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Fortsættes ...

DESCRIPTION

[0001] The invention relates to a recombinant bacterial host strain, particularly *E. coli*. The invention also relates to a method for producing a protein of interest in such a cell.

Background of the Invention

[0002] Bacterial cells, such as *E. coli*, are commonly used for producing recombinant proteins. There are many advantages to using bacterial cells, such as *E. coli*, for producing recombinant proteins particularly due to the versatile nature of bacterial cells as host cells allowing the gene insertion via plasmids. *E. coli* have been used to produce many recombinant proteins including human insulin.

[0003] Despite the many advantages to using bacterial cells to produce recombinant proteins, there are still significant limitations including the difficulty of producing protease sensitive proteins. Proteases play an important role in turning over old, damaged or mis-folded proteins in the *E. coli* periplasm and cytoplasm. Bacterial proteases act to degrade the recombinant protein of interest, thereby often significantly reducing the yield of active protein.

[0004] A number of bacterial proteases have been identified. In *E. coli* proteases including Protease III (ptr), DegP, OmpT, Tsp, prc, ptrA, ptrB, pepA-T, tsh, espc, eatA, clpP and lon have been identified.

[0005] Tsp (also known as Prc) is a 60kDa periplasmic protease. The first known substrate of Tsp was Penicillin-binding protein-3 (PBP3) (Determination of the cleavage site involved in C-terminal processing of penicillin-binding protein 3 of *Escherichia coli*; Nagasawa H, Sakagami Y, Suzuki A, Suzuki H, Hara H, Hirota Y. J Bacteriol. 1989 Nov;171(11):5890-3 and Cloning, mapping and characterization of the *Escherichia coli* Tsp gene which is involved in C-terminal processing of penicillin-binding protein 3; Hara H, Yamamoto Y, Higashitani A, Suzuki H, Nishimura Y. J Bacteriol. 1991 Aug;173 (15):4799-813) but it was later discovered that the Tsp was also able to cleave phage tail proteins and, therefore, it was renamed as Tail Specific Protease (Tsp) (Silber et al., Proc. Natl. Acad. Sci. USA, 89: 295-299 (1992)). Silber et al. (Deletion of the prc(tsp) gene provides evidence for additional tail-specific proteolytic activity in *Escherichia coli* K-12; Silber, K.R., Sauer, R.T.; Mol Gen Genet 1994 242:237-240) describes a prc deletion strain (KS1000) wherein the mutation was created by replacing a segment of the prc gene with a fragment comprising a Kan^r marker.

[0006] The reduction of Tsp (prc) activity is desirable to reduce the proteolysis of proteins of interest. However, it was found that cells lacking protease prc show thermosensitive growth at low osmolarity. Hara et al isolated thermoresistant revertants containing extragenic suppressor (spr) mutations (Hara et al., Microbial Drug Resistance, 2: 63-72 (1996)). Spr is an 18kDa

membrane bound periplasmic protease and the substrates of spr are Tsp and peptidoglycans in the outer membrane involved in cell wall hydrolysis during cell division. The spr gene is designated as UniProtKB/Swiss-Prot P0AFV4 (SPR_ECOLI).

[0007] Improved protease deficient strains comprising a mutant spr gene have been described. Chen et al describes the construction of *E. coli* strains carrying different combinations of mutations in prc (Tsp) and another protease, DegP, created by amplifying the upstream and downstream regions of the gene and ligating these together on a vector comprising selection markers and a sprW174R mutation (High-level accumulation of a recombinant antibody fragment in the periplasm of *Escherichia coli* requires a triple-mutant (Δ DegP Δ prc sprW174R) host strain (Chen C, Snedecor B, Nishihara JC, Joly JC, McFarland N, Andersen DC, Battersby JE, Champion KM. *Biotechnol Bioeng.* 2004 Mar 5;85(5):463-74). The combination of the Δ DegP, Δ prc and sprW174R mutations were found to provide the highest levels of antibody light chain, antibody heavy chain and F(ab')₂-LZ. EP1341899 discloses an *E. coli* strain that is deficient in chromosomal DegP and prc encoding proteases DegP and Prc, respectively, and harbors a mutant spr gene that encodes a protein that suppresses growth phenotypes exhibited by strains harboring prc mutants.

[0008] Other improved protease deficient strains containing mutations in both Tsp and spr have been described in WO2011/086136, and in WO 2012/013930.

[0009] Strains disclosed in WO02/48376 are lac⁻ and cannot grow in cultures where thymidine, fucose or maltose are employed as the carbon source. This can be a severe disadvantage for strains intended for use on a commercial scale. There may be further disadvantages associated with the strains, for example the lack of production of alkaline phosphatase. The latter is a periplasmic protein involved in phosphate utilization from culture media.

[0010] Certain proteins exhibit peptidyl-prolyl isomerase and/or isomerase activity and/or chaperone activity and have been found to provide advantageous properties when employed in cell lines employed for recombinant protein expression.

[0011] The present invention provides new bacterial strains carrying both Tsp and spr mutations and at least one gene encoding a protein or proteins capable of facilitating protein folding which provide advantageous means for producing recombinant proteins.

Summary of the Invention

[0012] Disclosed herein is a recombinant gram-negative bacterial cell comprising:

1. a. a mutant spr gene encoding a spr protein having a mutation at one or more amino acids selected from D133, H145, H157, N31, R62, I70, Q73, C94, S95, V98, Q99, R100, L108, Y115, V135, L136, G140, R144 and G147 and
2. b. a gene or genes capable of expressing or overexpressing one or more proteins

capable of facilitating protein folding, such as FkpA, Skp, SurA, PPIA and PPID

wherein the cell has reduced Tsp protein activity compared to a wild-type cell.

[0013] Further disclosed is a recombinant gram-negative bacterial cell encoding:

1. a. a mutant spr gene encoding a spr protein having a mutation at one or more amino acids selected from D133, H145, H157, N31, R62, I70, Q73, C94, S95, V98, Q99, R100, L108, Y115, V135, L136, G140, R144 and G147,
2. b. a gene or genes capable of expressing or overexpressing one or more proteins capable of facilitating protein folding, such as FkpA, Skp, SurA, PPIA and PPID,
3. c. a gene capable of expressing a protein of interest, for example an antibody or binding fragment thereof

wherein the cell has reduced Tsp protein activity compared to a wild-type cell and the remainder of cell genomic DNA is isogenic with the wild-type cell from which the recombinant cell was derived.

[0014] In one instance, the cell's genome is isogenic to a wild-type bacterial cell except for the mutated spr gene, the modification required to reduce Tsp protein activity compared to a wild-type cell and the gene or genes expressing a protein capable of facilitating protein folding.

[0015] Further disclosed herein is a recombinant gram-negative bacterial cell having reduced Tsp protein activity compared to a wild-type cell and comprising a mutant spr gene encoding a spr protein, wherein the cell's genome is isogenic to a wild-type bacterial cell except for the modification required to reduce Tsp protein activity compared to a wild-type cell, the mutated spr gene and the gene or genes introduced for expressing a protein capable of facilitating protein folding.

[0016] The cells disclosed herein show advantageous growth and protein production phenotypes.

[0017] Additionally disclosed herein is a method for producing a protein of interest comprising expressing the protein of interest in a recombinant gram-negative bacterial cell as defined above.

Brief Description of the Drawings

[0018]

Figure 1

shows the results of fermentations on the 5L scale performed with various combinations of host cells and "chaperone". W3110 is a wild-type *E coli* strain. The various combinations were: wild type with no chaperone; wild-type with FkpA and Skp; MXE016

mutant spr and Δ Tsp as published in WO2011/086136; MXE016 and FkpA; MXE016 and Skp; MXE016 and FkpA and Skp; MXE017 disclosed in WO2011/086136; MXE017 and FkpA and Skp

Figure 2

shows the results of feed rate variation experiments at post induction feed rates 5.4, 6.0 and 7.0g/h, for MXE016 the majority of the additional Fab' made at higher feed rates was lost in the supernatant.

Figures 3A,B

show cell viability (3A) and Fab' titres (3B) for MXE016 +/- FkpA.

Figure 4

shows the primary recovery data for 20L pilot scale production.

Figure 5

shows the primary recovery on SDS-PAGE stained gel under non-reducing conditions of a 20L pilot scale production. Other than the FkpA related bands the protein profile appears very similar between the two strains.

Figure 6

shows a His-tag western blot under non-reducing conditions for a 20L pilot scale process. Full length FkpA detected and corresponds to the ~30kDa band and no signal was detected in MXE016 alone as expected.

Figure 7A-C

shows various mutations in various genes

Figure 7D

shows a diagrammatic representation of the creation of a vector comprising a polynucleotide sequence encoding a light chain of an antibody (LC), a heavy chain of an antibody (HC), a FkpA polynucleotide sequence and/or Skp polynucleotide

Figure 8

shows various polynucleotide and amino acid sequences

Brief Description of the Sequences**[0019]**

SEQ ID NO:1 is the DNA sequence of the wild-type Tsp gene including the 6 nucleotides ATGAAC upstream of the start codon.

SEQ ID NO:2 is the amino acid sequence of the wild-type Tsp protein.

SEQ ID NO:3 is the DNA sequence of a mutated knockout Tsp gene including the 6 nucleotides ATGAAT upstream of the start codon.

SEQ ID NO:4 is the DNA sequence of the wild-type Protease III gene.

SEQ ID NO:5 is the amino acid sequence of the wild-type Protease III protein.

SEQ ID NO:6 is the DNA sequence of a mutated knockout Protease III gene.

SEQ ID NO:7 is the DNA sequence of the wild-type DegP gene.

SEQ ID NO:8 is the amino acid sequence of the wild-type DegP protein.

SEQ ID NO:9 is the DNA sequence of a mutated DegP gene.

SEQ ID NO:10 is the amino acid sequence of a mutated DegP protein.

SEQ ID NO: 11 is the sequence of the 5' oligonucleotide primer for the region of the mutated DegP gene comprising the Ase I restriction site.

SEQ ID NO: 12 is the sequence of the 3' oligonucleotide primer for the region of the mutated DegP gene comprising the Ase I restriction site.

SEQ ID NO: 13 is the sequence of the 5' oligonucleotide primer for the region of the mutated Tsp gene comprising the Ase I restriction site.

SEQ ID NO: 14 is the sequence of the 3' oligonucleotide primer for the region of the mutated Protease III gene comprising the Ase I restriction site.

SEQ ID NO: 15 is the sequence of the 5' oligonucleotide primer for the region of the mutated Protease III gene comprising the Ase I restriction site.

SEQ ID NO: 16 is the sequence of the 3' oligonucleotide primer for the region of the mutated Tsp gene comprising the Ase I restriction site.

SEQ ID NO: 17 is the DNA sequence of the wild-type spr gene.

SEQ ID NO: 18 is the sequence of the wild-type spr gene including the signal sequence which is the first 26 amino acid residues.

SEQ ID NO: 19 is the sequence of the non-mutated spr gene without the signal sequence.

SEQ ID NO: 20 is the nucleotide sequence of a mutated OmpT sequence comprising D210A and H212A mutations.

SEQ ID NO: 21 is the amino acid sequence of a mutated OmpT sequence comprising D210A and H212A mutations.

SEQ ID NO: 22 is the nucleotide sequence of a mutated knockout OmpT sequence.

SEQ ID NO: 23 shows the sequence of the OmpA oligonucleotide adapter.

SEQ ID NO: 24 shows the oligonucleotide cassette encoding intergenic sequence 1 (IGS1) for *E. coli* Fab expression.

SEQ ID NO: 25 shows the oligonucleotide cassette encoding intergenic sequence 2 (IGS2) for *E. coli* Fab expression.

SEQ ID NO: 26 shows the oligonucleotide cassette encoding intergenic sequence 3 (IGS3) for *E. coli* Fab expression.

SEQ ID NO: 27 shows the oligonucleotide cassette encoding intergenic sequence 4 (IGS4) for *E. coli* Fab expression.

SEQ ID NO: 28 is the DNA sequence of the wild-type FkpA gene.

SEQ ID NO: 29 is the protein sequence of the wild-type FkpA gene.

SEQ ID NO: 30 is the DNA sequence of the FkpA his tagged gene.

SEQ ID NO: 31 is the protein sequence of the FkpA his tagged gene.

SEQ ID NO: 32 is the DNA sequence of the wild-type skp gene.

SEQ ID NO: 33 is the protein sequence of the wild-type skp gene.

SEQ ID NO: 34 is the DNA sequence of the skp his tagged gene.

SEQ ID NO: 35 is the protein sequence of the skp his tagged gene.

SEQ ID NO: 36 to 74 show various amino acid and DNA sequences of FcRn antibodies or fragments thereof, which are suitable for expression in the cell line of the present invention. In particular SEQ ID NO: 50 is the amino acid sequence of the light chain variable region of an anti-FcRn antibody light chain 1519gH20 and SEQ ID NO:58 is the amino acid sequence of the heavy chain variable region of an anti-FcRn antibody heavy chain 1519gH20.

Detailed Description of the Preferred Embodiments of the Invention

[0020] The present inventors have provided improved recombinant gram-negative bacterial cells suitable for expressing a recombinant protein of interest.

[0021] In one embodiment the protein is an antibody or binding fragment thereof, in particular a therapeutic antibody.

[0022] In particular, the inventors have provided improved recombinant gram-negative bacterial cells suitable for expressing a recombinant protein of interest by incorporating one or more gene or genes, encoding a protein for facilitating protein folding, into gram-negative bacterial cells carrying a mutated Tsp gene and a mutated spr gene

[0023] In one embodiment the gene or genes, encoding the protein for facilitating protein folding, are integrated into the cells genome, for example to provide a stable cell line. In one embodiment a recombinant protein for expression (such as a therapeutic protein) is

transfected into a stable cell line to provide expression of the desired recombinant protein.

[0024] In one embodiment the gene or genes, encoding a protein for facilitating protein folding, are provided on one or more plasmids, for example the plasmids are transiently transfected into a cell to provide a cell line of the present disclosure.

[0025] In one embodiment the gene or genes, encoding a protein for facilitating protein folding, are provided on a plasmid also containing the coding sequence for a recombinant protein of interest.

[0026] In one embodiment the gene or genes, encoding a protein for facilitating protein folding, are provided on a plasmid that does not contain the coding sequence for a recombinant protein of interest.

[0027] In one embodiment the invention provides new strains having improved cell growth phenotype compared to wild-type bacterial cells and cells carrying just a mutated Tsp gene or a mutated Tsp and a mutated spr gene.

[0028] The cells of the present invention possess many advantages. The inventors have surprisingly found that cells according to the present disclosure may exhibit increased cell viability compared to a wild-type cell or a cell comprising a mutated Tsp gene and mutated spr gene.

[0029] Cell viability is of particular importance in practical terms because cells that are not viable tend to lyse and create DNA debris in the culture. This DNA debris increases the, difficulty, cost and expense of purifying the desired protein. Therefore minimizing the DNA debris from lysed non-viable cells is a significant issue in manufacturing recombinant proteins efficiently, see for example US 6,258,560.

[0030] Cell viability may be measured by any one of a number of routine techniques, for example employing a fluorescent dye and FACS analysis or similar.

[0031] Specifically, the cells according to the disclosure generally exhibit reduced cell lysis phenotype compared to cells carrying a mutated Tsp gene and a mutated spr gene.

[0032] Furthermore, the new strains may reduce leakage of protein from the cells and allow prolonged periplasmic accumulation compared to cells carrying a mutated Tsp gene and mutated spr gene. This is particularly important because, for example where total expression levels of target protein are similar but more protein is accumulated into the periplasm or less protein is accumulated in the supernatant because the strain is less leaky than cells with these less leaky properties will generally be more suitable for plant scale production because they facilitate protein recovery.

[0033] Further, the cells according to the present disclosure may exhibit increased yield of a

protein of interest compared to a wild-type bacterial cell or a cell comprising a mutated Tsp gene and a mutated spr gene in the absence of a gene or genes encoding a protein such as FkpA. The improved protein yield may be the periplasmic protein yield and/or the supernatant protein yield. In one embodiment the cells of the present invention show improved periplasmic protein yield compared to a cell carrying a mutated Tsp gene and mutated spr gene due to reduced leakage from the cell.

[0034] The recombinant bacterial cells may be capable of faster rate of production of a protein of interest and, therefore, the same quantity of a protein of interest may be produced in a shorter time compared to a wild-type bacterial cell or a cell comprising a mutated Tsp gene and a mutated spr gene. The faster rate of production of a protein of interest may be especially significant over the initial period of growth of the cell, for example over the first 5, 10, 20 or 30 hours post induction of protein expression.

[0035] The cells according to the present invention preferably express a maximum yield in the periplasm and/or media of approximately 1.0g/L, 1.5g/L, 1.8g/L, 2.0g/L, 2.4g/L, 2.5g/L, 3.0g/L, 3.5g/L or 4.0g/L of a protein of interest.

[0036] Additionally the expression of a protein or proteins that facilitates folding further optimizes the expression by maximizing the protein provided with proper folding. The skilled person is well aware that appropriate folding is essential for biological function and thus isolating protein with the desired folding is vitally important. This is particularly important when the protein is expressed in a gram-negative cell because the protein expressed will not be natural to cell and thus the cell may not automatically express the protein with the appropriate folding. Inappropriate folding may express itself as aggregation or other impurities. The isolation of the desired protein may require extensive purification, which has cost implications and may also result in a low yield of the desired protein. Maximizing the amount of properly folded protein expressed minimizes the amount of purification required and may optimize the useable yield and thus is advantageous.

[0037] Advantages associated with the expression of a protein that facilitates folding include one or more of the following: Higher titre (e.g. increased to about 1.05g/L in comparison to wild-type 0.5g/L); Higher viability at harvest (e.g. >95%); Increased titre with increasing feed rate (better prospects for process development); Higher titre at commercial production scales such as 20L scale and higher viability at harvest; and Easier clarification of extract, in particular at 20L scale.

[0038] The cells provided by the present invention have reduced protease activity of Tsp compared to a wild-type cell, which may reduce proteolysis of a protein of interest, particularly proteins of interest which are proteolytically sensitive to Tsp. Therefore, the cells provided by the present invention may provide higher yield of the intact proteins, preferably of the protein of interest and a lower yield, or preferably no proteolytic fragments of proteins, preferably of the protein of interest, compared to a wild-type bacterial cell.

[0039] Disclosed herein are cells that carry only the minimal mutations to the genome required to introduce the modifications according to the present disclosure. The bacterial cell may only differ from a wild-type bacterial cell by the one or more mutations to the spr gene and the modification required to reduce Tsp protein activity compared to a wild-type cell because for example the gene or genes encoding a protein for facilitating protein folding may be introduced transiently into the cell, such as on a plasmid. The cells disclosed herein do not carry any other mutations which may have deleterious effects on the cell's growth and/or ability to express a protein of interest.

[0040] Accordingly, one or more of the recombinant host cells disclosed herein may exhibit improved protein expression and/or improved growth characteristics compared to cells comprising further genetically engineered mutations to the genomic sequence. The cells disclosed herein are also more suitable for use to produce therapeutic proteins compared to cells comprising further disruptions to the cell genome.

[0041] The skilled person would easily be able to test a candidate cell clone to see if it has the desired yield of a protein of interest using methods well known in the art including a fermentation method, ELISA and protein G HPLC. Suitable fermentation methods are described in Humphreys D P, et al. (1997). Formation of dimeric Fabs in *E. coli*: effect of hinge size and isotype, presence of interchain disulphide bond, Fab' expression levels, tail piece sequences and growth conditions. *J. IMMUNOL. METH.* 209: 193-202; Backlund E. Reeks D. Markland K. Weir N. Bowering L. Larsson G. Fedbatch design for periplasmic product retention in *Escherichia coli*, *Journal Article. Research Support, Non-U.S. Gov't Journal of Biotechnology.* 135(4):358-65, 2008 Jul 31; Champion KM. Nishihara JC. Joly JC. Arnott D. Similarity of the *Escherichia coli* proteome upon completion of different biopharmaceutical fermentation processes. [*Journal Article*] *Proteomics.* 1(9):1133-48, 2001 Sep; and Horn U. Strittmatter W. Krebber A. Knupfer U. Kujau M. Wenderoth R. Muller K. Matzku S. Pluckthun A. Riesenberg D. High volumetric yields of functional dimeric miniantibodies in *Escherichia coli*, using an optimized expression vector and high-cell-density fermentation under non-limited growth conditions, *Journal Article. Research Support, Non-U.S. Gov't Applied Microbiology & Biotechnology.* 46(5-6):524-32, 1996 Dec. The skilled person would also easily be able to test secreted protein to see if the protein is correctly folded using methods well known in the art, such as protein G HPLC, circular dichroism, NMR, X-Ray crystallography and epitope affinity measurement methods.

[0042] The present invention will now be described in more detail.

[0043] The terms "protein" and "polypeptide" are used interchangeably herein, unless the context indicates otherwise. "Peptide" is intended to refer to 10 or less amino acids.

[0044] The terms "polynucleotide" includes a gene, DNA, cDNA, RNA, mRNA etc unless the context indicates otherwise.

[0045] 'Reduced activity' as employed herein refers to 'lower levels of enzymatic activity, such

as Tsp enzymic activity in comparison to the corresponding enzymic activity in a wild type strain when measured under comparable conditions in a suitable assay. In one embodiment the reduced activity is 50% or less, 40% or less, 30% or less, 20% or less, 10% or less or 5% or less of the enzymic activity of a wild-type comparator. In one embodiment the analysis to determine the levels of enzymic activity are performed concomitantly when the results are to be employed in a direct comparison.

[0046] Direct comparison as employed herein refers to where the numerical value of two or more results are compared for the purpose of evaluating if there is reduced activity as defined herein or ranking the activity results obtained from an assay.

[0047] As used herein, the term "comprising" in context of the present specification should be interpreted as "including".

[0048] Wild-type cell as employed herein employed interchangeably with non-mutated cell or control cell.

[0049] The non-mutated cell or control cell in the context of the present invention means a cell of the same type as the recombinant gram-negative cell of the invention wherein the cell has not been modified to carry the above reduce Tsp protein activity and to carry the mutant spr gene. For example, a non-mutated cell may be a wild-type cell and may be derived from the same population of host cells as the cells of the invention before modification to introduce any mutations.

[0050] The expressions "cell", "cell line", "cell culture" and "strain" are used interchangeably.

[0051] The expression "phenotype of a cell comprising a mutated Tsp gene" in the context of the present invention means the phenotype exhibited by a cell having a mutant Tsp gene. Typically cells comprising a mutant Tsp gene may lyse, especially at high cell densities. The lysis of these cells causes any recombinant protein to leak into the supernatant. Cells carrying mutated Tsp gene may also show thermosensitive growth at low osmolarity. For example, the cells exhibit no or reduced growth rate or the cells die in hypotonic media at a high temperature, such as at 40°C or more.

[0052] The term "isogenic" in the context of the present invention means that the genome of the cell of the present invention has substantially the same or the same genomic sequence compared to the wild-type cell from which the cell is derived except for a mutated spr gene and the modification required to reduce Tsp protein activity compared to a wild-type cell. In this embodiment the genome of the cell comprises no further non-naturally occurring or genetically engineered mutations. In one embodiment the cell according to the present invention may have substantially the same genomic sequence compared to the wild-type cell except for the mutated spr gene and the modification required to reduce Tsp protein activity compared to a wild-type cell taking into account any naturally occurring mutations which may occur. In one embodiment, the cell according to the present invention may have exactly the same genomic

sequence compared to the wild-type cell except for the mutated spr gene and the modification required to reduce Tsp protein activity compared to a wild-type cell.

[0053] The term "wild-type" in the context of the present invention means a strain of a gram-negative bacterial cell as it may occur in nature or may be isolated from the environment, which does not carry any genetically engineered mutations. An example of a wild-type strain of *E. coli* is W3110, such as W3110 K-12 strain.

[0054] Any suitable gram-negative bacterium may be used as the parental cell for producing the recombinant cell of the present invention. Suitable gram-negative bacterium include *Salmonella typhimurium*, *Pseudomonas fluorescens*, *Erwinia carotovora*, *Shigella*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii* and *E. coli*. Preferably the parental cell is *E. coli*. Any suitable strain of *E. coli* may be used in the present invention but preferably a wild-type W3110 strain, such as K-12 W3110, is used.

[0055] A drawback associated with the protease deficient bacterial strains previously created and used to express recombinant proteins is that they comprise additional mutations of genes involved in cell metabolism and DNA replication such as, for example *phoA*, *fhuA*, *lac*, *rec*, *gal*, *ara*, *arg*, *thi* and *pro* in *E. coli* strains. These mutations may have many deleterious effects on the host cell including effects on cell growth, stability, recombinant protein expression yield and toxicity. Strains having one or more of these genomic mutations, particularly strains having a high number of these mutations, may exhibit a loss of fitness which reduces bacterial growth rate to a level which is not suitable for industrial protein production. Further, any of the above genomic mutations may affect other genes in *cis* and/or in *trans* in unpredictable harmful ways thereby altering the strain's phenotype, fitness and protein profile. Further, the use of heavily mutated cells is not generally suitable for producing recombinant proteins for commercial use, particularly therapeutics, because such strains generally have defective metabolic pathways and hence may grow poorly or not at all in minimal or chemically defined media.

[0056] In one embodiment a cell according to the present invention is isogenic to a wild-type bacterial cell except for the mutated spr gene and the modification required to reduce Tsp protein activity compared to a wild-type cell. Only minimal mutations are made to the cell's genome to introduce the mutations. The cells do not carry any other mutations which may have deleterious effects on the cell's growth and/or ability to express a protein of interest. Accordingly, one or more of the recombinant host cells of the present invention may exhibit improved protein expression and/or improved growth characteristics compared to cells comprising further genetically engineered mutations to the genomic sequence. The cells provided by the present invention are also more suitable for use in the production of therapeutic proteins compared to cells comprising further disruptions to the cell genome.

[0057] In a preferred embodiment, the cell is isogenic to a wild-type *E. coli* cell, such as strain W3110, except for the mutated spr gene and the modification required to reduce Tsp protein activity compared to a wild-type cell.

[0058] The cell of the present invention may further differ from a wild-type cell by comprising a polynucleotide encoding the protein of interest. The polynucleotide sequence encoding the protein of interest may be exogenous or endogenous. The polynucleotide encoding the protein of interest may be contained within a suitable expression vector transformed into the cell and/or integrated into the host cell's genome. In the embodiment where the polynucleotide encoding the protein of interest is inserted into the host's genome, the cell of the present invention will also differ from a wild-type cell due to the inserted polynucleotide sequence encoding the protein of interest. Preferably the polynucleotide is in an expression vector in the cell thereby causing minimal disruption to the host cell's genome.

[0059] The spr protein is an *E. coli* membrane bound periplasmic protease.

[0060] The wild-type amino acid sequence of the spr protein is shown in SEQ ID NO:21 with the signal sequence at the N-terminus and in SEQ ID NO:22 without the signal sequence of 26 amino acids (according to UniProt Accession Number P0AFV4). The amino acid numbering of the spr protein sequence in the present invention includes the signal sequence. Accordingly, the amino acid 1 of the spr protein is the first amino acid (Met) shown in SEQ ID NO: 21.

[0061] The mutated spr gene is the cell's chromosomal spr gene.

[0062] The mutated spr gene encodes a spr protein capable of suppressing the phenotype of a cell further comprising a mutated Tsp gene. Cells carrying a mutated Tsp gene may have a good cell growth rate but one limitation of these cells is their tendency to lyse, especially at high cell densities. Accordingly the phenotype of a cell comprising a mutated Tsp gene is a tendency to lyse, especially at high cell densities. Cells carrying a mutated Tsp gene also show thermosensitive growth at low osmolality. However, the spr mutations carried by the cells of the present invention, when introduced into a cell having reduced Tsp activity suppress the reduced Tsp phenotype and, therefore, the cell exhibits reduced lysis, particularly at a high cell density. The growth phenotype of a cell may be easily measured by a person skilled in the art during shake flask or high cell density fermentation technique. The suppression of the cell lysis phenotype may be seen from the improved growth rate and/or recombinant protein production, particularly in the periplasm, exhibited by a cell carrying spr mutant and having reduced Tsp activity compared to a cell carrying the Tsp mutant and a wild-type spr.

[0063] The cells according to the present invention comprise a mutant spr gene encoding a spr protein having a mutation at one or more amino acids selected from N31, R62, I70, Q73, C94, S95, V98, Q99, R100, L108, Y115, D133, V135, L136, G140, R144, H145, G147 and H157, preferably a mutation at one or more amino acids selected from C94, S95, V98, Y115, D133, V135, H145, G147 and H157. In this embodiment, the spr protein preferably does not have any further mutations.

[0064] The mutation of one or more of the above amino acids may be any suitable missense mutation to one, two or three of the nucleotides encoding the amino acid. The mutation changes the amino acid residue to any suitable amino acid which results in a mutated spr

protein capable of suppressing the phenotype of a cell comprising a mutated Tsp gene. The missense mutation may change the amino acid to one which is a different size and/or has different chemical properties compared to the wild-type amino acid.

[0065] In one embodiment the mutant spr gene encodes an spr protein having one or more mutations selected from C94A, S95F, V98E, Y115F, D133A, V135D or G, H145A, G147C and H157A.

[0066] In one embodiment the mutation is to one, two or three of the catalytic triad of amino acid residues of C94, H145, and H157 (Solution NMR Structure of the NlpC/P60 Domain of Lipoprotein Spr from Escherichia coli Structural Evidence for a Novel Cysteine Peptidase Catalytic Triad, Biochemistry, 2008, 47, 9715-9717).

Accordingly, the mutated spr gene may comprise: a mutation to C94; or a mutation to H145; or a mutation to H157; or a mutation to C94 and H145; or a mutation to C94 and H157; or a mutation to H145 and H157; or a mutation to C94, H145 and H157.

[0067] In this embodiment, the spr protein preferably does not have any further mutations.

[0068] One, two or three of C94, H145 and H157 may be mutated to any suitable amino acid which results in a spr protein capable of suppressing the phenotype of a cell comprising a mutated Tsp gene. For example, one, two or three of C94, H145, and H157 may be mutated to a small amino acid such as Gly or Ala. Accordingly, the spr protein may have one, two or three of the mutations C94A, H145A and H157A. In one embodiment, the spr gene comprises the missense mutation C94A, which has been found to produce a spr protein capable of suppressing the phenotype of a cell comprising a mutated Tsp gene. In another embodiment, the spr gene comprises the missense mutation H145A, which has been found to produce a spr protein capable of suppressing the phenotype of a cell comprising a mutated Tsp gene.

[0069] The designation for a substitution mutant herein consists of a letter followed by a number followed by a letter. The first letter designates the amino acid in the wild-type protein. The number refers to the amino acid position where the amino acid substitution is being made, and the second letter designates the amino acid that is used to replace the wild-type amino acid.

In one embodiment the mutant spr protein comprises a mutation at one or more amino acids selected from N31, R62, I70, Q73, S95, V98, Q99, R100, L108, Y115, D133, V135, L136, G140, R144 and G147, preferably a mutation at one or more amino acids selected from S95, V98, Y115, D133, V135 and G147. In this embodiment, the spr protein preferably does not have any further mutations. Accordingly, the mutated spr gene may comprise: a mutation to N31; or a mutation to R62; or a mutation to 170; or a mutation to Q73; or a mutation to S95; or a mutation to V98; or a mutation to Q99; or a mutation to R100; or a mutation to L108; or a mutation to Y115; or a mutation to D133; or a mutation to V135; or a mutation to L136; or a mutation to G140; or a mutation to R144; or a mutation to G147.

In one embodiment the mutant spr protein comprises multiple mutations to amino acids: S95 and Y115; or N31, Q73, R100 and G140 ; or Q73, R100 and G140; or R100 and G140; or Q73

and G140; or Q73 and R100; or R62, Q99 and R144; or Q99 and R144.

[0070] One or more of the amino acids N31, R62, 170, Q73, S95, V98, Q99, R100, L108, Y115, D133, V135, L136, G140, R144 and G147 may be mutated to any suitable amino acid which results in a spr protein capable of suppressing the phenotype of a cell comprising a mutated Tsp gene. For example, one or more of N31, R62, 170, Q73, S95, V98, Q99, R100, L108, Y115, D133, V135, L136, G140 and R144 may be mutated to a small amino acid such as Gly or Ala.

[0071] In one embodiment the spr protein comprises one or more of the following mutations: N31Y, R62C, I70T, Q73R, S95F, V98E, Q99P, R100G, L108S, Y115F, D133A, V135D or V135G, L136P, G140C, R144C and G147C. In one embodiment the spr protein comprises one or more of the following mutations: S95F, V98E, Y115F, D133A, V135D or V135G and G147C. In this embodiment, the spr protein preferably does not have any further mutations.

[0072] In one embodiment the spr protein has one mutation selected from N31Y, R62C, I70T, Q73R, S95F, V98E, Q99P, R100G, L108S, Y115F, D133A, V135D or V135G, L136P, G140C, R144C and G147C. In this embodiment, the spr protein preferably does not have any further mutations.

In a further embodiment the spr protein has multiple mutations selected from: S95F and Y115F; N31Y, Q73R, R100G and G140C; Q73R, R100G and G140C; R100G and G140C; Q73R and G140C; Q73R and R100G; R62C, Q99P and R144C; or Q99P and R144C.

[0073] In one embodiment the mutated spr gene encodes a spr protein having a mutation C94A.

[0074] In one embodiment the mutated spr gene encodes a spr protein having a mutation V103E.

[0075] In one embodiment the mutated spr gene encodes a spr protein having a mutation D133A.

[0076] In one embodiment the mutated spr gene encodes a spr protein having a mutation V135D.

[0077] In one embodiment the mutated spr gene encodes a spr protein having a mutation V135A.

[0078] In one embodiment the mutated spr gene encodes a spr protein having a mutation H145A.

[0079] In one embodiment the mutated spr gene encodes a spr protein having a mutation G147C.

[0080] In one embodiment the mutated spr gene encodes a spr protein having a mutation H157A.

[0081] In one embodiment the mutant spr gene encodes a spr protein having a mutation selected from H145A, H157A and D133A.

[0082] In one embodiment of the present invention, any suitable mutation or mutations may be made to the spr gene which results in a spr protein capable of suppressing the phenotype of a cell comprising a mutated Tsp gene. Preferably, the spr protein may have one or more of the following mutations: N31Y, R62C, I70T, Q73R, C94A, S95F, V98E, Q99P, R100G, L108S, Y115F, D133A, V135D, V135G, L136P, G140C, R144C, H145A, G147C, H157A and W174R. In one embodiment the spr protein does not comprise the mutation W174R. Preferably, the spr gene comprises one or more mutations discussed above.

[0083] The cells according to the present invention have reduced Tsp protein activity compared to a wild-type cell. The expression "reduced Tsp protein activity compared to a wild-type cell" means that the Tsp activity of the cell is reduced compared to the Tsp activity of a wild-type cell. The cell may be modified by any suitable means to reduce the activity of Tsp.

[0084] In one embodiment the reduced Tsp activity is from modification of the endogenous polynucleotide encoding Tsp and/or associated regulatory expression sequences. The modification may reduce or stop Tsp gene transcription and translation or may provide an expressed Tsp protein having reduced protease activity compared to the wild-type Tsp protein.

[0085] In one embodiment an associated regulatory expression sequence is modified to reduce Tsp expression. For example, the promoter for the Tsp gene may be mutated to prevent expression of the gene.

[0086] In a preferred embodiment the cells according to the present invention carry a mutated Tsp gene encoding a Tsp protein having reduced protease activity or a knockout mutated Tsp gene.

[0087] Preferably the chromosomal Tsp gene is mutated.

