

(19) **DANMARK**

(10) **DK/EP 3068384 T3**



(12)

Oversættelse af europæisk patentskrift

Patent- og
Varemærkestyrelsen

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- (51) Int.Cl.: **A 61 K 31/191 (2006.01)** **A 61 K 31/164 (2006.01)** **A 61 K 33/26 (2006.01)**
A 61 K 39/02 (2006.01) **A 61 P 31/04 (2006.01)**
- (45) Oversættelsen bekendtgjort den: **2019-08-12**
- (80) Dato for Den Europæiske Patentmyndigheds bekendtgørelse om meddelelse af patentet: **2019-05-08**
- (86) Europæisk ansøgning nr.: **13709500.6**
- (86) Europæisk indleveringsdag: **2013-02-15**
- (87) Den europæiske ansøgnings publiceringsdag: **2016-09-21**
- (86) International ansøgning nr.: **GB2013050367**
- (87) Internationalt publikationsnr.: **WO2013121214**
- (30) Prioritet: **2012-02-16 GB 201202681** **2012-11-08 GB 201220158**
- (84) Designerede stater: **AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR**
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- (54) Benævnelse: **JERNKOMPLEKSER TIL REDUCERING AF GASTROINTESTINALKANAL-KOLONISERING MED CAMPYLOBACTER**
- (56) Fremdragne publikationer:
WO-A1-03/040351
WO-A2-2005/055944
WO-A2-2006/046017
BARCO A ET AL: "D-(-)-Quinic acid: a chiron store for natural product synthesis", TETRAHEDRON ASYMMETRY, PERGAMON PRESS LTD, OXFORD, GB, vol. 8, no. 21, 13 November 1997 (1997-11-13), pages 3515-3545, XP004115332, ISSN: 0957-4166, DOI: 10.1016/S0957-4166(97)00471-0

DESCRIPTION

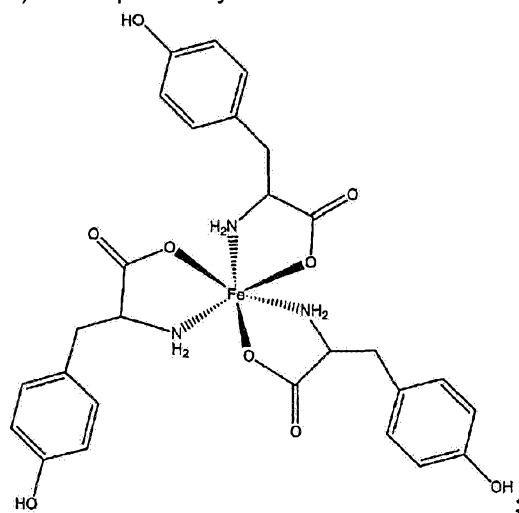
[0001] This invention relates to uses and methods of preventing or reducing the colonisation of the gastrointestinal tract of an animal with *Campylobacter*. In particular, it relates to reduction or prevention of colonisation of the gastrointestinal tract of poultry with *Campylobacter*.

[0002] *Campylobacter* are the commonest reported bacterial causes of gastroenteritis in the UK and industrialized world. *Campylobacter jejuni* (*C. jejuni*) is responsible for about 90% of *Campylobacter* infections, the majority of the remainder being caused by *C. coli*. *Campylobacter* form part of the natural gastrointestinal flora of many birds and domestic animals, but chickens are thought to constitute the largest source of human infection. Infected chickens are asymptomatic despite harbouring up to 10^8 colony forming units (cfu) per gram of intestinal content. Meat, in particular chicken meat, is often contaminated with intestinal contents including *Campylobacter* during slaughter. In humans, *Campylobacter* species cause diseases that vary in severity from mild watery diarrhoea to bloody dysentery. In a small subgroup of patients, the acute phase disease is followed by serious sequelae, including Guillain-Barre syndrome and reactive arthritis.

[0003] It is therefore of great interest to provide methods for reducing and preventing the risk of contamination of meat with *Campylobacter* and therefore the risk of human infection with *Campylobacter*. It is also of interest to provide new treatments for human infection with *Campylobacter* (campylobacteriosis).

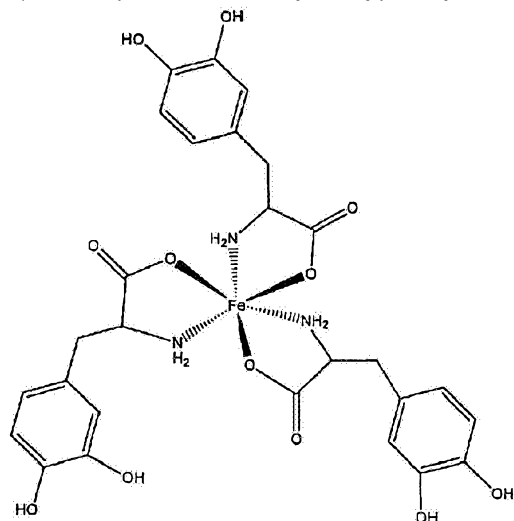
[0004] Accordingly, in accordance with Claim 1, the present invention provides a compound for use in a method of reducing the number of *Campylobacter* present in the gastrointestinal tract of an animal and thereby disinfecting the animal, wherein the compound is selected from the group consisting of:

a) a complex of tyrosine with Fe III



a) ferric quinate; and

b) a complex of 3,4 dihydroxyphenylalanine with Fe III



Optionally, the compound for use is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0005] In accordance with Claim 2, the present invention also provides for the use of a compound as defined above, for reducing the number of *Campylobacter* present in the gastrointestinal tract of a non-human animal and thereby disinfecting the animal, by a method comprising administering at least one compound as defined above, in an effective amount to said animal to reduce the number of *Campylobacter* present in the gastrointestinal tract of said animal, and then slaughtering the animal. Optionally, in use, the compound is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0006] In accordance with Claim 3, the present invention also provides a method for reducing the number of *Campylobacter* present in the gastrointestinal tract of said non-human animal, and thereby disinfecting the animal prior to slaughter, the method comprising: i) administering at least one compound as defined above in an effective amount to said animal to reduce the number of *Campylobacter* present in the gastrointestinal tract of said animal; and ii) slaughtering the animal. Optionally the compound for use is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0007] The present invention, in accordance with Claim 1, also provides a compound as defined above for use in a method of preventing or reducing the colonisation of the gastrointestinal tract of animals with *Campylobacter*. Optionally, the compound for use is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0008] In accordance with Claim 2, the present invention also provides for the use of a compound as defined above for preventing or reducing the colonisation of the gastrointestinal tract of non-human animals with *Campylobacter*, by a method comprising administering at

least one compound as defined above to said animal, and then slaughtering the animal. Optionally, in use, the compound is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0009] The present invention also provides, in accordance with Claim 1, a compound as defined above for use in a method of preventing *Campylobacter* from forming a biofilm in the gastrointestinal tract of an animal, or reducing the amount of biofilm formed by *Campylobacter* in the intestinal tract of an animal, and thereby disinfecting the animal. Optionally, the compound for use is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0010] In accordance with Claim 2, the present invention also provides for the use of a compound as defined above, for preventing *Campylobacter* from forming a biofilm in the gastrointestinal tract of a non-human animal, or reducing the amount of biofilm formed by *Campylobacter* in the intestinal tract of an animal, and thereby disinfecting the animal, by a method comprising administering at least one compound as defined above in an effective amount to said animal to prevent *Campylobacter* from forming a biofilm in the gastrointestinal tract of said animal or to reduce the amount of biofilm formed by *Campylobacter* in the intestinal tract of said animal, and then slaughtering the animal. Optionally, in use, the compound is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0011] In accordance with Claim 4, the present invention also provides a method for preventing *Campylobacter* from forming a biofilm in the gastrointestinal tract of a non-human animal, or reducing the amount of biofilm formed by *Campylobacter* in the intestinal tract of an animal, and thereby disinfecting the animal the method comprising: i) administering at least one compound as defined above in an effective amount to said animal to prevent *Campylobacter* from forming a biofilm in the gastrointestinal tract of said animal or to reduce the amount of biofilm formed by *Campylobacter* in the intestinal tract of said animal; and ii) slaughtering the animal. Optionally, the compound for use in the method is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0012] In accordance with Claim 5, the present invention also provides a compound as defined above for use in a method of preventing or reducing transmission of *Campylobacter* infection from one animal to another; wherein the method comprises administering the compound to said animals in an effective amount to prevent said *Campylobacter* from forming a biofilm in the gastrointestinal tract of said animal or to reduce the amount of biofilm formed by *Campylobacter* in the intestinal tract of said animal. Optionally, the compound for use is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0013] In accordance with Claim 6, the present invention also provides for the use of a compound as defined above for the prevention or reduction of transmission of *Campylobacter*

infection from one non-human animal to another; by a method comprising the administration of the compound to said animals in an effective amount to prevent said *Campylobacter* from forming a biofilm in the gastrointestinal tract of said animal or to reduce the amount of biofilm formed by *Campylobacter* in the intestinal tract of said animal, and then slaughtering the animals. Optionally, in use, the compound is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0014] The present invention also provides, in accordance with Claim 7, a method for preventing or reducing transmission of *Campylobacter* infection from one non-human animal to another prior to slaughter, for example preventing or reducing spread of *Campylobacter* infection within a flock or herd of animals, for example preventing spread of *Campylobacter* infection within a flock of chickens; said method comprising administering to said animals, for example said herd or flock of animals, for example said flock of chickens, at least one compound as defined above in an effective amount to prevent said *Campylobacter* from forming a biofilm in the gastrointestinal tract of said animal or to reduce the amount of biofilm formed by *Campylobacter* in the intestinal tract of said animal; and slaughtering the animals.

[0015] The uses and methods of the present invention may allow disinfection, prevention of biofilm formation and reduction of transmission of *Campylobacter* between animals by preventing or reducing adherence of *Campylobacter* to the gastrointestinal tract of said animals. This is advantageous because the fewer *Campylobacter* that are in the gastrointestinal tract of an animal at the time of slaughter, the lower the risk of contamination of meat from the animal with *Campylobacter*. The fewer *Campylobacter* that are in the gastrointestinal tract of an animal the lower the chance of the *Campylobacter* forming a biofilm in the gastrointestinal tract of the animal. The fewer *Campylobacter* that are in the gastrointestinal tract of an animal, the lower the chance that the *Campylobacter* will spread from one animal to another, for example within a herd or flock of animals.

[0016] Uses and methods of the present invention may be used to reduce the amount of colonisation of the gastrointestinal tract of any animal with *Campylobacter*. It is particularly advantageous to provide the compounds to animals that will be slaughtered for human consumption, such as, for example, cattle, sheep, pigs, goats, deer, fish, shellfish and poultry. Poultry includes birds that are used for human consumption such as chickens, geese, turkeys and ducks. It is particularly advantageous to use the compounds of the present invention to reduce or prevent colonisation of the gastrointestinal tract of poultry, in particular chickens, with *Campylobacter* because chickens are a leading source of human infection with *Campylobacter*.

[0017] *Campylobacter* are gram negative, spiral rod shaped bacteria with a single flagellum at one or both poles. They belong to the epsilon proteobacteria class and are closely related to *Helicobacter* and *Wolinella*. Although these species are related they have very different culture requirements and different hosts. *Campylobacter* species usually live in the gut of animals, in particular chickens while *Helicobacter* lives in the stomach of humans. Although fastidious in their culture requirements, *Campylobacter* species, particularly *C. jejuni* and *C. coli*, are important human pathogens, causing gastroenteritis of varying severity. Under normal

circumstances gastroenteritis is self-limiting, but sequelae associated with campylobacteriosis such as Guillain-Barre syndrome are potentially life threatening. There are many different reservoirs for *Campylobacter* but the most significant is contaminated meat, particularly poultry.

[0018] The number of *Campylobacter* in the gastrointestinal tracts of animals may be reduced by the uses and methods of the present invention. In one embodiment the number of colony forming units (cfu) of *Campylobacter* in the gastrointestinal tract of an animal treated with the compounds of the present invention may be reduced by 50%, by 60%, by 70%, by 80%, by 90% or by 100%. In one embodiment *Campylobacter* may be substantially eradicated from the gastrointestinal tract of animals treated by the uses or method of the present invention.

[0019] 10000 cfu of *Campylobacter* are enough for successful chicken colonization. 1000 cfu of *Campylobacter* are enough to infect a human and cause disease in a human. Therefore, an effective amount of a compound of the present invention is enough of the compound to reduce the number of *Campylobacter* in the gastrointestinal tract of an animal to a number that is unlikely to cause infection in humans. The number of cfu of *Campylobacter* that would be ingested by a human if they ate meat from an infected animal may be related to the number of *Campylobacter* in the gastrointestinal tract of the animal at the time of slaughter but also depends on other factors such as the amount of contamination of the meat with the contents of the gastrointestinal tract of the animal at the time of slaughter.

[0020] An effective amount of the compound of the present invention is enough of the compound to prevent colonisation of the gastrointestinal tract of the animal with *Campylobacter*.

[0021] In one embodiment the compounds of the present invention may make *Campylobacter* less virulent and less capable of infecting humans even if the total number of *Campylobacter* in the gastrointestinal tract does not decrease. In this embodiment administering a compound of the present invention to an animal may affect the metabolism of *Campylobacter* and make them less adaptive to the environment so that they can not colonize the gastrointestinal tract and are less likely to be transmitted to the other animals or to humans.

[0022] An effective amount of a compound provided to an animal should be enough to provide the required degree of reduction of *Campylobacter* colonisation. This may depend on the type of compound and/or the size of the animal. In one embodiment an effective amount of the compound may be 0.3 to 32 mg/day/kg bodyweight of the animal.

[0023] The uses and methods of the present invention preferably reduces colonisation of the gastrointestinal tract with *Campylobacter* species, for example *Campylobacter jejuni* or *Campylobacter coli*.

[0024] This is advantageous because *Campylobacter jejuni* is the commonest reported bacterial cause of gastroenteritis in the UK and industrialized world. *Campylobacter jejuni* (*C. jejuni*) is responsible for about 90% of *Campylobacter* infections, the majority of the remainder

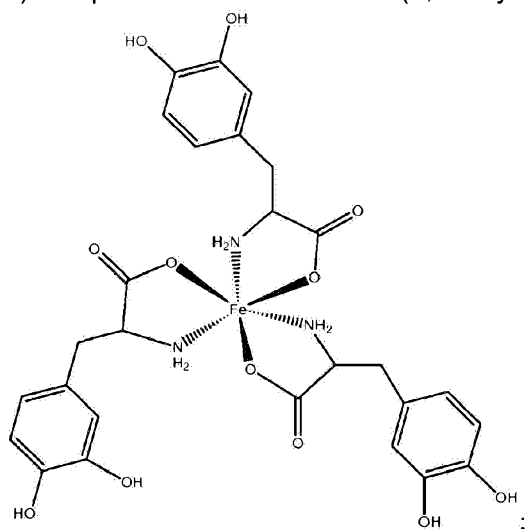
being caused by *C. coli*. *Campylobacter* form part of the natural gastrointestinal flora of many birds and domestic animals and there is therefore a high risk of contamination of the carcasses of these animals when they are slaughtered.

