrogen source to cell density.
- 15 7. The method of claim 5, wherein the complex nitrogen source comprises tryptone.
8. The method of claim 5, wherein the complex nitrogen source comprises peptone.
9. The method of claim 5, wherein the complex nitrogen source comprises
20 yeast extract.
10. The method of claim 1, wherein the culture medium is Superbroth.
11. The method of claim 10, wherein the Superbroth medium is doubly concentrated.
12. The method of claim 1, wherein the microorganism is transfected with a
25 recombinant DNA molecule encoding a heterologous polypeptide.
13. A method for preventing gluconoylation of a polypeptide expressed in *E. coli* comprising fermenting a K strain variety of *E. coli* for the expression of the polypeptide.
14. The method of claim 13, wherein the K strain demonstrates 100-fold
30 higher phosphogluconolactonase activity compared with B strain grown under the same conditions.
15. The method of claim 14, wherein the K strain is K-12.

16. A method for preventing gluconoylation of polypeptides expressed in a microorganism, comprising introducing DNA into the microorganism, wherein the DNA encodes a polypeptide that demonstrates 6-phosphogluconolactonase activity.
- 5 17. The method of claim 16, wherein the microorganism is *E. coli*.
18. The method of claim 16, wherein the DNA comprises DNA encoding a 6-phosphogluconolactonase enzyme.
19. The method of claim 18, wherein the DNA encoding the 6-phosphogluconolactonase enzyme has at least 70% sequence identity to DNA
- 10 encoding 6-phosphogluconolactonase from *Pseudomonas*.
20. The method of claim 19, wherein the *Pseudomonas* is *P. aeruginosa*.
21. The method of claim 18, wherein the DNA encoding the 6-phosphogluconolactonase enzyme has at least 90% sequence identity to SEQ ID NO:7.
- 15 22. The method of claim 18, wherein the DNA encoding the 6-phosphogluconolactonase enzyme has at least 95% sequence identity to SEQ ID NO:7.
23. The method of claim 18, wherein the 6-phosphogluconolactonase enzyme has an amino acid sequence having at least 90% sequence identity to
- 20 SEQ ID NO:8.
24. The method of claim 18, wherein the 6-phosphogluconolactonase enzyme has an amino acid sequence having at least 95% sequence identity to SEQ ID NO:8.
25. The method of claim 18, wherein the DNA encoding the 6-phosphogluconolactonase enzyme comprises the sequence set forth in SEQ ID
- 25 NO:7.
26. The method of claim 16, wherein the DNA is recombinant DNA.
27. The method of claim 16, wherein the DNA is transformed into the genomic DNA of the microorganism.
- 30 28. A microorganism capable of preventing gluconoylation of polypeptides.

29. The microorganism of claim 28, wherein the microorganism comprises DNA that encodes a polypeptide that demonstrates 6-phosphogluconolactonase activity.
30. The microorganism of claim 28, wherein the microorganism comprises
5 DNA that encodes 6-phosphogluconolactonase.
31. The microorganism of claim 28, wherein the DNA that encodes 6-phosphogluconolactonase has at least 90% sequence identity to DNA encoding a 6-phosphogluconolactonase enzyme from *Pseudomonas* and wherein the microorganism is not *Pseudomonas*.
- 10 32. The microorganism of claim 28, wherein the DNA that encodes 6-phosphogluconolactonase has at least 95% sequence identity to DNA encoding a 6-phosphogluconolactonase enzyme from *Pseudomonas* and wherein the microorganism is not *Pseudomonas*.
33. The microorganism of claim 31, wherein the DNA that encodes 6-
15 phosphogluconolactonase is from *P. aeruginosa*.
34. The microorganism of claim 28, wherein the microorganism is a strain of *E. coli*.
35. The microorganism of claim 31, wherein the microorganism is a strain of *E. coli* and wherein the DNA that encodes 6-phosphogluconolactonase is
20 incorporated into the genome of the microorganism.
36. An isolated polynucleotide comprising a polynucleotide having at least a 90% identity to the polynucleotide set forth in SEQ ID NO:7.
37. The isolated polynucleotide of claim 36, comprising a polynucleotide having at least a 90% identity to a polynucleotide encoding a polypeptide
25 comprising amino acids having at least 90% sequence identity to SEQ ID NO:8.
38. The isolated polynucleotide of claim 36, wherein the DNA encodes a protein demonstrating 6-phosphogluconolactonase activity.
39. The isolated polynucleotide of claim 36, wherein the DNA sequence is set forth in SEQ ID NO:7.
- 30 40. The isolated polynucleotide of claim 36, wherein the DNA sequence has at least 90% sequence identity to DNA encoding 6-phosphogluconolactonase from *P. aeruginosa*.

41. The isolated polynucleotide of claim 35, further comprising a polynucleotide that encodes human interleukin-18.
42. An isolated polynucleotide, comprising a polynucleotide having at least a 95% identity to the polynucleotide set forth in SEQ ID NO:7.
- 5 43. A method of improving polypeptide crystal formation comprising expressing said polypeptide according to the method of claim 1.
44. A method of improving polypeptide crystal formation comprising expressing said polypeptide according to the method of claim 16.
45. The method of claim 1, further comprising improving growth efficiency
10 wherein said polypeptide demonstrates an increased titer yield at fermentation stage compared with gluconoylated polypeptide.
46. The method of claim 16, further comprising improving growth efficiency wherein said polypeptide demonstrates an increased titer yield at the fermentation stage compared with gluconoylated polypeptide.
- 15 47. A method of producing a human interleukin comprising co-expressing said human interleukin in a microorganism with an enzyme having 6-Phosphogluconolactonase ("pgl") activity.
48. The method of claim 47, wherein the human interleukin is IL-18.
49. The method of claim 47, wherein the microorganism is *E. coli*.
- 20 50. The method of claim 49, wherein the pgl is encoded by a polynucleotide that is transformed into genome of said *E. coli*.
51. A method of producing a human interleukin comprising expressing said human interleukin in a microorganism that is grown in a rich culture medium.
52. The method of claim 51, wherein the human interleukin is IL-18.
- 25 53. The method of claim 51, wherein the microorganism is *E. coli*.
54. The method of claim 51, wherein the rich culture medium comprises phytone peptone.
55. The method of claim 51, wherein the rich culture medium comprises bacto yeast extract.
- 30 56. A microorganism completely free of infectious lambda phage expression.
57. The microorganism of claim 56, wherein lambda phage capsid structural protein, gpE, is deleted or disrupted.

58. The microorganism of claim 56, wherein the microorganism is *E. coli*.
59. The microorganism of claim 56, comprising a T7 RNA polymerase gene.