[0088] As used herein, "Tsp gene" means a gene encoding protease Tsp (also known as Prc) which is a periplasmic protease capable of acting on Penicillin-binding protein-3 (PBP3) and phage tail proteins. The sequence of the wild-type Tsp gene is shown in SEQ ID NO: 1 and the sequence of the wild-type Tsp protein is shown in SEQ ID NO: 2.

[0089] Reference to the mutated Tsp gene or mutated Tsp gene encoding Tsp, refers to either a mutated Tsp gene encoding a Tsp protein having reduced protease activity or a knockout mutated Tsp gene, unless otherwise indicated.

[0090] The expression "mutated Tsp gene encoding a Tsp protein having reduced protease

activity" in the context of the present invention means that the mutated Tsp gene does not have the full protease activity compared to the wild-type non-mutated Tsp gene.

[0091] Preferably, the mutated Tsp gene encodes a Tsp protein having 50% or less, 40% or less, 30% or less, 20% or less, 10% or less or 5% or less of the protease activity of a wild-type non-mutated Tsp protein. More preferably, the mutated Tsp gene encodes a Tsp protein having no protease activity. In this embodiment the cell is not deficient in chromosomal Tsp i.e. the Tsp gene sequence has not been deleted or mutated to prevent expression of any form of Tsp protein.

[0092] Any suitable mutation may be introduced into the Tsp gene in order to produce a protein having reduced protease activity. The protease activity of a Tsp protein expressed from a gram-negative bacterium may be easily tested by a person skilled in the art by any suitable method in the art, such as the method described in Keiler et al (Identification of Active Site Residues of the Tsp Protease* THE JOURNAL OF BIOLOGICAL CHEMISTRY Vol. 270, No. 48, Issue of December 1, pp. 28864-28868, 1995 Kenneth C. Keiler and Robert T. Sauer) wherein the protease activity of Tsp was tested.

[0093] Tsp has been reported in Keiler et al (*supra*) as having an active site comprising residues S430, D441 and K455 and residues G375, G376, E433 and T452 are important for maintaining the structure of Tsp. Keiler et al (*supra*) reports findings that the mutated Tsp genes S430A, D441A, K455A, K455H, K455R, G375A, G376A, E433A and T452A had no detectable protease activity. It is further reported that the mutated Tsp gene S430C displayed about 5-10% wild-type activity. Accordingly, the Tsp mutation to produce a protein having reduced protease activity may comprise a mutation, such as a missense mutation to one or more of residues S430, D441, K455, G375, G376, E433 and T452. Preferably the Tsp mutation to produce a protein having reduced protease activity may comprise a mutation, such as a missense mutation to one, two or all three of the active site residues S430, D441 and K455.

[0094] Accordingly the mutated Tsp gene may comprise: a mutation to S430; or a mutation to D441; or a mutation to K455; or a mutation to S430 and D441; or a mutation to S430 and K455; or a mutation to D441 and K455; or a mutation to S430, D441 and K455.

[0095] One or more of S430, D441, K455, G375, G376, E433 and T452 may be mutated to any suitable amino acid which results in a protein having reduced protease activity. Examples of suitable mutations are S430A, S430C, D441A, K455A, K455H, K455R, G375A, G376A, E433A and T452A. The mutated Tsp gene may comprise one, two or three mutations to the active site residues, for example the gene may comprise: S430A or S430C; and/or D441A; and/or K455A or K455H or K455R.

[0096] Preferably, the Tsp gene has the point mutation S430A or S430C.

[0097] The expression "knockout mutated Tsp gene" in the context of the present invention

means that the gene comprises one or more mutations which prevents expression of the Tsp protein encoded by the wild-type gene to provide a cell deficient in Tsp protein. The knockout gene may be partially or completely transcribed but not translated into the encoded protein. The knockout mutated Tsp gene may be mutated in any suitable way, for example by one or more deletion, insertion, point, missense, nonsense and frameshift mutations, to cause no expression of the protein. For example, the gene may be knocked out by insertion of a foreign DNA sequence, such as an antibiotic resistance marker, into the gene coding sequence.

[0098] In a preferred embodiment the Tsp gene is not mutated by insertion of a foreign DNA sequence, such as an antibiotic resistance marker, into the gene coding sequence. In this embodiment the Tsp gene may comprise a mutation to the gene start codon and/or one or more stop codons positioned downstream of the gene start codon and upstream of the gene stop codon thereby preventing expression of the Tsp protein. The mutation to the start codon may be a missense mutation of one, two or all three of the nucleotides of the start codon. Alternatively or additionally the start codon may be mutated by an insertion or deletion frameshift mutation. The Tsp gene comprises two ATG codons at the 5' end of the coding sequence, one or both of the ATG codons may be mutated by a missense mutation. The Tsp gene may be mutated at the second ATG codon (codon 3) to TCG. The Tsp gene may alternatively or additionally comprise one or more stop codons positioned downstream of the gene start codon and upstream of the gene stop codon. Preferably the knockout mutated Tsp gene comprises both a missense mutation to the start codon and one or more inserted stop codons. In a preferred embodiment the Tsp gene is mutated to delete "T" from the fifth codon thereby causing a frameshift resulting in stop codons at codons 11 and 16. In a preferred embodiment the Tsp gene is mutated to insert an Ase I restriction site to create a third in-frame stop codon at codon 21.

[0099] In a preferred embodiment the knockout mutated Tsp gene has the DNA sequence of SEQ ID NO: 3, which includes the 6 nucleotides ATGAAT upstream of the start codon. In one embodiment the mutated Tsp gene has the DNA sequence of nucleotides 7 to 2048 of SEQ ID NO:3.

[0100] In the present invention the cells also carry one or more genes capable of expressing or overexpressing one or more proteins capable of facilitating protein folding. Examples include proteins such as FkpA, Skp, SurA, PPIA and PPIB.

[0101] In one embodiment the protein for facilitating protein folding is FkpA, Skp or a combination thereof.

[0102] In one embodiment the protein for facilitating protein folding is selected from FkpA or a combination of FkpA and Skp.

[0103] FkpA is a peptidyl-prolyl cis-trans isomerase with the Swiss-Prot number P45523.

[0104] Skp is chaperone protein with the Swiss-Prot number P0AEU7.

[0105] The protein for facilitating protein folding may be encoded by a gene in the cells genome or transiently transfected therein, for example on a plasmid or a combination of the same, as appropriate.

[0106] The recombinant gram-negative bacterial cell of the invention does not comprise a recombinant polynucleotide encoding DsbC.

[0107] In one embodiment of the present invention the recombinant gram-negative bacterial cell further comprises a mutated DegP gene encoding a DegP protein having chaperone activity and reduced protease activity and/or a mutated ptr gene, wherein the mutated ptr gene encodes a Protease III protein having reduced protease activity or is a knockout mutated ptr gene and/or a mutated OmpT gene, wherein the mutated OmpT gene encodes an OmpT protein having reduced protease activity or is a knockout mutated OmpT gene.

[0108] In this embodiment the cell's genome is isogenic to a wild-type bacterial cell except for the above mutations.

[0109] As used herein, "DegP" means a gene encoding DegP protein (also known as HtrA), which has dual function as a chaperone and a protease (Families of serine peptidases; Rawlings ND, Barrett AJ. *Methods Enzymol.* 1994;244:19-61). The sequence of the non-mutated DegP gene is shown in SEQ ID NO: 7 and the sequence of the non-mutated DegP protein is shown in SEQ ID NO: 8.

[0110] At low temperatures DegP functions as a chaperone and at high temperatures DegP has a preference to function as a protease (A Temperature-Dependent Switch from Chaperone to Protease in a Widely Conserved Heat Shock Protein. *Cell*, Volume 97, Issue 3, Pages 339 - 347. Spiess C, Beil A, Ehrmann M) and The proteolytic activity of the HtrA (DegP) protein from *Escherichia coli* at low temperatures, Skorko-Glonek J et al *Microbiology* 2008, 154, 3649-3658).

[0111] In the embodiments where the cell comprises the DegP mutation the DegP mutation in the cell provides a mutated DegP gene encoding a DegP protein having chaperone activity but not full protease activity.

[0112] The expression "having chaperone activity" in the context of the present invention means that the mutated DegP protein has the same or substantially the same chaperone activity compared to the wild-type non-mutated DegP protein. Preferably, the mutated DegP gene encodes a DegP protein having 50% or more, 60% or more, 70% or more, 80% or more, 90% or more or 95% or more of the chaperone activity of a wild-type non-mutated DegP protein. More preferably, the mutated DegP gene encodes a DegP protein having the same chaperone activity compared to wild-type DegP.

[0113] The expression "having reduced protease activity" in the context of the present

invention means that the mutated DegP protein does not have the full protease activity compared to the wild-type non-mutated DegP protein. Preferably, the mutated DegP gene encodes a DegP protein having 50% or less, 40% or less, 30% or less, 20% or less, 10% or less or 5% or less of the protease activity of a wild-type non-mutated DegP protein. More preferably, the mutated DegP gene encodes a DegP protein having no protease activity. The cell is not deficient in chromosomal DegP i.e. the DegP gene sequences has not been deleted or mutated to prevent expression of any form of DegP protein.

[0114] Any suitable mutation may be introduced into the DegP gene in order to produce a protein having chaperone activity and reduced protease activity. The protease and chaperone activity of a DegP protein expressed from a gram-negative bacterium may be easily tested by a person skilled in the art by any suitable method such as the method described in Spiess et al wherein the protease and chaperone activities of DegP were tested on MalS, a natural substrate of DegP (A Temperature-Dependent Switch from Chaperone to Protease in a Widely Conserved Heat Shock Protein. *Cell*, Volume 97, Issue 3, Pages 339 - 347. Spiess C, Beil A, Ehrmann M) and also the method described in The proteolytic activity of the HtrA (DegP) protein from *Escherichia coli* at low temperatures, Skorko-Glonek J et al *Microbiology* 2008, 154, 3649-3658.

[0115] DegP is a serine protease and has an active center consisting of a catalytic triad of amino acid residues of His105, Asp135 and Ser210 (Families of serine peptidases, *Methods Enzymol.*, 1994, 244:19-61 Rawlings N and Barrett A). The DegP mutation to produce a protein having chaperone activity and reduced protease activity may comprise a mutation, such as a missense mutation to one, two or three of His105, Asp135 and Ser210.

[0116] Accordingly, the mutated DegP gene may comprise: a mutation to His105; or a mutation to Asp135; or a mutation to Ser210; or a mutation to His105 and Asp135; or a mutation to His105 and Ser210; or a mutation to Asp135 and Ser210; or a mutation to His105, Asp135 and Ser210.

[0117] One, two or three of His105, Asp135 and Ser210 may be mutated to any suitable amino acid which results in a protein having chaperone activity and reduced protease activity. For example, one, two or three of His105, Asp135 and Ser210 may be mutated to a small amino acid such as Gly or Ala. A further suitable mutation is to change one, two or three of His105, Asp135 and Ser210 to an amino acid having opposite properties such as Asp135 being mutated to Lys or Arg, polar His105 being mutated to a non-polar amino acid such as Gly, Ala, Val or Leu and small hydrophilic Ser210 being mutated to a large or hydrophobic residue such as Val, Leu, Phe or Tyr. Preferably, the DegP gene comprises the point mutation S210A, as shown in Figure 11c, which has been found to produce a protein having chaperone activity but not protease activity (A Temperature-Dependent Switch from Chaperone to Protease in a Widely Conserved Heat Shock Protein. *Cell*, Volume 97, Issue 3, Pages 339 - 347. Spiess C, Beil A, Ehrmann M).

[0118] DegP has two PDZ domains, PDZ1 (residues 260-358) and PDZ2 (residues 359-448),

which mediate protein-protein interaction (A Temperature-Dependent Switch from Chaperone to Protease in a Widely Conserved Heat Shock Protein. Cell, Volume 97, Issue 3, Pages 339 - 347. Spiess C, Beil A, Ehrmann M). In one embodiment of the present invention the degP gene is mutated to delete PDZ1 domain and/or PDZ2 domain. The deletion of PDZ1 and PDZ2 results in complete loss of protease activity of the DegP protein and lowered chaperone activity compared to wild-type DegP protein whilst deletion of either PDZ1 or PDZ2 results in 5% protease activity and similar chaperone activity compared to wild-type DegP protein (A Temperature-Dependent Switch from Chaperone to Protease in a Widely Conserved Heat Shock Protein. Cell, Volume 97, Issue 3, Pages 339 - 347. Spiess C, Beil A, Ehrmann M).

[0119] The mutated DegP gene may also comprise a silent non-naturally occurring restriction site, such as Ase I in order to aid in identification and screening methods, for example as shown in Figure 7C.

[0120] The preferred sequence of the mutated DegP gene comprising the point mutation S210A and an Ase I restriction marker site is provided in SEQ ID NO: 9 and the encoded protein sequence is shown in SEQ ID NO: 10.

[0121] In the embodiments of the present invention wherein the cell comprises a mutated DegP gene encoding a DegP protein having chaperone activity and reduced protease activity, one or more of the cells provided by the present invention may provide improved yield of correctly folded proteins from the cell relative to mutated cells wherein the DegP gene has been mutated to knockout DegP preventing DegP expression, such as chromosomal deficient DegP. In a cell comprising a knockout mutated DegP gene preventing DegP expression, the chaperone activity of DegP is lost completely whereas in the cell according to the present invention the chaperone activity of DegP is retained whilst the full protease activity is lost. In these embodiments, one or more cells according to the present invention have a lower protease activity to prevent proteolysis of the protein whilst maintaining the chaperone activity to allow correct folding and transportation of the protein in the host cell.

[0122] In these embodiments, one or more cells according to the present invention may have improved cell growth compared to cells carrying a mutated knockout DegP gene preventing DegP expression. Without wishing to be bound by theory improved cell growth maybe exhibited due to the DegP protease retaining chaperone activity which may increase capacity of the cell to process all proteins which require chaperone activity. Accordingly, the production of correctly folded proteins necessary for the cell's growth and reproduction may be increased in one or more of the cells of the present invention compared to cells carrying a DegP knockout mutation thereby improving the cellular pathways regulating growth. Further, known DegP protease deficient strains are generally temperature-sensitive and do not typically grow at temperatures higher than about 28°C. However, the cells according to the present invention are not temperature-sensitive and may be grown at temperatures of 28°C or higher, including temperatures of approximately 30°C to approximately 37°C, which are typically used for industrial scale production of proteins from bacteria.

[0123] In one embodiment of the present invention the cell carries a mutated ptr gene. As used herein, "ptr gene" means a gene encoding Protease III, a protease which degrades high molecular weight proteins. The sequence of the non-mutated ptr gene is shown in SEQ ID NO: 4 and the sequence of the non-mutated Protease III protein is shown in SEQ ID NO: 5.

[0124] Reference to the mutated ptr gene or mutated ptr gene encoding Protease III, refers to either a mutated ptr gene encoding a Protease III protein having reduced protease activity or a knockout mutated ptr gene, unless otherwise indicated.

[0125] The expression "mutated ptr gene encoding a Protease III protein having reduced protease activity" in the context of the present invention means that the mutated ptr gene does not have the full protease activity compared to the wild-type non-mutated ptr gene.

[0126] Preferably, the mutated ptr gene encodes a Protease III having 50% or less, 40% or less, 30% or less, 20% or less, 10% or less or 5% or less of the protease activity of a wild-type non-mutated Protease III protein. More preferably, the mutated ptr gene encodes a Protease III protein having no protease activity. In this embodiment the cell is not deficient in chromosomal ptr i.e. the ptr gene sequence has not been deleted or mutated to prevent expression of any form of Protease III protein.

[0127] Any suitable mutation may be introduced into the ptr gene in order to produce a Protease III protein having reduced protease activity. The protease activity of a Protease III protein expressed from a gram-negative bacterium may be easily tested by a person skilled in the art by any suitable method in the art.

[0128] The expression "knockout mutated ptr gene" in the context of the present invention means that the gene comprises one or more mutations thereby causing no expression of the protein encoded by the gene to provide a cell deficient in the protein encoded by the knockout mutated gene. The knockout gene may be partially or completely transcribed but not translated into the encoded protein. The knockout mutated ptr gene may be mutated in any suitable way, for example by one or more deletion, insertion, point, missense, nonsense and frameshift mutations, to cause no expression of the protein. For example, the gene may be knocked out by insertion of a foreign DNA sequence, such as an antibiotic resistance marker, into the gene coding sequence.

[0129] In a preferred embodiment the gene is not mutated by insertion of a foreign DNA sequence, such as an antibiotic resistance marker, into the gene coding sequence. Preferably the Protease III gene comprise a mutation to the gene start codon and/or one or more stop codons positioned downstream of the gene start codon and upstream of the gene stop codon thereby preventing expression of the Protease III protein.

[0130] A mutation to the target knockout gene start codon causes loss of function of the start codon and thereby ensures that the target gene does not comprise a suitable start codon at the start of the coding sequence. The mutation to the start codon may be a missense mutation

of one, two or all three of the nucleotides of the start codon. Alternatively or additionally the start codon may be mutated by an insertion or deletion frameshift mutation.

[0131] In a preferred embodiment the ptr gene is mutated to change the ATG start codon to ATT.

[0132] The knockout mutated ptr gene may alternatively or additionally comprise one or more stop codons positioned downstream of the gene start codon and upstream of the gene stop codon. Preferably the knockout mutated ptr gene comprises both a missense mutation to the start codon and one or more inserted stop codons.

[0133] The one or more inserted stop codons are preferably in-frame stop codons. However the one or more inserted stop codons may alternatively or additionally be out-of-frame stop codons. One or more out-of-frame stop codons may be required to stop translation where an out-of-frame start codon is changed to an in-frame start codon by an insertion or deletion frameshift mutation. The one or more stop codons may be introduced by any suitable mutation including a nonsense point mutation and a frameshift mutation. The one or more stop codons are preferably introduced by a frameshift mutation and/or an insertion mutation, preferably by replacement of a segment of the gene sequence with a sequence comprising a stop codon. For example an Ase I restriction site may be inserted, which comprises the stop codon TAA.

[0134] In a preferred embodiment the ptr gene is mutated to insert an in-frame stop codon by insertion of an Ase I restriction site, as shown in Figure 7A. In a preferred embodiment the knockout mutated ptr gene has the DNA sequence of SEQ ID NO: 6.

[0135] The above described knockout mutations are advantageous because they cause minimal or no disruption to the chromosomal DNA upstream or downstream of the target knockout gene site and do not require the insertion and retention of foreign DNA, such as antibiotic resistance markers, which may affect the cell's suitability for expressing a protein of interest, particularly therapeutic proteins. Accordingly, one or more of the cells according to the present invention may exhibit improved growth characteristics and/or protein expression compared to cells wherein the protease gene has been knocked out by insertion of foreign DNA into the gene coding sequence.

[0136] In one embodiment the cells according to the present invention carry a mutated OmpT gene. As used herein, "OmpT gene" means a gene encoding protease OmpT (outer membrane protease T) which is an outer membrane protease. The sequence of the wild-type non-mutated OmpT gene is SWISS-PROT P09169.

[0137] Reference to a mutated OmpT gene or mutated OmpT gene encoding OmpT, refers to either a mutated OmpT gene encoding a OmpT protein having reduced protease activity or a knockout mutated OmpT gene, unless otherwise indicated.

[0138] The expression "mutated OmpT gene encoding an OmpT protein having reduced

protease activity" in the context of the present invention means that the mutated OmpT gene does not have the full protease activity compared to the wild-type non-mutated OmpT gene. The mutated OmpT gene may encode an OmpT protein having 50% or less, 40% or less, 30% or less, 20% or less, 10% or less or 5% or less of the protease activity of a wild-type non-mutated OmpT protein. The mutated OmpT gene may encode an OmpT protein having no protease activity. In this embodiment the cell is not deficient in chromosomal OmpT i.e. the OmpT gene sequence has not been deleted or mutated to prevent expression of any form of OmpT protein.

[0139] Any suitable mutation may be introduced into the OmpT gene in order to produce a protein having reduced protease activity. The protease activity of a OmpT protein expressed from a gram-negative bacterium may be easily tested by a person skilled in the art by any suitable method in the art, such as the method described in Kramer et al (Identification of essential acidic residues of outer membrane protease OmpT supports a novel active site, FEBS Letters 505 (2001) 426-430) and Dekker et al (Substrate Specificity of the Integral Membrane Protease OmpT Determined by Spatially Addressed Peptide Libraries, Biochemistry 2001, 40, 1694-1701).

[0140] OmpT has been reported in Kramer et al (Identification of active site serine and histidine residues in Escherichia coli outer membrane protease OmpT FEBS Letters 2000 468, 220-224) discloses that substitution of serines, histidines and acidic residues by alanines results in ~10-fold reduced activity for Glu27, Asp97, Asp208 or His101, ~500-fold reduced activity for Ser99 and ~10000-fold reduced activity for Asp83, Asp85, Asp210 or His212. Vandeputte-Rutten et al (Crystal Structure of the Outer Membrane Protease OmpT from Escherichia coli suggests a novel catalytic site, The EMBO Journal 2001, Vol 20 No 18 5033-5039) as having an active site comprising a Asp83-Asp85 pair and a His212-Asp210 pair. Further Kramer et al (Lipopolysaccharide regions involved in the activation of Escherichia coli outer membrane protease OmpT, Eur. J. Biochem. FEBS 2002, 269, 1746-1752) discloses that mutations D208A, D210A, H212A, H212N, H212Q, G216K/K217G, K217T and R218L in loop L4 all resulted in partial or virtually complete loss of enzymatic activity.

[0141] Accordingly, the OmpT mutation to produce a protein having reduced protease activity may comprise a mutation, such as a missense mutation to one or more of residues E27, D43, D83, D85, D97, S99, H101 E111, E136, E193, D206, D208, D210, H212 G216, K217, R218 & E250.

[0142] One or more of E27, D43, D83, D85, D97, S99, H101 E111, E136, E193, D206, D208, D210, H212 G216, K217, R218 & E250 may be mutated to any suitable amino acid which results in a protein having reduced protease activity. For example, one or more of E27, D43, D83, D85, D97, S99, H101 E111, E136, E193, D206, D208, D210, H212 G216, K217, R218 & E250 may be mutated to alanine. Examples of suitable mutations are E27A, D43A, D83A, D85A, D97A, S99A, H101A E111A, E136A, E193A, D206A, D208A, D210A, H212A, H212N, H212Q, G216K, K217G, K217T, R218L & E250A. In one embodiment the mutated OmpT gene comprises D210A and H212A mutations. A suitable mutated OmpT sequence comprising

D210A and H212A mutations is shown in SEQ ID NO: 23.

[0143] The expression "knockout mutated OmpT gene" in the context of the present invention means that the gene comprises one or more mutations thereby causing no expression of the protein encoded by the gene to provide a cell deficient in the protein encoded by the knockout mutated gene. The knockout gene may be partially or completely transcribed but not translated into the encoded protein. The knockout mutated OmpT gene may be mutated in any suitable way, for example by one or more deletion, insertion, point, missense, nonsense and frameshift mutations, to cause no expression of the protein. For example, the gene may be knocked out by insertion of a foreign DNA sequence, such as an antibiotic resistance marker, into the gene coding sequence.

[0144] In one embodiment the OmpT gene comprises a mutation to the gene start codon and/or one or more stop codons positioned downstream of the gene start codon and upstream of the gene stop codon thereby preventing expression of the OmpT protein. The mutation to the start codon may be a missense mutation of one, two or all three of the nucleotides of the start codon. A suitable mutated knockout OmpT sequence is shown in SEQ ID NO: 24. Alternatively or additionally the start codon may be mutated by an insertion or deletion frameshift mutation.

[0145] In one embodiment the gram-negative bacterial cell according to the present invention does not carry a knockout mutated ompT gene, such as being deficient in chromosomal ompT.

[0146] In one embodiment the gram-negative bacterial cell according to the present invention does not carry a knockout mutated degP gene, such as being deficient in chromosomal degP. In one embodiment the gram-negative bacterial cell according to the present invention does not carry a mutated degP gene.

[0147] In one embodiment the gram-negative bacterial cell according to the present invention does not carry a knockout mutated ptr gene, such as being deficient in chromosomal ptr.

[0148] Many genetically engineered mutations including knockout mutations involve the use of antibiotic resistance markers which allow the selection and identification of successfully mutated cells. However, as discussed above, there are a number of disadvantages to using antibiotic resistance markers.

[0149] A further embodiment of the present invention the cell does not comprise an antibiotic resistance marker and overcomes the above disadvantages of using antibiotic resistance markers wherein the mutated Tsp gene, the mutated spr gene and optionally the mutated DegP gene and/or a mutated ptr gene and/or a mutated OmpT gene, are mutated to comprise one or more restriction marker sites. The restriction sites are genetically engineered into the gene and are non-naturally occurring. The restriction marker sites are advantageous because they allow screening and identification of correctly modified cells which comprise the required chromosomal mutations. Cells which have been modified to carry one or more of the mutated

protease genes may be analyzed by PCR of genomic DNA from cell lysates using oligonucleotide pairs designed to amplify a region of the genomic DNA comprising a non-naturally occurring restriction marker site. The amplified DNA may then be analyzed by agarose gel electrophoresis before and after incubation with a suitable restriction enzyme capable of digesting the DNA at the non-naturally occurring restriction marker site. The presence of DNA fragments after incubation with the restriction enzyme confirms that the cells have been successfully modified to carry the one or more mutated genes.

[0150] In the embodiment wherein the cell carries a knockout mutated ptr gene having the DNA sequence of SEQ ID NO: 6, the oligonucleotide primer sequences shown in SEQ ID NO: 17 and SEQ ID NO: 18 may be used to amplify the region of the DNA comprising the non-naturally occurring Ase I restriction site from the genomic DNA of transformed cells. The amplified genomic DNA may then be incubated with Ase I restriction enzyme and analyzed by gel electrophoresis to confirm the presence of the mutated ptr gene in the genomic DNA.

[0151] In the embodiment wherein the cell comprises a knockout mutated Tsp gene having the DNA sequence of SEQ ID NO: 3 or nucleotides 7 to 2048 of SEQ ID NO:3, the oligonucleotide primer sequences shown in SEQ ID NO: 15 and SEQ ID NO:16 may be used to amplify the region of the DNA comprising the non-naturally occurring Ase I restriction site from the genomic DNA of transformed cells. The amplified genomic DNA may then be incubated with Ase I restriction enzyme and analyzed by gel electrophoresis to confirm the presence of the mutated Tsp gene in the genomic DNA.

[0152] In the embodiment wherein the cell comprises a mutated DegP gene having the DNA sequence of SEQ ID NO: 9, the oligonucleotide primer sequences shown in SEQ ID NO: 19 and SEQ ID NO:20 may be used to amplify the region of the DNA comprising the non-naturally occurring Ase I restriction site from the genomic DNA of transformed cells. The amplified genomic DNA may then be incubated with Ase I restriction enzyme and analyzed by gel electrophoresis to confirm the presence of the mutated DegP gene in the genomic DNA.

[0153] The one or more restriction sites may be introduced by any suitable mutation including by one or more deletion, insertion, point, missense, nonsense and frameshift mutations. A restriction site may be introduced by the mutation of the start codon and/or mutation to introduce the one or more stop codons, as described above. This embodiment is advantageous because the restriction marker site is a direct and unique marker of the knockout mutations introduced.

[0154] A restriction marker site may be inserted which comprises an in-frame stop codon, such as an Ase I restriction site. This is particularly advantageous because the inserted restriction site serves as both a restriction marker site and a stop codon to prevent full transcription of the gene coding sequence. For example, in the embodiment wherein a stop codon is introduced to the ptr gene by introduction of an Ase I site, this also creates a restriction site, as shown in Figure 7A. For example, in the embodiment wherein a stop codon is introduced to the Tsp gene at codon 21 by introduction of an Ase I site, this also creates a restriction site, as shown

in Figure 7B.

[0155] A restriction marker site may be inserted by the mutation to the start codon and optionally one or more further point mutations. In this embodiment the restriction marker site is preferably an *EcoR* I restriction site. This is particularly advantageous because the mutation to the start codon also creates a restriction marker site. For example, in the embodiment wherein the start codon of the ptr gene is changed to ATT, this creates an *EcoR* I marker site, as shown in Figure 11a. For example, in the embodiment wherein the start codon (codon 3) of the Tsp gene is changed from ATG to TCG, as shown in Figure 1b, a further point mutation of codon 2 from AAC to AAT and mutation of codon 3 ATG to TCG creates an *EcoR* I restriction marker site, as shown in Figure 7B.

[0156] In the embodiment of the present invention wherein the cell carries a mutated OmpT gene, the one or more restriction sites may be introduced by any suitable mutation including by one or more deletion, insertion, point, missense, nonsense and frameshift mutations. For example, in the embodiment wherein the OmpT gene comprises the mutations D210A and H212A, these mutations introduce silent HindIII restriction site which may be used as a selection marker.

[0157] In the DegP gene or the spr gene, a marker restriction site may be introduced using silent codon changes. For example, an *Ase* I site may be used as a silent restriction marker site, wherein the TAA stop codon is out-of-frame, as shown in Figure 7C for the mutated DegP gene.

[0158] In the embodiments of the present invention, wherein the ptr gene and/or the Tsp gene are mutated to encode a Protease III or Tsp having reduced protease activity, one or more marker restriction sites may be introduced using silent codon changes.

[0159] The recombinant gram-negative bacterial cell according to the present invention may be produced by any suitable means. The skilled person knows of suitable techniques which may be used to replace a chromosomal gene sequence with a mutated gene sequence. Suitable vectors may be employed which allow integration into the host chromosome by homologous recombination.

[0160] Suitable gene replacement methods are described, for example, in Hamilton *et al* (New Method for Generating Deletions and Gene Replacements in Escherichia coli, Hamilton C. M. et al., Journal of Bacteriology Sept. 1989, Vol. 171, No. 9 p 4617-4622), Skorupski *et al* (Positive selection vectors for allelic exchange, Skorupski K and Taylor R. K., Gene, 1996, 169, 47-52), Kiel *et al* (A general method for the construction of Escherichia coli mutants by homologous recombination and plasmid segregation, Kiel J.A.K.W. et al, Mol Gen Genet 1987, 207:294-301), Blomfield *et al* (Allelic exchange in Escherichia coli using the Bacillus subtilis sacB gene and a temperature sensitive pSC101 replicon, Blomfield I. C. et al., Molecular Microbiology 1991, 5(6), 1447-1457) and Ried *et al*. (An nptI-sacB-sacR cartridge for constructing directed, unmarked mutations in Gram-negative bacteria by marker exchange-

eviction mutagenesis, Ried J. L. and Collmer A., Gene 57 (1987) 239-246). A suitable plasmid which enables homologous recombination/replacement is the pKO3 plasmid (Link et al., 1997, Journal of Bacteriology, 179, 6228-6237).

[0161] Successfully mutated strains may be identified using methods well known in the art including colony PCR DNA sequencing and colony PCR restriction enzyme mapping.

[0162] In the embodiment wherein the cell comprises two or more mutated chromosomal genes, the mutated genes may be introduced into the gram-negative bacterium on the same or different vectors.

[0163] In one embodiment the gram-negative bacterial cell according to the present invention does not carry a knockout mutated ompT gene, such as being deficient in chromosomal ompT.

[0164] In one embodiment the cells according to the present disclosure only contain the three characterizing mutations of mutated spr, reduced Tsp and express FkpA, Skp or a combination of FkpA and Skp.

[0165] In one embodiment the cell line according to the present disclosure consists of a mutated Tsp gene and a mutated spr gene, and an FkpA gene.

[0166] In one embodiment the cell line according to the present disclosure consists of a mutated Tsp gene and a mutated spr gene, and a Skp gene.

[0167] In one embodiment the cell line according to the present disclosure consists of a mutated Tsp gene and a mutated spr gene, an FkpA gene and a Skp gene.

[0168] In one embodiment the gene or genes capable of expressing or overexpressing one or more proteins capable of facilitating protein folding, such as FkpA, and Skp, are transiently transformed into the cell, for example in an expression vector optionally comprising a polynucleotide sequence encoding an antibody or binding fragment thereof.

[0169] In one embodiment the polynucleotide sequence encoding the antibody and the polynucleotide encoding FkpA and/or Skp are inserted into separate expression vectors.

[0170] For production of products comprising both heavy and light chains, the cell line may be transformed with two vectors, a first vector encoding a light chain polypeptide and a second vector encoding a heavy chain polypeptide. Alternatively, a single vector may be used, the vector including sequences encoding light chain and heavy chain polypeptides.

[0171] Alternatively, the polynucleotide sequence encoding the antibody and the polynucleotide encoding FkpA and/or Skp are inserted into one vector. Preferably the vector comprises the sequences encoding the light and heavy chain polypeptides of the antibody.

[0172] The present invention also provides an expression vector comprising a recombinant polynucleotide encoding FkpA and/or Skp and an antibody or an antigen binding fragment thereof specific for human FcRn. The expression vector is a multi-cistronic vector comprising the polynucleotide sequence encoding FkpA and/or Skp and the polynucleotide sequence encoding the antibody.

[0173] The multicistronic vector may be produced by an advantageous cloning method which allows repeated sequential cloning of polynucleotide sequences into a vector. The method uses compatible cohesive ends of a pair of restriction sites, such as the "AT" ends of *Ase I* and *Nde I* restriction sites. A polynucleotide sequence comprising a coding sequence and having compatible cohesive ends, such as a *AseI-NdeI* fragment, may be cloned into a restriction site in the vector, such as *Nde I*. The insertion of the polynucleotide sequence destroys the 5' restriction site but creates a new 3' restriction site, such as *NdeI*, which may then be used to insert a further polynucleotide sequence comprising compatible cohesive ends. The process may then be repeated to insert further sequences. Each polynucleotide sequence inserted into the vector comprises non-coding sequence 3' to the stop codon which may comprise an *Ssp I* site for screening, a Shine Dalgarno ribosome binding sequence, an A rich spacer and an *NdeI* site encoding a start codon.

[0174] A diagrammatic representation of the creation of a vector comprising a polynucleotide sequence encoding a light chain of an antibody (LC), a heavy chain of an antibody (HC), an FkpA polynucleotide sequences and a further polynucleotide sequence is shown in Figure 7d.

[0175] The cell according to the present invention preferably comprises an expression vector as defined above.

Further disclosed herein is an example wherein the cell also expresses one or more further proteins as follows: one or more proteins capable of facilitating protein folding, such as, *skp*, *SurA*, *PPiA* and *PPiD*; and optionally one or more protein capable of facilitating protein secretion or translocation, such as *SecY*, *SecE*, *SecG*, *SecYEG*, *SecA*, *SecB*, *FtsY* and *Lep*; the one or more further protein may be expressed from one or more polynucleotides inserted into the same vector as the polynucleotide encoding FkpA and/or the polynucleotide sequence encoding the antibody. Alternatively the one or more polynucleotides may be inserted into separate vectors.

[0176] The expression vector may be produced by inserting one or more expression cassettes as defined above into a suitable vector. Alternatively, the regulatory expression sequences for directing expression of the polynucleotide sequence may be contained in the expression vector and thus only the encoding region of the polynucleotide may be required to complete the expression vector.

[0177] The polynucleotide encoding FkpA and/or Skp and/or the polynucleotide encoding the antibody is suitably inserted into a replicable vector, typically an autonomously replicating expression vector, for expression in the cell under the control of a suitable promoter for the cell. Many vectors are known in the art for this purpose and the selection of the appropriate

vector may depend on the size of the nucleic acid and the particularly cell type.

[0178] Examples of expression vectors which may be employed to transform the host cell with a polynucleotide according to the invention include:

- a plasmid, such as pBR322 or pACYC184, and/or
- a viral vector such as bacterial phage
- a transposable genetic element such as a transposon

[0179] Such expression vectors usually comprise a plasmid origin of DNA replication, an antibiotic selectable marker, a promoter and transcriptional terminator separated by a multi-cloning site (expression cassette) and a DNA sequence encoding a ribosome binding site.