[0025] The compound used in the uses and methods of the present invention is preferably a compound that blocks the interaction of MOMP or FlaA on the surface of *Campylobacter* with the cells of gastrointestinal tract. Preferably the compound binds to MOMP or FlaA and competitively or non-competitively inhibits the binding of MOMP or FlaA on the *Campylobacter* with the cells of the gastrointestinal tract. Preferably the compound used in the present invention may bind to MOMP on the surface of *Campylobacter jejuni*. Preferably the compound used in the method of the present invention specifically binds to at least one of amino acid residues Arg³⁵², Lys²⁷⁸, Lys³⁸⁵, Asn²⁵⁸, Leu²⁹⁰, Tyr²⁹⁴, Phe³⁹⁵, Ile³³⁷, Arg³⁸¹, Asp²⁶¹ and Ser³⁹⁷ of MOMP. In another embodiment the compound of the present invention reduces the interaction between at least one of amino acid residues Arg³⁵², Lys²⁷⁸, Lys³⁸⁵, Asn²⁵⁸, Leu²⁹⁰, Tyr²⁹⁴, Phe³⁹⁵, Ile³³⁷, Arg³⁸¹, Asp²⁶¹ and Ser³⁹⁷ of MOMP and the gastrointestinal tract of an animal.

[0026] The compound used in the uses and methods of the present invention may be ferric quinate.

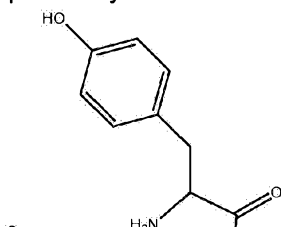
[0027] Alternatively, the compound used in the uses and methods of the present invention may have one of the following structures:

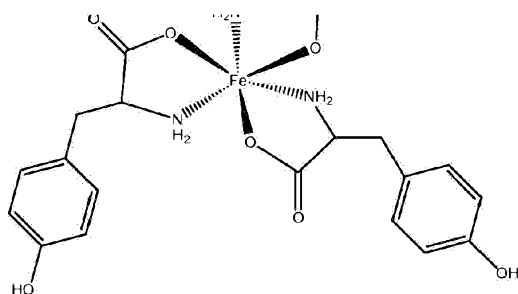
1. a) complex of DOPA with Fe III (3,4 dihydroxyphenylalanine)



or

2. b) complex of tyrosine with Fe III





[0028] The compound used in the uses and method of the present invention may be administered orally. This is advantageous because it is easy to administer compounds orally to animals. Oral administration is also a preferred method of administering a compound to ensure that it reaches the gastrointestinal tract.

[0029] Preferably the compound may be administered in an animal's feed or drinking water.

[0030] In the uses and methods of the present invention the compound may be administered to the animal at any time during its lifetime. In one embodiment the compound is administered to the animal at least once a day for a period of time before slaughter of the animal. For example the compound may be administered to the animal for between 1 and 10 days, preferably for between 1 and 8 days, between 1 and 6 days, between 1 and 4 days, before slaughter or for 2 or 1 days. In one embodiment a single dose of the compound may be administered to the animal between 1 and 4 days before slaughter. In one embodiment the compound may be administered to the animal every day for 3 days, 4 days or 5 days before slaughter. Chickens are often colonized by *Campylobacter* between 7 and 10 days before slaughter. Therefore in one embodiment the compound may be administered to a chicken less than 10 days before slaughter to disinfect the chicken and reduce colonisation of the gastrointestinal tract of the chicken before slaughter. In another embodiment the compound of the present invention may be administered to an animal before colonisation of the gastrointestinal tract of the animal with *Campylobacter* in order to prevent colonisation of the gastrointestinal tract of the animal with *Campylobacter*. In one embodiment the compound of the present invention is administered to a chicken more than 10 days before slaughter to prevent transmission of *Campylobacter* within a flock of chickens.

[0031] It is advantageous to administer the compound to the animal a short time before slaughter because the amount of *Campylobacter* in the gastrointestinal tract of the animal is reduced at the time of slaughter so that there is a lower risk of contamination of the carcass with *Campylobacter*.

[0032] In one embodiment of the present invention the compound may be administered to an animal at a dosage of 0.3-32 mg/day/kilo as a solution having a range of concentration from 34-340µM (0.02-0.2 g/L). A concentration of 0.2g/L has an effect on colonization during the first three days post-infection and also on the binding of *Campylobacter* to blood group

antigens which may be reduced by 60%. In another embodiment the compound may be administered at a concentration of 2g/L, which may prevent *Campylobacter* colonisation of the gastrointestinal tract of the animal and/or reduce the number of *Campylobacter* in the gastrointestinal tract of the animal to substantially zero.

[0033] The present invention also provides, in accordance with Claim 18, the use of a compound as defined above for reducing the amount of *Campylobacter* in meat by a method comprising the steps of: providing a non-human animal, or a flock or herd of non-human animals, with a compound as defined above; and preparing a meat product from the animal. Optionally, in use, the compound is in the form of an animal feed, animal drinking water, feed ingredient or feed supplement that comprises the compound.

[0034] In accordance with Claim 19, the present invention also provides a method for reducing the amount of *Campylobacter* in meat comprising the steps of:

Providing a non-human animal, or a flock or herd of non-human animals, with a compound as defined above; and preparing a meat product from the animal. The animal may be any type of animal, preferably a poultry bird, preferably a chicken.

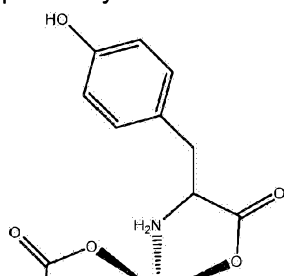
[0035] Compounds as defined above that are useful in the uses and methods of the present invention may be included in animal feed, as a feed ingredient or as a feed supplement. The animal feed, feed ingredient or feed supplement may be suitable for any animal, in particular animals that are to be slaughtered for human consumption, preferably poultry, more preferably chickens.

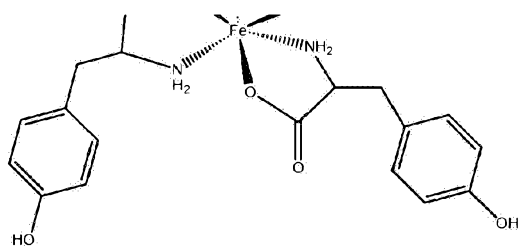
[0036] Compounds as defined above that are useful in the uses and methods of the present invention may be provided to an animal in liquid or solid form or as a powder. They may be included as an ingredient in feed or animal food or as an ingredient in a feed or food supplement. In one embodiment the compounds are provided to chickens in chicken feed or as a feed ingredient mixed with chicken feed.

[0037] A feed may be a food intended for or suitable for consumption by animals. A food or a foodstuff may be a food that is intended or suitable for consumption by humans.

[0038] Accordingly, the present invention also provides, in accordance with Claim 23, an animal feed, comprising a compound as a feed ingredient or as a feed supplement, wherein the animal feed is a food intended for or suitable for consumption by animals, and the compound is:

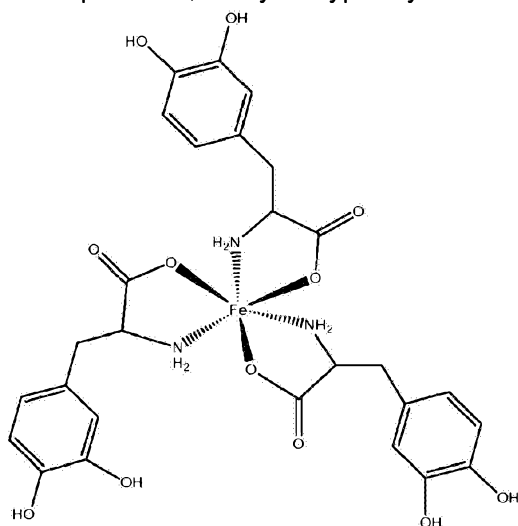
a complex of tyrosine with Fe III





wherein the animal feed comprises the compound in an amount effective to reduce or prevent the colonisation of the gastrointestinal tract of an animal with *Campylobacter*.

[0039] The present invention also provides, in accordance with Claim 24, an oral composition, animal feed or animal drinking water, comprising a compound that is:
a complex of 3,4 dihydroxyphenylalanine with Fe III



wherein the oral composition, animal feed, or animal drinking water comprises the compound in an amount effective to reduce or prevent the colonisation of the gastrointestinal tract of an animal with *Campylobacter*.

[0040] In accordance with Claim 27, the present invention also provides for the use of a compound, as defined by Claim 23 or 24, as a feed supplement or feed ingredient, in the manufacture of an animal feed, or as an additive in the manufacture of animal drinking water, as defined above.

[0041] In accordance with Claim 28, the present invention also provides a method for the manufacture of an animal feed or animal drinking water as defined above, wherein the method comprises the use of a compound, as defined by Claim 23 or 24, as a feed supplement or feed ingredient in the manufacture of the animal feed, or as an additive in the manufacture of animal drinking water.

[0042] The present invention provides, in accordance with Claim 29, a method of disinfecting a foodstuff or a food comprising administering a compound as defined above in an effective amount to the foodstuff to reduce the amount of *Campylobacter* in the foodstuff.

[0043] Likewise, in accordance with Claim 30, the present invention also provides for the use

of a compound as defined above for disinfecting a foodstuff, by administering an effective amount of the compound to the foodstuff to reduce the amount of *Campylobacter* in the foodstuff.

[0044] This is advantageous because it reduces the risk of infection with *Campylobacter* of humans who consume the foodstuff.

[0045] A foodstuff or a food may be for human consumption, in particular the food may be a meat product, for example a fresh meat product, a processed meat product, a chilled meat product, a frozen meat product or a cooked meat product. The meat product may be, for example a beef, lamb, pork, duck, chicken, goose, turkey, rabbit, fish or shellfish meat product. Preferably the meat product may be a poultry meat product, more preferably a chicken meat product.

[0046] The present invention also provides a compound as defined above for use in the prophylaxis or treatment of *Campylobacter* infection in humans. A compound as defined above may be used in the manufacture of a medicament for the prophylaxis or treatment of *Campylobacter* infection in humans.

[0047] The compound may be provided to humans to prevent or treat infection of humans with *Campylobacter* (campylobacteriosis). This is advantageous because the compounds prevent or reduce adhesion of *Campylobacter* to the epithelial cells in the gastrointestinal tract. This may prevent or reduce infection with *Campylobacter* because *Campylobacter* adheres to cells in the human gastrointestinal tract by docking onto human histo-blood group antigens that are expressed on the cells of the gastrointestinal tract. The compounds may compete with natural human histo-blood group antigens that are on the epithelial cells for binding of MOMP and FlaA and therefore reduce the amount of binding of *Campylobacter* to the cells.

[0048] The present application also discloses a method of treating or preventing *Campylobacter* infection in humans comprising administering to the human an effective amount of a compound as defined above.

[0049] The present application also discloses a kit comprising:

1. a) at least one compound as described in the present invention and optionally instructions for using the kit.

[0050] There now follows by way of example only a detailed description of the present invention with reference to the accompanying drawings, in which;

Figure 1 shows the competitive effect of the soluble glycoconjugates, *i.e.* H-II, Le^b or Le^y on attachment of strain NCTC11168 to a series of BgAs. **A)** An ELISA plate was coated with a selection of BgAs. Specific binding was calculated by subtracting the BSA (negative control)

values from the BgAg absorbance. Binding of strain NCTC11168 to BgAgS was inhibited significantly ($p < 0.05$) by pre-incubation of cells with soluble glycoconjugates prior to adding them to the ELISA plate. Error bars; mean of triplicate values $\pm$ SEM, number of repeating experiments was 3. Each group of bars, from left to right, NCTC11168, NCTC11168-H-II, NCTC11168-Leb, NCTC11168-Ley.

B) Identification of BgAg-binding proteins from strain NCTC11168 by using ReTagging method. Two proteins were identified at sizes of 45 and 59 kDa, corresponding to MOMP and FlaA, respectively.

Figure 2 shows **A)** Inhibition of binding of strain NCTC11168 to H-II glycoconjugate in the absence of an inhibitor (non-treated, NT) and in the presence of purified MOMP of Cj-281 (MOMP(-)), low binder strain). Purified MOMP from NCTC11168 (MOMP(+)), and pre-incubation of NCTC11168 bacterial cells with H-II glycoconjugate (H-II). Pre-treatment of all examined MOMP and H-II had significantly reduced ($p < 0.001$, ***) the bacterial binding to H-II antigen. In contrast, MOMP(-) had a lower effect compared with H-II or MOMP(+) due to the lower affinity for the H-II antigen. **B)** ELISA plate was coated with a selection of BgAgS. Specific binding was calculated by subtracting the BSA (negative control) values from the BgAg absorbance at 405 nm. Strain NCTC11168 and Cj-266 (high binder strain), and corresponding $\Delta flaA$ mutants, have been examined for binding to Le^b, H-II, H-I, Le^x and Le^a. t-test confirmed the reduction in binding seen with mutants are significant (Le^b; $p = 2.5E-05$, H-II; $p = 0.012$, H-I; $p = 0.001$, Le^x; $p = 0.029$ and Le^a; $p = 0.000$) in strain NCTC11168. However, Cj-266 $\Delta flaA$ mutation had no effect on binding, which indicates the binding capacity was compensated by MOMP protein. Each group of bars from left to right: NCTC11168, 11168- $\Delta flaA$, Cj-266, Cj-266 $\Delta flaA$. **C)** A double mutant (DM) of $\Delta flaA$ and single substitution of glycosylation site in MOMP protein (Thr²⁶⁸ was substituted with Gly) was constructed in both strain NCTC11168 and Cj-266, and the binding to Le^b H-I and H-II was examined. The binding was significantly reduced in NCTC11168-MOMP^{T/G} but the reduced binding was not significant in Cj-266-MOMP^{T/G}. Although, t-test confirmed the reduction in binding seen with NCTC11168-DM and Cj-266-DM the mutants are significant ($p < 0.05$). Each group of bars from left to right: Leb, H-II, H-1.

Figure 3 shows an overview of the mass spectrometry analysis by LC-MS/MS for both protein identification and glycosylated peptide characterization. **A)** Base peak chromatogram: Tryptic peptides are loaded on an on-line coupled C18 column and eluted into the mass spectrometer for analysis. **B** and **C)** MS precursor scan of the doubly charged glycosylated peptide at m/z 978.91 **C)** CID-MS/MS spectrum of the selected ion. **D)** Detection of glycan constituent of purified MOMP from different strains using biotinylated labeled lectins. **GSL II:** *Griffonia (Bandeiraea) simplicifolia* lectin II, **DSL:** *Datura Stramonium* lectin, **ECL:** *Erythrina cristagalli* lectin, **LEL:** *Lycopersicon esculentum* (tomato) lectin, **STL:** *Solanum tuberosum* (potato) lectin, **VVA:** *Vicia villosa* agglutinin and **Jacalin:** *Artocarpus integrifolia* lectin.

Jacalin lectin showed significant binding to NCTC11168 purified MOMP than the other used lectins. Jacalin lectin specifically recognizes Gal β 1-3GalNAc α 1-Ser/Thr (T-antigen) and/or GalNAc. **E)** Further analysis was revealed by using an antibody against the T-antigen to

confirm Jacalin specificity. MOMP(s) purified from strains 255, 281 (low binder clinical isolates) and MOMP^{T/G} didn't reveal significant binding to either Jacalin lectin or anti-T antigen compared with MOMP purified from strain NCTC11168 wild type. Error bars = mean of triplicate values $\pm$ SED, **No 2**. Two independent experiments (**P value**). For each pair of bars: left hand bar - Jacalin lectin, right hand bar - Anti-T-antigen.

Figure 4 shows a representation of MOMP (**A**, right) and glycosylated MOMP (**A**, left) in the approximate boundaries of the hydrophobic part of the outer membrane (OM). **B**), the superimposed lowest energy structure of MOMP (**green**) on the lowest energy structure of glycosylated MOMP (**magenta**) with RMSD of 1.291. Loops are shown in colours; β strands are green, **L1** (residues 41-60, red), **L2** (residues 87-109, magenta), **L3** (residues 128-147, orange), **L4** (residues 169-200 yellow) **L5** (residues 227-233, black), **L6** (residues 256-274, blue), **L7** (residues 296-333, gray), **L8** (residues 360-379, cyan) and **L9** (residues 399-414, purple).

Figure 5 shows a stereo cartoon of the MOMP backbone viewed from the extracellular side: β strands are green, L1 (red), L2 (magenta), L3 (orange), L4 (yellow) L5 (black) (L5), L6 (blue), L7 (gray), L8 (cyan) and L9 (purple) and its side view. The conformational changes in the glycosylate group induced by introduction of the ligands into the cavity of glycosylated MOMP. The complexes with Le^b (**A**) and H-II (**D**). In addition, hydrogen bonds shown in light blue involved in the interactions of MOMP (**B** and **E**) and its glycolysated form (**C** and **F**) with Le^b and H-II respectively in their active sites.

Figure 6 shows examples of compounds that can be used in the present invention.

Figure 7 shows the effect of a series of histo blood group antigens on biofilm formation. Comparison of biofilm formation between NCTC11168-WT, and corresponding mutants, Δ fla A and MOMP-T/G in presence and absence of free sugars. A) The most significant decrease in biofilm formation is seen in wild type strain compared to the mutants. However, the biofilm formation of MOMP268T/G strain is comparable to Δ flaA, which indicate that O-glycosylation of MOMP also play important role for this formation. For each group of bars from left to right: NCTC11168, NCTC11168 (sugar), MOMP-T/G, MOMP-T/G(sugar). B) Similar results were observed except for core-II, other examined sugars significantly reduced the biofilm formation. For each group of bars from left to right: NCTC11168, NCTC11168(sugar), Δ fla A, Δ fla A (sugar).

Figure 8 shows the lowest energy structure of MOMP from MD simulation with stereo cartoon of the MOMP backbone viewed from the extracellular side. MOMP forms hydrophilic channels through the outer membrane. The folding of β -barrel OMPs promotes trimer assembly and integration of the channel into the outer membrane. Moreover, two-dimensional crystallographic analysis showed that MOMP is structurally related to the family of trimeric bacterial porins.

CD spectroscopy analysis also demonstrated that the folded monomer mainly comprised β -sheet secondary structure, in agreement with the so called β -barrel structure of porins. MOMP folded monomers are able to form channels in artificial lipid bilayers with the same

conductance properties as monomers embedded into trimers, which suggests that the folded monomer is the functional unit of the MOMP porin.

Figure 9 shows molecules used in the modelling of molecules that bind to MOMP.

Figure 10 shows colonisation levels of chicks challenged with wild-type campylobacter strain NCT11168-0 or mutant campylobacter strain MOMP^{268T/G}.

Figure 11 shows Ferric-Quinate 1, 3, 4, 5-Tetrahydroxy Cyclohexan carboxylic acid

Figure 12 shows the inhibitory potential of Ferric Quinate Fe(QA)₃ on adherence of *C. jejuni* was analyzed by ELISA using BgAgs (Core-I, Core-II, H-I, H-II, Leb, Ley and Lex).

Figure 13 shows the inhibitory potential of Ferric Quinate Fe(QA)₃ on adherence of *C. jejuni* was analyzed by ELISA using BgAgs (Core-I, Core-II, H-I, H-II, Leb, Ley and Lex).

Figure 14 shows colonisation of chicks by *C. jejuni* 11168-0 following FeQ (0.034mM) treatment.

Figure 15 shows colonisation of chicks by *C. jejuni* 11168-0 following FeQ (0.34mM) treatment.

Figure 16 shows metagenomic analysis of population treated with FeQ Genus/species level.

Figure 17 shows metagenomic analysis of population treated with FeQ Phylum level.

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3. 3- Turnbaugh P, Ley R, Mahowald M, Magrini V, Mardis E, Gordon J (2006). "An obesity-associated gut microbiome with increased capacity for energy harvest". *Nature* 444 (7122): 1027-31. doi:10.1038/nature05414. PMID 17183312.

[0051] *Campylobacter jejuni* is an important cause of human food-borne gastroenteritis. Despite the high prevalence and medical importance of *C. jejuni* infection, fundamental aspects of pathogenesis remain poorly understood, in particular the detailed molecular interactions between host and pathogen. Human histo-blood group antigens (BgAgs) are often targeted by mucosal organisms as levers for adherence prior to invasion. Using a retagging approach, the corresponding surface-exposed BgAgs-binding adhesins of *C. jejuni* were identified as the major subunit protein of the flagella (FlaA) and the major outer membrane protein (MOMP). O-glycosylation of FlaA has previously been reported, and is required for filament assembly and for modulating flagella functionality. Purified MOMP like FlaA was O-glycosylated. The O-glycosylation was localised to Thr²⁶⁸ and suggested as Gal β ₁₋₃-(GalNAc)₃- α 1-Thr²⁶⁸. Site-

directed substitution of MOMP Thr²⁶⁸/Gly led to a significant reduction in binding to BgAgs. Furthermore, molecular dynamics (MD) simulation modelling techniques suggested that O-glycosylation of MOMP has a notable effect on the conformation of the protein. Thus, *C. jejuni* uses O-glycosylation of surface-exposed proteins to modulate the conformation and binding capability.

[0052] Prevention and treatment of human infection with *Campylobacter* and its consequences are hampered by a poor understanding of the detailed molecular interaction between the host and the pathogen.

[0053] Studies by the present inventors have shown that *C. jejuni* specifically bind all human BgAgs, and identified the bacterial ligands responsible for binding. These are the flagellin protein FlaA and the major outer membrane protein MOMP.

[0054] The present studies have also found that MOMP is O-glycosylated, and shares a common BgAg binding site with FlaA, which has already been shown to be O-glycosylated. Glycosylation of MOMP causes it to undergo conformational changes which alters its affinity for binding of, and hence recognition of, BgAgs compared with unglycosylated MOMP protein. Conformational MOMP epitopes are important in host immunity, and variation in surface-exposed regions probably occurs as a result of positive immune selection during infection. Identification of the protein glycosylation profile of *C. jejuni*, in the outer membrane is helpful in understanding the diverse pathogenicity of *C. jejuni* strains among different hosts.

[0055] The present studies have created an *in silico* model of glycosylated MOMP, which have been used to identify the amino acids which mediate the bacterial binding to BgAgs. The model and the amino acids that are essential for binding to BgAgs may be used to identify candidate drug targets. The model may also be used to predict which molecules will bind to MOMP and can reduce the adhesion of the *Campylobacter* carrying MOMP to cell walls.

[0056] The present studies have found that BgAgs can inhibit bacterial adhesion and biofilm formation and have identified molecules that can be used (a) for treatment of humans suffering from Campylobacteriosis; (b) to prevent colonisation of chickens with *Campylobacter ssp*; and (c) to eliminate chicken colonisation in infected flocks.

[0057] Previous attempts to reduce the risk of human infection with *Campylobacter ssp* involved the use of vaccines employing nucleic acids encoding *Campylobacter* proteins, in particular flagellin (US2007/249553).

[0058] This is completely different from the approach described by the present application which uses specific compounds to block the ligand binding site of the *Campylobacter* and hence inhibit *Campylobacter* adherence and colonisation in the chicken gastrointestinal tract.

[0059] In one embodiment, Ferric Quinate (Fe-Q) may be used in the present invention.

EXAMPLES

***C. jejuni* binds a wide range of human BgAgs.**

[0060] To determine the range and specificity of BgAgs that bind *C. jejuni*, Core-I, Core-II, H-I, H-II, Le^b, Le^x, and Le^y were immobilised in specialised 96-well ELISA plates and incubated with log-phase digoxigenin (Dig)-labelled *C. jejuni* strain NCTC11168. The strain bound to all the examined BgAgs, the degree varying only marginally between BgAgs (**S1-Fig.**).

[0061] Blood group antigens were obtained from IsoSep (Sweden). The lab strain (ATCC11168) was obtained from ATCC bank and the clinical strains from a collection belong to Prof. Julian M. Ketley (Department of Genetics, University of Leicester, Leicester LE1 7RH, UK).

[0062] Pre-incubation of bacteria or coated plates with soluble BgAgs inhibited the binding, confirming specificity (Fig. 1A). In addition, adhesion assays by co-culturing *C. jejuni* strain NCTC11168 and Caco-II cells were carried out. Soluble H-II caused significant reduction in bacterial binding to the host cells. In addition, the same range of immobilized BgAgs was used to test the ability of 39 clinical isolates of *C. jejuni*. All *C. jejuni* isolates bound to all examined BgAgs, albeit to a variable degree. Correlation analysis between each sugar and principal component analysis was performed. It enables a visualization of the correlations - the structurally closer the sugars are to each other, the more similar they are in terms of binding capacity.

[0063] The high degree of specificity by *H. pylori* BgAg-binding adhesions is in contrast to our findings with *C. jejuni*, which appears to bind to a wide range of related antigens. This may reflect the fact that *H. pylori* has a very restricted host range (infecting only humans), whereas *C. jejuni* is able to establish infection in a wide range of birds and mammals and may have gained an evolutionary advantage by broadening its specificity and maximising its survival in different hosts.

***C. jejuni* FlaA and MOMP mediate the binding to a wide range of human BgAgs.**

[0064] For identification and purification of BgAgs-binding bacterial adhesins, a retagging technique was used. Two generated protein bands in figure 1B identified by mass spectrometry as the major outer-membrane protein (MOMP, 45 kDa) and FlaA (the major flagella component, 59 kDa), respectively. The *C. jejuni* MOMP is a multifunctional porin and is essential for bacterial survival; it is predicted to comprise outer membrane-spanning beta strands separating periplasmic and surface-exposed loops. That it is encoded by the *porA* gene

which is extremely genetically diverse and the variability of the *porA* surface loops provides evidence that immune selection strongly influences the diversity of this protein. Interestingly, the greatest variation in both putative amino acid sequence and length was formed in loop 4.

[0065] MOMP was purified under native conditions from strain NCTC11168 and inhibition ELISA and confocal experiments showed that both purified MOMP and H-II significantly inhibited binding of NCTC11168 to H-II antigen (Fig. 2A).

[0066] Deletion mutant of $\Delta flaA$ in strains NCTC11168 and Cj-266 (a clinical isolate) were constructed. This had significantly reduced the binding capacity to all examined BgAgs except for Le^x in strain NCTC11168 (Fig. 2B). By contrast, $\Delta flaA$ deletion in strain Cj-266 didn't exhibit reduced binding to BgAgs (Fig. 2B), which indicated that MOMP *per se* is sufficient for adherence to BgAgs.

[0067] Invasive properties could be partially restored by centrifugation of the mutants onto the tissue culture cells, indicating that motility is a major, but not the only, factor involved. Here, we identified the corresponding *C. jejuni* adhesins, which mediate the bacterial binding to BgAgs.

Ability of MOMP^{268T/G} to colonise chicks

[0068] The ability of MOMP^{268T/G} to colonise chicks was determined. 6-weeks old birds (n=10 per group) were challenged with 3×10^3 cfu wild-type strain NCTC11168-O or its isogenic mutant MOMP^{268T/G} by oral gavage. Caecal colonisation levels were determined in birds from each group at 7 days post-challenge. The results show a significant reduction in the geometric mean colonisation levels in the caeca in the MOMP^{268T/G} group compared to the wild-type (See figure 10). In addition, the ability of the mutant strain to invade the chicken's liver was examined. The results showed that MOMP^{268T/G} was completely unable to invade compared to the wild-type strain. These results confirm the importance and biological relevance of MOMP glycosylation in the establishment of colonisation *in vivo*. Values less than 100 in Figure 10 are arbitrary figures, and no campylobacter was recovered.

Ferric Quinate; an inhibitor for *C. jejuni* adherence

[0069] A number of phenolic compounds, including caffeic and quinic acids (Baqar *et al.*), have been shown to have high levels of antioxidant activity and other potentially health-promoting effects *in vitro*. Also, quinic acid occurs in tea, coffee, fruits and vegetables. In particular, plants use the low molecular mass D-(-)-quinic acid (Baqar *et al.*) for mobilization of iron and further use of this metal by cellular structures in metabolic pathways (Menelaou *et al.*, 2009).

[0070] Ferric quinate Fe(QA)₃ was identified as having promising inhibitory effects *in vitro* and

in vivo on *C. jejuni* adhesion to BgAgs.

[0071] The inhibitory potential of Ferric Quinate Fe(QA)₃ on adherence of *C. jejuni* was analyzed by ELISA using BgAgs (Core-I, Core-II, H-I, H-II, Leb, Ley and Lex). *C. jejuni* was pre-incubated with 34 µM Fe(QA)₃ and specific inhibition was also analyzed by post-treatment of *C. jejuni* with Fe(QA)₃ which bound to BgAgs at the time. The result showed that Fe(QA)₃ conferred a 90% inhibition of binding, while Quinic Acid alone provided no inhibition of *C. jejuni* binding to all examined BgAgs. In addition the results from the bacterial culture (MH) containing Fe(QA)₃ approach also demonstrated reproducible inhibition of microbial adherence. In addition, the sequential passages (P) of bacteria to the new plate containing Fe(QA)₃ didn't cause any resistance concerning the binding abilities (see Figures 12 and 13).