[0180] The promoters employed in the present invention can be linked to the relevant polynucleotide directly or alternatively be located in an appropriate position, for example in a vector such that when the relevant polypeptide is inserted the relevant promoter can act on the same. In one embodiment the promoter is located before the encoding portion of the polynucleotide on which it acts, for example a relevant promoter before each encoding portion of polynucleotide. "Before" as used herein is intended to imply that the promoter is located at the 5 prime end in relation to the encoding polynucleotide portion.

[0181] The promoters may be endogenous or exogenous to the host cells. Suitable promoters include lac, tac, trp, phoA, lpp, Arab, tet and T7.

[0182] One or more promoters employed may be inducible promoters. In the embodiment wherein the polynucleotide encoding FkpA and/or Skp and the polynucleotide encoding the antibody are inserted into one vector, the nucleotide sequences encoding FkpA and the antibody may be under the control of a single promoter or separate promoters. In the embodiment wherein the nucleotide sequences encoding FkpA and/or Skp and the antibody are under the control of separate promoters, the promoter may be independently inducible promoters.

[0183] Promoters for use in bacterial systems also generally contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the polypeptide of interest. The promoter can be removed from the bacterial source DNA by restriction enzyme digestion and inserted into the vector containing the desired DNA.

[0184] The expression vector preferably also comprises a dicistronic message for producing the antibody or antigen binding fragment thereof as described in WO03/048208 or WO2007/039714 (the contents of which are incorporated herein by reference). Preferably the upstream cistron contains DNA coding for the light chain of the antibody and the downstream cistron contains DNA coding for the corresponding heavy chain, and the dicistronic intergenic sequence (IGS) preferably comprises a sequence selected from IGS1 (SEQ ID NO: 23), IGS2

(SEQ ID NO: 24), IGS3 (SEQ ID NO: 25) and IGS4 (SEQ ID NO: 26).

[0185] The terminators may be endogenous or exogenous to the host cells. A suitable terminator is *rrnB*.

[0186] Further suitable transcriptional regulators including promoters and terminators and protein targeting methods may be found in "Strategies for Achieving High-Level Expression of Genes in *Escherichia coli*" Savvas C. Makrides, Microbiological Reviews, Sept 1996, p 512-538.

[0187] The FkpA polynucleotide inserted into the expression vector preferably comprises the nucleic acid encoding the FkpA signal sequences and the FkpA coding sequence. The vector preferably contains a nucleic acid sequence that enables the vector to replicate in one or more selected host cells, preferably to replicate independently of the host chromosome. Such sequences are well known for a variety of bacteria.

[0188] In one embodiment the FkpA and/or Skp and/or the protein of interest comprises a histidine-tag at the N-terminus and/or C-terminus.

[0189] The antibody molecule may be secreted from the cell or targeted to the periplasm by suitable signal sequences. Alternatively, the antibody molecules may accumulate within the cell's cytoplasm. Preferably the antibody molecule is targeted to the periplasm.

[0190] The polynucleotide encoding the antibody may be expressed as a fusion with another polypeptide, preferably a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature polypeptide. The heterologous signal sequence selected should be one that is recognized and processed by the host cell. For prokaryotic host cells that do not recognize and process the native or a eukaryotic polypeptide signal sequence, the signal sequence is substituted by a prokaryotic signal sequence. Suitable signal sequences include OmpA, PhoA, LamB, PelB, DsbA and DsbC. In an embodiment where the cell comprises a polynucleotide sequence encoding a heavy chain of the antibody and a polynucleotide sequence encoding a light chain of the antibody, each polynucleotide may comprise a signal sequence, such as OmpA.

[0191] Construction of suitable vectors containing one or more of the above-listed components employs standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and re-ligated in the form desired to generate the plasmids required. General methods by which the vectors may be constructed, transfection methods and culture methods are well known to those skilled in the art. In this respect, reference is made to "Current Protocols in Molecular Biology", 1999, F. M. Ausubel (ed), Wiley Interscience, New York and the Maniatis Manual produced by Cold Spring Harbor Publishing.

[0192] Standard techniques of molecular biology may be used to prepare DNA sequences coding for the antibody. Desired DNA sequences may be synthesised completely or in part

using oligonucleotide synthesis techniques. Site-directed mutagenesis and polymerase chain reaction (PCR) techniques may be used as appropriate.

[0193] Embodiments of the invention described herein with reference to the polynucleotide apply equally to alternative embodiments of the invention, for example vectors, expression cassettes and/or host cells comprising the components employed therein, as far as the relevant aspect can be applied to same.

[0194] The cell according to the present invention may further comprise a polynucleotide sequence encoding a protein of interest. The polynucleotide sequence encoding the protein of interest may be exogenous or endogenous. The polynucleotide sequence encoding the protein of interest may be integrated into the host's chromosome or may be non-integrated in a vector, typically a plasmid.

[0195] In one embodiment the cell according to the present invention expresses a protein of interest. "Protein of interest" in the context of the present specification is intended to refer to polypeptide for expression, usually a recombinant polypeptide. However, the protein of interest may be an endogenous protein expressed from an endogenous gene in the host cell.

[0196] As used herein, a "recombinant polypeptide" refers to a protein that is constructed or produced using recombinant DNA technology. The protein of interest may be an exogenous sequence identical to an endogenous protein or a mutated version thereof, for example with attenuated biological activity, or fragment thereof, expressed from an exogenous vector. Alternatively, the protein of interest may be a heterologous protein, not normally expressed by the host cell.

[0197] The protein of interest may be any suitable protein including a therapeutic, prophylactic or diagnostic protein.

[0198] The skilled person would easily be able to test secreted protein to see if the protein is correctly folded using methods well known in the art, such as protein G HPLC, circular dichroism, NMR, X-Ray crystallography and epitope affinity measurement methods.

[0199] In one embodiment the protein of interest is useful in the treatment of diseases or disorders including immunological disorders and/or autoimmune diseases.

[0200] In one embodiment autoimmune disease is selected from acute disseminated encephalomyelitis (ADEM), acute necrotizing hemorrhagic leukoencephalitis, addison's disease, agammaglobulinemia, alopecia areata, amyloidosis, ANCA-associated vasculitis, ankylosing spondylitis, anti-GBM/Anti-TBM nephritis, antiphospholipid syndrome (APS), autoimmune angioedema, autoimmune aplastic anemia, autoimmune dysautonomia, autoimmune hepatitis, autoimmune hyperlipidemia, autoimmune immunodeficiency, autoimmune inner ear disease (AIED), autoimmune myocarditis, autoimmune pancreatitis, autoimmune retinopathy, autoimmune thrombocytopenic purpura (ATP), autoimmune thyroid

disease, autoimmune urticarial, axonal & neuronal neuropathies, balo disease, Behcet's disease, bullous pemphigoid, cardiomyopathy, Castleman disease, celiac disease, chagas disease, chronic fatigue syndrome, chronic inflammatory demyelinating polyneuropathy (CIDP), chronic recurrent multifocal osteomyelitis (CRMO), Churg-Strauss syndrome, cicatricial pemphigoid/benign mucosal pemphigoid, Crohn's disease, Cogans syndrome, cold agglutinin disease, congenital heart block, coxsackie myocarditis, CREST disease, essential mixed cryoglobulinemia, demyelinating neuropathies, dermatitis herpetiformis, dermatomyositis, Devic's disease (neuromyelitis optica), dilated cardiomyopathy, discoid lupus, Dressler's syndrome, endometriosis, eosinophilic angiocentric fibrosis, eosinophilic fasciitis, erythema nodosum, experimental allergic encephalomyelitis, Evans syndrome, fibromyalgia, fibrosing alveolitis, giant cell arteritis (temporal arteritis), glomerulonephritis, Goodpasture's syndrome, granulomatosis with polyangiitis (GPA) see Wegener's, Graves' disease, Guillain-Barre syndrome, Hashimoto's encephalitis, Hashimoto's thyroiditis, hemolytic anemia, Henoch-Schönlein purpura, herpes gestationis, hypogammaglobulinemia, idiopathic hypocomplementemic tubulointerstitial nephritis, idiopathic thrombocytopenic purpura (ITP), IgA nephropathy, IgG4-related disease, IgG4-related sclerosing disease, immunoregulatory lipoproteins, inflammatory aortic aneurysm, inflammatory pseudotumour, inclusion body myositis, insulin-dependent diabetes (type1), interstitial cystitis, juvenile arthritis, juvenile diabetes, Kawasaki syndrome, Kuttner's tumour, Lambert-Eaton syndrome, leukocytoclastic vasculitis, lichen planus, lichen sclerosus, ligneous conjunctivitis, linear IgA disease (LAD), Lupus (SLE), Lyme disease, chronic, mediastinal fibrosis, Ménière's disease, microscopic polyangiitis, Mikulicz's syndrome, mixed connective tissue disease (MCTD), Mooren's ulcer, Mucha-Habermann disease, multifocal fibrosclerosis, multiple sclerosis, myasthenia gravis, myositis, narcolepsy, neuromyelitis optica (Devic's), neutropenia, ocular cicatricial pemphigoid, optic neuritis, Ormond's disease (retroperitoneal fibrosis), palindromic rheumatism, PANDAS (Pediatric Autoimmune neuropsychiatric disorders associated with Streptococcus), paraneoplastic cerebellar degeneration, paraproteinemic polyneuropathies, paroxysmal nocturnal hemoglobinuria (PNH), Parry Romberg syndrome, Parsonage-Turner syndrome, pars planitis (peripheral uveitis), pemphigus vulgaris, periaortitis, periarthritis, peripheral neuropathy, perivenous encephalomyelitis, pernicious anemia, POEMS syndrome, polyarteritis nodosa, Type I, II, & III autoimmune polyglandular syndromes, polymyalgia rheumatica, polymyositis, postmyocardial infarction syndrome, postpericardiotomy syndrome, progesterone dermatitis, primary biliary cirrhosis, primary sclerosing cholangitis, psoriasis, psoriatic arthritis, idiopathic pulmonary fibrosis, pyoderma gangrenosum, pure red cell aplasia, Raynaud's phenomenon, reflex sympathetic dystrophy, Reiter's syndrome, relapsing polychondritis, restless legs syndrome, retroperitoneal fibrosis (Ormond's disease), rheumatic fever, rheumatoid arthritis, Riedel's thyroiditis, sarcoidosis, Schmidt syndrome, scleritis, scleroderma, Sjögren's syndrome, Sperm & testicular autoimmunity, stiff person syndrome, subacute bacterial endocarditis (SBE), Susac's syndrome, sympathetic ophthalmia, Takayasu's arteritis, temporal arteritis/giant cell arteritis, thrombotic, thrombocytopenic purpura (TTP), Tolosa-Hunt syndrome, transverse myelitis, ulcerative colitis, undifferentiated connective tissue disease (UCTD), uveitis, vasculitis, vesiculobullous dermatosis, vitiligo, Waldenström macroglobulinaemia, warm idiopathic haemolytic anaemia and Wegener's granulomatosis (now termed Granulomatosis with Polyangiitis (GPA)).

[0201] In one embodiment the neurological disorder is selected from chronic inflammatory demyelinating polyneuropathy (CIDP), Guillain-Barre syndrome, paraproteinemic polyneuropathies, neuromyelitis optica (NMO, NMO spectrum disorders or NMO spectrum diseases), and myasthenia gravis.

[0202] In one embodiment the immunology haematology disorder is selected from idiopathic thrombocytopenic purpura (ITP), thrombotic thrombocytopenic purpura (TTP), warm idiopathic haemolytic anaemia, Goodpasture's syndrome, and transplantation donor mismatch due to anti-HLA antibodies.

[0203] In one embodiment the disease is selected from myasthenia gravis, neuro- myelitis optica, CIDP, Guillaume-Barre Syndrome, Para-proteinemic Poly neuropathy, Refractory Epilepsy, ITP/TTP, hemolytic anemia, Goodpasture's Syndrome, ABO mismatch, Lupus nephritis, renal vasculitis, sclero-derma, fibrosing alveolitis, dilated cardio-myopathy, Grave's Disease, Type 1 diabetes, auto-immune diabetes, pemphigus, sclero-derma, lupus, ANCA vasculitis, dermatomyositis, Sjogren's disease and rheumatoid arthritis.

[0204] In one embodiment the dermatology disorder is selected from bullous pemphigoid, pemphigus vulgaris, ANCA-associated vasculitis and dilated cardiomyopathy.

[0205] In one embodiment the antibodies or fragments according to the present disclosure may be employed in prophylaxis or treatment of alloimmune diseases associated with allogenic organ or tissue transplantation or certain neonatal conditions.

[0206] The protein may be a proteolytically-sensitive polypeptide, i.e. proteins that are prone to be cleaved, susceptible to cleavage, or cleaved by one or more gram-negative bacterial, such as *E. coli*, proteases, either in the native state or during secretion. In one embodiment the protein of interest is proteolytically-sensitive to a protease selected from DegP, Protease III and Tsp. In one embodiment the protein of interest is proteolytically-sensitive to the protease Tsp. In one embodiment the protein of interest is proteolytically-sensitive to the proteases DegP and Protease III. In one embodiment the protein of interest is proteolytically sensitive to the proteases DegP and Tsp. In one embodiment the protein of interest is proteolytically-sensitive to the proteases Tsp and Protease III. In one embodiment the protein of interest is proteolytically sensitive to the proteases DegP, Protease III and Tsp.

[0207] Preferably the protein is a eukaryotic polypeptide.

[0208] The protein of interest expressed by the cells according to the invention may, for example be an immunogen, a fusion protein comprising two heterologous proteins or an antibody. Antibodies for use as the protein of interest include monoclonal, multi-valent, multi-specific, humanized, fully human or chimeric antibodies. The antibody can be from any species but is preferably derived from a monoclonal antibody, a human antibody, or a humanized fragment. The antibody can be derived from any class (e.g. IgG, IgE, IgM, IgD or IgA) or

subclass of immunoglobulin molecule and may be obtained from any species including for example mouse, rat, shark, rabbit, pig, hamster, camel, llama, goat or human. Parts of the antibody fragment may be obtained from more than one species for example the antibody fragments may be chimeric. In one example the constant regions are from one species and the variable regions from another.

[0209] The antibody may be a complete antibody molecule having full length heavy and light chains or a fragment thereof, e.g. VH, VL, VHH, Fab, modified Fab, Fab', F(ab')₂, Fv, scFv fragment, or a dual specificity antibody, such as a Fab-dAb or Fab-Fv, as described in WO2009/040562 and WO2010/035012.

[0210] In one embodiment the protein is a Fab'.

[0211] The antibody may be specific for any target antigen. The antigen may be a cell-associated protein, for example a cell surface protein on cells such as bacterial cells, yeast cells, T-cells, endothelial cells or tumour cells, or it may be a soluble protein. Antigens of interest may also be any medically relevant protein such as those proteins upregulated during disease or infection, for example receptors and/or their corresponding ligands. Particular examples of cell surface proteins include adhesion molecules, for example integrins such as β 1 integrins e.g. VLA-4, E-selectin, P selectin or L-selectin, CD2, CD3, CD4, CD5, CD7, CD8, CD11a, CD11b, CD18, CD19, CD20, CD23, CD25, CD33, CD38, CD40, CD40L, CD45, CDW52, CD69, CD134 (OX40), ICOS, BCMP7, CD137, CD27L, CDCP1, CSF1 or CSF1-Receptor, DPCR1, DPCR1, dudulin2, FLJ20584, FLJ40787, HEK2, KIAA0634, KIAA0659, KIAA1246, KIAA1455, LTBP2, LTK, MAL2, MRP2, nectin-like2, NKCC1, PTK7, RAIG1, TCAM1, SC6, BCMP101, BCMP84, BCMP11, DTD, carcinoembryonic antigen (CEA), human milk fat globulin (HMFG1 and 2), MHC Class I and MHC Class II antigens, KDR and VEGF, and where appropriate, receptors thereof.

[0212] Soluble antigens include interleukins such as IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8, IL-12, IL-13, IL-14, IL-16 or IL-17, such as IL17A and/or IL17F, viral antigens for example respiratory syncytial virus or cytomegalovirus antigens, immunoglobulins, such as IgE, interferons such as interferon α , interferon β or interferon γ , tumour necrosis factor TNF (formerly known as tumour necrosis factor- α), tumor necrosis factor- β , colony stimulating factors such as G-CSF or GM-CSF, and platelet derived growth factors such as PDGF- α , and PDGF- β and where appropriate receptors thereof. Other antigens include bacterial cell surface antigens, bacterial toxins, viruses such as influenza, EBV, HepA, B and C, bioterrorism agents, radionuclides and heavy metals, and snake and spider venoms and toxins.

[0213] In one embodiment the antigen is FcRn.

[0214] Antibodies for use in the present disclosure may be obtained using any suitable method known in the art. The FcRn polypeptide/protein including fusion proteins and mutants thereof, including cells (recombinantly or naturally) expressing the polypeptide (such as activated T cells) can be used to produce antibodies which specifically recognise FcRn. The polypeptide

may be the 'mature' polypeptide or a biologically active fragment or derivative thereof. The human protein is registered in Swiss-Prot under the number P55899. In one embodiment the immunogen is the FcRn alpha chain or a fragment thereof.

[0215] Polypeptides, for use to immunize a host, may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems or they may be recovered from natural biological sources. In the present application, the term "polypeptides" includes peptides, polypeptides and proteins. These are used interchangeably unless otherwise specified. The FcRn polypeptide may in some instances be part of a larger protein such as a fusion protein for example fused to an affinity tag.

[0216] Antibodies generated against the FcRn polypeptide may be obtained, where immunisation of an animal is necessary, by administering the polypeptides to an animal, preferably a non-human animal, using well-known and routine protocols, see for example Handbook of Experimental Immunology, D. M. Weir (ed.), Vol 4, Blackwell Scientific Publishers, Oxford, England, 1986). Many warm-blooded animals, such as rabbits, mice, rats, sheep, cows, camels or pigs may be immunized. However, mice, rabbits, pigs and rats are generally most suitable.

[0217] In one embodiment, the antibody may be used to functionally alter the activity of the antigen of interest. For example, the antibody may neutralize, antagonize or agonise the activity of said antigen, directly or indirectly or simply blocks binding of the normal ligand thereto.

[0218] The present invention also provides a recombinant gram-negative bacterial cell comprising a mutated Tsp gene, wherein the mutated Tsp gene encodes a Tsp protein having reduced protease activity or is a knockout mutated Tsp gene, a mutant spr gene encoding a mutant spr, a gene capable of expressing or overexpressing one or proteins capable of facilitating protein folding and a polynucleotide sequence encoding an antibody or an antigen binding fragment thereof specific for FcRn.

[0219] Various anti-FcRn antibodies and fragments are shown in sequences 36 to 74.

[0220] In one embodiment the heavy chain comprises 1, 2 or 3 CDRs independently selected from SEQ ID NO: 36, 37 and 38.

[0221] In one embodiment the light chain comprises 1, 2 or 3 CDRs independently selected from SEQ ID NO: 39, 40 and 41.

[0222] In one embodiment the antibody heavy chain comprises the sequence given in SEQ ID NO:36 for CDR-H1, the sequence given in SEQ ID NO:37 for CDR-H2 and the sequence given in SEQ ID NO:38 for CDRH3.

[0223] In one embodiment the antibody light chain comprises the sequence given in SEQ ID

NO:39 for CDR-L1, the sequence given in SEQ ID NO:40 for CDR-L2 and the sequence given in SEQ ID NO:41 for CDRL3.

[0224] In one embodiment the antibody heavy chain comprises the sequence given in SEQ ID NO:36 for CDR-H1, the sequence given in SEQ ID NO:37 for CDR-H2, the sequence given in SEQ ID NO:38 for CDRH3, the sequence given in SEQ ID NO:39 for CDR-L1, the sequence given in SEQ ID NO:40 for CDR-L2 and the sequence given in SEQ ID NO:41 for CDRL3.

[0225] In one embodiment the cell expresses an antibody molecule with a sequence disclosed herein.

[0226] Antibody molecules include antibodies and binding fragments thereof.

[0227] Suitably, the humanised antibody according to the present invention has a variable domain comprising human acceptor framework regions as well as one or more of the CDRs provided specifically herein. Thus, provided in one embodiment is a humanised antibody which binds human FcRn wherein the variable domains comprise human acceptor framework regions and non-human donor CDRs. In one example the light chain variable domain comprises the sequence given in SEQ ID NO:50 and the heavy chain variable domain comprises the sequence given in SEQ ID NO:58. In one example the light chain comprises the sequence given in SEQ ID NO:54 and the heavy chain comprises the sequence given in SEQ ID NO:62.

[0228] After expression, antibody fragments may be further processed, for example by conjugation to another entity such as an effector molecule.

[0229] The term effector molecule as used herein includes, for example, antineoplastic agents, drugs, toxins (such as enzymatically active toxins of bacterial or plant origin and fragments thereof e.g. ricin and fragments thereof) biologically active proteins, for example enzymes, other antibody or antibody fragments, synthetic or naturally occurring polymers, nucleic acids and fragments thereof e.g. DNA, RNA and fragments thereof, radionuclides, particularly radioiodide, radioisotopes, chelated metals, nanoparticles and reporter groups such as fluorescent compounds or compounds which may be detected by NMR or ESR spectroscopy. Effector molecular may be attached to the antibody or fragment thereof by any suitable method, for example an antibody fragment may be modified to attach at least one effector molecule as described in WO05/003171 or WO05/003170 (the contents of which are incorporated herein by reference). WO05/003171 or WO05/003170 also describe suitable effector molecules.

[0230] In one embodiment the antibody or fragment thereof, such as a Fab, is PEGylated to generate a product with the required properties, for example similar to the whole antibodies, if required. For example, the antibody may be a PEGylated anti-TNF- α Fab', as described in WO01/094585, preferably having attached to one of the cysteine residues at the C-terminal end of the heavy chain a lysyl-maleimide-derived group wherein each of the two amino groups of the lysyl residue has covalently linked to it a methoxypoly(ethyleneglycol) residue having a

molecular weight of about 20,000 Da, such that the total average molecular weight of the methoxypoly(ethyleneglycol) residues is about 40,000Da, more preferably the lysyl-maleimide-derived group is [1-[[[2-[[3-(2,5-dioxo-1-pyrrolidinyl)-1-oxopropyl]amino]ethyl]amino]-carbonyl]-1,5-pentanediy]bis(iminocarbonyl).

[0231] In one embodiment a Fab or Fab' according to the present disclosure is conjugated to a human serum albumin molecule or a starch molecule.

[0232] The cell may also comprise further polynucleotide sequences encoding one or more further proteins of interest.

[0233] Additionally disclosed herein are cells where one or more *E. coli* host proteins that in the wild type are known to co-purify with the recombinant protein of interest during purification are selected for genetic modification, as described in Humphreys et al. "Engineering of Escherichia coli to improve the purification of periplasmic Fab' fragments: changing the pI of the chromosomally encoded PhoS/PstS protein", Protein Expression and Purification 37 (2004) 109-118 and WO04/035792 (the contents of which are incorporated herein by reference). The use of such modified host proteins improves the purification process for proteins of interest, especially antibodies, produced in *E.coli* by altering the physical properties of selected *E.coli* proteins so they no longer co-purify with the recombinant antibody. Preferably the *E.coli* protein that is altered is selected from one or more of Phosphate binding protein (PhoS/PstS), Dipeptide binding protein (DppA), Maltose binding protein (MBP) and Thioredoxin.

[0234] In one example a physical property of a contaminating host protein is altered by the addition of an amino acid tag to the C-terminus or N-terminus. In a preferred embodiment the physical property that is altered is the isoelectric point and the amino acid tag is a poly-aspartic acid tag attached to the C-terminus. In one embodiment the *E.coli* proteins altered by the addition of said tag are Dipeptide binding protein (DppA), Maltose binding protein (MBP), Thioredoxin and Phosphate binding protein (PhoS/PstS). In one specific embodiment the pI of the *E. coli* Phosphate binding protein (PhoS/PstS) is reduced from 7.2 to 5.1 by the addition of a poly-aspartic acid tag (polyD), containing 6 aspartic acid residues to the C-terminus.

[0235] Also described is the modification of specific residues of the contaminating *E. coli* protein to alter its physical properties, either alone or in combination with the addition of N or C terminal tags. Such changes can include insertions or deletions to alter the size of the protein or amino acid substitutions to alter pI or hydrophobicity. These residues may be located on the surface of the protein. In embodiment particular example surface residues of the PhoS protein are altered in order to reduce the pI of the protein. Residues that have been implicated to be important in phosphate binding (Bass, US5,304,472) are avoided in order to maintain a functional PhoS protein. Preferably lysine residues that project far out of the surface of the protein or are in or near large groups of basic residues are targeted. In one example, the PhoS protein has a hexa poly-aspartic acid tag attached to the C-terminus whilst surface residues at the opposite end of the molecule are targeted for substitution. Preferably selected lysine residues are substituted for glutamic acid or aspartic acid to confer a greater potential pI

change than when changing neutral residues to acidic ones. The designation for a substitution mutant herein consists of a letter followed by a number followed by a letter. The first letter designates the amino acid in the wild-type protein. The number refers to the amino acid position where the amino acid substitution is being made, and the second letter designates the amino acid that is used to replace the wild-type amino acid. In preferred mutations of PhoS in the present invention lysine residues (K) 275, 107, 109, 110, 262, 265, 266, 309, 313 are substituted for glutamic acid (E) or glutamine (Q), as single or combined mutations, in addition lysine(K)318 may be substituted for aspartic acid (D) as a single or combined mutation. Preferably the single mutations are K262E, K265E and K266E. Preferably the combined mutations are K265/266E and K110/265/266E. More preferably, all mutations are combined with the polyaspartic acid (polyD) tag attached at the C-terminus and optionally also with the K318D substitution. In a further example the mutations result in a reduction in pI of at least 2 units. Preferably the mutations reduce the pI of PhoS from 7.2 to between about 4 and about 5.5. In one example the pI of the PhoS protein of *E. coli* is reduced from 7.2 to about 4.9, about 4.8 and about 4.5 using the mutations polyD K318D, polyD K265/266E and polyD K110/265/266E respectively.

[0236] The polynucleotide encoding the protein of interest may be expressed as a fusion with another polypeptide, preferably a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature polypeptide. The heterologous signal sequence selected should be one that is recognized and processed by the host cell. For prokaryotic host cells that do not recognize and process the native or a eukaryotic polypeptide signal sequence, the signal sequence is substituted by a prokaryotic signal sequence. Suitable signal sequences include OmpA, PhoA, LamB, PelB, DsbA and DsbC.

[0237] Construction of suitable vectors containing one or more of the above-listed components employs standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and re-ligated in the form desired to generate the plasmids required.

[0238] In one embodiment an expression cassette is employed in the present invention to carry the polynucleotide encoding the protein of interest which typically comprises one or more protein coding sequences encoding one or more proteins of interest and one or more regulatory expression sequences. The one or more regulatory expression sequences may include a promoter. The one or more regulatory expression sequences may also include a 3' untranslated region such as a termination sequence. Suitable promoters are discussed in more detail below.

[0239] In one embodiment, the cell according to the present invention comprises a vector, such as plasmid. The vector preferably comprises one or more of the expression cassettes as defined above.

[0240] In the embodiment where the protein of interest is an antibody comprising both heavy and light chains, the cell line may be transfected with two vectors, a first vector encoding a light chain polypeptide and a second vector encoding a heavy chain polypeptide. Alternatively, a

single vector may be used, the vector including sequences encoding light chain and heavy chain polypeptides.

[0241] The vector for use in the present invention may be produced by inserting an expression cassette as defined above into a suitable vector. Alternatively, the regulatory expression sequences for directing expression of the polynucleotide sequence encoding a protein of interest may be contained in the vector and thus only the encoding region of the polynucleotide may be required to complete the vector.

Examples of vectors which may be employed to transform the host cell with a polynucleotide according to the invention include: a plasmid, such as pBR322 or pACYC184, and/or a viral vector such as bacterial phage, a transposable genetic element such as a transposon.

[0242] Many forms of expression vector are available. Such vectors usually comprise a plasmid origin of DNA replication, an antibiotic selectable marker a promoter and transcriptional terminator separated by a multi-cloning site (expression cassette) and a DNA sequence encoding a ribosome binding site.

[0243] The promoters employed in the present invention can be linked to the relevant polynucleotide directly or alternatively be located in an appropriate position, for example in a vector such that when the relevant polypeptide is inserted the relevant promoter can act on the same. In one embodiment the promoter is located before the encoding portion of the polynucleotide on which it acts, for example a relevant promoter before each encoding portion of polynucleotide. "Before" as used herein is intended to imply that the promoter is located at the 5 prime end in relation to the encoding polynucleotide portion.

[0244] The promoters may be endogenous or exogenous to the host cells. Suitable promoters include lac, tac, trp, phoA, lpp, Arab, tet and T7.

[0245] One or more promoters employed may be inducible promoters.

[0246] Expression units for use in bacterial systems also generally contain a Shine-Dalgarno (S. D.) ribosome sequence operably linked to the DNA encoding the polypeptide of interest.

[0247] The expression vector preferably also comprises a dicistronic message for producing the antibody or antigen binding fragment thereof as described in WO 03/048208 or WO2007/039714 (the contents of which are incorporated herein by reference). Preferably the upstream cistron contains DNA coding for the light chain of the antibody and the downstream cistron contains DNA coding for the corresponding heavy chain, and the dicistronic intergenic sequence (IGS) preferably comprises a sequence selected from IGS1 (SEQ ID NO: 38), IGS2 (SEQ ID NO: 39), IGS3 (SEQ ID NO: 40) and IGS4 (SEQ ID NO: 41).

[0248] The terminators may be endogenous or exogenous to the host cells. A suitable terminator is rrnB.

[0249] Further suitable transcriptional regulators including promoters and terminators and protein targeting methods may be found in "Strategies for Achieving High-Level Expression of Genes in Escherichia coli" Savvas C. Makrides, Microbiological Reviews, Sept 1996, p 512-538.

[0250] The antibody molecule may be secreted from the cell or targeted to the periplasm by suitable signal sequences. Alternatively, the antibody molecules may accumulate within the cell's cytoplasm. Preferably the antibody molecule is targeted to the periplasm.

[0251] Embodiments of the invention described herein with reference to the polynucleotide apply equally to alternative embodiments of the invention, for example vectors, expression cassettes and/or host cells comprising the components employed therein, as far as the relevant aspect can be applied to same.

[0252] The present invention also provides a method for producing a recombinant protein of interest comprising expressing the recombinant protein of interest in a recombinant gram-negative bacterial cell as described above for the present invention.

[0253] The gram negative bacterial cell and protein of interest preferably employed in the method of the present invention are described in detail above.

[0254] When the polynucleotide encoding the protein of interest is exogenous the polynucleotide may be incorporated into the host cell using any suitable means known in the art. Typically, the polynucleotide is incorporated as part of an expression vector which is transformed into the cell. Accordingly, in one aspect the cell according to the present invention comprises an expression cassette comprising the polynucleotide encoding the protein of interest.

[0255] The polynucleotide sequence can be transformed into a cell using standard techniques, for example employing rubidium chloride, PEG or electroporation.

[0256] As further disclosed herein the method may also employ a selection system to facilitate selection of stable cells which have been successfully transformed with the polynucleotide encoding the protein of interest. The selection system typically employs co-transformation of a polynucleotide sequence encoding a selection marker. In one example, each polynucleotide transformed into the cell further comprises a polynucleotide sequence encoding one or more selection markers. Accordingly, the transformation of the polynucleotide encoding the protein of interest and the one or more polynucleotides encoding the marker occurs together and the selection system can be employed to select those cells which produce the desired proteins.

[0257] Cells able to express the one or more markers are able to survive/grow/multiply under certain artificially imposed conditions, for example the addition of a toxin or antibiotic, because of the properties endowed by the polypeptide/gene or polypeptide component of the selection system incorporated therein (e.g. antibiotic resistance). Those cells that cannot express the

one or more markers are not able to survive/grow/multiply in the artificially imposed conditions. The artificially imposed conditions can be chosen to be more or less vigorous, as required.

[0258] Any suitable selection system may be employed in the present invention. Typically the selection system may be based on including in the vector one or more genes that provides resistance to a known antibiotic, for example a tetracycline, chloramphenicol, kanamycin or ampicillin resistance gene. Cells that grow in the presence of a relevant antibiotic can be selected as they express both the gene that gives resistance to the antibiotic and the desired protein.

[0259] In one embodiment, the method according to the present invention further comprises the step of culturing the transformed cell in a medium to thereby express the protein of interest.

[0260] An inducible expression system or a constitutive promoter may be used is disclosed to express the protein of interest. Suitable inducible expression systems and constitutive promoters are well known in the art.

[0261] Any suitable medium may be used to culture the transformed cell. The medium may be adapted for a specific selection system, for example the medium may comprise an antibiotic, to allow only those cells which have been successfully transformed to grow in the medium.

[0262] The cells obtained from the medium may be subjected to further screening and/or purification as required. The method may further comprise one or more steps to extract and purify the protein of interest as required.

[0263] The polypeptide may be recovered from the strain, including from the cytoplasm, periplasm, or supernatant.

[0264] In one embodiment the antibody is isolated from the periplasm.

[0265] In one embodiment the post induction feed rate is in the range 5 to 7.5g/h, such as about 7g/h.

[0266] The specific method (s) used to purify a protein depends on the type of protein. Suitable methods include fractionation on immuno-affinity or ion-exchange columns; ethanol precipitation; reversed-phase HPLC; hydrophobic-interaction chromatography; chromatography on silica; chromatography on an ion-exchange resin such as S-SEPHAROSE and DEAE; chromatofocusing; ammonium-sulfate precipitation; and gel filtration.

[0267] Antibodies may be suitably separated from the culture medium and/or cytoplasm extract and/or periplasm extract by conventional antibody purification procedures such as, for example, protein A-Sepharose, protein G chromatography, protein L chromatography, thiophilic, mixed mode resins, His-tag, FLAGTag, hydroxylapatite chromatography, gel electrophoresis,

dialysis, affinity chromatography, Ammonium sulphate, ethanol or PEG fractionation/precipitation, ion exchange membranes, expanded bed adsorption chromatography (EBA) or simulated moving bed chromatography..

[0268] The method may also include a further step of measuring the quantity of expression of the protein of interest and selecting cells having high expression levels of the protein of interest.

[0269] The method may also include one or more further downstream processing steps such as PEGylation of the protein of interest, such as an antibody or antibody fragment.

[0270] One or more method steps described herein may be performed in combination in a suitable container such as a bioreactor.

The antibodies and fragments according to the present disclosure may be employed in treatment or prophylaxis.

Where technically appropriate embodiments of the invention may be combined. Embodiments are described herein as comprising certain features/elements. The disclosure also extends to separate embodiments consisting or consisting essentially of said features/elements. Technical references herein, such as patents & applications are incorporated herein by reference.

The present invention is further described by way of illustration only in the following examples, which refer to the accompanying Figures.

EXAMPLES

Example 1: Generation of Cell Lines

[0271] The generation of MXE016 and MXE017 is given in WO2011/086136.

[0272] Generation of plasmids for anti-FcRn Fab' expression and anti-FcRn Fab' with FkpA, anti-FcRn Fab' with skp and anti-FcRn Fab with both FkpA and skp expression

[0273] A plasmid was constructed containing both the heavy and light chain sequences of an anti-FcRn Fab (SEQ ID NOs: 63 and 55, respectively. Plasmid pTTOD 1519.g57 Fab', was constructed using conventional restriction cloning methodologies which can be found in Sambrook et al 1989, Molecular cloning: a laboratory manual. CSHL press, N.Y. The plasmid pTTOD 1519.g57 Fab' contained the following features; a strong *tac* promoter and *lac* operator sequence. The plasmid contained a unique EcoRI restriction site after the coding region of the Fab' heavy chain, followed by a non-coding sequence containing a strong ribosome binding site and then a unique NdeI restriction site.

[0274] The Fab light chain, heavy chain genes were transcribed as a single polycistronic

message. DNA encoding the signal peptide from the *E. coli* OmpA protein was fused to the 5' end of both light and heavy chain gene sequences, which directed the translocation of the polypeptides to the *E. coli* periplasm. Transcription was terminated using a dual transcription terminator *rrnB t1t2*. The *lacIq* gene encoded the constitutively expressed Lac I repressor protein. This repressed transcription from the *tac* promoter until de-repression was induced by the presence of allolactose or IPTG. The origin of replication used was p15A, which maintained a low copy number. The plasmid contained a tetracycline resistance gene for antibiotic selection.

[0275] Plasmid pTTOD 1519.g57 Fab' FkpA, an expression vector for the anti-FcRn Fab and FkpA (a periplasmic polypeptide), was constructed by ligating FkpA to the 3'end of the Fab' sequence of pTTOD 1519.g57 Fab' using the EcoRI and NdeI sites (See Figure 7d). The FkpA (SEQ ID NO:30) was synthetically constructed to remove 2 Puv II sites, an SfuI site, a BamHI site and an EcoRI, such that the new construct encoded for a 5' EcoRI site followed by a strong ribosome binding site, followed by the native start codon, signal sequence and mature sequence of FkpA, terminating in a C-terminal His tag and finally a strong ribosome binding site followed by a non-coding NdeI site. The EcoRI-NdeI restriction fragment was restricted and ligated into the expression vector such that all three polypeptides: Fab' light chain, Fab' heavy chain and FkpA were encoded on a single polycistronic mRNA.

[0276] Plasmid pTTOD 1519.g57 Fab' Skp, an expression vector for the anti-FcRn Fab and Skp (a periplasmic polypeptide), was constructed by ligating skp to the 3'end of the Fab' sequence of plasmid pTTOD 1519.g57 Fab' using the EcoRI and NdeI sites. The skp (SEQ ID NO:34) was synthetically constructed to remove 4 Pst I sites and an EcoRV site, such that the new construct encoded for a 5' EcoRI site followed by a strong ribosome binding site, followed by the native start codon, signal sequence and mature sequence of Skp, terminating in a C-terminal His tag and finally a strong ribosome binding site followed by a non-coding NdeI site. The EcoRI-NdeI restriction fragment was restricted and ligated into the expression vector such that all three polypeptides: Fab' light chain, Fab' heavy chain and skp were encoded on a single polycistronic mRNA.

[0277] Plasmid pTTOD 1519.g57 Fab' FkpA Skp an expression vector for the anti-FcRn Fab, FkpA and Skp (both periplasmic polypeptides), was constructed by ligating Skp into plasmid pTTOD 1519.g57 Fab' FkpA, at the 3'end of the FkpA sequence using the NdeI site. The Skp (SEQ ID NO:34) was synthetically constructed to remove 4 Pst I sites and an EcoRV site, such that the construct encoded for a 5' Ase I site including the native start codon, signal sequence and mature sequence of skp, terminating in a C-terminal His tag and finally a non-coding NdeI site. The AseI-NdeI restriction fragment was restricted and ligated into the expression vector such that all four polypeptides: Fab' light chain, Fab' heavy chain, FkpA and Skp were encoded on a single polycistronic mRNA.

[0278] Fermentation of pTTOD 1519.g57 Fab', pTTOD 1519.g57 Fab' FkpA, pTTOD 1519.g57 Fab' Skp and pTTOD 1519.g57 Fab' FkpA skp in *E.coli* W3110, MXE012 (*E. coli* W3110 spr H145A), MXE016 (*E. coli* W3110 ΔTsp, spr C94A) and MXE017 (*E. coli* W3110 ΔTsp, spr

H145A) The *E. coli* strains W3110, MXE012, MXE016 and MXE017 were transformed with the plasmids pTTOD 1519.g57 Fab', pTTOD 1519.g57 Fab' FkpA, pTTOD 1519.g57 Fab' Skp and pTTOD 1519.g57 Fab' FkpA Skp generated in Example 1. The transformation of the strains was carried out using the method found in Chung C.T et al Transformation and storage of bacterial cells in the same solution. PNAS 86:2172-2175 (1989). These transformed strains were tested for expression by fermentation.

[0279] Example 2: Effect of chaperones on Fab' expression: The strains shown in **Figure 1** were tested in 1L and 2.5L fermentation experiments comparing expression of Fab':

Growth medium, inoculum and fermentation steps. The fermentation process was initiated by preparing an inoculum from a vial of the cell bank and amplifying through several pre-culture stages (flask and reactors) before seeding of the production fermenter. In the production fermenter, the cells were grown in defined media to high density in batch and fed-batch mode. When the desired cell density was reached expression of the Fab' was induced by the addition of IPTG. The Fab' expression is targeted to the *E. coli* periplasmic space, where Fab' accumulates throughout the course of the induction phase. A carbon source feed was applied during the induction phase to control expression and cell growth. Temperature, dissolved oxygen (pO₂) and pH were controlled to maintain the culture within optimal culture conditions.

[0280] Measurement of biomass concentration and growth rate. Biomass concentration was determined by measuring the optical density of cultures at 600 nm.

[0281] Periplasmic Extraction. Cells were collected from culture samples by centrifugation. The supernatant fraction was retained (at -20°C) for further analysis. The cell pellet fraction was resuspended to the original culture volume in extraction buffer (100 mM Tris-HCl, 10 mM EDTA; pH 7.4). Following incubation at 60°C for approximately 10 to 12 hours the extract was clarified by centrifugation and the supernatant fraction used fresh or retained (at -20°C) for analysis.

[0282] Fab' quantification. Fab' concentrations in periplasmic extracts and culture supernatants were determined by using Protein G HPLC. A HiTrap Protein-G HP 1ml column (GE-Healthcare or equivalent) was loaded with analyte (approximately neutral pH, 30°C, 0.2µm filtered) at 2ml/min, the column was washed with 20mM phosphate, 50mM NaCl pH 7.4 and then Fab' was eluted using an injection of 50mM Glycine/HCl pH 2.7. Eluted Fab' was measured by A280 on an Agilent 1100 or 1200 HPLC system and quantified by reference to a standard curve of a purified Fab' protein of known concentration.

[0283] Figure 1 shows the results of 46 fermentations on the 5L scale performed with various combinations of host cells and "chaperone". W3110 is a wild-type *E coli* strain. The various combinations were: wild type with no chaperone, wild-type with FkpA and Skp, MXE016 mutant spr and Δ Tsp published in WO2011/086136, MXE016 and FkpA, MXE016 and Skp, MXE016 and FkpA and Skp, MXE017 disclosed in WO2011/086136, MXE017 and FkpA and Skp.

[0284] The results show that MXE016, MXE016 and FkpA, MXE016 and FkpA and Skp, and MXE017 and FkpA and Skp showed the best levels of expression.

Example 3: Effect of post induction feed rate

[0285] The effect of three different post induction feed rates 5.4, 6.0 and 7.0g/h was tested on MXE016 and MXE016 + FkpA.

[0286] **Growth medium, inoculum and fermentation steps.** The fermentation process was initiated by preparing an inoculum from a vial of the cell bank and amplifying through several pre-culture stages (flask and reactors) before seeding of the production fermenter. In the production fermenter, the cells were grown in defined media to high density in batch and fed-batch mode. When the desired cell density was reached expression of the Fab' was induced by the addition of IPTG. The Fab' expression is targeted to the *E. coli* periplasmic space, where Fab' accumulates throughout the course of the induction phase. A carbon source feed was applied during the induction phase to control expression and cell growth, in this experiment the feed rate set at three separate setpoints (shown in the figure). Temperature, dissolved oxygen (pO₂) and pH were controlled to maintain the culture within optimal culture conditions.

[0287] **Figure 2** shows strain MXE016 transformed with plasmids expressing either no chaperone or FkpA. The figure shows the effect of increasing the post-induction feed rate on Fab' production and retention in the periplasm both with and without FkpA. The data shows that when the feed rate is increased without FkpA expression the additional Fab' produced is lost to the supernatant. This is not the case with expression of FkpA where the additional Fab' produced at higher feed rates is retained within the periplasm resulting in a higher titre.

Example 4: Analysis of yield and cell viability

[0288] Figures 3A and B show effect on cell viability and Fab' titre in MXE016 transformed with plasmids expressing either no chaperone or FkpA at 20L scale. Figure 3A shows that cell viability is lower where no FkpA is present. 3b shows that Fab'titres were higher and less variable for MXE016 + FkpA.

[0289] Figure 4 shows the higher titre with MXE016+FkpA results in 30% more Fab' following primary Fab product recovery.

[0290] Figure 5 and 6 show SDS-PAGE and anti-his-tag western blots of samples from the primary recovery of MXE016 with no chaperone and MXE016 with FkpA expression.

[0291] Samples were loaded according to Fab' concentration with 1µg of Fab' loaded per lane. Gels were 4-20% Tris-Glycine Novex and were run under non-reducing conditions at 125V for

2 hours. Gels were stained with Sypro Ruby stain and imaged. The western blots were transferred to a PVDF membrane using an Invitrogen iBlot system and then blocked with 1% casein solution. The membranes were then probed with an anti-his HRP conjugate antibody (Novagen). The blots were then developed with ECL solution and imaged using an Amersham Life Sciences HyperProcessor.

SEQUENCE LISTING

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<130> G0164-WO

<150> GB1208367.1

<151> 2012-05-14

<160> 82

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tggaaagtgt gggagaacgt cagcgcgttg cagcaaacaa tgcccctgat gagtgaaaag	2880
aatgagtga	2889

<210> 7

<211> 1425

<212> DNA

<213> Escherichia coli

<400> 7

atgaaaaaaa ccacattagc actgagtgca ctggctctga gtttaggttt ggcgttatct	60
ccgctctctg caacggcggc tgagacttct tcagcaacga cagcccagca gatgccaaagc	120
cttgcacoga tgctcgaaaa ggtgatgcct tcagtggcca gcattaacgt agaaggtagc	180
acaaccgtta atacgcgcgc tatgccgcgt aatttccagc agttcttcgg tgatgattct	240
cogttctgcc aggaaggttc tccgttcag agctctccgt tctgccaggg tggccagggc	300
ggtaatgggtg gcggccagca acagaaatc atggcgctgg gttccggcgt catcattgat	360
gccgataaag gctatgtcgt caccaacaac caggttggtg ataacgcgac ggtcattaaa	420
gttcaactga gcgatggccg taagttcgac gcgaagatgg ttggcaaaga tccgcgctct	480
gatatcgcgc tgatccaaat ccagaacccg aaaaacctga ccgcaattaa gatggcggat	540
tctgatgcac tgcgcgtggg tgattacacc gtagegattg gtaaccogtt tggctcgggc	600
gagacggtaa cttccgggat tgtctctgcg ctggggcgta gcggcctgaa tgccgaaaac	660
tacgaaaact tcatccagac cgatgcagcg atcaaccgtg gtaactccgg tgggtcgcgtg	720
gttaacctga acggcgaaat gatcgggtatc aacaccgcga tcctcgacc ggacggcggc	780

```

aacatcggtgta tcggtttttgc tatcccgagt aacatggtga aaaacctgac ctgcgagatg      840
gtggaatacgc gccaggtgaa acgcggtgag ctgggtatta tggggactga gctgaactcc      900
gaactggcga aagcgatgaa agttgacgcc cagcgcggtg ctttcgtaag ccaggttctg      960
cctaattcct ccgctgcaaa agcgggcatt aaagcgggtg atgtgatcac ctactgaac     1020
ggtaagccga tcagcagctt tgccgcactg cgtgctcagg tgggtactat gccggtaggc     1080
agcaactga ccctgggctt actgcgcgac ggtaagcagg ttaacgtgaa cctggaactg     1140
cagcagagca gccagaatca ggttgattcc agctccatct tcaacggcat tgaaggcgt      1200
gagatgagca acaaaggcaa agatcagggc gtggtagtga acaacgtgaa aacgggcact      1260
ccggctgcgc agatcggcct gaagaaaggt gatgtgatta ttggcgcgaa ccagcaggca      1320
gtgaaaaaca tcgctgaact gcgtaaagtt ctgcacagca aaccgtctgt gctggcactc      1380
aacattcagc gcggcgacag caccatctac ctgttaatgc agtaa                        1425

```

<210> 8

<211> 474

<212> PRT

<213> Escherichia coli

<400> 8

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Met Lys Lys Thr Thr Leu Ala Leu Ser Ala Leu Ala Leu Ser Leu Gly
1           5           10           15

```

```

Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ala
           20           25           30

```

```

Thr Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys Val
35           40           45

```

```

Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val Asn
50           55           60

```

```

Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp Ser
65           70           75           80

```

```

Pro Phe Cys Gln Glu Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys Gln
85           90           95

```

```

Gly Gly Gln Gly Gly Asn Gly Gly Gly Gln Gln Gln Lys Phe Met Ala
100          105          110

```

```

Leu Gly Ser Gly Val Ile Ile Asp Ala Asp Lys Gly Tyr Val Val Thr
115          120          125

```

```

Asn Asn His Val Val Asp Asn Ala Thr Val Ile Lys Val Gln Leu Ser
130          135          140

```

```

Asp Gly Arg Lys Phe Asp Ala Lys Met Val Gly Lys Asp Pro Arg Ser
145          150          155          160

```

Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile
 165 170 175

Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala
 180 185 190

Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser Gly Ile Val
 195 200 205

Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe
 210 215 220

Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ser Gly Gly Ala Leu
 225 230 235 240

Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala
 245 250 255

Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met
 260 265 270

Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
 275 280 285

Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys
 290 295 300

Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
 305 310 315 320

Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
 325 330 335

Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala
 340 345 350

Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
 355 360 365

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

Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala
 385 390 395 400

Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val
 405 410 415

Lys Thr Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
 420 425 430

Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
 435 440 445

Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
 450 455 460

Gly Asp Ser Thr Ile Tyr Leu Leu Met Gln
465 470

<210> 9

<211> 1425

<212> DNA

<213> Artificial Sequence

<220>

<223> mutated DegP

<400> 9

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atgaaaaaaa ccacattagc actgagtgc ctggctctga gtttaggttt ggcgttatct      60
cgcctctctg caacggcggc tgagacttct tcagcaacga cagcccagca gatgccaagc      120
cttgaccoga tgctcgaaaa ggtgatgcct tcagtggtea gcattaacgt agaaggtagc      180
acaaccgtta atacgccgcg tatgccgcgt aatttccagc agttcttcgg tgatgattct      240
ccgttctgcc aggaagggtc tccgttccag agctctccgt tctgccaggg tggccagggc      300
ggtaatggtg gcggccagca acagaaattc atggcgctgg gttccggcgt catcattgat      360
gccgataaag gctatgtcgt caccaacaac cagcttgttg ataacgcgac ggtcattaaa      420
gttcaactga gcgatggcgg taagtctgac gcgaagatgg ttggcaaaga tccgcgctct      480
gatatcgcgc tgatccaaat ccagaacccg aaaaacctga ccgcaattaa gatggcggat      540
tctgatgcac tgcgcgtggg tgattacacc gtagcgattg gtaaccggtt tgggtctgggc      600
gagacggtaa cttccgggat tgtctctgcg ctggggcgta gcggcctgaa tgccgaaaac      660
tacgaaaact tcatccagac cgatgcagcg attaatcgtg gtaacgccgg tgggtgcgctg      720
gttaacctga acggcgaaact gatcgggtatc aacaccgcga tcctcgacc ggacggcggc      780
aacatcggtg tccgttttgc tatcccgagt aacatggtga aaaacctgac ctgcgagatg      840
gtggaatacg gccaggtgaa acgcgggtgag ctgggtatta tggggactga gctgaactcc      900
gaactggcga aagcgatgaa agttgacgcc cagcgcggtg ctttcgtaag ccaggttctg      960
cctaattcct ccgctgcaaa agcgggcatt aaagcgggtg atgtgatcac ctactgaac      1020
ggtaagccga tcagcagctt tgccgcactg cgtgctcagg tgggtactat gccggtaggc      1080
agcaaaactga ccctgggctt actgcgcgac ggtaagcagg ttaacgtgaa cctggaactg      1140
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gagatgagca acaaaggcaa agatcagggc gtggtagtga acaacgtgaa aacgggcact      1260
ccggtctgcg agatcgccct gaagaaaggt gatgtgatta ttggcgcgaa ccagcaggca      1320
gtgaaaaaca tcgctgaact gcgtaaagtt ctgcacagca aaccgtctgt gctggcactc      1380
aacattcagc gcggcgacag caccatctac ctgttaatgc agtaa      1425

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<210> 10

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated DegP

<400> 10

Met Lys Lys Thr Thr Leu Ala Leu Ser Ala Leu Ala Leu Ser Leu Gly
 1 5 10 15

Leu Ala Leu Ser Pro Leu Ser Ala Thr Ala Ala Glu Thr Ser Ser Ala
 20 25 30

Thr Thr Ala Gln Gln Met Pro Ser Leu Ala Pro Met Leu Glu Lys Val
 35 40 45

Met Pro Ser Val Val Ser Ile Asn Val Glu Gly Ser Thr Thr Val Asn
 50 55 60

Thr Pro Arg Met Pro Arg Asn Phe Gln Gln Phe Phe Gly Asp Asp Ser
 65 70 75 80

Pro Phe Cys Gln Glu Gly Ser Pro Phe Gln Ser Ser Pro Phe Cys Gln
 85 90 95

Gly Gly Gln Gly Gly Asn Gly Gly Gly Gln Gln Gln Lys Phe Met Ala
 100 105 110

Leu Gly Ser Gly Val Ile Ile Asp Ala Asp Lys Gly Tyr Val Val Thr
 115 120 125

Asn Asn His Val Val Asp Asn Ala Thr Val Ile Lys Val Gln Leu Ser
 130 135 140

Asp Gly Arg Lys Phe Asp Ala Lys Met Val Gly Lys Asp Pro Arg Ser
 145 150 155 160

Asp Ile Ala Leu Ile Gln Ile Gln Asn Pro Lys Asn Leu Thr Ala Ile
 165 170 175

Lys Met Ala Asp Ser Asp Ala Leu Arg Val Gly Asp Tyr Thr Val Ala
 180 185 190

Ile Gly Asn Pro Phe Gly Leu Gly Glu Thr Val Thr Ser Gly Ile Val
 195 200 205

Ser Ala Leu Gly Arg Ser Gly Leu Asn Ala Glu Asn Tyr Glu Asn Phe
 210 215 220

Ile Gln Thr Asp Ala Ala Ile Asn Arg Gly Asn Ala Gly Gly Ala Leu
 225 230 235 240

Val Asn Leu Asn Gly Glu Leu Ile Gly Ile Asn Thr Ala Ile Leu Ala
 245 250 255

Pro Asp Gly Gly Asn Ile Gly Ile Gly Phe Ala Ile Pro Ser Asn Met
 260 265 270

Val Lys Asn Leu Thr Ser Gln Met Val Glu Tyr Gly Gln Val Lys Arg
275 280 285

Gly Glu Leu Gly Ile Met Gly Thr Glu Leu Asn Ser Glu Leu Ala Lys
290 295 300

Ala Met Lys Val Asp Ala Gln Arg Gly Ala Phe Val Ser Gln Val Leu
305 310 315 320

Pro Asn Ser Ser Ala Ala Lys Ala Gly Ile Lys Ala Gly Asp Val Ile
325 330 335

Thr Ser Leu Asn Gly Lys Pro Ile Ser Ser Phe Ala Ala Leu Arg Ala
340 345 350

Gln Val Gly Thr Met Pro Val Gly Ser Lys Leu Thr Leu Gly Leu Leu
355 360 365

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

Gln Asn Gln Val Asp Ser Ser Ser Ile Phe Asn Gly Ile Glu Gly Ala
385 390 395 400

Glu Met Ser Asn Lys Gly Lys Asp Gln Gly Val Val Val Asn Asn Val
405 410 415

Lys Thr Gly Thr Pro Ala Ala Gln Ile Gly Leu Lys Lys Gly Asp Val
420 425 430

Ile Ile Gly Ala Asn Gln Gln Ala Val Lys Asn Ile Ala Glu Leu Arg
435 440 445

Lys Val Leu Asp Ser Lys Pro Ser Val Leu Ala Leu Asn Ile Gln Arg
450 455 460

Gly Asp Ser Thr Ile Tyr Leu Leu Met Gln
465 470

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' oligonucleotide primer for the region of the mutated DegP gene comprising the Ase I restriction site

<400> 11

ctgcctgcga ttttcgccgg aacg 24

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligonucleotide primer for the region of the mutated DegP gene comprising the Ase I restriction site

<400> 12

cgcatggtac gtgccacgat atcc 24

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> the 5' oligonucleotide primer for the region of the mutated Tsp gene comprising the Ase I restriction site

<400> 13

gggaaatgaa cctgagcaaa acgc 24

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligonucleotide primer for the region of the mutated Protease III gene comprising the Ase I restriction site

<400> 14

gggaaaggcg gcggaaccgc ctag 24

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' oligonucleotide primer for the region of the mutated Protease III gene comprising the Ase I restriction site

<400> 15

ctactgtgcc agcgggtggta atgg 24

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligonucleotide primer for the region of the mutated Tsp gene comprising the Ase I restriction site

<400> 16

gcatcataat tttctttta cctc 24

<210> 17

<211> 564

<212> DNA

<213> Artificial Sequence

<220>

<223> wild-type spr gene

<400> 17

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atggtcaaat ctcaaccgat tttgagatat atcttgcgcg ggattccgcg gattgcagta      60
gcggttctgc tttctgcatg tagtgcaaat aacaccgcaa agaatatgca tcctgagaca      120
cgtgcagtggt gtagtgaaac atcatcactg caagcttctc aggatgaatt tgaaaacctg      180
gttcgtaatg tcgacgtaaa atcgcggaatt atggatcagt atgctgactg gaaaggcgta      240
cgttatcgtc tgggcggcag cactaaaaaa ggtatcgatt gttctggttt cgtacagcgt      300
acattccgtg agcaatttgg cttagaactt ccgcgttoga cttacgaaca gcaggaaatg      360
ggtaaattctg tttccgcgag taatttgctt acgggtgatt tagttctggt ccgtgccggt      420
tcaacgggac gccatgtcgg tatttatatc ggcaacaatc agtttgtcca tgcttccacc      480
agcagtgggtg ttattatttc cagcatgaat gaaccgtact ggaagaagcg ttacaacgaa      540
gcacgccggg ttctcagccg cagc      564

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<210> 18

<211> 188

<212> PRT

<213> Escherichia coli

<400> 18

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Met Val Lys Ser Gln Pro Ile Leu Arg Tyr Ile Leu Arg Gly Ile Pro
1           5           10           15

Ala Ile Ala Val Ala Val Leu Leu Ser Ala Cys Ser Ala Asn Asn Thr
20           25           30

Ala Lys Asn Met His Pro Glu Thr Arg Ala Val Gly Ser Glu Thr Ser
35           40           45

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

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-- -- --
 Asp Val Lys Ser Arg Ile Met Asp Gln Tyr Ala Asp Trp Lys Gly Val
 65 70 75 80

Arg Tyr Arg Leu Gly Gly Ser Thr Lys Lys Gly Ile Asp Cys Ser Gly
 85 90 95

Phe Val Gln Arg Thr Phe Arg Glu Gln Phe Gly Leu Glu Leu Pro Arg
 100 105 110

Ser Thr Tyr Glu Gln Gln Glu Met Gly Lys Ser Val Ser Arg Ser Asn
 115 120 125

Leu Arg Thr Gly Asp Leu Val Leu Phe Arg Ala Gly Ser Thr Gly Arg
 130 135 140

His Val Gly Ile Tyr Ile Gly Asn Asn Gln Phe Val His Ala Ser Thr
 145 150 155 160

Ser Ser Gly Val Ile Ile Ser Ser Met Asn Glu Pro Tyr Trp Lys Lys
 165 170 175

Arg Tyr Asn Glu Ala Arg Arg Val Leu Ser Arg Ser
 180 185

<210> 19

<211> 162

<212> PRT

<213> Escherichia coli

<400> 19

Cys Ser Ala Asn Asn Thr Ala Lys Asn Met His Pro Glu Thr Arg Ala
 1 5 10 15

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

Asn Leu Val Arg Asn Val Asp Val Lys Ser Arg Ile Met Asp Gln Tyr
 35 40 45

Ala Asp Trp Lys Gly Val Arg Tyr Arg Leu Gly Gly Ser Thr Lys Lys
 50 55 60

Gly Ile Asp Cys Ser Gly Phe Val Gln Arg Thr Phe Arg Glu Gln Phe
 65 70 75 80

Gly Leu Glu Leu Pro Arg Ser Thr Tyr Glu Gln Gln Glu Met Gly Lys
 85 90 95

Ser Val Ser Arg Ser Asn Leu Arg Thr Gly Asp Leu Val Leu Phe Arg
 100 105 110

Ala Gly Ser Thr Gly Arg His Val Gly Ile Tyr Ile Gly Asn Asn Gln
 115 120 125

Phe Val His Ala Ser Thr Ser Ser Gly Val Ile Ile Ser Ser Met Asn
 130 135 140

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

Arg Ser

<210> 20

<211> 954

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence of a mutated OmpT sequence comprising D210A and H212A mutations

<400> 20

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tctaccgaga ctttatcggt tactcctgac aacataaatg cggacattag tcttggaact      120
ctgagcggaa aaacaaaaga gcgtgtttat ctagccgaag aaggaggccg aaaagtcagt      180
caactcgact ggaaattcaa taacgctgca attattaaag gtgcaattaa ttgggatttg      240
atgccccaga tatctatcgg ggctgctggc tggacaactc tcggcagccg aggtggcaat      300
atggtcgatc aggactggat ggattccagt aaccccgga cctggacgga tgaaagtaga      360
cacctgata cacaactcaa ttatgccaac gaatttgatc tgaatatcaa aggttggtc      420
ctcaacgaac ccaattaccg cctgggactc atggccgat atcaggaaag ccgttatagc      480
tttacagcca gaggtggttc ctatatctac agttctgagg agggattcag agatgatata      540
ggctccttcc cgaatggaga aagagcaatc ggctacaaac aacgttttaa aatgccctac      600
attggcttga ctggaagtta tcgttatgaa gattttgaac tcggtggcac atttaaatac      660
agcggctggg tggaatcatc tgataacgct gaagcttatg acccgggaaa aagaatcact      720
tatcgcagta aggtcaaaga ccaaaattac tattctgttg cagtcaatgc aggttattac      780
gtcacaccta acgaaaagt ttatgttgaa ggcgcatgga atcgggttac gaataaaaaa      840
ggtaatactt cactttatga tcacaataat aacacttcag actacagcaa aaatggagca      900
ggtatagaaa actataactt catcactact gctggtctta agtacacatt ttaa          954

```

<210> 21

<211> 317

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated OmpT sequence comprising D210A and H212A mutations

<400> 21

Met Arg Ala Lys Leu Leu Gly Ile Val Leu Thr Thr Pro Ile Ala Ile
 1 5 10 15

Ser Ser Phe Ala Ser Thr Glu Thr Leu Ser Phe Thr Pro Asp Asn Ile
 20 25 30
 Asn Ala Asp Ile Ser Leu Gly Thr Leu Ser Gly Lys Thr Lys Glu Arg
 35 40 45
 Val Tyr Leu Ala Glu Glu Gly Gly Arg Lys Val Ser Gln Leu Asp Trp
 50 55 60
 Lys Phe Asn Asn Ala Ala Ile Ile Lys Gly Ala Ile Asn Trp Asp Leu
 65 70 75 80
 Met Pro Gln Ile Ser Ile Gly Ala Ala Gly Trp Thr Thr Leu Gly Ser
 85 90 95
 Arg Gly Gly Asn Met Val Asp Gln Asp Trp Met Asp Ser Ser Asn Pro
 100 105 110
 Gly Thr Trp Thr Asp Glu Ser Arg His Pro Asp Thr Gln Leu Asn Tyr
 115 120 125
 Ala Asn Glu Phe Asp Leu Asn Ile Lys Gly Trp Leu Leu Asn Glu Pro
 130 135 140
 Asn Tyr Arg Leu Gly Leu Met Ala Gly Tyr Gln Glu Ser Arg Tyr Ser
 145 150 155 160
 Phe Thr Ala Arg Gly Gly Ser Tyr Ile Tyr Ser Ser Glu Glu Gly Phe
 165 170 175
 Arg Asp Asp Ile Gly Ser Phe Pro Asn Gly Glu Arg Ala Ile Gly Tyr
 180 185 190
 Lys Gln Arg Phe Lys Met Pro Tyr Ile Gly Leu Thr Gly Ser Tyr Arg
 195 200 205
 Tyr Glu Asp Phe Glu Leu Gly Gly Thr Phe Lys Tyr Ser Gly Trp Val
 210 215 220
 Glu Ser Ser Asp Asn Ala Glu Ala Tyr Asp Pro Gly Lys Arg Ile Thr
 225 230 235 240
 Tyr Arg Ser Lys Val Lys Asp Gln Asn Tyr Tyr Ser Val Ala Val Asn
 245 250 255
 Ala Gly Tyr Tyr Val Thr Pro Asn Ala Lys Val Tyr Val Glu Gly Ala
 260 265 270
 Trp Asn Arg Val Thr Asn Lys Lys Gly Asn Thr Ser Leu Tyr Asp His
 275 280 285
 Asn Asn Asn Thr Ser Asp Tyr Ser Lys Asn Gly Ala Gly Ile Glu Asn
 290 295 300

Tyr Asn Phe Ile Thr Thr Ala Gly Leu Lys Tyr Thr Phe
 305 310 315

<210> 22

<211> 954

<212> DNA

<213> Artificial Sequence

<220>

<223> mutated knockout OmpT sequence

<400> 22

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attcgggcga aacttctggg aatagtcctg acaacccta ttgcgatcag ctcttttgct      60
totaccgaga ctttatcggt tactcctgac aacataaatg cggacattag tottggaact      120
ctgagcggaa aaacaaaaga gcgtgtttat ctagccgaag aaggaggccg aaaagtcagt      180
caactcgact ggaaattcaa taacgctgca attattaaag gtgcaattaa ttgggatttg      240
atgccccaga tatctatcgg ggctgctggc tggacaactc tcggcagccg aggtggcaat      300
atggtcgatc aggactggat ggattccagt aaccccgga cctggacgga tgaaagtaga      360
caccctgata cacaactcaa ttatgccaac gaatttgatc tgaatatcaa aggctggctc      420
ctcaacgaac ccaattaccg cctgggactc atggccgat atcaggaaag ccgttatagc      480
tttacagcca gaggtggttc ctatatctac agttctgagg agggattcag agatgatatc      540
ggctccttcc cgaatggaga aagagcaatc ggctacaaac aacgttttaa aatgccctac      600
attggcttga ctggaagtta tcgttatgaa gattttgaac tcggtggcac atttaaatac      660
agcggctggg tggaatcacc tgataacgat gaacactatg acccgggaaa aagaatcact      720
tatcgcagta aggtcaaaga caaaattac tattctgttg cagtcaatgc aggttattac      780
gtcacacctc acgcaaaagt ttatgttgaa ggcgatgga atcgggttac gaataaaaaa      840
ggtaataact cactttatga tcacaataat aacacttcag actacagcaa aaatggagca      900
ggtatagaaa actataactt catcactact gctggtctta agtacacatt ttaa          954

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<210> 23

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> OmpA oligonucleotide adapter

<400> 23

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cgattgaatg gagaacttga attcgggcga aacttctggg aatag      45
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<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide cassette encoding intergenic sequence 1 (IGS1) for E. coli Fab expression

<400> 24

aagttttaat agaggagagt gttaatgaag aag 33

<210> 25

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> the oligonucleotide cassette encoding intergenic sequence 2 (IGS2) for E. coli Fab expression.