[0072] To further clarify the growth-effect properties of Fe(QA)₃, we investigated the effect of adding Fe(QA)₃ to the culture medium. Supplementation with the different concentrations of Fe(QA)₃, (34 and 340 µM) did not affect the growth of *C. jejuni* NCTC11168 strain.

[0073] These inhibitory properties against *C. jejuni* adherence to BgAgs were analyzed *in vivo*. Ferric Quinate was used as an additive to water (0.034-0.34 mM) and as an inhibitor of *C. jejuni* NCTC11168 strain adherence to, and thus colonization, in the chicken intestinal tract. 6-weeks old birds (n=10 per group) were challenged with $3 \times 10^{3-5}$ cfu wild-type strain NCTC11168-O by oral gavage. Caecal colonisation levels were determined in birds from each group at 3 and 7 days post-challenge.

[0074] The complex reduced significantly the adhesion of *C. jejuni* (2-3 Log at 0.34 mM concentration) to the intestinal mucosa and epithelial lining by inhibiting the binding between bacterial adhesins, such as MOMP (confirmed by model), may FlaA, and the corresponding binding sites in the host intestinal epithelium see Figures 14 and 15.

[0075] In a Metagenomic analysis of population treated with FeQ at a Genus/species level a difference can be seen between FeQ treated and non-treated birds at day 7, there is a shift in the population with increase of *Bacterioidetes* phylum, especially *Bacteroides feacalis* (1, 2, 3).

MOMP is O-glycosylated.

[0076] *Campylobacter* specifically modify their flagellar proteins with O-linked glycans that can constitute up to 10% of the protein mass. These modifications are necessary for flagellum assembly, and thus affect secretion of virulence-modulating proteins, bacterial colonization of the gastrointestinal tract, autoagglutination and biofilm formation.

[0077] MOMP was purified from strains NCTC11168 and Cj-281 under native conditions and analysed by Nanoflow LC-MS/MS FT/ICR following in-gel protein digestion as described in A. Shevchenko, M. Wilm, O. Vorm, M. Mann, Anal Chem 68, 850 (Mar 1, 1996). The migration of

trypsin-digested MOMP peptides from both strains was essentially identical except for one peptide corresponding to amino acids 268-278, corresponding to the predicted loop 6: the strain NCTC11168 peptide showed a greater mass; MS/MS analysis confirmed that glycosylation of Thr-268 with a Hex-(HexN-acetylamine)₃ (where Hex can be Glucose or Galactose) was responsible for the observed shift (Fig. 3A, B and C). FASTA sequence alignment of clinical isolates indicated that Thr-268 on loop 6 of strain NCTC11168 appears to be conserved in 52% of isolates.

[0078] Site-directed substitution of Thr²⁶⁸ to Gly was carried out on MOMP of strain NCTC11168 and a clinical isolate Cj-266 (yielding MOMP^{268T/G}, **S5**-Table). This substitution caused a clear shift in the protein's migration, strongly suggesting the loss of its glycosylation (**S5**). The ability of this mutant to bind to a range of BgAgs in an ELISA assay was examined and it was shown to have a reduction in binding to each of examined BgAgs (Fig. 2A). Also, a reduced biofilm formation was observed, which indicates that O-glycosylation of MOMP plays an important role in this context (**S8**-Fig. A and B).

The role of PglB and PseD transferases on MOMP glycosylation.

[0079] Flagellin is the only O-glycosylated *C. jejuni* protein to have been reported and glycans constitute ca. 10% to this protein's weight. The predominant O-glycans attached to the *Campylobacter* flagellum are derivatives of pseudaminic acid or legionaminic acid, which are C9 sugars that are related to sialic acids. In addition, the related human gastric pathogen *H. pylori* also O-glycosylates its flagella with Pse, similarly to *C. jejuni*, and modification is required for bacterial motility and flagellar assembly.

[0080] Interestingly, specific loss of Pse5Am due to mutation of the Pse biosynthesis A gene (*pseA*) in *C. jejuni* subsp. *jejuni* 81-176 resulted in loss of auto-agglutination and reduced adherence to and invasion of intestinal epithelial cells *in vitro*, and reduced virulence in the ferret model.

[0081] Also, PseD as a putative PseAm transferase showed that mutation in *pseD* lacked PseAm on flagellin and failed to auto-agglutinate.

[0082] The general protein glycosylation (Pgl) pathway involves several key "Pgl" enzymes, of which PglB is critical for protein N-glycosylation *i.e.* transfer of the first glycan molecules to the target proteins at specific Asn residues.

[0083] In order to evaluate the contribution of PseD and PglB transferases on *C. jejuni* MOMP glycosylation and its role on bacterial binding activity, a *pglB* deletion mutant was created in strain Cj81-176 and *pseD* deletion in strain NCTC11168; *pglB* deletion had no detectable impact on MOMP gel migration, glycan staining (data not shown), or bacterial binding to any of the examined BgAgs (**S7**-Fig. A). However, strain NCTC11168-*pseD* deletion resulted a

significant reduction in binding to all examined BgAs and biofilm formation (data not shown).

[0084] These findings indicate that *C. jejuni* strain NCTC11168 encodes a transferase that is involved in post-translational modification of protein, which plays an important role in bacterial adhesion and reveals unusual post-translational modifications; an O-linked Hex-(HexNAc)₃ at Thr²⁶⁸. These post-translational modifications might undergo phase variation and may also vary in structure from one generation of *C. jejuni* to the next, and have a function in immune escape. Moreover, these findings provide new insights into MOMP structure and resolve long-standing issues regarding the adhesion molecules which mediate the bacterial binding to the BgAgs. The pathogenesis and study of the effects on processes such as colonization, invasion, and the ability to stimulate the host inflammatory response remain to be elucidated.

Determination of MOMP glycan composition.

[0085] Lectin kit was used for determination of the MOMP glycosylation constituent. The kit consists of 7 different lectins with overlapping specificity. The purified NCTC11168-MOMP in lectin array revealed significant binding to Jacalin lectin and in a lesser extent to GSL and LEL (Fig. 3D). Among the galactose-specific lectins, the lectin from *Artocarpus integrifolia*, known in the literature as Jacalin, exhibits specificity toward human tumour specific Thomsen-Friedenreich disaccharide (T-antigen, Gal β ₁₋₃GalNAc α ₁-Ser/Thr).

[0086] Moreover, to confirm the Jacalin binding specificity, monoclonal anti- T-antigen was used against purified MOMP isolated from different strains (NCTC11168-MOMP, NCTC11168 MOMP^{268T/G} and two clinical isolates with low binding activity; Cj281 and Cj-255). Figure 3E shows that anti-T antigen antibody and Jacalin lectin reacted specifically with purified NCTC11168-MOMP. The observation that NCTC11168-MOMP interacts with Jacalin and anti-T antigen but not MOMP isolated from low binder strains and NCTC11168 MOMP^{268T/G} (Fig. 3E) indicates that strain NCTC11168-MOMP is likely to be the O-linked trimeric form of T-antigen (Gal β ₁₋₃GalNAc β ₁₋₄GalNAc β ₁₋₄GalNAc α ₁-Thr²⁶⁸).

[0087] Glycosylation of MOMP with T-antigen presented herein provides an important insight on the role of glycosylation for *C. jejuni* binding activity to Lewis antigens and in MOMP immunogenicity. Further determination of the other N- and O-glycosylated outer membrane proteins may shed light into the development of a glycoconjugate based vaccine in the future.

The role of glycan in MOMP binding to BgAgs

[0088] The advances in computer technology and new modelling techniques have facilitated simulations of peptide folding at the atomic level. Although gram-negative bacteria possess quite different homology in primary sequences of their porins, they are remarkably similar in

their beta-barrel structure. Hence, we employed the beta-barrel structure from *Comamonas acidovorans* (1E54.pdb) as a template and constructed our model based on this assumption. In order to understand better the role of MOMP glycosylation in *C. jejuni* binding to the BgAgs, here we present the construction and molecular dynamic properties of MOMP and its glycosylated form.

[0089] The initial structure was constructed and showed to have 9 loops and 18 beta-strands. The lowest energy structure obtained from molecular dynamics (MD) simulations at 300 Kelvin (K). This structure was glycosylated at residue 268 with a glycosyl group. The lowest energy structure of glycosylated MOMP (gly-MOMP) obtained from MD simulations was superimposed on the lowest energy structure of MOMP to see the conformational changes induced by the introduction of glycosylation as presented in Figure 4B. It shows that the major changes occur in loops 4, 6 and 7 constructed roughly of 169-200, 256-274 and 296-333 residues where loop 6 bears the glycosyl group. However, it shows that a small change appears in the barrels. The approximate boundaries of two proteins in the hydrophobic part of the outer membrane are indicated by horizontal lines as represented in Figure 4A. Interestingly, the galactosyl residue has a favourable interaction with Arg³²⁸ residue as indicated in Figure 4 but upon complex with H-II the glycosylated residue undergoes considerable conformational changes where this interaction vanishes and the group tends to move towards loop 4 to interact with Thr¹⁸⁶ and 187 (Fig. 4A). In contrast, this conformational change did not occur in the case of gly-MOMP with Le^b.

[0090] The MOMP protein has a canal-like cavity, which is expected to be capable of accommodating very large molecules. A mimic of Lewis antigen, type-1 Lewis carbohydrate determinant (Le^b) and type-2 H-II antigen were docked into the cavity of MOMP and gly-MOMP. These complexes were computed for MD simulations. The introduction of the ligands within the cavity of MOMP leads to a remarkable effect on conformational changes in the loops, especially in loops 4 and 7. These two loops are the longest among the rest and obviously undergo significant conformational changes compared with others. Interestingly, it was found that gly-MOMP has a relatively stable structure since it shows that only loop 7 slightly undergoes conformational changes upon this complex. This may mean that glycosylation enhances the stability of the protein and allow it to be immunologically inert through molecular mimicry of its host.

[0091] Corresponding MOMP amino acids, which mediate binding to Le^b and H-II antigens.

The interactions involved in the complexes of both proteins with Le^b and H-II are represented in Figure 5A-F. The channel of these barrel proteins largely contains arginine and lysine residues, which are likely responsible for the recognition of these sugars. It is apparent that gly-MOMP has favourable interactions with Le^b compared to MOMP. The residues Arg³⁵², Lys²⁷⁸ and 385 seems to be the major contributor in the interaction of the glycosylated protein with Le^b via hydrogen bonds whereas only the residues Asn²⁵⁸ and Lys²⁷⁸ are involved in the interaction of MOMP with Le^b. The residues 352 and 385 are the members of the beta-barrel

7, which are the part of loop 7. This loop, as mentioned earlier, mostly undergoes conformation changes during the molecular dynamic simulation (Fig. 4B). The glycosyl group interacts with this loop, thus leading to favourable conformational change for the interaction, and consequently resulting in a well-orientation of these residues to interact with Le^b. The glycosyl group is sandwiched between loops 4 and 7, probably influencing the dynamics of these loops, thus contributing to the binding ability of the protein. Calculations also show that the glycosylated protein has more favourable van der Waals (vdw) interactions compared with MOMP. It appears that the residues Leu²⁹⁰, Tyr²⁹⁴, Phe³⁹⁵ and Ile³³⁷ are well-located over the hydrophobic surface of Le^b in the complex of gly-MOMP compared with MOMP (Fig. 5B and C). This is reflected in 67 kcal/mol vdw energy difference between two complexes. It seems that H-II is bound to proteins with a similar mode to Le^b. The residues Lys²⁷⁸, Arg³⁵² and 381 are involved in the complex of both proteins with H-II (Fig 5E and F). The only difference is in the residues Asp²⁶¹ and Ser³⁹⁷, the first is involved in the complex of MOMP and the second in gly-MOMP. The very large binding energy obtained for the complex of H-II by MMPBSA could not be explained but it still shows that gly-MOMP binds to H-II better than MOMP itself.

[0092] The other outcome gathered from MD calculations is the conformation and alignment of the ligands within the cavities of two proteins. They show that both ligands have different conformational orientations in the active sites of the proteins.

[0093] In conclusion, although MD simulations were carried out in short MD simulation time and in implicit salvation medium, it still shows that glycosylation of major outer membrane proteins provides better conformational changes and consequently affinity for binding and hence recognition of Lewis antigens compared with its parent protein. Conformational MOMP epitopes are important in host immunity, and variation in surface-exposed regions probably occurs as a result of positive immune selection during infection. *porA* diversity has been exploited in genotyping studies using highly discriminatory nucleotide sequences to identify potentially epidemiologically linked cases of clinical manifestations of *C. jejuni* infection. Interestingly, the host immune response has been suggested to play a role in defining the more antigenically homogeneous clonal complexes, and this could also reflect niche adaptation. For example, alignment of MOMP sequences isolated from human and chicken associated strains demonstrates that they differ predominantly at loop 4, therefore variation of loop 4 could influence the bacterial binding ability and consequently niche adaptation.

[0094] Moreover, identification of protein glycosylation profile of *C. jejuni*, mainly those related to outer membrane, are fundamental to understanding the diverse pathogenicity of *C. jejuni* strains among different hosts. The model can be mined for sub-networks of biological interest, such as essential amino acid that suggest candidate drug targets. Importantly, some low confidence interactions may be found to be biologically significant by experimental validation.

[0095] The model for *C. jejuni* interaction to Le^b and H-II antigens mediated by MOMP generated here substantially increases our knowledge about the protein and its glycosylation and the role in interactions detected thus far for the *C. jejuni* outer membrane.

[0096] Thus, the structural glycobiology will play a key role in unravelling other glycan structures that mediate the host-bacteria interaction through MOMP/FlaA proteins, contributing decisively for identification and validation of new glycan receptors for these bacterial lectins. This information will be of major importance for the improvement and design of new therapies to overcome the *C. jejuni* infection.

Biofilm formation

[0097] Auto-agglutination (AAG) has been demonstrated to be critical for virulence for a variety of pathogens, and can play a role in adherence, microcolony formation, biofilm formation, and resistance to acid and phagocytosis. In two previous studies on AAG of *C. jejuni* (N. Misawa, M. J. Blaser, Infect Immun 68, 6168 (Nov, 2000) and N. J. Golden, D. W. Acheson, Infect Immun 70, 1761 (Apr, 2002)), there appeared to be an association with adherence or invasion of intestinal epithelial cells.