<400> 25

aagttttaat agaggggagt gttaaaatga agaag 35

<210> 26

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide cassette encoding intergenic sequence 3 (IGS3) for E. coli Fab expression

<400> 26

aagctttaat agaggagagt gttgaggagg aaaaaaaaaat gaagaaa 47

<210> 27

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide cassette encoding intergenic sequence 4 (IGS4) for E. coli Fab expression

<400> 27

aagctttaat agaggagagt gttgacgagg attatataat gaagaaa 47

<210> 28

<211> 810

<212> DNA

<213> Escherichia coli

<400> 28

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atgaaatcac tgtttaaagt aacgctgctg gcgaccacaa tggccgttgc cctgcatgca      60
ccaatcactt ttgctgctga agctgcaaaa cctgctacag ctgctgacag caaagcagcg      120
ttcaaaaatg acgatcagaa atcagcttat gcactgggtg cctcgctggg tcgttacatg      180
gaaaactctc taaaagaaca agaaaaactg ggcatcaaac tggataaaga tcagctgac      240
gctggtgttc aggatgcatt tgctgataag agcaaactct ccgaccaaga gatcgaacag      300
actctacaag cattcgaagc tcgctgaag tcttctgctc aggcgaagat ggaaaaagac      360
gcggtcgata acgaagcaaa aggtaaagag taccgcgaga aatttgccaa agagaaaggt      420
gtgaaaacct cttcaactgg tctggtttat caggtagtag aagccggtaa aggcgaagca      480
ccgaagaca gcgatactgt tgtagtgaac taaaaaggta cgctgatcga cggtaaagag      540
ttcgacaact cttacaccgg tgggtgaaccg ctttctttcc gtctggacgg tgttatcccg      600
ggttggacag aaggtctgaa gaacatcaag aaaggcggta agatcaaact ggttattcca      660
ccagaactgg cttacggcaa agcgggtgtt ccggggatcc caccgaattc taccctggtg      720
tttgacgtag agctgctgga tgtgaaacca gcgccgaagg ctgatgcaaa gccggaagct      780
gatgcgaaag ccgcagattc tgctaaaaaa      810

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<210> 29

<211> 270

<212> PRT

<213> Escherichia coli

<400> 29

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

Ala Leu His Ala Pro Ile Thr Phe Ala Ala Glu Ala Ala Lys Pro Ala
20          25          30

Thr Ala Ala Asp Ser Lys Ala Ala Phe Lys Asn Asp Asp Gln Lys Ser
35          40          45

Ala Tyr Ala Leu Gly Ala Ser Leu Gly Arg Tyr Met Glu Asn Ser Leu
50          55          60

Lys Glu Gln Glu Lys Leu Gly Ile Lys Leu Asp Lys Asp Gln Leu Ile
65          70          75          80

Ala Gly Val Gln Asp Ala Phe Ala Asp Lys Ser Lys Leu Ser Asp Gln
85          90          95

Glu Ile Glu Gln Thr Leu Gln Ala Phe Glu Ala Arg Val Lys Ser Ser
100         105         110

Ala Gln Ala Lys Met Glu Lys Asp Ala Ala Asp Asn Glu Ala Lys Gly
115         120         125

Lys Glu Tyr Arg Glu Lys Phe Ala Lys Glu Lys Gly Val Lys Thr Ser

```

130 135 140
 Ser Thr Gly Leu Val Tyr Gln Val Val Glu Ala Gly Lys Gly Glu Ala
 145 150 155 160
 Pro Lys Asp Ser Asp Thr Val Val Val Asn Tyr Lys Gly Thr Leu Ile
 165 170 175
 Asp Gly Lys Glu Phe Asp Asn Ser Tyr Thr Arg Gly Glu Pro Leu Ser
 180 185 190
 Phe Arg Leu Asp Gly Val Ile Pro Gly Trp Thr Glu Gly Leu Lys Asn
 195 200 205
 Ile Lys Lys Gly Gly Lys Ile Lys Leu Val Ile Pro Pro Glu Leu Ala
 210 215 220
 Tyr Gly Lys Ala Gly Val Pro Gly Ile Pro Pro Asn Ser Thr Leu Val
 225 230 235 240
 Phe Asp Val Glu Leu Leu Asp Val Lys Pro Ala Pro Lys Ala Asp Ala
 245 250 255
 Lys Pro Glu Ala Asp Ala Lys Ala Ala Asp Ser Ala Lys Lys
 260 265 270

<210> 30

<211> 828

<212> DNA

<213> Artificial Sequence

<220>

<223> the FkpA tagged gene

<400> 30

atgaaatcac tgtttaaagt aacgctgctg gcgaccacaa tggccggttc cctgcacgca	60
ccaatcactt ttgctgctga agctgcaaaa cctgctactg ctgctgacag caaagcagcg	120
ttcaaaaatg acgatcagaa atcagcttat gcactgggtg cctcgctggg tcgttacatg	180
gaaaactctc taaaagaaca agaaaactg ggcatacaac tggataaaga tcaactgatc	240
gctggtgttc aggatgcatt tgctgataag agcaaaactct ccgaccaaga gatcgaacag	300
actctacaag catttgaagc tcgcgtgaag tcttctgctc aggcgaagat ggaaaaagac	360
gcggtctgata acgaagcaaa aggtaaagag taccgcgaga aatttgccaa agagaaaggt	420
gtgaaaacct cttcaactgg tctggtttat caggtagtag aagccggtaa aggcgaagca	480
ccgaaagaca gcgatactgt tgtagtgaac tacaaaggta cgctgatcga cggtaaagag	540
ttcgacaact cttacacccg tgggtgaaccg ctttctttcc gtctggacgg tgttatcccg	600
ggttggacag aaggtctgaa gaacatcaag aaaggcggta agataaaact ggttattcca	660
ccagaactgg cttacggcaa agcgggtgtt ccggggatcc caccaaattc taccctggtg	720
tttgcacata aactactcaa tataaaacca acacccaaga ctgatcaaa acccaaaact	780

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gatgcgaaag cgcgagattc tgctaaaaaa caccatcacc atcaccac
828

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<210> 31

<211> 276

<212> PRT

<213> Artificial Sequence

<220>

<223> FkpA his tagged gene

<400> 31

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

Ala Leu His Ala Pro Ile Thr Phe Ala Ala Glu Ala Ala Lys Pro Ala
20          25          30

Thr Ala Ala Asp Ser Lys Ala Ala Phe Lys Asn Asp Asp Gln Lys Ser
35          40          45

Ala Tyr Ala Leu Gly Ala Ser Leu Gly Arg Tyr Met Glu Asn Ser Leu
50          55          60

Lys Glu Gln Glu Lys Leu Gly Ile Lys Leu Asp Lys Asp Gln Leu Ile
65          70          75          80

Ala Gly Val Gln Asp Ala Phe Ala Asp Lys Ser Lys Leu Ser Asp Gln
85          90          95

Glu Ile Glu Gln Thr Leu Gln Ala Phe Glu Ala Arg Val Lys Ser Ser
100         105         110

Ala Gln Ala Lys Met Glu Lys Asp Ala Ala Asp Asn Glu Ala Lys Gly
115         120         125

Lys Glu Tyr Arg Glu Lys Phe Ala Lys Glu Lys Gly Val Lys Thr Ser
130         135         140

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

Pro Lys Asp Ser Asp Thr Val Val Val Asn Tyr Lys Gly Thr Leu Ile
165         170         175

Asp Gly Lys Glu Phe Asp Asn Ser Tyr Thr Arg Gly Glu Pro Leu Ser
180         185         190

Phe Arg Leu Asp Gly Val Ile Pro Gly Trp Thr Glu Gly Leu Lys Asn
195         200         205

Ile Lys Lys Gly Gly Lys Ile Lys Leu Val Ile Pro Pro Glu Leu Ala
210         215         220

Tyr Gly Lys Ala Gly Val Pro Gly Ile Pro Pro Asn Ser Thr Leu Val

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[illegible]

<210> 32
<211> 486
<212> DNA
<213> Escherichia coli

<400> 32	
gtgaaaaagt ggttattagc tgcaggtctc ggtttagcac tggcaacttc tgctcaggcg	60
gctgacaaaa ttgcaatcgt caacatgggc agcctgttcc agcaggtagc gcagaaaacc	120
ggtgtttcta acacgctgga aatgagttc aaaggcgtg ccagcgaact gcagcgatg	180
gaaaccgatc tgcaggctaa aatgaaaaag ctgcagtcca tgaaagcggg cagcgatcgc	240
actaagctgg aaaaagacgt gatggctcag cgccagactt ttgctcagaa agcgcaggct	300
tttgagcagg atcgcgcacg tcgttccaac gaagaacgcg gcaaactggt tactcgtatc	360
cagactgctg tgaaatccgt tgccaacagc caggatatcg atctggttgt tgatgcaaac	420
gccgttgctt acaacagcag cgatgtaaaa gacatcactg ccgacgtact gaaacaggtt	480
aaataa	486

<210> 33
<211> 161
<212> **PRT**
<213> Escherichia coli

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<400> 33
Met  Lys  Lys  Trp  Leu  Leu  Ala  Ala  Gly  Leu  Gly  Leu  Ala  Leu  Ala  Thr
 1          5          10          15

Ser  Ala  Gln  Ala  Ala  Asp  Lys  Ile  Ala  Ile  Val  Asn  Met  Gly  Ser  Leu
          20          25          30

Phe  Gln  Gln  Val  Ala  Gln  Lys  Thr  Gly  Val  Ser  Asn  Thr  Leu  Glu  Asn
          35          40          45

Glu  Phe  Lys  Gly  Arg  Ala  Ser  Glu  Leu  Gln  Arg  Met  Glu  Thr  Asp  Leu
 50          55          60

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

Thr  Lys  Leu  Glu  Lys  Asp  Val  Met  Ala  Gln  Arg  Gln  Thr  Phe  Ala  Gln
          85          90          95

```

Lys Ala Gln Ala Phe Glu Gln Asp Arg Ala Arg Arg Ser Asn Glu Glu
 100 105 110

Arg Gly Lys Leu Val Thr Arg Ile Gln Thr Ala Val Lys Ser Val Ala
 115 120 125

Asn Ser Gln Asp Ile Asp Leu Val Val Asp Ala Asn Ala Val Ala Tyr
 130 135 140

Asn Ser Ser Asp Val Lys Asp Ile Thr Ala Asp Val Leu Lys Gln Val
 145 150 155 160

Lys

<210> 34

<211> 501

<212> DNA

<213> Artificial Sequence

<220>

<223> skip his tagged gene

<400> 34

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atgaaaaagt ggttattagc cgcaggtctc ggtttagcac tggcaacttc tgctcaggcg      60
gctgacaaaa ttgcaatcgt caacatgggc agcctgttcc agcaggtagc gcagaaaacc      120
ggtgtttcta acacgctgga aaatgagttc aaaggccgtg ccagcgaact ccagcgtatg      180
gaaaccgatc tccaggctaa aatgaaaaag ctgcaatcca tgaaagcggg cagcgatcgc      240
actaagctgg aaaaagacgt gatggctcag cgccagactt ttgctcagaa agcgcaggct      300
tttgagcagg atcgcgcacg tcgttccaac gaagaacgog gcaaactggg tactcgtatc      360
cagactgctg tgaaatccgt tgccaacagc caggaaatcg atctggttgt tgatgcaaac      420
gccgttgctt acaacagcag cgatgtaaaa gacatcactg ccgacgtact gaaacagggt      480
aaacaccatc accatcacca c                                          501

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<210> 35

<211> 167

<212> PRT

<213> Artificial Sequence

<220>

<223> skip his tagged gene

<400> 35

Met Lys Lys Trp Leu Leu Ala Ala Gly Leu Gly Leu Ala Leu Ala Thr
 1 5 10 15

Ser Ala Gln Ala Ala Asp Lys Ile Ala Ile Val Asn Met Gly Ser Leu
 20 25 30

Phe Gln Gln Val Ala Gln Lys Thr Gly Val Ser Asn Thr Leu Glu Asn
35 40 45

Glu Phe Lys Gly Arg Ala Ser Glu Leu Gln Arg Met Glu Thr Asp Leu
50 55 60

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

Thr Lys Leu Glu Lys Asp Val Met Ala Gln Arg Gln Thr Phe Ala Gln
85 90 95

Lys Ala Gln Ala Phe Glu Gln Asp Arg Ala Arg Arg Ser Asn Glu Glu
100 105 110

Arg Gly Lys Leu Val Thr Arg Ile Gln Thr Ala Val Lys Ser Val Ala
115 120 125

Asn Ser Gln Glu Ile Asp Leu Val Val Asp Ala Asn Ala Val Ala Tyr
130 135 140

Asn Ser Ser Asp Val Lys Asp Ile Thr Ala Asp Val Leu Lys Gln Val
145 150 155 160

Lys His His His His His His
165

<210> 36

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CA170 1519 Ab CDRH1

<400> 36

Gly Phe Thr Phe Ser Asn Tyr Gly Met Val
1 5 10

<210> 37

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CA170_1519 Ab CDRH2

<400> 37

Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg Asp Ser Val Lys
1 5 10 15

Gly

<210> 38

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CA170_1519 Ab CDRH3

<400> 38

Gly	Ile	Val	Arg	Pro	Phe	Leu	Tyr
1				5			

<210> 39

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> CA170_1519 Ab CDRL1

<400> 39

Lys	Ser	Ser	Gln	Ser	Leu	Val	Gly	Ala	Ser	Gly	Lys	Thr	Tyr	Leu	Tyr
1				5					10					15	

<210> 40

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CA170_1519 Ab CDRL2

<400> 40

Leu	Val	Ser	Thr	Leu	Asp	Ser
1				5		

<210> 41

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CA170_1519 Ab CDRL3

<400> 41

Leu	Gln	Gly	Thr	His	Phe	Pro	His	Thr
1				5				

<210> 42

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Rat Ab 1519 VL region

<400> 42

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Arg Ser Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
50 55 60

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

Arg Arg Val Glu Ala Asp Asp Leu Gly Val Tyr Tyr Cys Leu Gln Gly
85 90 95

Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 43

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Rat Ab 1519 VL region

<400> 43

gatgtttgta tgaccagac tccactgtct ttgtcggttg cccttggaca accagcctcc	60
atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg	120
ttatttcaga ggtccggcca gtctccaaag cgactaatct atctgggtgtc cacactggac	180
tctggaattc ctgatagggt cagtggcagt ggagcagaga cagattttac tcttaaaatc	240
cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtac acattttcct	300
cacacgtttg gagctgggac caagctggaa ttgaaa	336

<210> 44

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Rat Ab 1519 VL region

<400> 44

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

Gly Thr Ser Gly Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser
 20 25 30

Val Ala Leu Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
 35 40 45

Leu Val Gly Ala Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Arg
 50 55 60

Ser Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp
 65 70 75 80

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ala Glu Thr Asp Phe
 85 90 95

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

Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Ala Gly Thr Lys
 115 120 125

Leu Glu Leu Lys
 130

<210> 45

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Rat Ab 1519 VL region

<400> 45

atgatgagtc ctgccagtt cctgtttctg ctgatgctct ggattcaggg aaccagtggg 60
 gatgttgtga tgaccagac tccactgtct ttgtcggttg cccttggaca accagcctcc 120
 atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata tttgtattgg 180
 ttatttcaga ggtccggcca gtctccaaag cgactaatct atctgggtgac cacactggac 240
 tctggaattc ctgatagggt cagtggcagt ggagcagaga cagattttac tcttaaaatc 300
 cgcagagtgg aagccgatga tttgggagtt tattactgct tgcaaggtag acattttcct 360
 cacacgtttg gagctgggac caagctggaa ttgaaa 396

<210> 46

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Rat Ab 1519 VH region

<400> 46

Glu Val Pro Leu Val Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Arg
1 5 10 15

Ser Met Lys Leu Ser Cys Val Val Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met Val Trp Val Arg Gln Ala Pro Lys Lys Gly Leu Glu Trp Val
35 40 45

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

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

Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser
115

<210> 47

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> Rat Ab 1519 VH region

<400> 47

gaggtgccgc tgggtggagtc tgggggcggc tcagtgcagc ctgggagggtc catgaaactc	60
tctgtgtag tctcaggatt cactttcagt aattatggca tgggtctgggt ccgccaggct	120
ccaaagaagg gtctggagtg ggtcgcatat attgattctg atggtgataa tacttactac	180
cgagattccg tgaagggccg attcactatc tccagaaata atgcaaaaag caccctatat	240
ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggtatt	300
gtccggccct ttctctattg gggccaagga accacgggtca ccgtctcg	348

<210> 48

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Rat Ab 1519 VH region

<400> 48

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

Val Arg Cys Glu Val Pro Leu Val Glu Ser Gly Gly Gly Ser Val Gln
20 25 30

Pro Gly Arg Ser Met Lys Leu Ser Cys Val Val Ser Gly Phe Thr Phe
35 40 45

Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Lys Lys Gly Leu

50 55 60

Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ala Lys Ser
85 90 95

Thr Leu Tyr Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Thr
100 105 110

Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln
115 120 125

Gly Thr Thr Val Thr Val Ser
130 135

<210> 49

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Rat Ab 1519 VH region

<400> 49

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gtgccgctgg tggagtctgg gggcggctca gtgcagcctg ggaggtccat gaaactctcc	120
tgtgtagtct caggattcac ttccagtaat tatggcatgg tctgggtccg ccaggctcca	180
aagaagggtc tggagtgggt cgcataatatt gattctgatg gtgataatac ttactaccga	240
gattccgtga agggccgatt cactatctcc agaaataatg caaaaagcac cctatatttg	300
caaatggaca gtctgaggtc tgaggacacg gccacttatt actgtacaac agggattgtc	360
cggccctttc tctattgggg ccaaggaacc acggtcaccg tctcg	405

<210> 50

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> 1519 gL20 V-region

<400> 50

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

Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu Val Gly Ala
20 25 30

Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln Lys Pro Gly Lys Ala
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu Asp Ser Gly Ile Pro
50 55 60

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
65 70 75 80

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly
85 90 95

Thr His Phe Pro His Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 51

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> 1519 gL20 V-region

<400> 51

gatatccaga tgacccagag tccaagcagt ctctccgccg gcgtaggcga tcgtgtgact 60
attacctgta aaagctccca gtccctggtg ggtgcaagcg gcaaaacctc cctgtactgg 120
ctcttccaga aaccggggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat 180
agcggtatcc cgtctcggtt ctccggtagc ggtagcggta ccgaattcac gctgaccatt 240
agctccctcc agccggagga ctttgctacc tattactgcc tccagggcac tcattttccg 300
cacactttcg gccagggtac caaactggaa atcaaaa 336

<210> 52

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> 1519 gL20 V-region

<400> 52

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

Thr Val Ala Gln Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln
35 40 45

Ser Leu Val Gly Ala Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln
50 55 60

Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu
65 70 75 80

Asp Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
100 105 110

Tyr Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Gln Gly Thr
115 120 125

Lys Leu Glu Ile Lys
130

<210> 53

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> 1519 gL20 V-region

<400> 53

atgaaaaaga cagctatcgc aattgcagtg gccttggtcg gtttcgctac cgtagcgcaa	60
gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg	120
actattacct gtaaaagctc ccagtccttg gtgggtgcaa gcggcaaaac ctacctgtac	180
tggctcttcc agaaaccggg caaagctccg aaacgcctga tctatctggt gtctaccctg	240
gatagcggta ttccgtctcg tttctccggt agcggtagcg gtaccgaatt cacgctgacc	300
attagctccc tccagccgga ggactttgct acctattact gcctccaggg cactcatttt	360
cgcacactt tcggccaggg taccaaactg gaaatcaaa	399

<210> 54

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> 1519 gL20 light chain (V + constant)

<400> 54

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

Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Val	Gly	Ala
		20					25					30			

Ser	Gly	Lys	Thr	Tyr	Leu	Tyr	Trp	Leu	Phe	Gln	Lys	Pro	Gly	Lys	Ala
		35					40					45			

Pro	Lys	Arg	Leu	Ile	Tyr	Leu	Val	Ser	Thr	Leu	Asp	Ser	Gly	Ile	Pro
	50					55					60				

Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile
65					70					75					80

Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Gly
				85					90					95	

Thr	His	Phe	Pro	His	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110		

Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
		115					120					125			

Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
	130					135					140				

Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
145					150					155					160

Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
			165						170					175	

Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
			180					185					190		

Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
		195					200					205			

Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys
	210					215				

<210> 55

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> 1519 gL20 light chain (V + constant)

<400> 55

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gatatccaga tgacccagag tccaagcagt ctctccgcca gcgtaggcga tcgtgtgact      60
attacctgta aaagctccca gtccctgggtg ggtgcaagcg gcaaaacctt cctgtactgg      120
ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctgggtgc taccctggat      180
agcgggtattc cgtctcgttt ctccggtagc ggtagcggta ccgaattcac gctgaccatt      240
agctccctcc agccggagga ctttgctacc tattactgcc tccagggcac tcattttccg      300
cacactttcg gccagggtac caaactggaa atcaaacgta cggtagcggc cccatctgtc      360
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg      420
ctgaataact tctatcccag agaggccaaa gtacagtggg aggtggataa cgccctccaa      480
tcgggtaact ccagagagag tgtcacagag caggacagca aggacagcac ctacagcctc      540
agcagcacc c tgacgctgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa      600
gtcaccatc agggcctgag ctcaccagta acaaaaagtt ttaatagagg ggagtgt      657

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<210> 56

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> 1519 gL20 light chain

<400> 56

```

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

Thr Val Ala Gln Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20          25          30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln
35          40          45

Ser Leu Val Gly Ala Ser Gly Lys Thr Tyr Leu Tyr Trp Leu Phe Gln
50          55          60

Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Leu Val Ser Thr Leu
65          70          75          80

Asp Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
85          90          95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
100         105         110

Tyr Cys Leu Gln Gly Thr His Phe Pro His Thr Phe Gly Gln Gly Thr
115         120         125

Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
130         135         140

```

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
145 150 155 160

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
165 170 175

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

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
195 200 205

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
210 215 220

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235 240

<210> 57

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> 1519 gL20 light chain

<400> 57

atgaaaaaga cagctatcgc aattgcagtg gccttggtcg gtttcgctac cgtagcgcaa	60
gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg	120
actattacct gtaaaagctc ccagtccttg gtgggtgcaa gcggcaaaac ctacctgtac	180
tggctcttcc agaaaccggg caaagctccg aaacgcctga tctatctggt gtctaccctg	240
gatagcggta ttccgtctcg tttctccggt agcggtagcg gtaccgaatt caegctgacc	300
attagctccc tccagcogga ggactttgct acctattact gcctccaggg cactcatttt	360
ccgcacactt tcggccaggg taccaaactg gaaatcaaac gtacggtagc ggccccatct	420
gtcttcacat tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc	480
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc	540
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc	600
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc	660
gaagtcaccc atcagggcct gagctcacca gtaacaaaaa gttttaatag aggggagtgt	720

<210> 58

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> 1519 gH2O V-region

<400> 58

Glu Val Pro Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser
115

<210> 59

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> 1519 gH2O V-region

<400> 59

gaggttccgc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc	60
tcttgtgcag tatctggctt cacgttctcc aactacgcta tgggtgtgggt tcgtcaggct	120
ccaggtaaag gtctggaatg ggtggcgatat attgactccg acggcgacaa cacctactat	180
cgcgactctg tgaaaggctc cttcaccatt tcccgcgata acgccaatc cagcctgtac	240
ctgcagatga acagcctgcg tgetgaagat actgcggtgt actattgcac cactggcatc	300
gtgcgtccgt ttctgtattg gggtcagggt accctcgtaa ctgtctcg	348

<210> 60

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> 1519 gH2O V-region

<400> 60

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

Thr Val Ala Gln Ala Glu Val Pro Leu Val Glu Ser Gly Gly Gly Leu
20 25 30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
35 40 45

Thr Phe Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

Gly Leu Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr
65 70 75 80

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

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

Ala Val Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser
130 135

<210> 61

<211> 411

<212> DNA

<213> Artificial Sequence

<220>

<223> 1519 gH2O V-region

<400> 61

atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa	60
gctgagggttc cgctgggtcga gtctggaggc gggcttgtcc agcctggagg gagcctgcgt	120
ctctcttgtg cagtatctgg cttcacgttc tccaactacg gtatggtgtg ggttcgtcag	180
gctccaggta aaggtctgga atgggtggcg tatattgact ccgacggcga caacacctac	240
tatcgcgact ctgtgaaagg tcgcttcacc atttcccgcg ataacgccaa atccagcctg	300
tacctgcaga tgaacagcct gcgtgctgaa gatactgcgg tgtactattg caccactggc	360
atcgtgcgtc cgtttctgta ttgggggtcag ggtaccctcg ttactgtctc g	411

<210> 62

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> 1519gH20 Fab' heavy chain (V + human gamma-1 CH1 + hinge)

<400> 62

Glu	Val	Pro	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Val	Ser	Gly	Phe	Thr	Phe	Ser	Asn	Tyr
		20						25					30		

Gly	Met	Val	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

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

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Ser	Ser	Leu	Tyr
65					70					75					80

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Thr	Thr	Gly	Ile	Val	Arg	Pro	Phe	Leu	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
			100					105					110		

Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
		115					120					125			

Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys
	130					135					140				

Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
145					150					155					160

Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
				165					170					175	

Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
			180					185					190		

Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn
		195					200					205			

Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His
	210					215					220				

Thr	Cys	Ala	Ala
225			

<210> 63

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> 1519gH20 Fab' heavy chain (V + human gamma-1 CH1 + hinge)

<400> 63

```

gaggttccgc tggtcgagtc tggaggcggg cttgtccagc ctggaggag cctgcgtctc      60
tcttgtgcag tatctggctt cacgttctcc aactacggta tgggtgggt tcgtcaggct      120
ccaggtaaag gtctggaatg ggtggcgat attgactccg acggcgacaa cacctactat      180
cgcgactctg tgaaaggctg cttcaccatt tcccgcgata acgccaatc cagcctgtac      240
ctgcagatga acagcctgcg tgctgaagat actgcggtgt actattgcac cactggcatc      300
gtgcgtccgt ttctgtattg gggtcagggt accctcgta ctgtctcgag cgcttctaca      360
aagggcccat cggctctccc cctggcacc tctccaaga gcacctctgg gggcacagcg      420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca      480
ggcgccctga ccagcgcgct gcacaccttc ccggctgtcc tacagtcttc aggactctac      540
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc      600
aacgtgaatc acaagccag caacaccaag gtcgacaaga aagttgagcc caaatcttgt      660
gacaaaactc acacatgcgc cgcg                                           684

```

<210> 64

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> 1519 gH20 Fab' heavy chain

<400> 64

```

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

Thr Val Ala Gln Ala Glu Val Pro Leu Val Glu Ser Gly Gly Gly Leu
20        25        30

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe
35        40        45

Thr Phe Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys
50        55        60

Gly Leu Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr
65        70        75        80

Tyr Arg Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85        90        95

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

Ala Val Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp
115       120       125

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Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 225 230 235 240

Cys Asp Lys Thr His Thr Cys Ala Ala
 245

<210> 65

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<223> 1519 gH20 Fab' heavy chain

<400> 65

atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa	60
gctgagggtc cgctgggtcga gtctggaggc gggcttgctc agcctggagg gagcctgcgt	120
ctctcttggtg cagtatctgg ctccacgttc tccaactacg gtatggtgtg ggttcgtcag	180
gctccaggta aaggtctgga atgggtggcg tatattgact ccgacggcga caacacctac	240
tatcgcgact ctgtgaaagg tcgcttcacc atttcccgcg ataacgccaa atccagcctg	300
tacctgcaga tgaacagcct gcgtgctgaa gatactgcgg tgtactattg caccactggc	360
atcgtgcgtc cgtttctgta ttgggggtcag ggtaccctcg ttactgtctc gagcgcttct	420
acaaagggcc catcggtctt cccctggca ccctcctcca agagcacctc tgggggcaca	480
gcgccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	540
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc	600
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	660
tgcaacgtga atcacaagcc cagcaacacc aagggtcgaca agaaagttga gcccaaattct	720
tgtgacaaaa ctcacacatg cgccgcg	747

<210> 66

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> 1519gH20 IgG4 heavy chain (V + human gamma-4P constant)

<400> 66

Glu	Val	Pro	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Val	Ser	Gly	Phe	Thr	Phe	Ser	Asn	Tyr
		20						25					30		

Gly	Met	Val	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35						40					45			

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

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Ser	Ser	Leu	Tyr
65					70					75					80

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	

Thr	Thr	Gly	Ile	Val	Arg	Pro	Phe	Leu	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
			100					105					110		

Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
		115					120					125			

Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys
	130					135					140				

Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
145					150					155					160

Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
				165					170					175	

Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
		180						185					190		

Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn
		195					200					205			

Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro
	210					215					220				

Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
225					230					235					240

Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
			245						250					255	

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
 260 265 270
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285
 Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 305 310 315 320
 Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 325 330 335
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
 340 345 350
 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 355 360 365
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 370 375 380
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 385 390 395 400
 Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
 405 410 415
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 420 425 430
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440

<210> 67

<211> 1939

<212> DNA

<213> Artificial Sequence

<220>

<223> 1519gH20 IgG4 heavy chain (V + human gamma-4P constant, exons)

<400> 67

gaggtaccac ttgtggaag cggaggaggt cttgtgcagc ctggaggaag tttacgtctc	60
tcttgtgctg tgtctggctt cacttctcc aattacgga tggtctgggt cagacaagca	120
cctggaaggt gtcttgaatg ggtggcctat attgactctg acggggacaa cacctactat	180
cgggattccg tgaaaggacg cttcacaatc tcccgagata acgccaagag ctcactgtac	240
ctgcagatga atagcctgag agccgaggat actgccgtgt actattgcac aacgggaatc	300
gttaggcctt ttctgtactg gggacagggc accttgggta ctgtctcgag cgcttctaca	360

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aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 600
aacgtagatc acaagcccag caacaccaag gtggacaaga gagtgggtga gaggccagca 660
caggggaggga ggggtgtctgc tggaagccag gctcagccct cctgcctgga cgcaccccg 720

ctgtgcagcc ccagcccagg gcagcaaggc atgccccatc tgtctcctca cccggaggcc 780
tctgaccacc cactcatgc ccagggagag ggtcttctgg atttttccac caggctccgg 840
gcagccacag gctggatgcc cctaccccag gccctgcgca tacaggggca ggtgctgcgc 900
tcagacctgc caagagccat atccgggagg accctgcccc tgacctaac ccacccaaa 960
ggccaaactc tccactccct cagctcagac accttctctc ctcccagatc tgagtaactc 1020
ccaatcttct ctctgcagag tccaaatatg gtccccatg cccaccatgc ccaggtaagc 1080
caaccagggc ctgcgccctc agctcaaggc gggacagggt ccctagagta gctgcatcc 1140
agggacaggc cccagccggg tgctgacgca tccacctcca tctcttctc agcacctgag 1200
ttcctggggg gaccatcagt ctctctgttc cccccaaaac ccaaggacac tctcatgac 1260
tcccgagccc ctgaggtcac gtgcgtgggt gtggacgtga gccaggaaga ccccgaggtc 1320
cagttcaact ggtacgtgga tggcgtggag gtgcataatg ccaagacaaa gccgcgggag 1380
gagcagttca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 1440
ctgaacggca aggagtacaa gtgcaaggtc tccaacaaag gcctcccgtc ctccatcgag 1500
aaaaccatct ccaaagccaa aggtggggacc caccgggtgc gaggggccaca tggacagagg 1560
tcagctcggc ccacctctg ccctgggagt gaccgctgtg ccaacctctg tccctacagg 1620
gcagccccga gagccacagg tgtacacct gcccccaccc caggaggaga tgaccaagaa 1680
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<400> 68

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Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Gly
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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
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Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
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Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Ser Gly Gly Gly Gly
210 215 220

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
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Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser Trp Tyr
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<211> 1041

<212> DNA

<213> Artificial Sequence

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<213> Artificial Sequence

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 165 170 175
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 180 185 190
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 195 200 205
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
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 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Ser
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 245 250 255
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 Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn Phe
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Tyr Glu Ala Ser Lys Leu Thr Ser Gly Val Pro Ser Arg Phe Ser Gly
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<210> 71

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<212> DNA

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<210> 72

<211> 357

<212> PRT

<213> Artificial Sequence

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<223> 1519gH20 FabFv heavy chain

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 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln Gly Thr Leu
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Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Ser Gly Gly Gly
 210 215 220

Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Glu Val Gln Leu
 225 230 235 240

Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
 245 250 255

Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Asn Tyr Ala Ile Asn Trp
 260 265 270

Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Ile Gly Ile Ile Trp
 275 280 285

Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly Arg Phe Thr
 290 295 300

Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser
 305 310 315 320

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<213> Artificial Sequence

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<211> 376

<212> PRT

<213> Artificial Sequence

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35 40 45

Ser Asn Tyr Gly Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Tyr Ile Asp Ser Asp Gly Asp Asn Thr Tyr Tyr Arg
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser
85 90 95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Thr Thr Gly Ile Val Arg Pro Phe Leu Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
145 150 155 160

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
165 170 175

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
195 200 205

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
210 215 220

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Ser
225 230 235 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser Glu
245 250 255

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
260 265 270

Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Asn Tyr Ala
275 280 285

Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Ile Gly
290 295 300

Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly
305 310 315 320

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln
325 330 335

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<211> 66

<212> DNA

<213> Artificial Sequence

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<211> 19

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<400> 77

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<210> 78

<211> 66

<212> DNA

<213> Artificial Sequence

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<400> 81

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<210> 82

<211> 66

<212> DNA

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<400> 82

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ttaagt                                           66
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REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

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- [WO2007039714A](#) [0184] [0247]
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- [WO05003170A](#) [0229] [0229]
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- **CHUNG C.T et al.** Transformation and storage of bacterial cells in the same solution *PNAS*, 1989, vol. 86, 2172-2175 [\[0278\]](#)

P A T E N T K R A V

1. Rekombinant gram-negativ bakteriecelle omfattende:

a. et mutant spr-gen kodende for et spr-protein, som har en mutation i en eller flere aminosyrer valgt blandt D133, H145, H157, N31, R62, 170, Q73, C94, S95, V98, Q99, R100, L108, Y115, V135, L136, G140, R144 og G147 og

b. en ekspressionsvektor omfattende et gen, som udtrykker eller overudtrykker et eller flere proteiner, der er i stand til at lette proteinfoldning valgt blandt FkpA, Skp eller en kombination af FkpA og Skp,

hvor cellen har reduceret Tsp proteinaktivitet i forhold til en vildtype-celle, og hvor cellen ikke omfatter et rekombinant polynukleotid kodende for DsbC, og hvor bakteriecellen er isogen til en vildtype-E. coli-celle, bortset fra det muterede spr-gen og den modifikation, der kræves for at reducere Tsp-proteinaktivitet i forhold til en vildtype-celle.

2. Celle ifølge krav 1, hvor det mutante spr-gen koder for et spr-protein med en eller flere mutationer valgt blandt D133A, H145A, H157A, N31Y, R62C, I70T, Q73R, C94A, S95F, V98E, Q99P, R100G, L108S, Y115F, V135D, V135G, L136P, G140C, R144C og G147C.

3. Celle ifølge krav 1, hvor det mutante spr-gen koder for et spr-protein med mutationerne C94 og H145A.

4. Celle ifølge krav 1, hvor det mutante spr-gen koder for et spr-protein med en mutation valgt blandt D133A, H145A og H157A.

5. Celle ifølge krav 1, hvor det mutante spr-gen koder for et spr-protein med en mutation valgt blandt C94A.

6. Celle ifølge ethvert af de foregående krav, hvor det mutante spr-gen er integreret i cellens genom.

7. Celle ifølge ethvert af de foregående krav, hvor et gen kodende for et protein, som er i stand til at lette proteinfoldning, midlertidigt transficeres i cellen.

8. Celle ifølge ethvert af de foregående krav, hvor proteinet, som er i stand til at lette proteinfoldning, er FkpA.

9. Celle ifølge ethvert af de foregående krav, hvor cellen desuden omfatter et eller flere af de følgende muterede gener:

et muteret DegP-gen, der koder for et DegP-protein, der har chaperonaktivitet og reduceret proteaseaktivitet;

b. et muteret ptr-gen, hvor det muterede ptr-gen koder for et Protease III-protein med reduceret proteaseaktivitet eller er et deaktiveret ptr-gen; og

c. et muteret OmpT-gen, hvor det muterede OmpT-gen koder for et OmpT-protein med reduceret proteaseaktivitet eller er et deaktiveret OmpT-gen.

10. Celle ifølge ethvert af de foregående krav, hvor cellen omfatter et muteret Tsp-gen, som koder for et Tsp-protein, der har reduceret proteaseaktivitet eller er et deaktiveret Tsp-gen.

11. Celle ifølge ethvert af de foregående krav, hvor cellen har et deaktiveret Tsp-gen, som omfatter en mutation til genstartkodonet og / eller et eller flere stopkodoner placeret nedstrøms for genstartkodonet og opstrøms for genstopkodonet.
12. Celle ifølge krav 11, hvor det deaktiverede Tsp-gen omfatter et restriktionsmærke
5 kørested skabt af en missense-mutation til genstartkodonet og eventuelt en eller flere yderligere punktmutationer.
13. Celle ifølge krav 12, hvor det deaktiverede Tsp-gen omfatter SEQ ID NO: 3.
14. Celle ifølge ethvert af de foregående krav, hvor cellen er E. coli.
15. Celle ifølge krav 14, hvor E. coli er stamme K12 eller W3110.
- 10 16. Celle ifølge ethvert af de foregående krav, hvor cellen omfatter en polynukleotidsekvens kodende for et protein af interesse valgt blandt et antistof eller et antigenbindende fragment deraf.
17. Celle ifølge krav 16, hvor antistoffet eller det antigenbindende fragment deraf er specifikt for FcRn.
- 15 18. Fremgangsmåde til fremstilling af et protein af interesse, der omfatter at dyrke en rekombinant gram-negativ bakteriecelle ifølge ethvert af kravene 1 til 17 i et kulturmedium under betingelser, der er effektive til at udtrykke det rekombinante protein af interesse og at udvinde det rekombinante protein af interesse fra periplasmaet af den rekombinante gram-negative bakteriecelle og / eller dyrkningsmediet.
- 20 19. Fremgangsmåde ifølge krav 18, hvor fremgangsmåden yderligere omfatter at udvinde proteinet af interesse fra cellen.
20. Fremgangsmåde ifølge krav 19, hvor proteinet af interesse udvindes fra periplasmaet og / eller supernatanten.

DRAWINGS

Figure 1

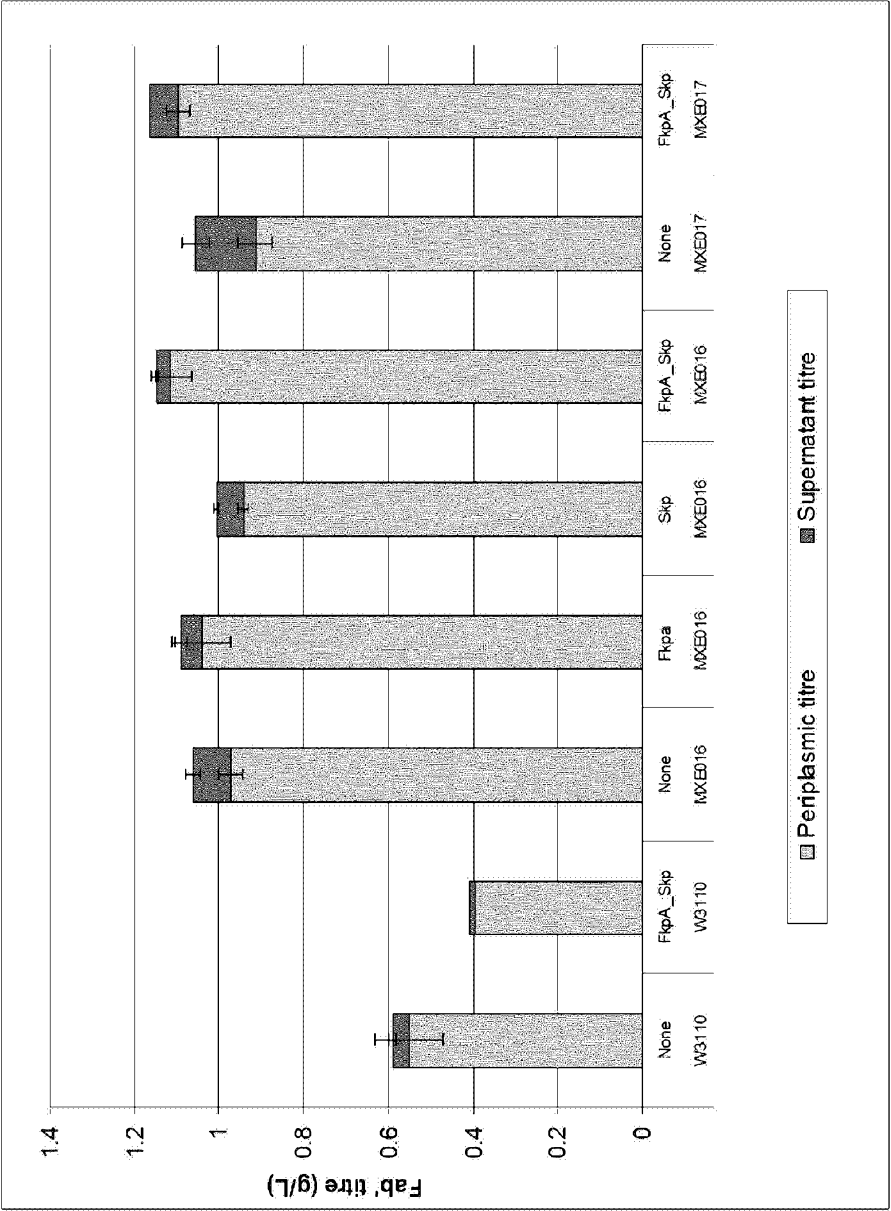


Figure 2 Feed Rate Variation Experiments

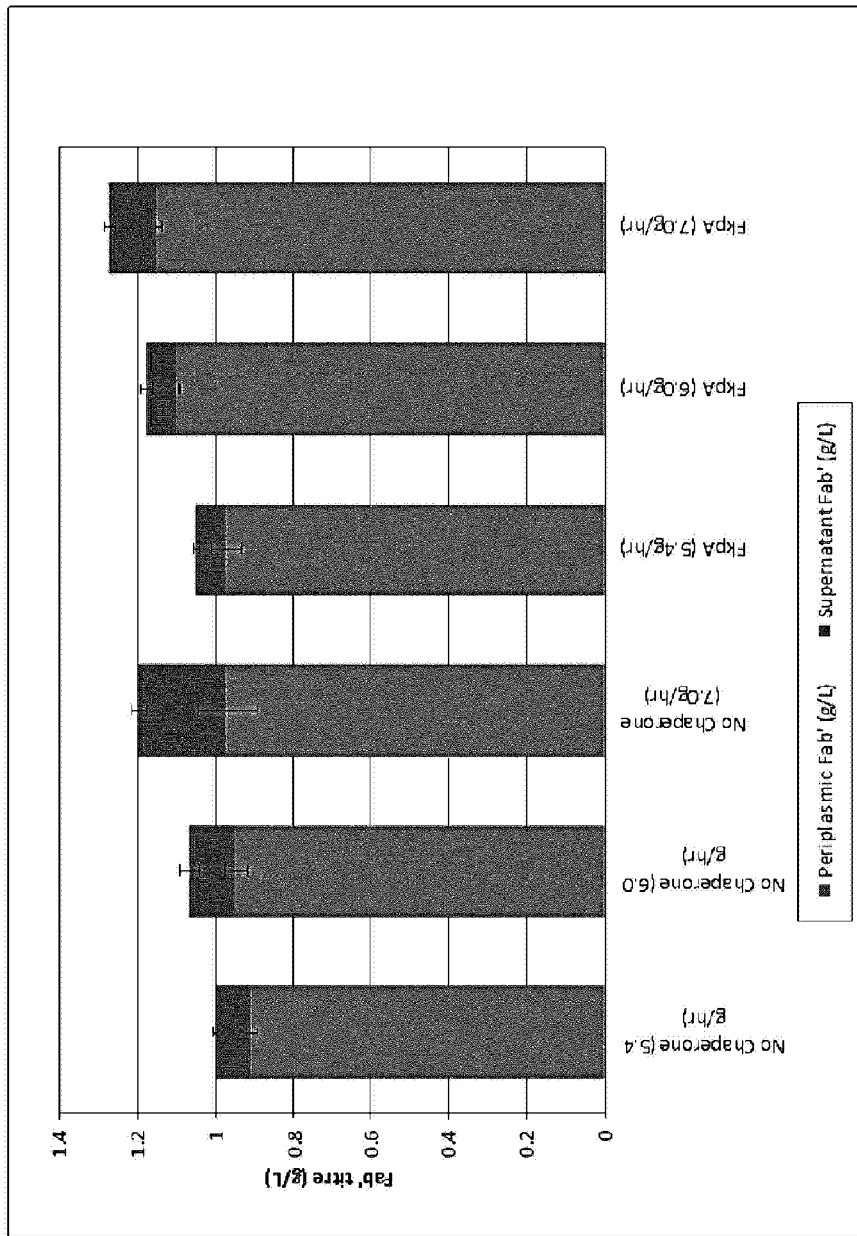


Figure 3A Cell Viability

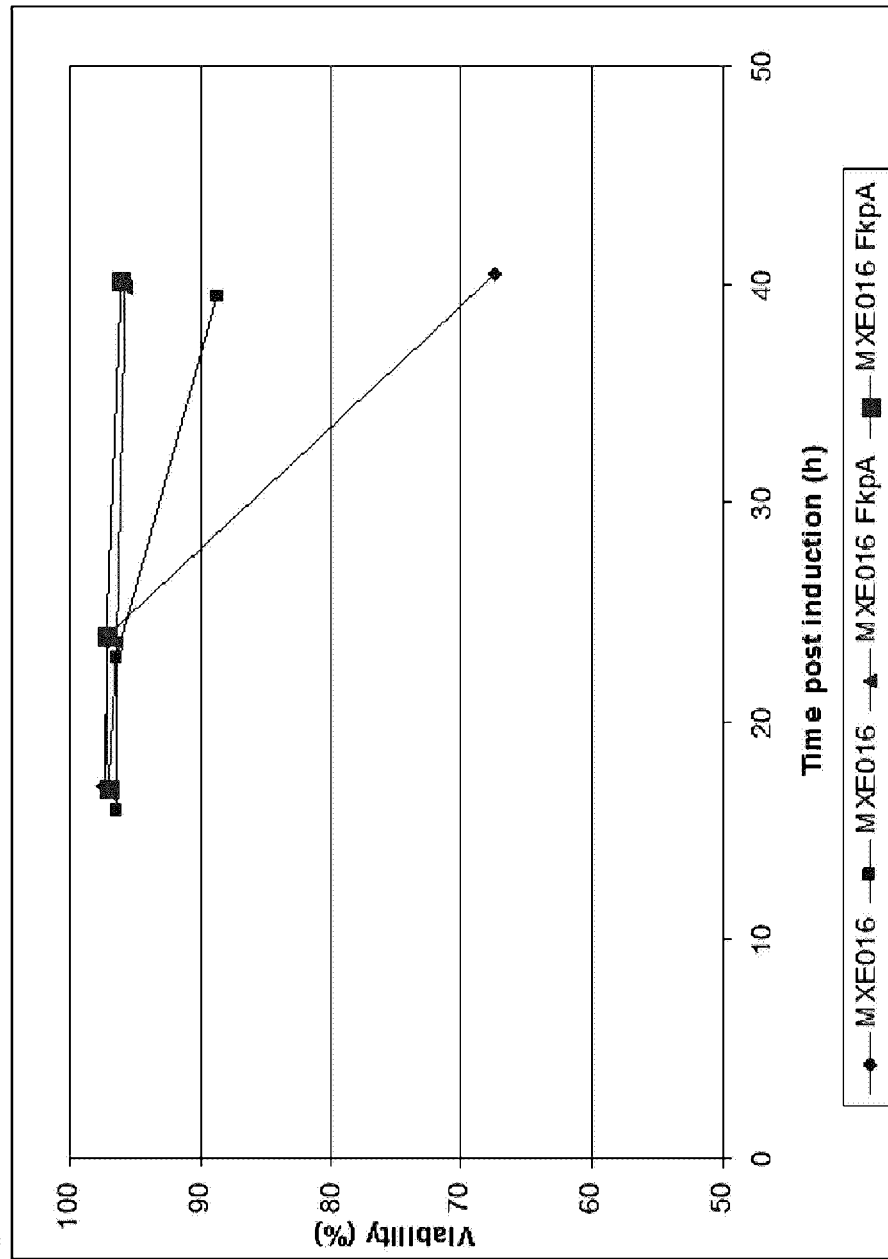


Figure 3B

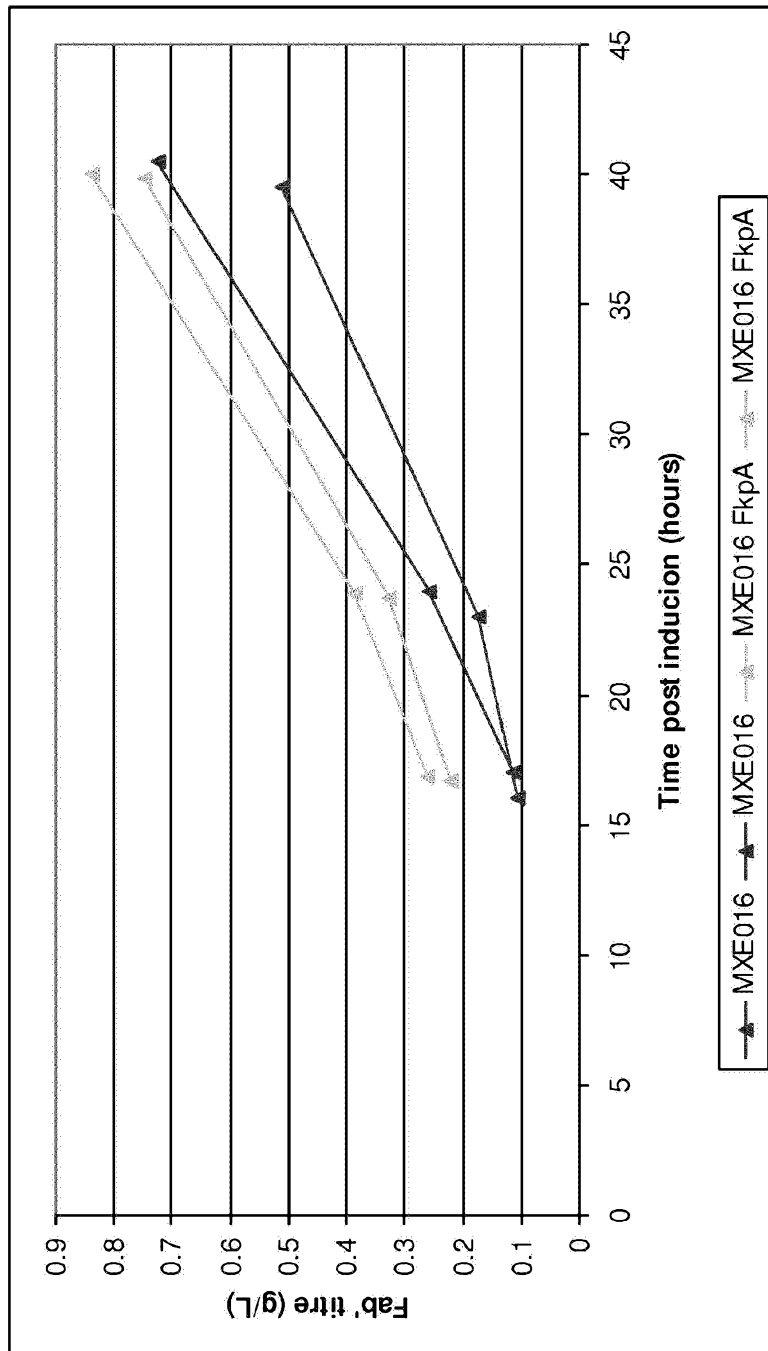


Figure 4 Harvest from 20 Litre Pilot Scale Productions and Primary Recovery for “MXE016” Cell Lines

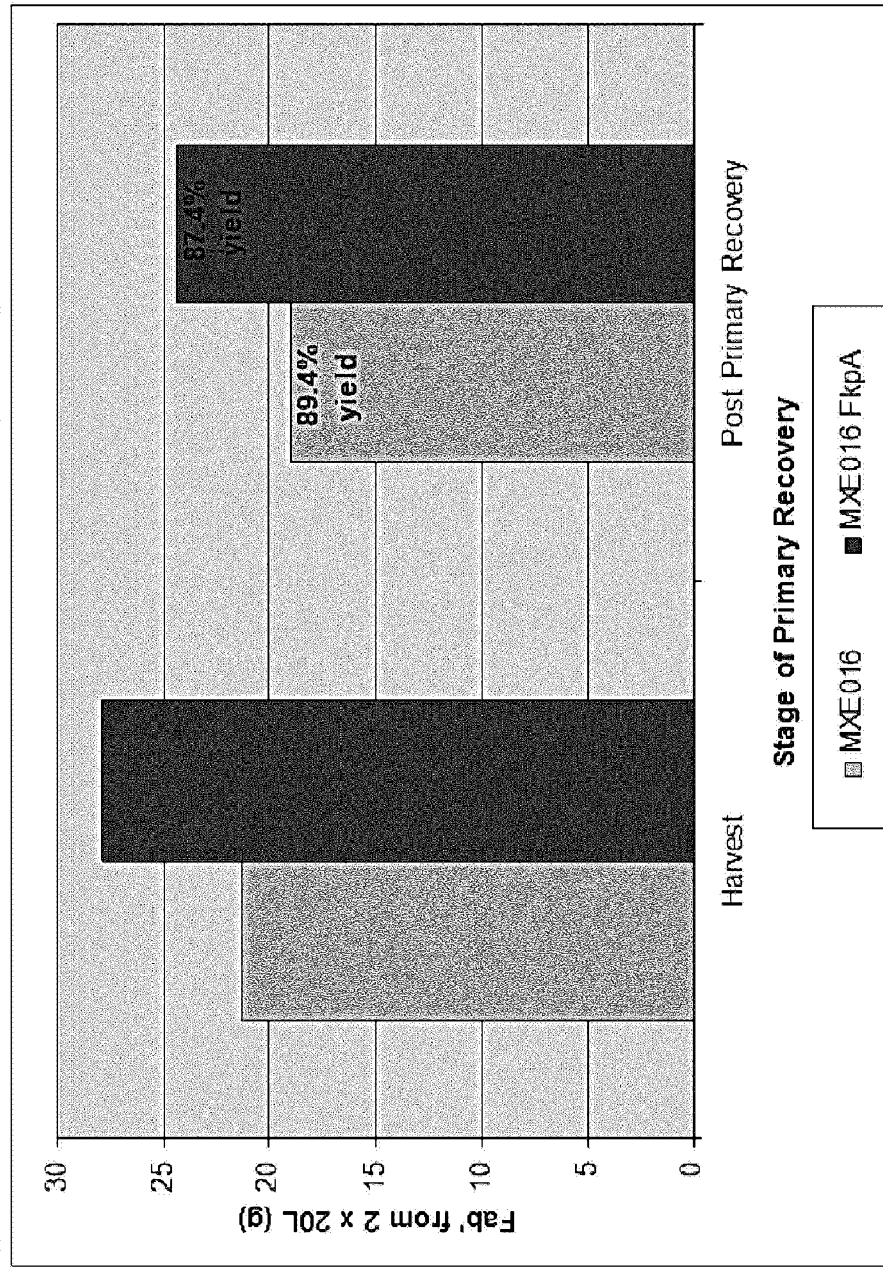
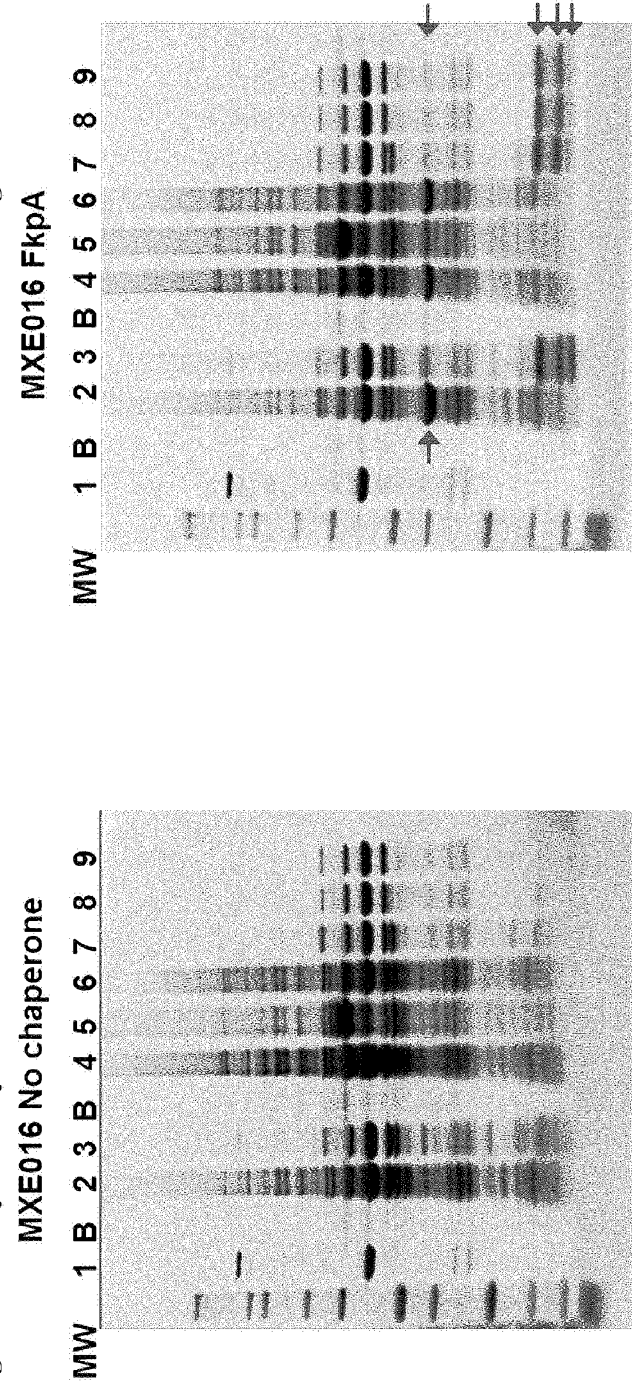
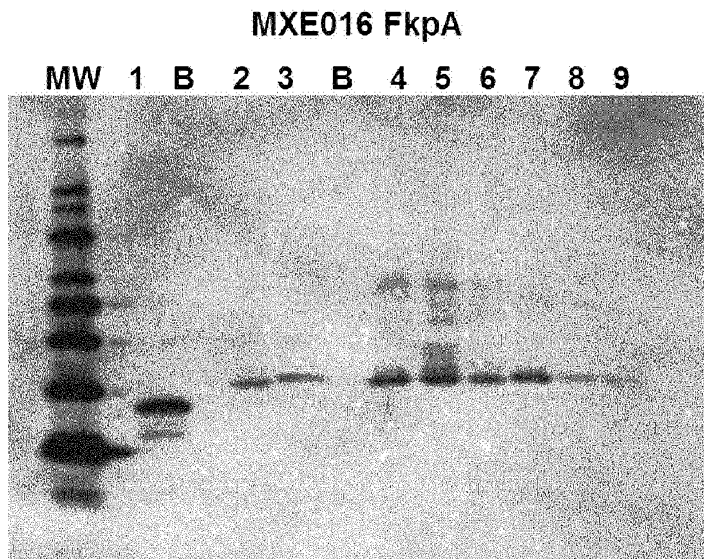


Figure 5 Primary Recovery From 20 Litre Batch Run on SDS-PAGE Stained Gel Under Non-Reducing Conditions



- 1 – X Fab' Standard;
- 2 - 30°C small scale extract;
- 3 - 60°C small scale extract;
- 4 – Supernatant of heavy phase;
- 5 – Light phase
- 6 – Post buffer addition;
- 7 – Post extraction;
- 8 – Post extract centrifugation
- 9 – Post filtration

Figure 6 Western Blot Under Non-Reducing Conditions for a 20 L Pilot Scale Batch

- 1 – His-tag positive control (DsbC)
- 2 - 30°C small scale extract
- 3 - 60°C small scale extract
- 4 – Supernatant of heavy phase
- 5 – Light phase
- 6 – Post buffer addition
- 7 – Post extraction
- 8 – Post extract centrifugation
- 9 – Post filtration

Figure 7A Mutation in Various Genes**Wild type ptr (protease III) 5' (SEQ ID NOs 81 and 82)**

```

      * M P R S T W F K A L L L L V
TGA ATG CCC CGC AGC ACC TGG TTC AAA GCA TTA TTG TTG TTA GTT

      A L W A P L S
GCC CTT TGG GCA CCC TTA AGT

```

Mutated Δ ptr (protease III) 5' (SEQ ID NOs 79 and 80)

```

      EcoR I
      ~~~~~
      * I P R S T W F K A L L L L V
TGA ATT CCC CGC AGC ACC TGG TTC AAA GCA TTA TTG TTG TTA GTT

                        Ase I
                        ~~~~~
      A L W A H * C
GCC CTT TGG GCA CAT TAA TGT

```

Figure 7B**Wild type Tsp 5' (SEQ ID NOs 75 and 76)**

```

      M N M F F R L T A L A G L L A
ATG AAC ATG TTT TTT AGG CTT ACC GCG TTA GCT GGC CTG CTT GCA

      I A G Q T F A
ATA GCA GGC CAG ACC TTC GCT

```

Mutated Δ Tsp 5' (SEQ ID NOs 77 and 78)

```

      EcoR I
      ~~~~~
      M N S F L G L P R * L A C L Q
ATG AAT TCG TTT TTA GGC TTA CCG CGT TAG CTG GCC TGC TTG CAA

                        Ase I
                        ~~~~~
      * Q A R H * L
TAG CAG GCC AGA CAT TAA TTG

```

Figure 7C

Wild type DegP

202	D	A	A	I	N	R	G	N	S	G	G
949	GAT	GCA	GCG	ATC	AAC	CGT	GGT	AAC	TCC	GGT	GGT

Mutated DegP S210A

				<i>Ase I</i>							
				~~~~~							
202	D	A	A	I	N	R	G	N	<b>A</b>	G	G
949	GAT	GCA	GCG	<b>ATT AAT</b>	CGT	GGT	AAC	<b>GCC</b>	GGT	GGT	

Figure 7D Gene Insertion

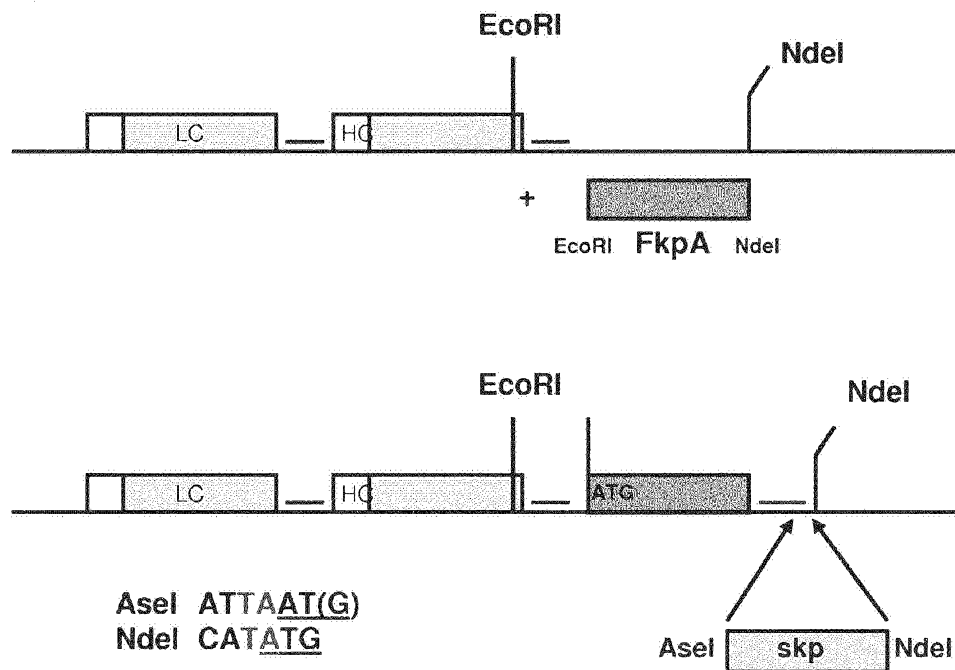


**FIGURE 8A** SEQ ID NO:1 is the DNA sequence of the wild-type Tsp gene including the 6 nucleotides ATGAAC upstream of the start codon.

ATGAACATGTTTTTTAGGCTTACCGCGTTAGCTGGCCTGCTTGCAATAGCAGGCCAGACCTTCGCTGTAGAA  
GATATCACGCGTGCTGATCAAATTCGGTATTAAAGGAAGAGACGCAGCATGCGACGGTAAAGTGAGCGCGTA  
ACGTCGCGCTTCACCCGTTCTCATTATCGCCAGTTCGACCTCGATCAGGCATTTTCGGCCAAAATCTTTGAC  
CGCTACCTGAATCTGCTCGATTACAGCCACAACGTGCTGCTGGCAAGCGATGTTGAACAGTTCGCGAAAAAG  
AAAACCGAGTTAGGCGATGAAGTTCAGGCAAACTCGACGTTTTCTACGATCTCTACAATCTGGCGCAA  
AAGCGCCGTTTTGAGCGTTACAGTACGCTTTGTCTGCTAGTGGAAAAGCCGATGGATTTACCGGCAACGAC  
ACTTATAACCTTGACCGCAGCAAAGCGCCCTGGCCGAAAAACGAGGCTGAGTTGAACGCGCTGTGGACAGT  
AAAGTCAAATTCGACGAGTTAAGCCTGAAGCTGACAGGAAAAACGGATAAAGAAATTCGTGAAACCCCTGACT  
CGCCGCTACAAATTTGCCATTTCGTCTGCTGGCGCAAACCAACAGCGAAGATGTTTTCTCGCTGGCAATGACG  
CGCTTTGCGCGTGAAATCGACCCGCATACCAACTATCTTTCCCGCGTAATACCGAACAGTTC AACACTGAA  
ATGAGTTTTGTCTGCTGGAAGGTATTGGCGCAGTGCTGCAAATGGATGATGACTACACCGTTATCAATTCGATG  
GTGGCAGGTGGTCCGGCAGCGAAGAGTAAAGCTATCAGCGTTGGTGACAAAATTGTCTGGTGTGGTCAAACA  
GGCAAGCCGATGGTTGACGTGATTGGCTGGCGTCTTGATGATGTTGGTTGCCTTAATTAAGGCGCCGAGGGC  
AGTAAAGTTCTGCTCGGAAATTTTACCTGCTGGTAAAGGGACCAAGACCCGTAAGTGAACGTTGACCCGTGAA  
CGTATTCGTCTCGAAGACCGCGCGGTTAAAATGTCTGGTGAAGACCGTCGGTAAAGAGAAAGTCGGCGTGCTG  
GATATTCGGGCTTCTATGTGGGTTTGACAGACGATGTCAAAGTGCAACTGCAGAACTGGAAAAACAGAAT  
GTCAGCAGCGTCATCATCGACCTGCGTAGCAATGGCGGTGGGGCGTTAACTGAAGCCGTATCGCTCTCCGGT  
CTGTTTATTCTCGCGGTCCCATTGTTCAAGGTCCGCGATAACAACGGCAAGGTTTCGTGAAGATAGCGATAAC  
GACGGACAGGTTTTCTATAAAGGCCCGCTGGTGGTGCTGGTTGACCGCTTCAGTGCTTCGGCTTCAGAAATC  
TTTGCCGCGGCAATGCAGGATTACGGTCTGCGCTGGTTGTGGTGAACCGACGTTTGGTAAAGGCACCGCTT  
CAGCAATACCGTTTATTGAACCGTATTTACGATCAGATGTTACGTCCTGAATGGCCAGCGCTGGGTTCTGTG  
CAGTACACGATCCAGAAATTTCTATCGCGTTAACGCGCGCAGTACGCAACGTAAGGCGTAACGCCAGACATC  
ATCATGCCGACGGTAATGAAGAAACGGAACUGGTTGAGAAATTCGAAGATAACCGCTGCCGTGGGATAGC  
ATTGATGCCGCGACTTATGTGAAATCAGGAGATTTAACGGCCTTTGAACCGGAGCTGCTGAAGGAACATAAT  
GCGCGTATCGCGAAAGATCCTGAGTTCCAGAACATCATGAAGGATATCGCGCGCTTCAACGCTATGAAGGAC  
AAGCGCAATATCGTTTCTCTGAATTACGCTGTGCGTGAGAAAGAGAATAATGAAGATGATGCGACGCGTCTG  
GCGCGTTTGAACGAACGCTTTAAACGCGAAGGTAAACCGGAGTTGAAGAACTGGATGATCTACCGAAAGAT  
TACCAGGAGCCGGATCCTTATCTGGATGAGACGGTGAATATCGCACTCGATCTGGCGAAGCTTGAAAAAGCC  
AGACCCGCGGAACAACCCGCTCCCGTCAAGTAA

**FIGURE 8B** SEQ ID NO:2 is the amino acid sequence of the wild-type Tsp protein.

MFRLTALAGLLAIAGQTFAVEDITRADQIPVLKEETQHATVSRVTSRFRSHYRQFDLDQAFSAKIFDRY  
LNLLDYSHNVLLASDVEQFAKKKTELGDRLSGKLDVFYDLYNLAQKRRFERYQYALSVLEKPMDFTGNDTY  
NLDRSKAPWPKNEAEINALWDSKVKFDELSLKLTKGTDKEIRETLTRYKFAIRRLAQTNSEDFVSLAMTAF  
AREIDPHTNYLSPRNTEQFNTEMSLSLEGI GAVLQMDDDYTVINSMVAGGPAKSKAISVGDKIVGVGQTGX  
PMVDVIGWRLDDVVALIKGPKGSKVRLEILPAGKGTKTRTVTLTRERIRLEDRAVKMSVKTVGKEKVGVLDI  
PGFYVGLTDDVKVQLQKLEKQNVSSVIDLRSNGGGALTEAVSLSGLFIPAG?IVQVRDNNNGKVREDSDTDG  
QVFYKGPLVVLVDRFSASASEIFAAAMQDYGRALVVGEPTFGKGTVQQYRSLNRIYDQMLRPEWPALGVSQY  
TIQKFYRVNGGSTQRKGVTPDIIMPTGNEETETGEKFEDNALPWDSIDAATYVKSGLTAFEPELLKEHMA  
IAKDPEFQNMKDIARENAMKDKRNIVSLNYAVREKENNEDDATRLARLNERFKREGKPELKKLDDLPKDYQ  
EPDPYLDETVNIALDLAKLEKARPAEQPAPVK*

**FIGURE 8C**

SEQ ID NO:3 is the DNA sequence of a mutated knockout Tsp gene including the 6 nucleotides ATGAAT upstream of the start codon.

```

ATCAATTCGTTTTTACCCCTTACCCCGTTACCTGCCCTGCTTGAATACCAAGCCAGACATTAATTGTACAAC
ATATCACGCGTGCTGATCAAAATTCGGGTATTAAAGGAAGAGACGCAGCATGCGACGGTAAGTGAGCGCGTAA
CGTGGCGCTTACCCCGTTCTCATTATCGCCAGTTCGACCTCGATCAGCCATTTTCGGCCAAAATCTTTGACC
GCTACCTGAATCTGCTCGATTACAGCCACAACGTGCTGCTGGCAAGCGATGTTGAACAGTTCGCGAAAAAGA
AAACCGAGTTAGGCGATGAAGTGCCTTCAGGCAAACCTCGACGTTTTCTACGATCTCTACAATCTGGCGCAA
AGCGCCGTTTTGAGCGTTACCAGTACGCTTTGTCCGTACTGGAAAAGCCGATGGATTTCACCGGCAACGACA
CTTATAACCTTGACCGCAGCAAAGCGCCCTGGCCGAAAAACGAGGCTGAGTTGAACGCGCTGTGGGACAGTA
AAGTCAAAATTCGACGAGTTAAGCCTGAAGCTGACAGGAAAAACGGATAAAGAAATTCGTGAAACCCTGACTC
GCCGCTACAAATTTGCCATTCTGCTGCTGGCGCAAACCAACAGCGAAGATGTTTTCTCGCTGGCAATGACGG
CGTTTGGCGGTGAAATCGACCCGCATACCAACTATCTTTCCCGCGTAATACCGAACAGTTCAACACTGAAA
TGAGTTTGTGCTGGGAAGGTATTGGCGCAGTGCTGCAAAATGGATGATGACTACACCGTTATCAATTTCGATGG
TGGCAGGTGGTCCGGCAGCGAAGAGTAAAGCTATCAGCGTTGGTGACAAAATTGTCCGTTGGTCAAACAG
GCAAGCCGATGGTTGACGTGATTGGCTGGCGTCTTGATGATGTGGTTGCCCTAATTAAAGGGCCGAAGGGCA
GTAAAGTTCGTCTGGAATTTTACCTGCTGGTAAAGGGACCAAGACCGTACTGTAACTTGACCCGTGAA
GTATTCGTCTCGAAGACCGCGCGGTAAATATGTCGGTGAAGACCGTCCGTAAAGAGAAAGTCGGCGTGCTGG
ATATTCGGGCTTCTAATGTGGGTTTGACAGACGATGTCAAAGTGCAACTGCAGAACTGGAAAAACAGAATG
TCAGCAGCGTCATCATCGACCTGCGTAGCAATGGCGGTGGGGCGTTAACTGAAGCCGTATCGCTCTCCGGTC
TGTTTATTCTCGCGGTCCTTGTTCAGGTCCGCGATAACAACGGCAAGGTTTCGTGAAGATAGCGATACCG
ACGACAGGTTTTCTATAAAGGCCGCTGGTGGTGTGGTTGACCGCTTCAGTGCTTCGGCTTCAGAAATCT
TTGCCGCGCAATGCAGGATTACGGTCTGCGCTGGTTGTGGGTGAACCGACGTTTGGTAAAGGCACCGTTC
AGCAATACCGTTCATTGAACCGTATTACGATCAGATGTTACGTCTGAAATGGCCAGCGCTGGGTTCTGTGC
AGTACACGATCCAGAAATTTCTATCGCGTTAACGGCGGCAGTACGCAACGTAAAGGCGTAACGCCAGACATCA
TCAATGCCGACGGTAATGAAGAAACCGAAACGGGTGAGAAATTCGAACATAACGCGCTGCCGTGGGATAGCA
TTGATGCCGCGACTTATGTGAATCAGGAGATTTAACGGCTTTGAACCGGAGCTGCTGAAGGAACATAATG
CGCTATCGCGAAAGATCCTGAGTCCAGAACATCATGAAGGATATCCCGCGCTTCAACGCTATGAAGGACA
AGCGCAATATCGTTTCTCTGAATTACGCTGTGCGTGAGAAAGAGAATAATGAAGATGATGCGACGCGTCTGG
CGGTTTGAACGAACGCTTTAAACGCGAAGGTAACCGGAGTTGAAGAACTGGATGATCTACCGAAAGATT
ACGAGGAGCCGGATCCTTATCTGGATGAGACGGTGAATATCGCACTCCATCTGGCGAAGCTTGAAAAAGCCA
GACCCGCGGAACAACCCGCTCCCGTCAAGTAA

```

SEQ ID NO:4 is the DNA sequence of the wild-type Protease III gene.