[0098] The impact of *flaA* mutation and/or MOMP-T/G substitution on biofilm was examined. Biofilms were generated over 48h on polystyrene plates at 42°C under microaerophilic conditions, and stained with crystal violet before they were assessed by opacity measurement, using an ELISA reader at A₅₉₅. In control samples without sugar added, biofilm formation of strain NCTC11168-Δ*flaA* deletion and MOMP^{T/G} were significantly lower than wild type strain (WT). Already known from previous studies, O-linked glycosylation of flagellin is necessary for proper assembly of flagella filaments, also *flaA* mutation leads to reduction in biofilm formation due to reduced motility. To determine the role of host BgAgs in inhibiting biofilm formation, various antigens were added into the media inoculated with different strains. A reduced biofilm formation was observed in the presence of free sugar structures in media; most dramatic drop is seen in WT. For wild type strain, the H-II produced the highest reduction by 90% and followed by Le^b structure with 80% compared with other examined BgAgs. Probably, the greater reduction is due to the higher affinity, which effects the equilibrium equation, and requires longer time for detachment of free sugar from surface molecules and prevents the biofilm formation. Although, the stronger binding affinity more interruption in biofilm formation. These data suggest that BgAgs compete with AAG and biofilm determinants on flagellin and MOMP, also confirmed the validity of the model and underlined the critical role of O-glycosylation in biofilm formation (**Figure 7**-Figure A and B).

This experiment was repeated and same pattern was achieved. Taking in account that position of plate might affect growth; we added the samples and its control in identical position on different plates. In addition, we took an aliquot from each sample and grow on CCDA, it showed that growth were equal in all.

The lowest energy structure of MOMP protein.

[0099] Functional and structural studies of outer membrane proteins from Gram-negative bacteria are frequently carried out using refolded proteins. Although several structures of bacterial OMPs (outer membrane proteins) are now available, a large number of these proteins are still structurally and functionally poorly characterized. A model was generated for *C. jejuni* MOMP to study the effect of glycosylation on MOMP conformation and also the role of it in bacterial binding activity. The model may be used for predicting the functions of uncharacterized proteins and for mapping functional pathways in *C. jejuni* and other prokaryotes. The data can provide a framework for understanding dynamic biological processes, such as the *C. jejuni* primary attachment to histo-blood group antigens.

Alignment of *porA* from different bacterial isolates

[0100] CLUSTAL W (1.81) multiple sequence alignment using BLOSUM weight matrix, of *Campylobacter jejuni* major outer membrane sequences downloaded from the Uniprot Database (<http://www.uniprot.org/>). Also, three non-binder (NB) and three high binder (HB) clinical isolates were added into this series (in house sequencing). Amino acid positions refer to positions in strain NCTC11168 (**P80672**).

The alignment showed the major contributors of the interaction of the glycosylated MOMP with Le^b via hydrogen bonds are residues 352 (Arg), 381 (Arg), and 278 (Lys), whereas only the residues 352 and 278 are involved in the interaction of non-glycosylated MOMP with Le^b. Amino acid sequence alignments indicating MOMP active sites of *C. jejuni* isolates from different patients has been sufficiently stable for this purpose. Interestingly, residue 278 (Lys) is semi-conserved in 16 isolates and was substituted by Arg which is able to mediate the binding through hydrogen bond in similar fashion as residues 381(Arg) and 352(Arg).

[0101] In addition, alignment of these sequences also demonstrates that they differ predominantly at loop 4 but the binding pocket between loop 4 and 7 is relatively conserved. A definitive study on MOMP host association would require glycosylation analysis data for isolates from a wide variety of hosts. A complicating factor in exploring these relationships for all *C. jejuni* may be their ability to colonize multiple hosts and thereby undergo exposure to many different immune responses.

Moreover, the glycosylation site Thr²⁶⁸ in the MOMP proteins was conserved in 52% of bacterial isolates aligned in this study, which indicate the importance role of Thr in 268 position.

Alignment of *porA* from different *C. jejuni* isolates.

[0102] CLUSTAL W (1.81) multiple sequence alignment using BLOSUM weight matrix, of *Campylobacter jejuni* major outer membrane sequences downloaded from the Uniprot Database (<http://www.uniprot.org/>). Also, three non-binder (NB) and three high binder (HB) clinical isolates were added into this series from in house sequencing. Amino acid positions

referred to in this application relate to the amino acid positions in strain NCTC11168 (P80672)
SEQ ID No. 1.

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<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>
VATSVIAGKQ	QLNLIWTDNA	IDGLVGTGVK	VVNSIDGLT	LAAFAVDSFM	AAEQCADLLE
<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>
HSNISTTSNQ	APFKVDSVGN	LYGAAAVGSY	DLAGGQFNPO	LWLAYWDQVA	FFYAVDAAYS
<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>	<u>290</u>	<u>300</u>
TTIFDGINWT	LEGAYLGNSL	DSELDDKTHA	NGNLFALKGS	IEVNGWDASL	GGLYYGDKEK
<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>	<u>360</u>
ASTVVIEDQG	NLGSLLAGEE	IFYTTGSRLN	GDTGRNIFGY	VTGGYTFNET	VRVGADFVYG
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GTKTEAANHL	GGGKKLEAVA	RVDYKYSPLK	NFSAFYSYVN	IDQGVNTNES	ADHSTVRLQA
LYKF					

[0103] Annotation with "***", ":", "." refers to identical, conserved, semi-conserved amino acid substitutions respectively.

SEQUENCE LISTING

[0104]

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<120> Reduction of gastrointestinal tract colonisation by Campylobacter

<130> JA58052P.WOP

<140> PCT/GB2013/050367

<141> 2013-02-15

<150> GB 1202681.1

<151> 2012-02-16

<150> GB 1220158.8

<151> 2012-11-08

<160> 46

<170> PatentIn version 3.5

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Asp Leu Leu Glu His Ser Asn Ile Ser Thr Thr Ser Asn Gln Ala Pro
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195 200 205

Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
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Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser
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Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
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Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
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Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
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Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala Gly
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Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
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Val Gly Thr Gly Val Lys Val Val Asn Asn Ser Ile Asp Gly Leu Thr
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Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
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Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
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Ala Asn Gly Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
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Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala Gly
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 Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
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 260 265 270
 Asn Leu Phe Ala Leu Lys Gly Ser Ile Glu Val Asn Gly Trp Asp Ala
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 Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn
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 His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
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 Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
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Ala Asn Gly Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
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Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala Gly
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Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Val Asp Gly Leu
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Asp Leu Leu Gly Gln Ser Thr Ile Ser Thr Thr Gln Asn Ala Ala Pro
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Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
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Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
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Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser
 225 230 235 240

Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu
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Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn Gly
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410

420

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Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn
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His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
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Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
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Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
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Ala Asn Gly Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
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Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala Gly
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Val Gly Thr Gly Ile Lys Val Val Asn Asn Ser Ile Asp Gly Leu Thr
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Leu Ala Ala Phe Ala Val Asp Ser Phe Met Ala Glu Glu Gln Gly Ala
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Asp Leu Leu Gly Gln Ser Thr Ile Ser Thr Thr Gln Asn Ala Ala Pro
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Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
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Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
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Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser
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Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu
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Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn Gly
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Asn Leu Phe Ala Leu Lys Gly Ser Ile Glu Val Asn Gly Trp Asp Ala
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Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn
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His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
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Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
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Arg Leu Gln Ala Leu Tyr Lys Phe
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Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asp His
50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
65 70 75 80

Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
85 90 95

Ala Asn Gly Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

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

Leu Ala Ala Phe Ala Val Asp Ser Phe Met Ala Glu Glu Gln Gly Ala
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Asp Leu Leu Gly Gln Ser Thr Ile Ser Thr Thr Gln Asn Ala Ala Pro
180 185 190

Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
195 200 205

Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
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Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser
 225 230 235 240

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

Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn Gly
 260 265 270

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

Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
 290 295 300

Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
 305 310 315 320

Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
 325 330 335

Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Ile Val Arg
 340 345 350

Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn
 355 360 365

His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
 370 375 380

Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
 385 390 395 400

Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Xaa Thr Val
 405 410 415

Arg Leu Gln Ala Leu Tyr Lys Phe
 420

<210> 9

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 9

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
 35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asn His
 50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
 65 70 75 80

Lys Ala Phe Ile Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
 85 90 95

Ala Asn Gly Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
 100 105 110

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

Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Val Asp Gly Leu
 130 135 140

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

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

Asp Leu Leu Gly Lys Ser Thr Ile Ser Thr Thr Gln Lys Ala Ala Pro
 180 185 190

Phe Gln Ala Asp Ser Leu Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
 195 200 205

Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
 210 215 220

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

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

Gly Asn Ser Leu Asp Ser Glu Leu Asn Asp Lys Arg His Ala Asn Gly
 260 265 270

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

Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
 290 295 300

Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
 305 310 315 320

Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
 325 330 335

Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
340 345 350

Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Thr Asn
355 360 365

His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
370 375 380

Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
385 390 395 400

Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val
405 410 415

Arg Leu Gln Ala Leu Tyr Lys Phe
420

<210> 10

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 10

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asp His
50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
65 70 75 80

Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
85 90 95

Ala Asn Gly Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Val Asp Gly Leu
130 135 140

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

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

Asp Leu Leu Gly Gln Ser Thr Ile Ser Thr Thr Gln Lys Ala Ala Pro
 180 185 190
 Phe Gln Ala Asp Ser Leu Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
 195 200 205
 Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
 210 215 220
 Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser
 225 230 235 240
 Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu
 245 250 255
 Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Arg His Ala Asn Gly
 260 265 270
 Asn Leu Phe Ala Leu Lys Gly Ser Ile Glu Val Asn Gly Trp Asp Ala
 275 280 285
 Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
 290 295 300
 Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
 305 310 315 320
 Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
 325 330 335
 Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
 340 345 350
 Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Thr Asn
 355 360 365
 His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
 370 375 380
 Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
 385 390 395 400
 Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val
 405 410 415
 Arg Leu Gln Ala Leu Tyr Lys Phe
 420

<210> 11

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 11

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
 35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asp His
 50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
 65 70 75 80

Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
 85 90 95

Ala Asn Gly Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
 100 105 110

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

Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Val Asp Gly Leu
 130 135 140

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

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

Asp Leu Leu Gly Gln Ser Thr Ile Ser Thr Thr Gln Lys Ala Ala Pro
 180 185 190

Phe Gln Ala Asp Ser Leu Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
 195 200 205

Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
 210 215 220

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

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

Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn Gly
 260 265 270

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

Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
 290 295 300

Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
 305 310 315 320

Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
 325 330 335

Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
 340 345 350

Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Thr Asn
 355 360 365

His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
 370 375 380

Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
 385 390 395 400

Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val
 405 410 415

Arg Leu Gln Ala Leu Tyr Lys Phe
 420

<210> 12

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 12

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
 35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asp His
 50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
 65 70 75 80

Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
 85 90 95

Ala Asn Gly Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
 100 105 110

Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala Gly
 115 120 125 130 135 140 145 150

115	120	125
Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Val Asp Gly Leu 130	135	140
Val Gly Thr Gly Ile Lys Val Val Asn Asn Ser Ile Asp Gly Leu Thr 145	150	155 160
Leu Ala Ala Phe Ala Val Asp Ser Phe Met Ala Glu Glu Gln Gly Thr 165	170	175
Asp Leu Leu Gly Gln Ser Thr Ile Ser Thr Thr Gln Asn Thr Ala Pro 180	185	190
Phe Gln Ala Asp Ser Leu Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly 195	200	205
Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala 210	215	220
Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser 225	230	235 240
Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu 245	250	255
Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Arg His Ala Asn Gly 260	265	270
Asn Leu Phe Ala Leu Lys Gly Ser Ile Glu Val Asn Gly Trp Asp Ala 275	280	285
Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val 290	295	300
Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu 305	310	315 320
Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn 325	330	335
Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg 340	345	350
Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Thr Asn 355	360	365
His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr 370	375	380
Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn 385	390	395 400
Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val 405	410	415
Arg Leu Gln Ala Leu Tyr Lys Phe		

420

<210> 13

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 13

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
 35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asp His
 50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
 65 70 75 80

Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
 85 90 95

Ala Asn Gly Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
 100 105 110

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

Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Val Asp Gly Leu
 130 135 140

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

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

Asp Leu Leu Gly Gln Ser Thr Ile Ser Thr Thr Gln Asn Thr Ala Leu
 180 185 190

Phe Gln Ala Asp Ser Leu Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
 195 200 205

Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
 210 215 220

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

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

Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Arg His Ala Asn Gly
 260 265 270
 Asn Leu Phe Ala Leu Lys Gly Ser Ile Glu Val Asn Gly Trp Asp Ala
 275 280 285
 Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
 290 295 300
 Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
 305 310 315 320
 Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
 325 330 335
 Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
 340 345 350
 Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Thr Asn
 355 360 365
 His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
 370 375 380
 Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
 385 390 395 400
 Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val
 405 410 415
 Arg Leu Gln Ala Leu Tyr Lys Phe
 420
 <210> 14
 <211> 425
 <212> PRT
 <213> Campylobacter jejuni
 <400> 14
 Met Lys Leu Val Lys Leu Ser Leu Val Ala Ala Leu Ala Ala Gly Ala
 1 5 10 15
 Phe Ser Ala Ala Asn Ala Thr Pro Leu Glu Glu Ala Ile Lys Asp Val
 20 25 30
 Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
 35 40 45
 Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asp His
 50 55 60
 Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
 65 70 75 80
 Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
 85 90 95

Ala Asn Gly Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
 100 105 110

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

Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Val Asp Gly Leu
 130 135 140

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

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

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

Pro Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val
 195 200 205

Gly Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu
 210 215 220

Ala Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr
 225 230 235 240

Ser Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr
 245 250 255

Leu Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Thr Thr His Ala Asn
 260 265 270

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

Ala Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr
 290 295 300

Val Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu
 305 310 315 320

Glu Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg
 325 330 335

Asn Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val
 340 345 350

Arg Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala
 355 360 365

Asn His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp
 370 375 380

Tyr Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val
 385 390 395 400

Asn Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr
 405 410 415

Val Arg Leu Gln Ala Leu Tyr Lys Phe
 420 425

<210> 15

<211> 425

<212> PRT

<213> Campylobacter jejuni

<400> 15

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
 35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His
 50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
 65 70 75 80

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

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

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

Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
 130 135 140

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

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

Asp Leu Leu Gly His Ser Asn Ile Ser Thr Thr Ser Lys Gln Ala Pro
 180 185 190

Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
 195 200 205

Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
 210 215 220 225

210 215 220

Tyr Trp Asp Gln Val Thr Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser

225 230 235 240

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

Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn Gly
260 265 270

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

Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
290 295 300

Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
305 310 315 320

Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
325 330 335

Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
340 345 350

Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Ala
355 360 365

Asn His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp
370 375 380

Tyr Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val
385 390 395 400

Asn Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr
405 410 415

Val Arg Leu Gln Ala Leu Tyr Lys Phe
420 425

<210> 16
<211> 424
<212> PRT
<213> Campylobacter jejuni

<400> 16
Met Lys Leu Val Lys Leu Ser Leu Val Ala Ala Leu Ala Ala Gly Ala
1 5 10 15

Phe Ser Ala Ala Asn Ala Thr Pro Leu Glu Glu Ala Ile Lys Asp Val

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
 35 40 45
 Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His
 50 55 60
 Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
 65 70 75 80
 Lys Ala Phe Ile Gln Phe Asp Tyr Asn Ala Val Asp Gly Gly Thr Gly
 85 90 95
 Val Asp Asn Val Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln Leu
 100 105 110
 Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala Gly
 115 120 125
 Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
 130 135 140
 Val Gly Thr Gly Val Lys Val Val Asn Asn Ser Ile Asp Gly Leu Thr
 145 150 155 160
 Leu Ala Ala Phe Ala Ala Asp Ser Phe Met Ala Ala Glu Gln Gly Ala
 165 170 175
 Asp Leu Leu Gly His Ser Thr Thr Ser Thr Thr Gln Ala Thr Ala Pro
 180 185 190
 Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
 195 200 205
 Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
 210 215 220
 Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser
 225 230 235 240
 Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu
 245 250 255
 Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn Gly
 260 265 270
 Asn Leu Phe Ala Leu Lys Gly Thr Ile Glu Val Asn Gly Trp Asp Ala
 275 280 285
 Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
 290 295 300
 Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
 305 310 315 320
 Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
 325 330 335

Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
340 345 350

Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn
355 360 365

His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
370 375 380

Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
385 390 395 400

Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val
405 410 415

Arg Leu Gln Ala Leu Tyr Lys Phe
420

<210> 17

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 17

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His
50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asp Phe
65 70 75 80

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

Val Asp Asn Val Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
130 135 140

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

Leu Ala Ala Phe Ala Ala Asn Ser Phe Met Ala Ala Glu Glu Glu Ala

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

Asp Leu Leu Gly His Ser Thr Thr Ser Thr Thr Gln Ala Thr Ala Pro
180                               185                               190

Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
195                               200                               205

Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
210                               215                               220

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

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

Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn Gly
260                               265                               270

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

Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
290                               295                               300

Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
305                               310                               315                               320

Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
325                               330                               335

Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
340                               345                               350

Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn
355                               360                               365

His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
370                               375                               380

Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
385                               390                               395                               400

Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val
405                               410                               415

Arg Leu Gln Ala Leu Tyr Lys Phe
420

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<210> 18

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 18

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
 35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asp His
 50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
 65 70 75 80

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

Val Asp Asn Val Thr Asn Thr Glu Lys Gly Leu Phe Val Arg Gln Leu
 100 105 110

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

Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
 130 135 140

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

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

Asp Leu Leu Glu His Ser Thr Ile Ser Thr Thr Gln Asn Ala Ala Pro
 180 185 190

Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
 195 200 205

Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
 210 215 220

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

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

Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn Gly
 260 265 270

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

Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
 290 295 300

Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
305 310 315 320

Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
325 330 335

Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
340 345 350

Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn
355 360 365

His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
370 375 380

Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
385 390 395 400

Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val
405 410 415

Arg Leu Gln Ala Leu Tyr Lys Phe
420

<210> 19

<211> 425

<212> PRT

<213> Campylobacter jejuni

<400> 19

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His
50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
65 70 75 80

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

Val Asp Asn Val Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
 130 135 140

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

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

Asp Leu Leu Gly His Ser Asn Ile Ser Thr Thr Asn Ala Asn Gln Ala
 180 185 190

Pro Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val
 195 200 205

Gly Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu
 210 215 220

Ala Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr
 225 230 235 240

Ser Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr
 245 250 255

Leu Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn
 260 265 270

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

Ala Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr
 290 295 300

Val Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu
 305 310 315 320

Glu Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg
 325 330 335

Asn Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val
 340 345 350

Arg Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala
 355 360 365

Asn His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp
 370 375 380

Tyr Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val
 385 390 395 400

Asn Leu Asp Gln Gly Ala Asn Thr Asn Glu Ser Ala Asp His Ser Thr
 405 410 415

Val Arg Leu Gln Ala Leu Tyr Lys Phe
 420 425

420

425

<210> 20

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 20

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His
50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
65 70 75 80

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

Val Asp Asn Val Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
130 135 140

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

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

Asp Leu Leu Gly His Ser Asn Ile Ser Thr Thr Pro Asn Gln Ala Pro
180 185 190

Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly

195

200

205

Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
210 215 220

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

Thr Thr Ile Phe Asn Glv Ile Asn Trp Thr Leu Glu Glv Ala Tyr Leu

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      245              250              255
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Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn Gly
      260              265              270

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

Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
      290              295              300

Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
      305              310              315              320

Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
      325              330              335

Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
      340              345              350

Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Asp Thr Ala
      355              360              365

His Val Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asn Tyr
      370              375              380

Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
      385              390              395              400

Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val
      405              410              415

Arg Leu Gln Ala Leu Tyr Lys Phe
      420

<210> 21
<211> 425
<212> PRT
<213> Campylobacter jejuni

<400> 21
Met Lys Leu Val Lys Leu Ile Leu Val Ala Ala Leu Ala Ala Gly Ala
 1              5              10              15

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
      35              40              45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His
      50              55              60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
      65              70              75              80

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

Val Asp Asn Val Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
130 135 140

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

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

Asp Leu Leu Gly His Arg Asn Ile Ser Thr Ile Thr Pro Asn Gln Ala
180 185 190

Pro Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val
195 200 205

Gly Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu
210 215 220

Ala Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr
225 230 235 240

Ser Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr
245 250 255

Leu Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn
260 265 270

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

Ala Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr
290 295 300

Val Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu
305 310 315 320

Glu Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg
325 330 335

Asn Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val
340 345 350

Arg Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Asp Thr
355 360 365

Ala His Val Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp
370 375 380

Tyr Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val
385 390 395 400

Asn Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr
405 410 415

Val Arg Leu Gln Ala Leu Tyr Lys Phe
420 425

<210> 22

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 22

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His
50 55 60

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

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

Val Asp Asn Val Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
130 135 140

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

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

Asp Leu Leu Gly His Ser Asn Ile Ser Thr Thr Ser Asn Gln Val Pro
180 185 190

Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly
195 200 205

Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
 210 215 220
 Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser
 225 230 235 240
 Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu
 245 250 255
 Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Lys Thr His Ala Asn Gly
 260 265 270
 Asn Leu Phe Ala Leu Lys Gly Thr Ile Glu Val Asn Gly Trp Asp Ala
 275 280 285
 Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
 290 295 300
 Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu
 305 310 315 320
 Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
 325 330 335
 Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
 340 345 350
 Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn
 355 360 365
 His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
 370 375 380
 Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
 385 390 395 400
 Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val
 405 410 415
 Arg Leu Gln Ala Leu Tyr Lys Phe
 420

<210> 23

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 23

Met Lys Leu Val Lys Leu Ser Leu Val Ala Ala Leu Ala Ala Gly Ala
 1 5 10 15
 Phe Ser Ala Ala Asn Ala Thr Pro Leu Glu Glu Ala Ile Lys Asp Val
 20 25 30
 Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp

35	40	45
Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His		
50	55	60
Lys Tyr Arg Ala Gln Val Asn Phe Gly Ala Ala Ile Ala Asp Asn Phe		
65	70	75
Lys Ala Phe Ile Gln Phe Asp Tyr Asn Ala Val Asp Gly Gly Thr Gly		
	85	90
Val Asp Asn Val Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln Leu		
	100	105
Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala Gly		
	115	120
Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu		
	130	135
Val Gly Thr Gly Val Lys Val Val Asn Asn Ser Ile Asp Gly Leu Thr		
	145	150
Leu Ala Ala Phe Ala Ala Asp Ser Phe Met Ala Ala Glu Gln Gly Ala		
	165	170
Asp Leu Leu Gly His Ser Asn Ile Ser Thr Thr Ser Asn Gln Ala Pro		
	180	185
Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly		
	195	200
Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala		
	210	215
Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser		
	225	230
Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu		
	245	250
Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Gln Ala His Ala Asn Gly		
	260	265
Asn Leu Phe Ala Leu Lys Gly Thr Ile Glu Val Asn Gly Trp Asp Ala		
	275	280
Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val		
	290	295
Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu		
	305	310
Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn		
	325	330
Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg		
	340	345

Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn
 355 360 365

His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
 370 375 380

Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
 385 390 395 400

Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val
 405 410 415

Arg Leu Gln Ala Leu Tyr Lys Phe
 420

<210> 24

<211> 425

<212> PRT

<213> Campylobacter jejuni

<400> 24

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
 35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His
 50 55 60

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

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

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

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

Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
 130 135 140

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

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

Asp Leu Leu Gly His Ser Asn Thr Ser Thr Ala Thr Pro Asn Gln Ala
 180 185 190
 Pro Phe Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val
 195 200 205
 Gly Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu
 210 215 220
 Ala Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr
 225 230 235 240
 Ser Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr
 245 250 255
 Leu Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Thr Thr His Ala Asn
 260 265 270
 Gly Asn Leu Phe Ala Leu Lys Gly Thr Ile Glu Val Asn Gly Trp Asp
 275 280 285
 Ala Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr
 290 295 300
 Val Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu
 305 310 315 320
 Glu Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg
 325 330 335
 Asn Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val
 340 345 350
 Arg Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala
 355 360 365
 Ser His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp
 370 375 380
 Tyr Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val
 385 390 395 400
 Asn Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr
 405 410 415
 Val Arg Leu Gln Ala Leu Tyr Lys Phe
 420 425

<210> 25

<211> 423

<212> PRT

<213> Campylobacter jejuni

<400> 25

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His
50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
65 70 75 80

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

Val Asp Asn Val Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

Lys Gln Gln Leu Asn Phe Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
130 135 140

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

Leu Ala Ala Phe Ala Val Asp Ser Phe Met Ala Ala Glu Gln Ala Glu
165 170 175

Leu Leu Gly His Ser Asn Ile Ser Thr Thr Ser Asn Gln Ala Pro Phe
180 185 190

Lys Val Asp Ser Val Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly Ser
195 200 205

Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr
210 215 220

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

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

Asn Ser Ile Asp Ser Glu Leu Asp Asp Thr Thr His Thr Asn Gly Asn
260 265 270

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

Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val Val
290 295 300

Ile Glu Asp Gln Gly Asn Leu Ser Ser Leu Leu Ala Gly Glu Glu Ile
305 310 315 320

Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn Ile
325 330 335

Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg Val
340 345 350

Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala Ser His
355 360 365

Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr Lys
370 375 380

Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Leu
385 390 395 400

Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser Thr Val Arg
405 410 415

Leu Gln Ala Leu Tyr Lys Phe
420

<210> 26

<211> 417

<212> PRT

<213> Campylobacter jejuni

<400> 26

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
35 40 45

Lys Asn Phe Val Asn Asn Ser Asn Leu Asn Asn Asn Lys Gln Asp His
50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
65 70 75 80

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

Val Asp Asn Ala Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

Lys Gln Gln Leu Asn Leu Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu
130 135 140

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

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

Asp Leu Leu Gly His Asn Gly Ser Gln Phe Asn Pro Asp Ser Ile Gly
180 185 190

Asn Leu Tyr Gly Ala Ala Ala Val Gly Ser Tyr Asp Leu Ala Gly Gly
195 200 205

Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Trp Asp Gln Val Ala Phe
210 215 220

Phe Tyr Ala Leu Asp Ala Ser Tyr Ser Thr Thr Ile Phe Asp Gly Ile
225 230 235 240

Asn Trp Thr Leu Glu Gly Ala Tyr Leu Gly Asn Ser Val Asp Ser Asp
245 250 255

Leu Asp Ser Thr Arg Tyr Ala Asn Gly Asn Phe Phe Ala Leu Lys Gly
260 265 270

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

Gly Asp Lys Glu Lys Ala Ser Thr Val Ile Ile Asp Asp Gln Gly Asn
290 295 300

Leu Ser Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr Thr Gly Ser
305 310 315 320

Arg Leu Asn Gly Asp Thr Gly Arg Asn Ile Phe Gly Tyr Val Thr Gly
325 330 335

Gly Tyr Thr Phe Asn Glu Thr Val Arg Val Gly Ala Asp Phe Val Tyr
340 345 350

Gly Gly Thr Lys Thr Glu Ala Ala Asn His Leu Gly Gly Gly Lys Lys
355 360 365

Leu Glu Ala Val Ala Arg Val Asp Tyr Lys Tyr Ser Pro Lys Leu Asn
370 375 380

Phe Ser Ala Phe Tyr Ser Tyr Val Asn Leu Asp Gln Gly Val Asn Thr
385 390 395 400

Asn Glu Ser Ala Asp His Ser Thr Val Arg Leu Gln Ala Leu Tyr Lys
405 410 415

Phe

<210> 27

<211> 417

<212> PRT

<213> Campylobacter jejuni

<400> 27

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Thr Phe Asp
 35 40 45

Lys Asn Trp Gly Thr Pro Asn Ser Asn Leu Asn Asp Ser Lys Gln Asp
 50 55 60

His Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn
 65 70 75 80

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

Gly Val Asp Asn Lys Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln
 100 105 110

Leu Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala
 115 120 125

Gly Lys Gln Gln Leu Asn Ile Ile Trp Thr Asp Asn Gly Val Asp Gly
 130 135 140

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

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

Ser Asp Leu Val Gly Ala Asn Asn Thr Phe Lys Val Asp Ser Ile Gly
 180 185 190

Asn Leu Tyr Gly Ala Ala Ala Val Gly Ser Tyr Asp Leu Ala Gly Gly
 195 200 205

Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Trp Asp Gln Val Ala Phe
 210 215 220

Phe Tyr Ala Val Asp Ala Ala Tyr Ser Thr Thr Ile Phe Asp Gly Ile
 225 230 235 240

Asn Trp Thr Leu Glu Gly Ala Tyr Leu Gly Asn Ser Val Asp Ser Asp
 245 250 255

Leu Asn Ser Ala Glu His Ala Asn Gly Asn Leu Phe Ala Leu Lys Gly

260 265 270
 Ser Ile Glu Val Asn Gly Trp Asp Ala Ser Leu Gly Gly Leu Tyr Tyr
 275 280 285
 Gly Asp Lys Glu Lys Ala Ser Thr Val Val Ile Glu Asp Gln Gly Asn
 290 295 300
 Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr Thr Gly Ser
 305 310 315 320
 Arg Leu Asn Gly Asp Thr Gly Arg Asn Ile Phe Gly Tyr Val Thr Gly
 325 330 335
 Gly Tyr Thr Phe Asn Glu Thr Val Arg Val Gly Ala Asp Phe Val Tyr
 340 345 350
 Gly Gly Thr Lys Thr Glu Ala Ala Ser His Leu Gly Gly Gly Lys Lys
 355 360 365
 Leu Glu Ala Val Ala Arg Val Asp Tyr Lys Tyr Ser Pro Lys Leu Asn
 370 375 380
 Phe Ser Ala Phe Tyr Ser Tyr Val Asn Leu Asp Gln Gly Val Asn Thr
 385 390 395 400
 Asn Glu Ser Ala Asp His Ser Thr Val Arg Leu Gln Ala Leu Tyr Lys
 405 410 415
 Phe
 <210> 28
 <211> 418
 <212> PRT
 <213> Campylobacter jejuni
 <400> 28
 Met Lys Leu Val Lys Leu Ser Leu Val Ala Ala Leu Ala Ala Gly Ala
 1 5 10 15
 Phe Ser Ala Ala Asn Ala Thr Pro Leu Glu Glu Ala Ile Lys Asp Val
 20 25 30
 Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Thr Phe Asp
 35 40 45
 Lys Asn Trp Gly Thr Pro Asn Ser Asn Leu Asn Asp Ser Lys Gln Asp
 50 55 60
 His Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn
 65 70 75 80
 Phe Lys Ala Phe Ile Gln Phe Asp Tyr Asn Ala Val Asp Gly Gly Thr
 85 90 95