```

ATGCCCCGAGCACCTCGTTCAAAGCATTATTGTTGTTAGTTGCCCTTTGGGCACCCCTTAAGTCAGGCAGAA
ACGCGATGGCAGCGGATTCAGGAAACCATCCGTAAAAGTGATAAAGATAACCGCCAGTATCAGGCTATACGT
CTGGATAACGGTATGGTGGTCTTGCTGGTTTTCTGATCCGCGAGGCAGTTAAATCGCTCTCGCGCTGGTGGTG
CCCGTTGGGTGCTGGAAGATCCCGAGGCGTACCAGGGGCTGGCACATTACCTTGAACATATGAGTCTGATG
GGGTCGAAAAAGTACCCGACGGCTGACAGTCTGGCCGAATATCTCAAAATGCACGGCGGTAGTCACAAATGCC
AGCACTGCGCCGTATCGCACGGCTTTCTATCTGGAAGTTGAGAACGACGCGCTTGCTTGGTGGCGGTAGACCGC
CTGGCCGATGCTATTGCTGAACCTTTGCTCGACAAGAAATATGCCGAACGTGAGCGTAATGCGGTGAACGCT
GAATTAACCATGGCGGTACGCGTGACGGGATGCGCATGGCACAGGTCAGCGCAGAAACCATTAAACCCGGCA
CACCCCGGTTCAAAGTTTTCTGGTGGTAACCTCGAAACTTTAAGCGACAAACCTGGTAATCCGGTGCAGCAG
GCGCTGAAAGATTCCACGAGAAGTACTATTCCGCCAATTTGATGAACGCGGTTATTTACAGTAATAAACCG
CTGCCGGAGTTGGCAAAAATGGCGGCGGACACCTTTGGTTCGCGTGCCGAACAAAGAGAGCAAAAAACCGGAA
ATCACCGTGCCGGTAGTCACCGACGCGCAAAAGGGCATTATCATTCAATTACGTCCCTGCGCTGCCGCGTAAA
GTGTTGCGCGTTGAGTTTCGCATCGATAACAACCTCAGCGAAGTTCCGTAGTAAAACCGATGAATTGATTACC
TATCTGATTGGCAATCGCAGCCCAGGTACACTTTCTGACTGGCTGCAAAAGCAGGGATTAGTTGAGGGCATT
AGCGCCAACTCCGATCCTATCGTCAACGGCAACAGCGGCGTATTAGCGATCTCTGCGCTTTAACCGATAAA
GGCCTGGCTAATCGCGATCAGGTTGTGGCGGCAATTTTATGCTATCTCAATCTGTTACGTGAAAAAGGCATT

```

**FIGURE 8C continued**

GATAACAATACTTCGATGAACTGGCGAATGTGCTGGATATCGACTTCCGTTATCCGTCGATCACCCTGAT  
 ATGGATTACGTCGAATGGCTGGCAGATACCATGATTGCGCTTCCTGTTGAGCATACGCTGGATGCAGTCAAT  
 ATTGCCGATCGGTACCATGCTAAAGCAGTAAAGGAACGCTCTGGCGATGATGACGCCGAGAATGCGCGTATC  
 TGGTATATCAGCCCGAAAGAGCCGCACAAACAAACGCGTTACTTTGTCTGATGCGCCGTATCAGGTCGATAAA  
 ATCAGCGCACAACTTTGCGCGACTGGCAGAAAAAGCCGCGACATTGCGCTCTCTTTGCCAGAGCTTAAC  
 CCTTATATTCCIGATGATTTCTCGCTGATTAAGTCAGAGAAGAAATACGACCATCCAGAGCTGATTGTTGAT  
 GAGTCGAATCTGCGCGTGGTGTATGCGCCAAGCCGTTATTTTGCCAGCGAGCCCAAAGCTGATGTCAGCCTG  
 ATTTTGCGTAATCCGAAAGCCATGGACAGCGCCCGCAATCAGGTGATGTTTGCGCTCAATGATTATCTCGCA  
 GGGCTGGCGCTIGATCAGTTAAGCAACCAGGCGTCGGTTGGTGGCATAAGTTTTTCCACCAACGCTAACAAAC  
 GGCTTATGGTIAATGCTAATGGTTACACCCAGCGCTCTGCCGAGCTGTTCCAGGCATTGCTCGAGGGGTAC  
 TTTAGCTATACCGCTACGGAAGATCAGCTTGAGCAGGCGAAGTCTCTGGTATAACCAGATGATGGATTCCGCA  
 GAAAAGGGTAAAGCGTTTGAGCAGGCGATTATGCCCGCGCAGATGCTCTCGCAAGTGCCGTACTTCTCGCGA  
 GATGAACGGCGIAAAATTTTGGCCCTCCATTACGTTGAAAGAGGTGCTGGCCTATCGCGACGCGCTAAAAATCA  
 GGGGCTCGACCAGAGTTTATGGTTATCGGCAACATGACCGAGGCCAGGCAACACGCTGGCAGCGGATGTG  
 CAAAAACAGTTGGGCGCTGATGGTTCAGAGTGGTGTGCAAAACAAAGATGTAGTGGTCGATAAAAAACAATCC  
 GTCATCTTTGAAAAAGCCGGTAACAGCACCGACTCCGCACTGGCAGCGGTATTTGTACCGACTGGCTACGAT  
 GAATACACCAGCTCAGCCTATAGCTCTCTGTTGGGGCAGATCGTACAGCCGTGGTTCTACAATCAGTTGCGT  
 ACCGAAGAACAATTGGGCTATGCCGTGTTTGCGTTTCCAATGAGCGTGGGGCGTCAGTGGGGCATGGGCTTC  
 CTTTTGCAAAGCAATGATAAACAGCCTTCATTCTTGTGGGAGCGTTACAAGGCGTTTTTCCCAACCGCAGAG  
 GCAAAATTGCGAGCGATGAAGCCAGATGAGTTTGGCGAAATCCAGCAGGCGGTAATTACCCAGATGCTGCAG  
 GCACCGCAACCGCTCGCGGAAGAAGCATCGAAGTTAAGTAAAGATTTCGATCGCGGCAATATGCGCTTCGAT  
 TCGCGTGATAAAATCGTGGCCAGATAAACTGCTGACGCCGCAAAAACTTGCTGATTCTTCCATCAGGCG  
 GTGGTCGAGCCCGAAGGCATGGCTATTTCTGTCGAGATTTCGGCAGCCAGAACGGGAAGCCGAATATGTA  
 CACCCTGAAGGCTGGAAGTGTGGGAGAACGTGACGCGCTTGACAGCAACAATGCCCTGATGAGTGAAAAG  
 AATGAGTGA

SEQ ID NO:5 is the amino acid sequence of the wild-type Protease III protein.

MPRSTWFKALLLLVALWAPLSQAETGWQPIQETIRKSDKDNRYQAIRLDNGMVVLLVSDPQAVKSLSALVV  
 PVGSLEDPEAYQGLAHYLEHMSLMGSKKYPQADSLAEYLMHGGSHNASTAPYRTAFYLEVENDALPGAVDR  
 LADAIAPRLDDKKYERERNAVNAELTMARTRDGMRMAQVSAETINPAHPGSKFSGGNLETLSDKPGNPVQQ  
 ALKDFHEKYYSANLMKAVIYSNKPLPELAKMAADTFGRVPNKESKKPEITVPVVTDAQKGIIHYVPALPRK  
 VLRVEFRIDNNSAKFRSKTDELITYLIGNRSPGTLSDWLQKQGLVEGISANSPIVNGNSGVLAISASLTDK  
 GLANRDQVVAIFSYLNLREKIDKQYFDELANVLDIDFRYPSITRDMDYVEWLADTMIRVPVEHTLDAVN  
 IADRYDAKAVKERLAMMTPQNARIWYISPKEPHNKTAIFYVDAPYQVDKISAQTFADWQKKAADIALSLPELN  
 PYIPDDFSLIKSEKKYDHPELIVDESNLRVVYAPSRYFASEPKADVSLILRNPAMDSARNQVMFALNDYLA  
 GLALDQLSNQASVGGISFSTNANNGLMVNANGYTQRLPQLFQALLEGYFSYTATEDQLEQAKSWYNQMDSA  
 EKGAFEQAIMFAQMLSQVPYFSRDERRKILPSITLKEVLAYRDALKSGARPEFMVIGNMTEAQATTLARDV  
 QKQLGADGSEWCRNKDVVDKKQSVIFEKAGNSTDSALAAVFVPTGYDEYTSSAYSLLGQIVQPFYFNQLR  
 TEEQLGYAVFAFPM SVGRQWGMGFLQSNQKQPSFLWERYKAFFPTAEAKLRAMPDEFAQIQQAVITQMLQ  
 APQTLGEEASKLSKDFDRGNMRFDSRDKIVAQIKLLTPQKLADFFHQAVVEPQGMALISQISGSQNGKAEEYV  
 HPEGWKVWENVSAQQTMPLMSEKNE*

**FIGURE 8D**

SEQ ID NO:6 is the DNA sequence of a mutated knockout Protease III gene.

```

ATTCCCCGAGCACCCTGGTTCAAAGCATTATTGTTGTTAGTTGCCCTTTGGGCACATTAATGTCAGGCAGAA
ACGGGATGGCAGCCGATTACAGGAAACCATCCGTAAAAGTGATAAAGATAACGCCAGTATCAGGCTATACGT
CTGGATAACGGTATGGTGGTCTTGCTGGTTTCTGATCCGCAGGCAGTTAAATCGCTCTCGGCGCTGGTGGTG
CCCGTTGGGTCGCTGGAAGATCCCGAGGCGTACCAGGGGCTGGCACATTACCTTGAACATATGAGTCTGATG
GGGTCGAAAAAGTACCCGAGGCTGACAGTCTGGCCGAATATCTCAAAATGCACGGCGGTAGTCACAAATGCC
AGCACTGCGCCGTATCGCACGGCTTTCTATCTGGAAGTTGAGAACGACGCCTTGCTGGTGCGGTAGACCGC
CTGGCCGATGCTATTGCTGAACCTTTGCTCGACAAGAAATATGCCGAACGTGAGCGTAATGCGGTGAACGCT
GAATTAACCATGGCGCGTACGCGTGACGGGATGCGCATGGCACAGSTCAGCGCAGAAACCATTAACCCGGCA
CACCCCGGTTCAAAGTTTTCTGGTGGTAACCTCGAAACCTTAAGCGACAAACCTGGTAATCCGGTGCAGCAG
GCGCTGAAAGATTTCCACGAGAAGTACTATTCCGCCAATTTGATGAAGGCGGTTATTTACAGTAATAAACCG
CTGCCGGAGTTGGCAAAAATGGCGGCGGACACCTTTGGTCGCGTGCCGAACAAAGAGAGCAAAAAACCGGAA
ATCACCGTGCCGGTAGTCCACCGACGCGCAAAAGGGCATTATCATTTCATTACGTCCCTGCGCTGCCGCGTAAA
GTGTTGCGCGTTGAGTTTTCGCATCGATAACAACCTCAGCGAAGTTCCGTAGTAAACCCGATGAATTGATTACC
TATCTGATTGGCAATCGCAGCCCAGGTACACTTTCTGACTGGCTGCAAAAGCAGGGATTAGTTGAGSGCATT
AGCGCCAACTCCGATCCTATCGTCAACGGCAACAGCGGCGTATTAGCGATCTCTGCGCTTTAACCGATAAA
GGCCTGGCTAATCGCGATCAGGTTGTGGCGGCAATTTTTAGCTATCTCAATCTGTTACGTGAAAAAGGCATT
GATAACAATACTTCGATGAACCTGGCGAATGTGCTGGATATCGACTTCCGTTATCCGTGATCACCCGTGAT
ATGGATTACGTCGAATGGCTGGCAGATACCATGATTGCGGTTCCGTGTTGAGCATACGCTGGATGCAGTCAAT
ATTGCCGATCGGTACGATGCTAAAGCAGTAAAGGAACGCTCTGGCGATGATGACGCCGAGAAATGCGCGTATC
TGGTATATCAGCCCCGAAAGAGCCGACACAAACAAACGGCTTACTTTGTCGATGCGCGGTATCAGGTCGATAAA
ATCAGCGCACAAACTTTGCGCGACTGGCAGAAAAAAGCCGCGGACATTGCGCTCTCTTTGCCAGAGCTTAAC
CCTTATATTCTGATGATTTCTCGCTGATTAAGTCAGAGAAGAAATACGACCATCCAGAGCTGATTGTTGAT
GAGTCGAATCTGCGCGTGGTGTATGCGCCAAGCCGTTATTTTGCCAGCGAGCCCAAAGCTGATGTCAGCCTG
ATTTTGCGTAATCCGAAAGCCATGGACAGCGCCCGCAATCAGGTGATGTTTGCGCTCAATGATTATCTCGCA
GGGCTGGCGCTTGATCAGTTAAGCAACCCAGGCGTCGGTTGGTGGCATAAGTTTTTCCACCAACGCTAACAA
GGCCTTATGGTTAATGCTAATGGTTACACCCAGCGCTCTGCCGAGCTGTTCCAGGCATTGCTCGAGGGGTAC
TTTAGCTATACCGCTACGGAAGATCAGCTTGAGCAGGCGAAGTCCTGGTATAACCAGATGATGGATTCCGCA
GAAAAGGGTAAAGCGTTTGAGCAGGCGATTATGCCGCGCAGATGCTCTCGCAAGTGCCGTACTTCTCGCGA
GATGAACGGCGTAAATTTTGCCCTCCATTACGTTGAAAGAGGTGCTGGCCTATCGCGACGCCTTAAATCA
GGGGCTCGACCAGAGTTTATGGTTATCGGCAACATGACCGAGGCCAGGCAACAACGCTGGCACGCGATGTG
CAAAAACAGTTGGGCGCTGATGGTTCAGAGTGGTGTGCAAAACAAAGATGTAGTGGTCGATAAAAAACAATCC
GTCATCTTTGAAAAAGCCGGTAACAGCACCGACTCCGCACTGGCAGCGGTATTTGTACCGACTGGCTACGAT
GAATACACCAGCTCAGCCTATAGCTCTCTGTTGGGGCAGATCGTACAGCCGTGGTTCTACAAATCAGTTGCGT
ACCGAAGAACAATTTGGGCTATGCCGTGTTTGGCTTTCCAATGAGCGTGGGGCGTCAGTGGGSCATGGGCTTC
CTTTTGCAAGCAATGATAAACAGCCTTCATTCTTGTTGGGAGCGTTACAAGGCGTTTTTCCCAACCGCAGAG
GCAAAATTGCGAGCGATGAAGCCAGATGAGTTTTCGCAATCCAGCAGGCGGTAATTACCCAGATGCTGCAG
GCACCGCAACGCTCGGCGAAGAAGCATCGAAGTTAAGTAAAGATTTGATCGCGGCAATATGCGCTTCGAT
TCGCGTGATAAAATCGTGGCCAGATAAACTGCTGACGCCGCAAAACTTGCTGATTTCTTCCATCAGGCG
GTGGTCGAGCCGCAAGGCATGGCTATTTCTGTCGAGATTTCCGCGAGCCAGAACGGGAAAGCCGAATATGTA
CACCTGAAGGCTGGAAAGTGTGGGAGAACGTACGCGCGTTGCAGCAACAATGCCCTGATGAGTGAAGAG
AATGAGTGA

```

**FIGURE 8E**

SEQ ID NO:7 is the DNA sequence of the wild-type DegP gene.

```
ATGAAAAAAACCACATTAGCACTGAGTGCACTGGCTCTGAGTTTAGGTTTGGCGTTATCTCCGCTCTCTGCA
ACGGCGGCTGAGACTTCTTCAGCAACGACAGCCCAGCAGATGCCAAGCCTTGCACCGATGCTCGAAAAGGTG
ATGCCTTCAGTGGTCAGCATTAAACGTAGAAGGTAGCACAAACCGTTAATACGCCCGGTATGCCGCGTAATTTT
CAGCAGTTCTTCGGTGATGATTCTCCGTTCTGCCAGGAAGTTCTCCGTTCCAGAGCTCTCCGTTCTGCCAG
GGTGGCCAGGGCGGTAATGGTGGCGGCCAGCAACAGAAATTCATGGCGCTGGGTTCGGGCGTCATCATTTGAT
GCCGATAAAGGCTATGTCTGTACCAACAACCACTGTTGTTGATAACGCGACGGTCATTAAAGTTCAACTGAGC
GATGGCCGTAAGTTCGACGCGAAGATGGTTGGCAAAGATCCGCGCTCTGATATCGCGCTGATCCAAATCCAG
AACCCGAAAAACCTGACCGCAATTAAGATGGCGGATTCTGATGCACTGCGCGTGGGTGATTACACCGTAGCG
ATTGGTAACCCGTTTGGTCTGGGCGAGACGGTAACCTCCGGGATTGTCTCTGCGCTGGGGCGTAGCGGCCTG
AATGCCGAAAACTACGAAAACTTCATCCAGACCGATGCAGCGATCAACCGTGGTAACTCCG3TGGTGGCGCTG
GTTAACCTGAACGGCGAACTGATCGGTATCAACACCGCGATCCTCGCACCGGACGGCGGCAACATCGGTATC
GGTTTTGCTATCCCGAGTAACATGGTGAAAAACCTGACCTCGCAGATGGTGGAATACGGCCAGGTGAAACGC
GGTGAGCTGGGTATTTATGGGGACTGAGCTGAACTCCGAACCTGGCGAAAGCGATGAAAGTTGACGCCCGACGCG
GGTGCTTTTCGTAAGCCAGGTTCTGCC'FAATT'CTCCGCTGCAAAAGCGGGCATTAAAGCGGGTGTATGTGATC
ACCTCACTGAACGGTAAGCCGATCAGCAGCTTTGCCGCACTGCGTGCTCAGGTGGGTACTATGCCG3TAGGC
AGCAAACCTGACCCCTGGGCTTACTGCGCGACGGTAAGCAGGTTAACGTGAACCTGGAACCTGCAGCAGAGCAGC
CAGAATCAGGTTGATTCCAGCTCCATCTTCAACGGCAT'GAAGGCGCTGAGATGAGCAACAAAGGCAAGAT
CAGGGCGTGGTAGTGAACAACGTGAAAACGGGCACTCCGGCTGCGCAGATCGGCCTGAAGAAAGGTGATGTG
ATTATTGGCGCGAACCAGCAGGCAGTGAAAAACATCGCTGAACTGCGTAAAGTTCTCGACAGCAACCCGTCT
TGCTGGCACTCAACATTCAGCGCGGCGACAGCACCATCTACCTGTTAATGCAGTAA
```

SEQ ID NO:8 is the amino acid sequence of the wild-type DegP protein.

```
MKKTTLALSALALS LGLALSPLSATAAETSSATTAQMPSLAPMLEKVMPSVVSINVEGSTTVNTPRMPRNF
QQFFGDDSPFCQEGSPFQSSPFCQGGQGGNGGGQQQKFMALGSGV I I DADKGYVVTNNHVVDNATVIKVL
DGRKFDKAMVGKDPRSDIALIQINPKNLTAIKMADSDALRVGDTVAIGNPFGI.GETVTS3IVSALGRSGL
NAENYENFIQTDAATNRGNSGGALVNLNGELIGINTAILAPDGGNIGIGFAI?SNMVKNLTSQMVEYQVVK
GELGIMGTELNSELAKAMKVDAQRGAFVSQVLPNSSAAKAGIKAGDVITSLNGKPISSFAALRAQVGTMPVG
SKLTLGLLRDGDQVNVNLELQQSSQNQVDSSSIFNGIEGAEMSNKGDQGVVNVNVKTGT3PAAQIGLKKGDV
TIGANQQAVKNIAELRKVLDSKPSVIAINIQRGDSTIYIIMQ
```

SEQ ID NO:9 is the DNA sequence of a mutated DegP gene.

```
ATGAAAAAAACCACATTAGCACTGAGTGCACTGGCTCTGAGTTTAGGTTTGGCGTTATCTCCGCTCTCTGCA
ACGGCGGCTGAGACTTCTTCAGCAACGACAGCCCAGCAGATGCCAAGCCTTGCACCGATGCTCGAAAAGGTG
ATGCCTTCAGTGGTCAGCATTAAACGTAGAAGGTAGCACAAACCGTTAATACGCCCGGTATGCCGCGTAATTTT
CAGCAGTTCTTCGGTGATGATTCTCCGTTCTGCCAGGAAGTTCTCCGTTCCAGAGCTCTCCGTTCTGCCAG
GGTGGCCAGGGCGGTAATGGTGGCGGCCAGCAACAGAAATTCATGGCGCTGGGTTCGGGCGTCATCATTTGAT
GCCGATAAAGGCTATGTCTGTACCAACAACCACTGTTGTTGATAACGCGACGGTCATTAAAGTTCAACTGAGC
GATGGCCGTAAGTTCGACGCGAAGATGGTTGGCAAAGATCCGCGCTCTGATATCGCGCTGATCCAAATCCAG
AACCCGAAAAACCTGACCGCAATTAAGATGGCGGATTCTGATGCACTGCGCGTGGGTGATTACACCC3TAGCG
ATTGGTAACCCGTTTGGTCTGGGCGAGACGGTAACCTCCGGGATTGTCTCTGCGCTGGGGCGTAGCGGCCTG
AATGCCGAAAACTACGAAAACTTCATCCAGACCGATGCAGCGATTAATCGTGGTAACGCCCGTGGTGGCGCTG
GTTAACCTGAACGGCGAACTGATCGGTATCAACACCGCGATCCTCGCACCGGACGGCGGCAACATCGGTATC
GGTTTTGCTATCCCGAGTAACATGGTGAAAAACCTGACCTCGCAGATGGTGGAATACGGCCAGGTGAAACGC
GGTGAGCTGGGTATTATGGGGACTGAGCTGAACTCCGAACCTGGCGAAAGCGATGAAAGTTGACGCCCGAGCGC
GGTGCTTTTCGTAAGCCAGGTTCTGCC'TAAT'CTCCGCTGCAAAAGCGGGCATTAAAGCGGGTGTATGTGATC
ACCTCACTGAACGGTAAGCCGATCAGCAGCTTTGCCGCACTGCGTGCTCAGGTGGGTACTATGCCG3TAGGC
AGCAAACCTGACCCCTGGGCTTACTGCGCGACGGTAAGCAGGTTAACGTGAACCTGGAACCTGCAGCAGAGCAGC
CAGAATCAGGTTGATTCCAGCTCCATCTTCAACGGCAT'GAAGGCGCTGAGATGAGCAACAAAGGCAAGAT
CAGGGCGTGGTAGTGAACAACGTGAAAACGGGCACTCCGGCTGCGCAGATCGGCCTGAAGAAAGGTGATGTG
ATTATTGGCGCGAACCAGCAGGCAGTGAAAAACATCGCTGAACTGCGTAAAGTTCTCGACAGCAACCCGTCT
TGCTGGCACTCAACATTCAGCGCGGCGACAGCACCATCTACCTGTTAATGCAGTAA
```

**FIGURE 8F**

SEQ ID NO:10 is the amino acid sequence of a mutated DegP protein.

MKKTTLALSALALSGLALSPLSATAAETSSATTAQQMPSLAPMLEKVMPSVVSINVEGSTTVNTPRMPRNF  
QQFFGDDSPFCQEGSPFQSSPFCQGGQGGNGGGQQQKFMALGSGVIIDADKGYVVTNNHVVDNATVIKVQLS  
DGRKFDKAMVGKDPKSDIALIQINPKNLTAIKMADSDALRVGDYTVAGNPFCLGETVTSQIVSALGRSGL  
NAENYENFIQTDAAINRGNAGGALVNLNDELIGINTAILAPDGGNIGIGFAIPSNMVKNLTSQMVEYGQVQR  
GELGIMGTELNSELAKAMKVDAQRGAFVSQVLPNSSAAKAGIKAGDVITSLNGKPISSFAALRAQVGTMPVG  
SKLTLGLLRDGKQVNVNLELQSSQNQVDSSSIFNGIEGAEMSNKGDQGVVVNNVKTGTPAAQIGLKKGDV  
IIGANQQAVKNIAELRKVLDSKPSVLALNIQRGDSTIYLLMQ

SEQ ID NO: 11 is the sequence of the 5' oligonucleotide primer for the region of the mutated DegP gene comprising the Ase I restriction site.

CTGCCTGCGATTTTCGCCGGAACG

SEQ ID NO: 12 is the sequence of the 3' oligonucleotide primer for the region of the mutated DegP gene comprising the Ase I restriction site.

CGCATGGTACGTGCCACGATATCC

SEQ ID NO: 13 is the sequence of the 5' oligonucleotide primer for the region of the mutated Tsp gene comprising the Ase I restriction site.

GGGAAATGAACCTGAGCAAAACGC

SEQ ID NO: 14 is the sequence of the 3' oligonucleotide primer for the region of the mutated Protease III gene comprising the Ase I restriction site.

GGGAAAGGCGCGGAACCGCCTAG

SEQ ID NO: 15 is the sequence of the 5' oligonucleotide primer for the region of the mutated Protease III gene comprising the Ase I restriction site.

CTACTGTGCCAGCGGTGGTAATGG

SEQ ID NO: 16 is the sequence of the 3' oligonucleotide primer for the region of the mutated Tsp gene comprising the Ase I restriction site.

GCATCATAATTTCTTTTACCTC

SEQ ID NO: 17 is the DNA sequence of the wild-type spr gene.

ATGGTCAAATCTCAACCGATTTTGAGATATATCTTGCGCGGGATTCCCGCGATIGCAGTAGCGGTTCTGCTT  
TCTGCATGTAGTGCAAATAACACCGCAAAGAATATGCATCCTGAGACACGTGCAGTGGGTAGTGAAACATCA  
TCACTGCAAGCTTCTCAGGATGAATTTGAAAACCTGGTTCGTAATGTCGACGTAAAATCGCGAATTATGGAT  
CAGTATGCTGACTGGAAGGCGTACGTTATCGTCTGGGCGGCAGCACTAAAAAGGTATCGATTGTTCTGGT  
TTCGTACAGCGTACATTCCGTGAGCAATTTGGCTTAGAACTTCCGCGTTCGACTACGAACAGCAGGAAATG  
GGTAAATCTGTTTCCCGCAGTAATTTGCGTACGGGTGATTTAGTTCTGTTCCGTGCCGGTTCAACGGGACGC  
CATGTCCGTTATTTATATCGGCAACAATCAGTTTGTCCATGCTTCCACCAGCAGTGGTGTATTATTTCCAGC  
ATGAATGAACCGTACTGGAAGAAGCGTTACAACGAAGCACGCCGGGTCTCAGCCGCAGC

**FIGURE 8G**

SEQ ID NO: 18 is the amino acid sequence of the wild-type spr gene including the signal sequence which is the first 26 amino acid residues.

MVKSQFILRYILRGIPAIIVAVLLSACSANNTAKNMHPETRAVGSETSSLQASQDEFENLVRNVDVKSRI  
MDQYADWKGVRYRLGGSTKKGIDCSGFVQRTFREQFGLLELPSTYEQQEMGKSVSRNLRTGDLVLF  
FRAGSTGRHVGIYIGNNQFVHASTSSGVIISSMNEPYWKKRYNEARRVLSRS

SEQ ID NO: 19 the non-mutated spr gene without the signal sequence.

CSANNIAKNMHPETRAVGSETSSLQASQDEFENLVRNVDVKSRI  
MDQYADWKGVRYRLGGSTKKGIDCSGFVQRTFREQFGLLELPSTYEQQEMGKSVSRNLRTGDLVLF  
FRAGSTGRHVGIYIGNNQFVHASTSSGVIISSMNEPYWKKRYNEARRVLSRS

SEQ ID NO: 20 a mutated OmpT sequence comprising D210A and H212A mutations.

ATGCGGCGGAACTTCTGGGAATAGTCCTGACAACCCCTATTGCGATCAGCTCTTTTGCTTCTACCGAGACT  
TTATCGTTTACTCCTGACAACATAAATGCGGACATTAGTCTTGGAACCTCTGAGCGGAAAAACAAAGAGCGT  
GTTTATCTAGCCGAAGAAGGAGGCGGAAAAGTCAGTCAACTCGACTGGAAATTCAATAACGCTGCAATTATT  
AAAGGTGCAATTAATTGGGATTTGATGCCCCAGATATCTATCGGGGCTGCTGGCTGGACAACTCTCGGCAGC  
CGAGGTGGCAATATGGTCGATCAGGACTGGATGGATTCCAGTAACCCCGGAACCTGGACGGATGAAAGTAGA  
CACCTGATACACAACCTCAATTATGCCAACGAATTGATCTGAATATCAAAGGCTGGCTCCTCAACGAACCC  
AATTACCGCCTGGGACTCATGGCCGATATCAGGAAAGCCGTTATAGCTTTACAGCCAGAGGTGGTTCCCTAT  
ATCTACAGTTCTGAGGAGGGATTGAGAGATGATATCGGCTCCTTCCCGAATGGAGAAAGAGCAATCGGCTAC  
AAACAACGTTTTAAATGCCCTACATTGGCTTGACTGGAAGTTATCGTATGAAGATTTGAACTCGGTGGC  
ACATTAAATACAGCGGCTGGGTGGAATCATCTGATAACGCTGAAGCTTATGACCCGGGAAAAAGAATCACT  
TATCGCAGTAAGGTCAAAGACCAAAATTACTATTCTGTTGCAGTCAATGCAGGTTATTACGTCACACCTAAC  
GCAAAAGTTTATGTTGAAGGCGCATGGAATCGGGTTACGAATAAAAAAGGTAATACTTCACTTTATGATCAC  
AATAATAACACTTCAGACTACAGCAAAAATGGAGCAGGTATAGAAAACATAACTTCATCACTACTGCTGGT  
CTTAAGTACACATTTTAA

SEQ ID NO: 21 a mutated OmpT sequence comprising D210A and H212A mutations.

MRAKLLGIVLTTPAIISSFASTETLSFTPDNINADISLGTLSGKTKERVYLAEEGGRKVSQLDWKFNNAAII  
KGAINWDLMPQISIGAGWTTLGSRGNMVDQDWMDSNPGTWTDSESRHPDTQLNYANEFDLNKGWLLINEP  
NYRLGLMAGYQESRYSFTARGGSYIYSSEEGFRDDIGSFPNGERAIGYKQRFKMPYIGLTGSYRYEDFELGG  
TFKYSCWVESSDNAEAYDPGKRITYRSKVKDQNYYSVAVNAGYYVTPNAKVYVEGAWNRVTNKKGNTSLYDH  
NNNTSDYSKNGAGIENYNFITTAGLKYTF

SEQ ID NO: 22 is the nucleotide sequence of a mutated knockout OmpT sequence.

ATTGCGCGGAACTTCTGGGAATAGTCCTGACAACCCCTATTGCGATCAGCTCTTTTGCTTCTACCGAGACT  
TTATCGTTTACTCCTGACAACATAAATGCGGACATTAGTCTTGGAACCTCTGAGCGGAAAAACAAAGAGCGT  
GTTTATCTAGCCGAAGAAGGAGGCGGAAAAGTCAGTCAACTCGACTGGAAATTCAATAACGCTGCAATTATT  
AAAGGTGCAATTAATTGGGATTTGATGCCCCAGATATCTATCGGGGCTGCTGGCTGGACAACTCTCGGCAGC  
CGAGGTGGCAATATGGTCGATCAGGACTGGATGGATTCCAGTAACCCCGGAACCTGGACGGATGAAAGTAGA  
CACCTGATACACAACCTCAATTATGCCAACGAATTGATCTGAATATCAAAGGCTGGCTCCTCAACGAACCC  
AATTACCGCCTGGGACTCATGGCCGATATCAGCAAAACCCCTTATAGCTTTACAGCCAGAGCTGGTTCCCTAT  
ATCTACAGTTCTGAGGAGGGATTGAGAGATGATATCGGCTCCTTCCCGAATGGAGAAAGACCAATCGGCTAC  
AAACAACGTTTTAAATGCCCTACATTGGCTTGACTGGAAGTTATCGTATGAAGATTTGAACTCGGTGGC  
ACATTAAATACAGCGGCTGGGTGGAATCATCTGATAACGCTGAACACTATGACCCGGGAAAAAGAATCACT  
TATCGCAGTAAGGTCAAAGACCAAAATTACTATTCTGTTGCAGTCAATGCAGGTTATTACGTCACACCTAAC  
GCAAAAGTTTATGTTGAAGGCGCATGGAATCGGGTTACGAATAAAAAAGGTAATACTTCACTTTATGATCAC  
AATAATAACACTTCAGACTACAGCAAAAATGGAGCAGGTATAGAAAACATAACTTCATCACTACTGCTGGT  
CTTAAGTACACATTTTAA

**FIGURE 8H**

SEQ ID NO: 23 shows the sequence of the OmpA oligonucleotide adapter.  
CGATTGAATGGAGAACTTGAATTCGGGCGAAACTTCTGGGAATAG

SEQ ID NO: 24 shows a cassette encoding intergenic sequence 1 (IGS1) for E. coli Fab expression.  
AAGTTTTAATAGAGGAGAGTGTTAATGAAGAAG

SEQ ID NO: 25 shows the oligonucleotide cassette encoding intergenic sequence 2 (IGS2) for E. coli Fab expression.  
AAGTTTTAATAGAGGGGAGTGTAAAAATGAAGAAG

SEQ ID NO: 26 shows a cassette encoding intergenic sequence 3 (IGS3) for E. coli Fab expression.  
AAGCTTTAATAGAGGAGAGTGTGAGGAGGAAAAAATGAAGAAA

SEQ ID NO: 27 shows a cassette encoding intergenic sequence 4 (IGS4) for E. coli Fab expression.  
AAGCTTTAATAGAGGAGAGTGTGACGAGGATTATATAATGAAGAAA

SEQ ID NO: 28 is the DNA sequence of the wild-type FkpA gene.

ATGAAATCACTGTTTAAAGTAACGCTGCTGCGCACCACAATGGCCGTTGCCCTGCATGCACCAATCACTTTT  
GCTGCTGAAGCTGCAAAACCTGCTACAGCTGCTGACAGCAAAGCAGCGTTCAAAAATGACGATCAGAAATCA  
GCTTATGCACTGGGTGCCTCGCTGGGTCGTACATGGAAAACCTCTCTAAAAGAACAGAAAAACTGGGCATC  
AAACTGGATAAAGATCAGCTGATCGCTGGTCTTCAGGATGCATTTGCTGATAAGAGCAAACCTCTCCGACCAA  
GAGATCGAACAGACTCTACAAGCATTCGAAGCTCGCGTGAAGTCTTCTGCTCAGGCGAAGATGGAAAAAGAC  
GCGGCTGATAACGAAGCAAAAGGTAAAGAGTACCGCGAGAAATTTGCCAAAGAGAAAGGTGTGAAAACCTCT  
TCAAAGTGGTCTGGTTTATCAGGTAGTAGAAGCCGGTAAAGGCGAAGCACCAGAAAGACAGCGATACTGTTGTA  
GTGAAGTACAAAGGTACGCTGATCGACGGTAAAGAGTTCGACAACCTTTACACCCGTGGTGAACCGCTTTCT  
TTCCGTCTGGACGGTGTATCCCGGGTTGGACAGAAGGTCTGAAGAACATCAAGAAAGGCGGTAAGATCAAA  
CTGGTTATTCACACAGAACTGGCTTACGGCAAAGCGGTGTTCGGGGGATCCACCGAATTTCTACCTGGTG  
TTTGACGTAGAGCTGCTGGATGTGAAACCAAGCGCCGAAGGCTGATGCAAAGCCGGAAGCTGATGCGAAAGCC  
GCAGATTCTGCTAAAAAA

SEQ ID NO: 29 is the protein sequence of the wild-type FkpA gene.

MKSLFKVTLTATMAVALHAPITFAAEAAKPATAADSKAAFKNDDQKSAYALGASLGRYMENS LKEQEKLGI  
KLDKDQLIAGVQDAFADKSKLSDQEIEQTLQAFEARVKSSAQAKMEKDAADNEAKGKEYREKFAKEKGVKTS  
STGLVYQVVEAGKEAPKSDTVVNYKGTLDGKEFDNSYTRGEPLSFRLDGVI PGWTEGLKNIKKGGKIK  
LVIPPELAYGKAGVPGIPPNSTLVFDVELLDVKPAPKADAKPEADAKAADS AKK

SEQ ID NO: 30 is the DNA sequence of the FkpA his tagged gene.

ATGAAATCACTGTTTAAAGTAACGCTGCTGCGCACCACAATGGCCGTTGCCCTGCACGCACCAATCACTTTT  
GCTGCTGAAGCTGCAAAACCTGCTACTGCTGCTGACAGCAAAGCAGCGTTCAAAAATGACGATCAGAAATCA  
GCTTATGCACTGGGTGCCTCGCTGGGTCGTACATGGAAAACCTCTCTAAAAGAACAGAAAAACTGGGCATC  
AAACTGGATAAAGATCAACTGATCGCTGGTCTTCAGGATGCATTTGCTGATAAGAGCAAACCTCTCCGACCAA  
GAGATCGAACAGACTCTACAAGCATTTGAAGCTCGCGTGAAGTCTTCTGCTCAGGCGAAGATGGAAAAAGAC  
GCGGCTGATAACGAAGCAAAAGGTAAAGAGTACCGCGAGAAATTTGCCAAAGAGAAAGGTGTGAAAACCTCT  
TCAAAGTGGTCTGGTTTATCAGGTAGTAGAAGCCGGTAAAGGCGAAGCACCAGAAAGACAGCGATACTGTTGTA  
GTGAAGTACAAAGGTACGCTGATCGACGGTAAAGAGTTCGACAACCTTTACACCCGTGGTGAACCGCTTTCT  
TTCCGTCTGGACGGTGTATCCCGGGTTGGACAGAAGGTCTGAAGAACATCAAGAAAGGCGGTAAGATAAAA  
CTGGTTATTCACACAGAACTGGCTTACGGCAAAGCGGTGTTCGGGGGATCCACCAAATTTCTACCTGGTG  
TTTGACGTAGAGCTGCTGGATGTGAAACCAAGCGCCGAAGGCTGATGCAAAGCCGGAAGCTGATGCGAAAGCC  
GCAGATTCTGCTAAAAAACACCATCACCATCACCAC

**FIGURE 8I**

SEQ ID NO: 31 is the protein sequence of the FkpA his tagged gene.

MKSLFKVTLTLLATMAVALHAPITFAAEAAKPATAADSKAAFKNDDQKSAYALGASLGRYMENSLKEQEKLGI  
KLDKDLIAGVQDAFADKSKLSDOEIEOTLOAFEARVKSSAQAKMEKDAADNEAKGKEYREKFAKEKGVKTS  
STGLVYQVVEAGKGEAPKSDTVVVNYKGTLLDGKEFDNSYTRGEPLSFRLDGVIPCWTEGLKNIKKGGKIX  
LVIPPELAYGKAGVPGIPPNSTLVFDVELLDVKPAPKADAKPEADAKAADSARKHHHHHH

SEQ ID NO: 32 is the DNA sequence of the wild-type *skp* gene.

GTGAAAAAGTGGTTATTAGCTGCAGGTCTCGGTTTAGCACTGGCAACTTCTGCTCAGGCGGCTGACAAAATT  
GCAATCGTCAACATGGGCAGCCTGTTCCAGCAGGTAGCGCAGAAAACCGGTGTTTCTAACACGCTGGAAAAT  
GAGTTCAAAGGCCGTGCCAGCGAACTGCAGCGTATGGAAACCGATCTGCAGGCTAAAATGAAAAAGCTGCAG  
TCCATGAAAGCGGGCAGCGATCGCACTAAGCTGGAAAAAGACGTGATGGCTCAGCGCCAGACTTTTGCTCAG  
AAAGCGCAGGCTTTTGAGCAGGATCGCGCACGTCGTTCCAACGAAGAACGCGGCAAACCTGGTTACTCGTATC  
CAGACTGCTGTGAAATCCGTTGCCAACAGCCAGGATATCGATCTGGTTGTTGATGCAAACGCGCTTGTCTAC  
AACAGCAGCGATGTAAAGACATCACTGCCGACGTACTGAAACAGGTTAAATAA

SEQ ID NO: 33 is the protein sequence of the wild-type *skp* gene.

MKKWLLAAGLGLALATSAQAADKIAIVNMGSLFQQVAQKTGVSNTLENEFKGRASELQRMETDLQAKMKKLQ  
SMKAGSDRTKLEKDVMAQRQTFAQKAQAFEQDRARRSNEERGKLVTRIQTAVKSVANSQDIDLVDANAVAY  
NSSDVKDITADVLKQVK

SEQ ID NO: 34 is the DNA sequence of the *skp* his tagged gene.

ATGAAAAAGTGGTTATTAGCCGCAGGTCTCGGTTTAGCACTGGCAACTTCTGCTCAGGCGGCTGACAAAATT  
GCAATCGTCAACATGGGCAGCCTGTTCCAGCAGGTAGCGCAGAAAACCGGTGTTTCTAACACGCTGGAAAAT  
GAGTTCAAAGGCCGTGCCAGCGAACTCCAGCGTATGGAAACCGATCTCCAGGCTAAAATGAAAAAGCTGCAA  
TCCATGAAAGCGGGCAGCGATCGCACTAAGCTGGAAAAAGACGTGATGGCTCAGCGCCAGACTTTTGCTCAG  
AAAGCGCAGGCTTTTGAGCAGGATCGCGCACGTCGTTCCAACGAAGAACGCGGCAAACCTGGTTACTCGTATC  
CAGACTGCTGTGAAATCCGTTGCCAACAGCCAGGAAATCGATCTGGTTGTTGATGCAAACGCGCTTGTCTAC  
AACAGCAGCGATGTAAAGACATCACTGCCGACGTACTGAAACAGGTTAAACACCATCACCATCACCAC

SEQ ID NO: 35 is the protein sequence of the *skp* his tagged gene.

MKKWLLAAGLGLALATSAQAADKIAIVNMGSLFQQVAQKTGVSNTLENEFKGRASELQRMETDLQAKMKKLQ  
SMKAGSDRTKLEKDVMAQRQTFAQKAQAFEQDRARRSNEERGKLVTRIQTAVKSVANSQEIDLVDANAVAY  
NSSDVKDITADVLKQVKHHHHHH

**CA170_1519 Ab sequences****CDRH1**

GETFSNYGMV

SEQ ID NO: 36

**CDRH2**

YIDSDGDNITYRDSVKG

SEQ ID NO: 37

**CDRH3**

GIVRPFLY

SEQ ID NO: 38

**CDRL1**

KSSQSLVGASGKTYLY

SEQ ID NO: 39

**CDRL2**

LVSTLDS

SEQ ID NO: 40

**CDRL3**

LQGTTFPHT

SEQ ID NO: 41

**FIGURE 8J**

**Rat Ab 1519 VL region** SEQ ID NO: 42  
 DVVMTQTPLS LSVALGQPAS ISCKSSQSLV GASGKTYLYW LFQRSGQSPK RLIYLVSTLD  
 SGIPDRFSGS GAETDFTLKI RRVEADDLGV YYCLQGTHFP HTFGAGTKLE LK

**Rat Ab 1519 VL region** SEQ ID NO: 43  
 gatgttggtga tgaccagac tccactgtct ttgtcgggtg cccttggaca accagcctcc  
 atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata ttgtattgg  
 ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgta cacaetggac  
 tctggaattc ctgatagggt cagtggcagt ggagcagaga cagattttac tcttaaaatc  
 cgcagagtgg aagccgatga ttggggagtt tattactgct tgcaaggtag acattttcct  
 cacacgtttg gagctgggac caagctggaa ttgaaa

**Rat Ab 1519 VL region with signal sequence underlined and italicised** SEQ ID NO: 44  
*MMSPAQFLFLMLNIQGTSG*DVVMTQTPLSLSVALGQPASISCKSSQSLVGASGKTYLYWLFQRSGQSPK  
 RLIYLVSTLD SGIPDRFSGSGAETDFTLKIRRVEADDLGVYYCLQGTHFPHTFGAGTKLELK

**Rat Ab 1519 VL region with signal sequence underlined and italicised** SEQ ID NO: 45  
*atgatgagtc ctgcccagtt cctgtttctg ctgatgctct ggattcaggg aaccagtgg*  
 gatgttggtga tgaccagac tccactgtct ttgtcgggtg cccttggaca accagcctcc  
 atctcttgca agtcaagtca gagcctcgta ggtgctagtg gaaagacata ttgtattgg  
 ttatttcaga ggtccggcca gtctccaaag cgactaatct atctggtgta cacaetggac  
 tctggaattc ctgatagggt cagtggcagt ggagcagaga cagattttac tcttaaaatc  
 cgcagagtgg aagccgatga ttggggagtt tattactgct tgcaaggtag acattttcct  
 cacacgtttg gagctgggac caagctggaa ttgaaa

**Rat Ab 1519 VH region** SEQ ID NO: 46  
 EVPLVESGGG SVQPGRSMKL SCVVS GFTFS NYGMVWVRQA PKKGLEWVAY IDSDGDNITYY  
 RDSVKGRFTI SRNNAKSTLY LQMDSLRSED TATYYCTTGI VRPFLYWGGQ TTVTVS

**Rat Ab 1519 VH region** SEQ ID NO: 47  
 gaggtgccgc tgggtggagtc tgggggcggc tcagtgcagc ctggggaggtc catgaaactc  
 tctgtgtag tctcaggatt cactttcagt aattatggca tgggtctgggt ccgccaggct  
 ccaaagaagg gtctggagtg ggtcgcataat attgattctg atggtgataa tacttactac  
 cgagattccg tgaaggcccg attcactatc tccagaaata atgcaaaaag caccctatat  
 ttgcaaatgg acagtctgag gtctgaggac acggccactt attactgtac aacagggtt  
 gtccggccct ttctctattg gggccaagga accacgggtc cegtctcg

**Rat Ab 1519 VH region with signal sequence underlined and italicised** SEQ ID NO: 48  
*MDISLSLAFL VLFIKVRC*E VPLVESGGGS VQPGRSMKLS CVVS GFTFSN YGMVWVRQAP  
 KKGLEWVAYI DSDGDNITYYR DSVKGRFTIS RNNAKSTLYL QMDSLRSED TATYYCTTGIV  
 RPFLYWGGQT TTVTVS

**Rat Ab 1519 VH region with signal sequence underlined and italicised** SEQ ID NO: 49  
*atggacatca gtctcagctt ggctttcctt gtctttttca taaaagggtg ccggtgtgag*  
 gtgccgctgg tggagtctgg gggcggctca gtgcagcctg ggaggtccat gaaactctcc  
 tgtgtagctc caggattcac tttcagtaat tatggcatgg tctgggtccg ccaggctcca  
 aagaagggtc tggagtgggt cgcataatatt gattctgatg gtgataatac ttactaccga  
 gattccgtga agggccgatt cactatctcc agaaataatg caaaaagcac cctatatttg  
 caaatggaca gtctgaggtc tgaggacacg gccacttatt actgtacaac agggattgtc  
 cggcccttctc tctattgggg ccaaggaaac acggtcaccg tctcg

## FIGURE 8K

## 1519 gL20 V-region SEQ ID NO: 50

DIQMTQSPSS LSASVGDRVT ITCKSSQSLV GASGKTYLYW LFQKPGKAPK RLIYLVSTLD  
SGIPSRFSGS GSGTEFTLTI SSLQPEDFAT YYCLQGTHFP HTFGQGTKLE IK

## 1519 gL20 V-region SEQ ID NO: 51

gatatccaga tgaccacagag tccaagcagt ctctccgccca gcgtaggcga tcgtgtgact  
attacctgta aaagctccca gtccctggtg ggtgcaagcg gcaaaacctc cctgtactgg  
ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat  
agcggtatcc cgtctcggtt ctccggtagc ggtagcggta ccgaattcac gctgaccatt  
agctccctcc agccggagga ctttgcctac tattactgcc tccagggcac tcattttccg  
cacactttcg gccagggtac caaactggaa atcaaa

## 1519 gL20 V-region with signal sequence underlined and italicized SEQ ID NO: 52

*MKKTATAIAVALAGFATVAQ*ADIQMTQSPSSLSASVGDRVTITCKSSQSLVGASGKTYLYWLFQKPGKAPK  
RLIYLVSTLDSGIPSRFSGSGSGTEFTLTISLQPEDFATYYCLQGTHFPHTFGQGTKLEIK

## 1519 gL20 V-region with signal sequence underlined and italicized SEQ ID NO: 53

*atgaaaaaga cagctatcgc aattgcagtg gccttggtcg gtttcgctac cgtagcgcga*  
*gctgatatcc agatgaccca gagtccaagc agtctctccg ccagcgtagg cgatcgtgtg*  
actattacct gtaaaagctc ccagtcctcg gtgggtgcaa gcggcaaaac ctacctgtac  
tggtctttcc agaaacgggg caaagctccg aaacgcctga tctatctggt gtctacctg  
gatagcggta ttccgtctcg tttctccggt agcggtagcg gtaccgaatt cagcgtgacc  
attagctccc tccagcggga ggactttgct acctattact gcctccaggg cactcatttt  
ccgcacactt tcggccaggg taccaaactg gaaatcaaa

## 1519 gL20 light chain (V + constant) SEQ ID NO: 54

DIQMTQSPSS LSASVGDRVT ITCKSSQSLV GASGKTYLYW LFQKPGKAPK RLIYLVSTLD  
SGIPSRFSGS GSGTEFTLTI SSLQPEDFAT YYCLQGTHFP HTFGQGTKLE IKRTVAAPSV  
FIFPPSDEQL KSGTASVVCL LNNFYPREAK VQWKVDNALQ SGNSQESVTE QDSKDSTYSL  
SSTLTLSKAD YEKHKVYACE VTHQGLSSPV TKSFNREGC

## 1519 gL20 light chain (V + constant) SEQ ID NO: 55

gatatccaga tgaccacagag tccaagcagt ctctccgccca gcgtaggcga tcgtgtgact  
attacctgta aaagctccca gtccctggtg ggtgcaagcg gcaaaacctc cctgtactgg  
ctcttccaga aaccgggcaa agctccgaaa cgcctgatct atctggtgtc taccctggat  
agcggtatcc cgtctcggtt ctccggtagc ggtagcggta ccgaattcac gctgaccatt  
agctccctcc agccggagga ctttgcctac tattactgcc tccagggcac tcattttccg  
cacactttcg gccagggtac caaactggaa atcaaacgta cggtagcggc cccatctgtc  
ttcatcttcc cgcctctgta tgagcagttg aaatctggaa ctgcctctgt tgtgtgectg  
ctgaataact tctatcccag agaggccaaa gtacagtggg aggtggataa cgcctcccaa  
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc  
agcagcacc ctagcgtgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa  
gtcaccctcc agggcctgag ctaccagta acaaaaagtt ttaatagagg ggagtgt

## 1519 gL20 light chain with signal sequence underlined and italicized SEQ ID NO: 56

*MKKTATAIAV ALAGFATVAQ*ADIQMTQSPSLSASVGDRVITITCKSSQSLVGASGKTYLY  
WLFQKPGKAPKRLIYLVSTLDSGIPSRFSGSGSGTEFTLTISLQPEDFAITYYCLQGTHF  
PHTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREA KVQWKVDNAL  
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYIEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 8L

1519 gL20 light chain with signal sequence underlined and italicized SEQ ID NO: 57

atgaaaaaga cagctatcgc aattgcagtg gccttggetg gtttcgctac cgtagcgcaa  
gctgatatcc agatgaccca gagccaagc agtctctccg ccagcgtagg cgatcgtgtg  
 actattacct gtaaaagctc ccagtcctcg gtgggtgcaa gcggcaaaac ctacctgtac  
 tggctcttcc agaaaccggg caaagctccg aaacgcctga tctatctggt gtctaccctg  
 gatagcggta ttcggtctcg tttctccggt agcggtagcg gtaccgaatt cacgctgacc  
 attagctccc tccagccgga ggactttgct acctattact gcctccaggg cactcatttt  
 ccgcacactt tcggccaggg taccaaactg gaaatcaaac gtacggtagc ggccccatct  
 gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttggtgtg  
 ctgtgtaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc  
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cactacagc  
 ctacgcagca cctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc  
 gaagtcaccc atcagggcct gagctcacca gtaacaaaaa gttttaatag aggggagtgt

1519 gH20 V-region SEQ ID NO: 58

EVPLVESGGG LVQPGGSLRL SCAVSGFTFS NYGMVWVRQA PGKGLEWVAY IDSDGDNTYY  
 RDSVKGRFTI SRDnakssly LQMNSLRAED TAVYYCTTGI VRPFLYWGQG TLVTVS

1519 gH20 V-region SEQ ID NO: 59

gaggttccgc tggtcgagtc tggaggcggg cttgtccagc ctggagggag cctgcgtctc  
 tcttgtagcag tatctggctt caggttctcc aactacggta tgggtggtgtg tgcctaggct  
 ccaggtaaaag gtctggaatg ggtggcgtat attgactccg acggcgacaa cacctactat  
 cgcgactctg tgaaggtcgc cttcaccatt tccgcgcgata acgccaatc cagcctgtac  
 ctgcagatga acagcctgcg tgcgtaagat actgcggtgt actattgcac cactggcatc  
 gtgcgtccgt ttctgtattg gggtcagggt accctcgtaa ctgtctcg

1519 gH20 V-region with signal sequence underlined and italicized SEQ ID NO: 60

MKKTATATAV ALAGFATVAQ AEVPLVESGG GLVQPGGSLR LSCAVSGFTF SNYGMVWVRQ  
 APGKGLEWVA YIDSDGDNTY YRDSVKGRFT ISRDnakssl YLQMNSLRAE DTAVYYCTTG  
 IVRPFLYWGQ GTLVTVS

1519 gH20 V-region with signal sequence underlined and italicized SEQ ID NO: 61

atgaagaaga ctgctatagc aattgcagtg gcgctagctg gtttcgccac cgtggcgcaa  
gctgaggttc cgctggctga gtctggaggc gggcttgctc agcctggagg gagcctgcgt  
 ctctcttggt cagtatctgg cttcacgttc tccaaactac gtatggtgtg ggttcgtcag  
 gctccaggta aaggctctga atgggtggcg tatattgact ccgacggcga caacacctac  
 tatcgcgact ctgtgaaagg tcgcttcacc atttcccgcg ataacgccaa atccagcctg  
 tacctgcaga tgaacagcct gcgtgctgaa gatactgcgg tgtactattg caccactggc  
 atcgtgcgtc cgtttctgta ttggggtcag ggtacctcg ttactgtctc g

1519gH20 Fab' heavy chain (V + human gamma-1 CH1 + hinge) SEQ ID NO: 62

EVPLVESGGG LVQPGGSLRL SCAVSGFTFS NYGMVWVRQA PGKGLEWVAY IDSDGDNTYY  
 RDSVKGRFTI SRDnakssly LQMNSLRAED TAVYYCTTGI VRPFLYWGQG TLVTVSSAST  
 KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  
 SLSSVTVTPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKHTCAA

## FIGURE 8M

1519gH20 Fab' heavy chain (V + human gamma-1 CH1 + hinge) SEQ ID NO: 63

gagggtccgc tggctcagtc tggaggcggg cttgtccagc ctggaggag cctgcgtctc  
 tcttgtgcag tatctggctt cacgttctcc aactacggta tgggtgtgggt tggtcaggct  
 ccaggtaaag gtctggaatg ggtggcgat attgactccg acggcgacaa cacctactat  
 cgcgactctg tgaaaggctg cttcaccatt tcccgcgata acgccaatc cagcctgtac  
 ctgcagatga acagcctgcg tgcetgaagat actgcgggtg actattgcac cactggcacc  
 gtgcgtccgt ttctgtattg gggtcagggt accctcgta ctgtctcgag cgtttctaca  
 aagggcccat cgggtcttccc cctggcaccc tccccaaga gcacctctgg gggcacagcg  
 gccctgggct gectgggtcaa ggactacttc ccogaaccgg tgacggtgtc gtggaactca  
 ggcgccctga ccagcgcggt gcacaccttc ccggctgtcc tacagtctc aggactctac  
 tccctcagca gcgtgggtgac cgtgccctcc agcagcttg gcacccagac ctacatctgc  
 aacgtgaatc acaagccag caacaccaag gtcgacaaga aagttgagcc caaatcttgt  
 gacaaaactc acacatgcgc cgcg

1519gH20 Fab' heavy chain with signal sequence underlined and italicized SEQ ID NO: 64

*MKKTALIAIAV* *ALAGFATVAQ* *AEVPLVESGG* GLVQPGGSLR LSCAVSGFTF SNYGMVWVRQ APGKGLEWVA  
 YIDSDGDNTRY YRDSVKGRFT ISRDNAKSSL YLQMNSLRAE DTAVYYCTTG IVRPFYWGQ GTLTVSSAS  
 TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTWSN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP  
 SSSLGTQTYI CNVNHKPSNT KVDKKVEPKS CDKTHCA

1519gH20 Fab' heavy chain with signal sequence underlined and italicized SEQ ID NO: 65

*atgaagaaga* *ctgctatagc* *aattgcagtg* *gcgctagctg* *gtttcgccac* *cgtggcgcaa*  
*gctgaggttc* cgctggctga gtctggaggg gggcttgctc agcctggagg gaggctgcgt  
 ctctcttggt cagtatctgg cttcacgttc tccaaactac gtatgggtgt ggttcgtcag  
 gctccaggta aagggtctga atgggtggcg tatattgact ccgacggcga caacacctac  
 tatcgcgact ctgtgaaagg tcgcttcacc atttcccgcg ataacgcca atccagcctg  
 tacctgcaga tgaacagcct gcgtgctgaa gatactgcgg tgtactattg caccactggc  
 atcgtgcgtc cgtttctgta ttggggctcag ggtaccctcg ttactgtctc gagegttct  
 acaaagggcc catcggtctt cccctggcga cctcctcca agagcacctc tgggggcaca  
 gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac  
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tctacagtc ctcaggactc  
 tactccctca gcagcgtggt gaccgtgcc tccagcagct tgggcacca gacctacatc  
 tgcaacgtga atcacaagcc cagcaacacc aaggtcgaca agaaagttga gcccgaatct  
 tgtgacaaaa ctcacacatg cgcgcgcg

1519gH20 IgG4 heavy chain (V + human gamma-4P constant) SEQ ID NO: 66

EVPLVESGGG LVQPGGSLRL SCAVSGFTFS NYGMVWVRQA PGKGLEWVAY IDSDGDNTRY  
 RDSVKGRFTI SRDNAKSSLY LQMNSLRAED TAVYYCTTGI VRPFYWGQG TLTVSSAST  
 KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  
 SLSSVVTVPSS SSLGKTITCTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  
 PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  
 SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  
 SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  
 SCSVMHEALH NHYTQKSLSL SLGK

**FIGURE 8N**

1519gH20 IgG4 heavy chain (V + human gamma-4P constant, exons underlined) SEQ ID NO: 67

gaggtaccacttctgtggaagcggagaggtcttctgtgcaagcctggaggaagtttacgtctctcttctgtctgtgtctggtt  
caccttctccaattacggaatggtctgggtcagacaagcacctggaaaggggtcttgaatgggtggcctatatgtactctg  
acggggacaaacacctactatcgggattccgtgaaaggacgcttcacaatctcccgagataacgccaagagctcactgtac  
ctgcagatgaatagcctgagagccgaggatactgcccgtgtactattgcacaacgggaatcgttaggccttttctgtactg  
gggacagggcaccttgggtactgtctcgagcgttctacaaagggcccatccgtcttccccctggcgccctgctccagga  
gcacctccgagagcacagccgcccctggggtgcctggtaaggactacttccccgaaccggtgacggtgtcgtggaactca  
ggegcectgaccagcggcgtgcaacaccttcccggtgtgctctacagtcctcaggactctactccctcagcagcgtggtgac  
cgtgccctccagcagcttgggcacgaagacctacacctgcacaagcccagcaacaccaaggtggacaagagagttggtga  
gaggccagcacaggaggagggtgtctgtgtggaagccaggctcagccctcctgcttgacgcaccccggctgtgcaagcc  
ccagcccagggcagcaaggcatgccccatctgtctctcaccggaggcctctgaccacccactcatgcccaggagag  
ggtcttctggatttttccaccaggctccgggcagccacaggctggatgccctaccccaggccctgcgcatacaggggca  
ggtgtcgtcagacctgccaagagccatataccgggaggacctgcccctgacctaaagccaccccaagccaaactc  
tccactccctcagctcagacacaccttctctctccagactctagtaactcccaatcttctctctgcagagtcacaaatag  
gtcccccatgccaccatgccaggtgaagcaacccaggcctgcctctcagctcaaggcgggacaggtgccttagagta  
gcctgcctcagggacaggcccccagccgggtgtgtgacgcacacacctcctcttctcagcacctgagttctctggggg  
gacctcagcttctctgttccccccaaaacccaaggacactctcatgatctcccggaacctgaggtcacgtgcgtggtg  
gtggacgtgagccaggaagaccccaggttccagttcactggttactggtgagtggtggtgaggtgcatatgccaaagacaaa  
gcccggggaggagcagttcaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggtggaacgca  
aggagtacaagtgaaggctctccaacaaaggcctcccgctcctccatcgagaaaaacatctccaaagccaaaggtgggacc  
cacgggtgtcgagggccacatggacagaggtcagctcgcccacacctctgcccctgggagtgacgcgtgtgccaacctctg  
tccctacagggcagccccgagagccacaggtgtacacctgccccatcccaggaggagatgaccaagaaccagggtcagc  
ctgcctggcgtggtcaaaaggcttctaccccagcgacatcgccgtggagtgggagagcaatgggcagccgggacaacacta  
caagaccacgcctcccgctgctggactcagcggctccttcttctctacagcaggctaacggtggacaagagcaggtggc  
aggagggaatgtcttctcctatgctccgtgatgcagaggctctgcacaaccactacacagaagagcctctcctgtct  
ctgggtaaa

## 1519gL20 FabFv light chain SEQ ID NO: 68

DIQMTQSPSS LSASVGRDVT ITCKSSQSLV GASGKTYLYW LFQKPGKAPK RLIYLVSTLD  
 SGIPSRFSGS GSGTEFTLTI SSLQPEDFAT YYCLQGTHFP HTFGQGTKLE IKRTVAAPSV  
 FIFPPSDEQL KSGTASVVCL LNNFYPREAK VQWKVDNALQ SGNSQESVTE QDSKDYSTSL  
 SSTLTLSKAD YEKHKVYACE VTHQGLSSPV TKSFNREGCS GGGGSGGGGS GGGGSDIQMT  
 QSPSSVSASV GDRVITICQS SPSVWSNFLS WYQQKPGKAP KLLIYEASKL TSGVPSRFSG  
 SSGSTDFTLT ISSLQPEDFA TYCGGGYSS ISLTTFGCGT KVEIKRT

## 1519gL20 FabFv light chain SEQ ID NO: 69

gatatccaga tgacccagag cccatctagc ttatccgcct ccgttgggtga tcgcgtgaca  
 attacgtgta agagctccca atctctcgtg ggtgoaagtg gcaagacctc tctgtactgg  
 ctcttttcaga agcctcgcaa ggcaaccaaa ccgctgatct atctggtgtc tacccttgac  
 tctgggatac cgtcacgatt ttccggatcc gggagcggaa ctgagttcac actcacgatt  
 tcatcgctgc aacccgagga ctttgcctacc tactactgcc tgcaaggcac tcatttccct  
 cacactttcg gcagcgggac aaaactcgaa atcaaacgta cggtagcggc cccatctgtc  
 tcatcttcc cgcctatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgctg  
 ctgaataact tctatcccag agaggccaaa gtacagtggg aggtggataa cgcctccaa  
 tgggtaact cccagcagag tgtcacagag caggacagca aggacagcac ctacagcctg  
 agcagcacc tgcagctgtc taaagcagac tacgagaaac acaaagtgtc cgcctgcgaa  
 gtcacccatc agggcctgag ctaccagta acaaaaagt ttaatagagg ggagtgtagc  
 ggtggcgggtg gcagtcgtgg gggaggtccc ggaggtggcg gttcagacat acaaatgacc  
 cagagtcctt catcgctatc cgcgtccgtt ggcgataggg tgactattac atgtcaaagc  
 tctcctagcg tctggagcaa ttttctatcc tggatcaac agaaaccggg gaaggctcca  
 aaacttctga tttatgaag ctcgaaactc accagtggag ttccgtcaag attcagtggc  
 tctggatcag ggacagactt cagcttgaca atcagttcgc tgcaaccaga ggactttgag  
 acctactatt gtggctgagg ttacagtagc ataagtgaac cgacatttgg gtgcggtact  
 aagggtgaaa tcaaacgtac c

**FIGURE 80****1519gL20 FabFv light chain with signal sequence underlined and italicised SEQ ID NO: 70**

*MSVPTQVLGLLLWLTDARCDIQMTQSPSSLSASVGDRTITCKSSQSLVGASGKTYLYWLFQKPGKAPKRRLIYLV*  
 STLDSPGIPSRFSGSGSGTEFTLTISLQPEDFATYYCLOGTHFPHTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSSGGGSGGGGSGGGGSDIQMTQSPSSVSASVGDRTITCQSSPSVWSNFLSWYQQKPGKAPKLLIYEASKLTSQVPSRFSGSGSGTDFTLTISLQPEDFATYYCGGYSISDTTFCGCTKVEIKRT

**1519gL20 FabFv light chain with signal sequence underlined and italicised SEQ ID NO: 71**

*atgtctgtccccaccaagtcctcggactcctgctactctggcttacagatgccagatgccgatatccagatg*  
 acccagagcccatctagcttatccgcttcggttggtgacgctgacaattacgtgtaagagctcccaatctctcgtgggtgcaagtgccaagacctatctgtactggctctttcagaagcctggcaaggcaccaaaacggctgatctatctggtgtctaccccttgactctgggataccgctcacgattttccggatctgggagcgggaactgagttcacactcacgatttcacgctgcaacccgaggactttgctacctactactgctgcaaggcactcatttccctcacactttcgggtccaggggacaaaactcgaaatcaaacgtacggtagcggcccatctgtcttcattctccgccatctgatgagcagttgaaatctggaaactgctctgtgtgtgctgctgaataacttctatccagagaggccaaagtacagtggaaggtggataaacgcccctccaatcgggtaactccagggagagtggtcacagagcaggacagcaaggacagcactacagcctgagcagcaccctgacgctgtctaaagcagactacgagaaacacaaagtgtacgctgcaagtcaccccatcaggcctgagctcacagtaacaaaaagttttaatagaggggagtgtagcgggtggcgggtggcagtggtgggggaggctccggagggtggcggttcagacatacaaatgaccagagtccttcatcggtatccgctccgttggcgatagggtgactattacatgtcaaagctctcctagcgtctggagcaattttctactcctggtatcaacagaaacccgggaaggctccaaaacttctgatttatgaagcctcgaaactcacagtgaggttccgtcaagattcagtggtctctggatcagggacagacttcacgttgacaatcagttcgtctgcaaccaagggaactttgcgacctactattgtggtggagggttacagtagcataagtgatacgacatttgggtgcgggtactaagggtggaaatcaaacgtacc

**1519gH20 FabFv heavy chain SEQ ID NO: 72**

EVPLVESGGGLVQPGGSLRLSCAVSGFTFSNYGMVWRQAPGKGLEWVAYIDSDGDNITYYRDSVKGRFTISRDNKSSLYLQMNSLRAEDTAVYYCTTGIVRPFYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCSGGGSGGGGTGGGGSEVQLLESGGGLVQPGGSLRLSCAVSGIDLSNYAINWVRQAPGKCLEWIGIIWASGTTFYATWAKGRFTISRDNKNTVYLQMNSLRAEDTAVYYCARTVPGYSTAPYFDLWGQGLTVTVSS

**1519gH20 FabFv heavy chain SEQ ID NO: 73**

gaggtaccacttgtggaaagcggaggaggtcttctgtgcagcctggagggaagtttacgtctctcttctgtgctgtgtcttggttccaccttctccaattacggaatgggtctgggtcagacaagcactggaaagggctcttgaatgggtggcctatattgactctgacggggacaacacctactatcgggattccgpgaaaggacgcttcacaatctcccgagataacgccaaagactcactgtacctgcagatgaatagcctgagagccgaggatactgcccgtgactatttgcacaaagggaatcgttaggccttttctgtactggggacagggeaccttgggtactgtctcgagcgcgtccacaaggggcccatcgggtctccccctggcaccctcctccaagagcaacctctgggggcacagcggccctgggtctgctggtcaaggactacttccccgaaccagtgaagggtgtcgtggaaactcaggtgcccgtgaccagcggcgttcacaccttccgggtgtcctacagttctcaggactctactccctgagcagcgtgggtgaccgtgcccctccagcagcttgggcacccagacctacatctgcaacgtgaatcacaaagccagcaacaccaaaggtcgataagaaagttgagcccaaatcttgtagtgagggtgggggtcagggtggaggcgggacgggtggaggtggcagcagaggttcaactgcttgagttctggaggaggcctagtcacgctggagggaagcctgctctctctctgtgagtaagcggcatcgactgagcaatttacgcatcaactgggtgagacaagctccggggaagtggttagaatggatcgggtataataggccagtgaggacgaccttttatgtacatgggcgaaagggaaggtttacaattagccgggacaaatagcaaaaacaccgtgtatctccaaatgaactccttgcgagcagaggacacggcgggtgtactattgtgctcgcactgtcccggttatagcactgcaacctacttcgatctgtggggacaagggaacctgggtgactgtttcaagt

**1519gH20 FabFv heavy chain with signal sequence underlined and italicised SEQ ID NO: 74**

*MEWSWVFLFFLSVTTGVHSEVPLVESGGGLVQPGGSLRLSCAVSGFTFSNYGMVWRQAPGKGLEWVAYIDSDGDNITYYRDSVKGRFTISRDNKSSLYLQMNSLRAEDTAVYYCTTGIVRPFYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCSGGGSGGGGTGGGGSEVQLLESGGGLVQPGGSLRLSCAVSGIDLSNYAINWVRQAPGKCLEWIGIIWASGTTFYATWAKGRFTISRDNKNTVYLQMNSLRAEDTAVYYCARTVPGYSTAPYFDLWGQGLTVTVSS*