Gly Val Asp Asn Lys Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln
 100 105 110
 Leu Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala
 115 120 125
 Gly Lys Gln Gln Leu Asn Ile Ile Trp Thr Asp Asn Gly Val Asp Gly
 130 135 140
 Leu Val Gly Thr Gly Ile Lys Val Val Asn Asn Ser Ile Asp Gly Leu
 145 150 155 160
 Thr Leu Ala Ala Phe Ala Val Asp Ser Phe Met Ala Ala Glu Gln Gly
 165 170 175
 Ser Asp Leu Val Gly Ala Asn Asn Ser Thr Phe Lys Val Asp Ser Ile
 180 185 190
 Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly Ser Tyr Asp Leu Ala Gly
 195 200 205
 Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Trp Asp Gln Val Ala
 210 215 220
 Phe Phe Tyr Ala Leu Asp Val Ser Tyr Ser Thr Thr Ile Phe Asp Gly
 225 230 235 240
 Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu Gly Asn Ser Leu Asp Ser
 245 250 255
 Glu Leu Asn Asp Lys Thr Tyr Ala Asn Gly Asn Leu Phe Ala Leu Lys
 260 265 270
 Gly Ser Ile Glu Val Asn Gly Trp Asp Ala Ser Leu Gly Gly Leu Tyr
 275 280 285
 Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val Ala Ile Glu Asp Gln Gly
 290 295 300
 Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr Thr Gly
 305 310 315 320
 Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn Ile Phe Gly Tyr Val Thr
 325 330 335
 Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg Val Gly Ala Asp Phe Val
 340 345 350
 Tyr Gly Gly Thr Lys Thr Glu Ala Ala Gly His Leu Gly Gly Gly Lys
 355 360 365
 Lys Leu Glu Ala Val Ala Arg Val Asp Tyr Lys Tyr Ser Pro Lys Leu
 370 375 380
 Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Leu Asp Gln Gly Val Asn
 385 390 395 400

Thr Asn Glu Ser Ala Asp His Ser Thr Val Arg Leu Gln Ala Leu Tyr
 405 410 415

Lys Phe

<210> 29

<211> 418

<212> PRT

<213> Campylobacter jejuni

<400> 29

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Thr Phe Asp
 35 40 45

Lys Asn Trp Gly Thr Pro Asn Ser Asn Leu Asn Asp Ser Lys Gln Asp
 50 55 60

His Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn
 65 70 75 80

Phe Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Val Asp Gly Gly Thr
 85 90 95

Gly Val Asp Asn Ala Thr Asn Ala Gln Lys Gly Phe Phe Val Arg Gln
 100 105 110

Leu Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala
 115 120 125

Gly Lys Gln Gln Leu Asn Ile Ile Trp Thr Asp Asn Gly Ile Asp Gly
 130 135 140

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

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

Ser Asp Leu Val Gly His Asn Gly Ser Gln Phe Asn Pro Asp Ser Ile
 180 185 190

Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly Ser Tyr Asp Leu Ala Gly
 195 200 205

Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Trp Asp Gln Val Ala
 210 215 220

Phe Phe Tyr Ala Leu Asp Ala Ser Tyr Ser Thr Thr Ile Phe Asp Gly
 225 230 235 240

Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu Gly Asn Ser Val Asp Ser
245 250 255

Asp Leu Asp Ser Ala Lys Tyr Ala Asn Gly Asn Leu Phe Ala Leu Lys
260 265 270

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

Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val Val Ile Glu Asp Gln Gly
290 295 300

Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr Thr Gly
305 310 315 320

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

Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg Val Gly Ala Asp Phe Val
340 345 350

Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn His Leu Gly Gly Gly Lys
355 360 365

Lys Leu Glu Ala Val Ala Arg Val Asp Tyr Lys Tyr Ser Pro Lys Leu
370 375 380

Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Leu Asp Gln Gly Val Asn
385 390 395 400

Thr Asn Glu Ser Ala Asp His Ser Thr Val Arg Leu Gln Ala Leu Tyr
405 410 415

Lys Phe

<210> 30

<211> 418

<212> PRT

<213> Campylobacter jejuni

<400> 30

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Thr Phe Asp
35 40 45

Lys Asn Trp Gly Thr Pro Asn Ser Asn Leu Asn Asp Ser Lys Gln Asp
50 55 60

His Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn
65 70 75 80

Phe Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Val Asp Gly Gly Thr
85 90 95

Gly Val Asp Asn Ala Thr Asn Ala Gln Lys Gly Phe Phe Val Arg Gln
100 105 110

Leu Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala
115 120 125

Gly Lys Gln Gln Leu Asn Ile Ile Trp Thr Asp Asn Gly Ile Asp Gly
130 135 140

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

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

Ser Asp Leu Val Gly His Asn Gly Ser Gln Phe Asn Pro Asp Ser Ile
180 185 190

Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly Ser Tyr Asp Leu Ala Gly
195 200 205

Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Trp Asp Gln Val Ala
210 215 220

Phe Phe Tyr Ala Leu Asp Ala Ser Tyr Ser Thr Thr Ile Phe Asp Gly
225 230 235 240

Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu Gly Asn Ser Val Asp Ser
245 250 255

Asp Leu Asp Ser Ala Arg Tyr Ala Asn Gly Asn Leu Phe Ala Leu Lys
260 265 270

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

Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val Val Ile Glu Asp Gln Gly
290 295 300

Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr Thr Gly
305 310 315 320

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

Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg Val Gly Ala Asp Phe Val
340 345 350

Tyr Gly Gly Thr Lys Thr Glu Ala Ala Asn His Leu Gly Gly Gly Lys
 355 360 365

Lys Leu Glu Ala Val Ala Arg Val Asp Tyr Lys Tyr Ser Pro Lys Leu
 370 375 380

Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Leu Asp Gln Gly Val Asn
 385 390 395 400

Thr Asn Glu Ser Ala Asp His Ser Thr Val Arg Leu Gln Ala Leu Tyr
 405 410 415

Lys Phe

<210> 31

<211> 418

<212> PRT

<213> Campylobacter jejuni

<400> 31

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Thr Phe Asp
 35 40 45

Lys Asn Trp Gly Thr Pro Asn Ser Asn Leu Asn Asp Ser Lys Gln Asp
 50 55 60

His Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn
 65 70 75 80

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

Gly Val Asp Asn Ala Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln
 100 105 110

Leu Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala
 115 120 125

Gly Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Ile Asp Gly
 130 135 140

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

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

Ser Asp Leu Val Gly His Asn Gly Ser Lys Phe Ser Pro Asp Ser Ile
 180 185 190

Gly Asn Leu Tyr Gly Ala Ala Ala Val Gly Ser Tyr Asp Leu Ala Gly
195 200 205

Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Trp Asp Gln Val Ala
210 215 220

Phe Phe Tyr Ala Leu Asp Ala Ser Tyr Ser Thr Thr Ile Phe Asp Gly
225 230 235 240

Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu Gly Asn Ser Val Asp Ser
245 250 255

Asp Leu Asn Ser Ala Glu Tyr Ala Asn Gly Asn Leu Phe Ala Leu Lys
260 265 270

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

Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val Val Ile Glu Asp Gln Gly
290 295 300

Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr Thr Gly
305 310 315 320

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

Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg Val Gly Ala Asp Phe Val
340 345 350

Tyr Gly Gly Thr Lys Thr Glu Ala Thr Thr His Leu Gly Gly Gly Lys
355 360 365

Lys Leu Glu Ala Val Ala Arg Val Asp Tyr Lys Tyr Ser Pro Lys Leu
370 375 380

Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Leu Asp Gln Gly Val Asn
385 390 395 400

Thr Asn Glu Ser Ala Asp His Ser Thr Val Arg Leu Gln Ala Leu Tyr
405 410 415

Lys Phe

<210> 32

<211> 426

<212> PRT

<213> Campylobacter jejuni

<400> 32

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
35 40 45

Lys Asn Phe Leu Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asp His
50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
65 70 75 80

Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Val Asp Gly Gly Thr Gly
85 90 95

Val Asp Asn Ala Thr Asn Ala Glu Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

Lys Gln Gln Leu Asn Ile Ile Trp Thr Asp Asn Gly Val Asp Gly Leu
130 135 140

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

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

Asp Leu Leu Gly Gln Ser Thr Tyr Val Ser Asn Asp Lys Asn Asn Asn
180 185 190

Asp Ser Phe Lys Leu Asp Ser Ile Gly Asn Leu Tyr Gly Ala Ala Ala
195 200 205

Val Gly Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp
210 215 220

Leu Ala Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala
225 230 235 240

Tyr Ser Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala
245 250 255

Tyr Leu Gly Asn Ser Leu Asp Ser Glu Leu Asp Asp Arg Thr Tyr Ala
260 265 270

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

Asp Ala Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser
290 295 300

Thr Val Val Ile Glu Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly
305 310 315 320

325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

Glu Glu Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly
325 330 335

Arg Asn Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr
340 345 350

Val Arg Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala
355 360 365

Val Gly His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val
370 375 380

Asp Tyr Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr
385 390 395 400

Val Asn Leu Asp Gln Gly Val Asn Thr Asn Glu Ser Ala Asp His Ser
405 410 415

Thr Val Arg Leu Gln Ala Leu Tyr Lys Phe
420 425

<210> 33

<211> 424

<212> PRT

<213> Campylobacter jejuni

<400> 33

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
35 40 45

Lys Asn Phe Ile Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asp His
50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
65 70 75 80

Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Thr Gly
85 90 95

Val Asp Asn Ala Thr Asn Ala Gln Lys Gly Leu Phe Val Arg Gln Leu
100 105 110

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

Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Ile Asp Gly Leu
130 135 140

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

Leu Ala Ala Phe Ala Val Asp Ser Phe Met Ala Glu Glu Gln Gly Ala
 165 170 175
 Asp Leu Leu Gly His Ser Asn Ile Ser Ser Ala Asn Asn Ser Ala Pro
 180 185 190
 Phe Lys Leu Asp Ser Ile Gly Asn Leu Tyr Gly Gly Ala Ala Val Gly
 195 200 205
 Ser Tyr Glu Phe Leu Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala
 210 215 220
 Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr Ser
 225 230 235 240
 Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr Leu
 245 250 255
 Gly Asn Ser Ile Asp Ser Glu Leu Asp Lys Thr Thr His Thr Asn Gly
 260 265 270
 Asn Leu Phe Ala Leu Arg Gly Ser Val Glu Leu Asn Gly Trp Asp Ala
 275 280 285
 Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr Val
 290 295 300
 Val Ile Glu Asp Gln Gly Asn Ile Gly Ser Leu Leu Ala Gly Glu Glu
 305 310 315 320
 Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg Asn
 325 330 335
 Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val Arg
 340 345 350
 Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Thr Ala Gly
 355 360 365
 His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
 370 375 380
 Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
 385 390 395 400
 Leu Asp Glu Gly Val Asn Thr Lys Glu Ser Ala Asp His Ser Thr Val
 405 410 415
 Arg Leu Gln Ala Leu Tyr Lys Phe
 420

<210> 34

<211> 425

<212> PRT

<213> Campylobacter jejuni

<400> 34

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Gly Asn Phe Asp
 35 40 45

Lys Asn Phe Ile Asn Asn Ser Asn Leu Asn Asn Ser Lys Gln Asp His
 50 55 60

Lys Tyr Arg Ala Gln Val Asn Phe Ser Ala Ala Ile Ala Asp Asn Phe
 65 70 75 80

Lys Ala Phe Val Gln Phe Asp Tyr Asn Ala Ala Asp Gly Gly Tyr Gly
 85 90 95

Ala Asn Glu Ile Lys Asn Asp Gln Lys Gly Leu Phe Val Arg Gln Leu
 100 105 110

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

Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Ile Asp Gly Leu
 130 135 140

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

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

Asp Leu Leu Gly His Ser Asn Ile Ser Ser Ala Lys Pro Asn Ile Ala
 180 185 190

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

Gly Ser Tyr Glu Phe Leu Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu
 210 215 220

Ala Tyr Trp Asp Gln Val Ala Phe Phe Tyr Ala Val Asp Ala Ala Tyr
 225 230 235 240

Ser Thr Thr Ile Phe Asp Gly Ile Asn Trp Thr Leu Glu Gly Ala Tyr
 245 250 255

Leu Gly Asn Ser Ile Asp Ser Glu Leu Asp Asp Lys Thr His Thr Asn
 260 265 270

Gly Asn Leu Phe Ala Leu Arg Gly Ser Val Glu Leu Asn Gly Trp Asp
 275 280 285

Ala Ser Leu Gly Gly Leu Tyr Tyr Gly Asp Lys Glu Lys Ala Ser Thr
 290 295 300
 Val Val Ile Glu Asp Gln Gly Asn Ile Gly Ser Leu Leu Ala Gly Glu
 305 310 315 320
 Glu Ile Phe Tyr Thr Thr Gly Ser Arg Leu Asn Gly Asp Thr Gly Arg
 325 330 335
 Asn Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val
 340 345 350
 Arg Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Glu Ala Ala
 355 360 365
 Asn His Leu Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp
 370 375 380
 Tyr Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val
 385 390 395 400
 Asn Leu Asp Glu Gly Val Asn Thr Lys Glu Ser Ala Asp His Ser Thr
 405 410 415
 Val Arg Leu Gln Ala Leu Tyr Lys Phe
 420 425
 <210> 35
 <211> 420
 <212> PRT
 <213> Campylobacter jejuni
 <400> 35
 Met Lys Leu Val Lys Leu Ser Leu Val Ala Ala Leu Ala Ala Gly Ala
 1 5 10 15
 Phe Ser Ala Ala Asn Ala Thr Pro Leu Glu Glu Ala Ile Lys Asp Val
 20 25 30
 Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Thr Ser Asn Asp Trp
 35 40 45
 Ser Asn Ala Asn Phe Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys
 50 55 60
 Tyr Arg Ala Gln Val Asn Phe Gly Ala Ala Ser Ala Asp Asn Phe Lys
 65 70 75 80
 Ala Phe Val Gln Phe Asp Tyr Ser Gln Ala Asp Gly Gly Tyr Gly Ala
 85 90 95
 Asp Ser Ile Ser Asn Thr Ser Asp Thr Leu Ser Val Arg Gln Leu Tyr

100	105	110
Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala Gly Lys 115 120 125		
Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Ile Asp Gly Leu Val 130 135 140		
Gly Thr Gly Ile Lys Val Val Asn Asn Ser Ile Asp Gly Leu Thr Leu 145 150 155 160		
Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Glu Val Pro Ala Thr Thr 165 170 175		
Thr Asn Gly Phe Asn Lys Gly Asn Val Asn Gly Asp Gly Asp Val Ser 180 185 190		
Ser Ala Leu Asp Trp Ser Lys Asn Ile Tyr Gly Ala Ala Ala Ile Gly 195 200 205		
Ser Tyr Asp Leu Ile Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala 210 215 220		
Tyr Met Ser Asp Asn Ala Phe Leu Tyr Ala Leu Asp Ala Ala Tyr Ser 225 230 235 240		
Thr Thr Ile Phe Asp Gly Ile Asn Trp Ser Ile Glu Gly Ala Tyr Leu 245 250 255		
Gly Asn Ser Val Asp Asn Lys Leu Lys Asp Arg Leu Asp Ala Ala Asn 260 265 270		
Gly Asn Phe Phe Ala Leu Arg Gly Thr Val Glu Val Asn Gly Trp Asp 275 280 285		
Ala Ser Leu Gly Gly Leu Tyr Tyr Gly Lys Lys Asp Lys Ala Thr Val 290 295 300		
Thr Thr Ile Glu Asp Gln Gly Asn Ile Gly Ser Leu Leu Ala Gly Glu 305 310 315 320		
Glu Ile Phe Tyr Thr Arg Gly Ser Asn Leu Asn Gly Asp Ile Gly Arg 325 330 335		
Asn Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr Val 340 345 350		
Arg Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Asn Ile Ile 355 360 365		
Gly Gly Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr Lys 370 375 380		
Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Val 385 390 395 400		

Asp Thr Asp Pro Glu Ser Thr His His Asp Ala Val Arg Leu Gln Ala
 405 410 415

Leu Tyr Lys Phe
 420

<210> 36

<211> 421

<212> PRT

<213> Campylobacter jejuni

<400> 36

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Thr Ser Asn Asp Trp
 35 40 45

Ser Asn Ala Asn Phe Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys
 50 55 60

Tyr Arg Ala Gln Val Asn Phe Ser Gly Ala Ile Ser Asp Asn Phe Lys
 65 70 75 80

Ala Phe Val Gln Phe Asp Tyr Asn Ser Gln Asp Gly Gly Tyr Gly Ala
 85 90 95

Asp Ser Ile Ser Asn Thr Ser Asp Thr Leu Ser Val Arg Gln Leu Tyr
 100 105 110

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

Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Ile Asp Gly Leu Val
 130 135 140

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

Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Glu Val Pro Ala Thr Thr
 165 170 175

Thr Asn Gly Asn Phe Asn Lys Gly Asn Val Asn Gly Asp Gly Asp Val
 180 185 190

Ser Ser Ala Leu Asp Trp Ser Lys Asn Ile Tyr Gly Ala Ala Ala Ile
 195 200 205

Gly Ser Tyr Asp Ile Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu
 210 215 220

Ala Tyr Met Ser Asp Asn Ala Phe Leu Tyr Ala Leu Asp Ala Ala Tyr
 225 230 235 240

225 230 235 240
 Ser Thr Thr Ile Phe Asp Gly Ile Asn Trp Ser Ile Glu Gly Ala Tyr
 245 250 255
 Leu Gly Asn Ser Val Asp Asn Lys Leu Lys Asp Arg Leu Asp Ala Ala
 260 265 270
 Asn Gly Asn Phe Phe Ala Leu Arg Gly Thr Val Glu Val Asn Gly Trp
 275 280 285
 Asp Ala Ser Leu Gly Gly Leu Tyr Tyr Gly Lys Lys Asp Lys Ala Thr
 290 295 300
 Val Thr Thr Ile Glu Asp Gln Gly Asn Ile Gly Ser Leu Leu Ala Gly
 305 310 315 320
 Glu Glu Ile Phe Tyr Thr Arg Gly Ser Asn Leu Asn Gly Asp Ile Gly
 325 330 335
 Arg Asn Ile Phe Gly Tyr Val Thr Gly Gly Tyr Thr Phe Asn Glu Thr
 340 345 350
 Val Arg Val Gly Ala Asp Phe Val Tyr Gly Gly Thr Lys Thr Asn Ile
 355 360 365
 Ile Gly Gln Gly Gly Lys Lys Leu Glu Ala Val Ala Arg Val Asp Tyr
 370 375 380
 Lys Tyr Ser Pro Lys Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn
 385 390 395 400
 Val Asp Thr Asp Pro Glu Ser Thr His His Asp Ala Val Arg Leu Gln
 405 410 415
 Ala Leu Tyr Lys Phe
 420
 <210> 37
 <211> 431
 <212> PRT
 <213> Campylobacter jejuni
 <400> 37
 Met Lys Leu Val Lys Leu Ser Leu Val Ala Ala Leu Ala Ala Ser Ala
 1 5 10 15
 Phe Ser Ala Ala Asn Ala Thr Pro Leu Glu Glu Ala Ile Lys Asp Ile
 20 25 30
 Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Ser Ser Asn Pro Trp
 35 40 45
 Ser Asn Ala Asn Phe Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys
 50 55 60
 Met Ser Ile Glu Val Ser Phe Gln Glu Ile Thr Ser Ser Ser Phe Tyr

Tyr Arg Ala Gln Val Asn Phe Ser Gly Ala Ile Ser Asp Asn Phe Lys
 65 70 75 80
 Ala Phe Val Gln Phe Asp Tyr Asn Ser Gln Asp Gly Gly Tyr Gly Ala
 85 90 95
 Asp Ser Ile Ser Asn Thr Ser Asp Thr Leu Ser Val Arg Gln Leu Tyr
 100 105 110
 Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala Gly Lys
 115 120 125
 Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu Val
 130 135 140
 Gly Thr Gly Ile Lys Val Val Asn Asn Ser Ile Asp Gly Leu Thr Leu
 145 150 155 160
 Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Ala Ser Asp Thr Thr Val
 165 170 175
 Thr Ile Thr Gln Asp Asn Ser Gln Lys Ile Thr Gly Val Gln Phe Asn
 180 185 190
 Arg Gly Asn Pro Lys Gly Asp Ser Asp Val Ser Gly Ala Leu Asp Trp
 195 200 205
 Ser Lys Asn Ile Tyr Gly Ala Ala Ala Ile Gly Ser Tyr Asp Ile Ala
 210 215 220
 Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Met Ser Asp Asn
 225 230 235 240
 Ala Phe Leu Tyr Ala Leu Asp Ala Thr Tyr Ser Thr Thr Ile Phe Asp
 245 250 255
 Gly Ile Asn Trp Thr Ile Glu Gly Ala Tyr Leu Gly Asn Ser Val Asp
 260 265 270
 Asn Lys Leu Lys Asp Arg Leu Asp Ala Ala Asn Gly Asn Phe Phe Ala
 275 280 285
 Leu Arg Gly Thr Val Glu Val Asn Gly Trp Asp Ala Ser Leu Gly Gly
 290 295 300
 Leu Tyr Tyr Gly Lys Lys Asp Lys Ile Thr Val Thr Thr Ile Glu Asp
 305 310 315 320
 Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr
 325 330 335
 Arg Gly Ser Asn Leu Asn Gly Asp Leu Gly Arg Asn Ile Phe Gly Tyr
 340 345 350
 Val Thr Gly Gly Tyr Thr Phe Asn Glu Ala Val Arg Val Gly Ala Asp
 355 360 365

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

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

Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Val Asp Thr Asp Pro Glu
405 410 415

Ser Thr His His Asp Ala Val Arg Leu Gln Ala Leu Tyr Lys Phe
420 425 430

<210> 38

<211> 431

<212> PRT

<213> Campylobacter jejuni

<400> 38

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Ser Ser Asn Pro Trp
35 40 45

Ser Asn Ala Asn Phe Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys
50 55 60

Tyr Arg Ala Gln Val Asn Phe Ser Gly Ala Ile Ser Asp Asn Phe Lys
65 70 75 80

Ala Phe Val Gln Phe Asp Tyr Asn Ser Gln Asp Gly Gly Tyr Gly Ala
85 90 95

Asp Ser Ile Ser Asn Thr Ser Asp Thr Leu Ser Val Arg Gln Leu Tyr
100 105 110

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

Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu Val
130 135 140

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

Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Ala Ser Asp Thr Thr Val
165 170 175

Thr Ile Thr Gln Asp Asn Ser Gln Lys Ile Thr Gly Val Gln Phe Asn
180 185 190

Arg Gly Asn Pro Lys Gly Asp Ser Asp Val Ser Gly Ala Leu Asp Trp
195 200 205

Ser Lys Asn Ile Tyr Gly Ala Thr Ala Ile Gly Ser Tyr Asp Ile Ala
210 215 220

Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Met Ser Asp Asn
225 230 235 240

Ala Phe Leu Tyr Ala Leu Asp Ala Thr Tyr Ser Thr Thr Ile Phe Asp
245 250 255

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

Asn	Lys	Leu	Lys	Asp	Arg	Leu	Asp	Ala	Ala	Asn	Gly	Asn	Phe	Phe	Ala
		275					280					285			

Leu	Arg	Gly	Thr	Val	Glu	Val	Asn	Gly	Trp	Asp	Ala	Ser	Leu	Gly	Gly
290						295					300				

Leu Tyr Tyr Gly Lys Lys Asp Lys Ile Thr Val Thr Thr Ile Glu Asp
305 310 315 320

Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr
325 330 335

Arg Gly Ser Asn Leu Asn Gly Asp Leu Gly Arg Asn Ile Phe Gly Tyr
340 345 350

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

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

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

Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Val Asp Thr Asp Pro Glu
405 410 415

Ser Thr His His Asp Ala Val Lys Leu Gln Ala Leu Tyr Lys Phe
420 425 430

<210> 39

$\langle 211 \rangle$ 431

<212> PRT

<213> Campylobacter jejuni

<400> 39

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

Phe Ser Ala Ala Asn Ala Thr Pro Leu Glu Glu Ala Ile Lys Asp Ile

20	25	30
Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Ser Ser Asn Pro Trp		
35	40	45
Ser Asn Ala Asn Phe Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys		
50	55	60
Tyr Arg Ala Gln Val Asn Phe Ser Gly Ala Ile Ser Asp Asn Phe Lys		
65	70	75
Ala Phe Val Gln Phe Asp Tyr Asn Ser Gln Asp Gly Gly Tyr Gly Thr		
85	90	95
Asp Ser Ile Ser Asn Thr Ser Asp Thr Leu Thr Val Arg Gln Leu Tyr		
100	105	110
Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val Ile Ala Gly Lys		
115	120	125
Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Ile Asp Gly Leu Val		
130	135	140
Gly Thr Gly Val Lys Val Val Asn Asn Ser Ile Asp Gly Leu Thr Leu		
145	150	155
Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Ala Ser Asp Thr Thr Val		
165	170	175
Thr Ile Thr Gln Asp Ser Asn Gln Lys Ile Thr Gly Val Gln Phe Asn		
180	185	190
Arg Gly Asn Pro Lys Gly Asp Ser Asp Val Ser Gly Ala Leu Asp Trp		
195	200	205
Ser Lys Asn Ile Tyr Gly Ala Ala Ala Ile Gly Ser Tyr Asp Ile Ala		
210	215	220
Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Met Ser Asp Asn		
225	230	235
Ala Phe Leu Tyr Ala Leu Asp Ala Ala Tyr Ser Thr Thr Ile Phe Asp		
245	250	255
Gly Ile Asn Trp Thr Ile Glu Gly Ala Tyr Leu Gly Asn Ser Val Asp		
260	265	270
Asn Lys Leu Lys Asp Arg Leu Asp Ala Ala Asn Gly Asn Phe Phe Ala		
275	280	285
Leu Arg Gly Thr Val Glu Val Asn Gly Trp Asp Ala Ser Leu Gly Gly		
290	295	300
Leu Tyr Tyr Gly Lys Lys Asp Lys Ile Thr Val Thr Thr Ile Glu Asp		
305	310	315
		320

Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr
325 330 335

Arg Gly Ser Asn Leu Asn Gly Asp Leu Gly Arg Asn Ile Phe Gly Tyr
340 345 350

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

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

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

Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Val Asp Thr Asp Pro Glu
405 410 415

Ser Thr His His Asp Ala Val Arg Leu Gln Ala Leu Tyr Lys Phe
420 425 430

<210> 40

<211> 431

<212> PRT

<213> Campylobacter jejuni

<400> 40

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

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20 25 30

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Ser Ser Asn Pro Trp
35 40 45

Ser Asn Ala Asn Phe Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys
50 55 60

Tyr Arg Ala Gln Val Asn Phe Ser Gly Ala Ile Ser Asp Asn Phe Lys

65 70 75 80

Ala Phe Val Gln Phe Asp Tyr Asn Ser Gln Asp Gly Gly Tyr Gly Thr
85 90 95

Asp Ser Ile Ser Asn Thr Ser Asp Thr Leu Thr Val Arg Gln Leu Tyr
100 105 110

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

Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Val Asp Gly Leu Val
130 135 140

Gly Thr Gly Ile Lys Val Val Asn Asn Ser Ile Asp Gly Leu Thr Leu
 145 150 155 160
 Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Ala Ser Asp Thr Thr Val
 165 170 175
 Thr Ile Thr Gln Asn Ser Ser Gln Lys Ile Thr Gly Val Gln Phe Asn
 180 185 190
 Arg Gly Asn Pro Lys Gly Asp Gly Asp Val Ser Gly Ala Leu Asp Trp
 195 200 205
 Ser Lys Asn Ile Tyr Gly Ala Ala Ala Ile Gly Ser Tyr Asp Ile Thr
 210 215 220
 Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Met Ser Asp Asn
 225 230 235 240
 Ala Phe Leu Tyr Ala Leu Asp Ala Ala Tyr Ser Thr Thr Ile Phe Asp
 245 250 255
 Gly Ile Asn Trp Ser Ile Glu Gly Ala Tyr Leu Gly Asn Ser Val Asp
 260 265 270
 Asn Lys Leu Lys Asp Arg Leu Gly Val Ala Asn Gly Asn Phe Phe Ala
 275 280 285
 Leu Arg Gly Thr Val Glu Val Asn Gly Trp Asp Ala Ser Leu Gly Gly
 290 295 300
 Leu Tyr Tyr Gly Lys Lys Asp Lys Val Thr Val Thr Thr Ile Glu Asp
 305 310 315 320
 Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr
 325 330 335
 Arg Gly Ser Asn Leu Asn Gly Asp Leu Gly Arg Asn Ile Phe Gly Tyr
 340 345 350
 Val Thr Gly Gly Tyr Thr Phe Asn Glu Ala Val Arg Val Gly Ala Asp
 355 360 365
 Phe Val Tyr Gly Gly Thr Lys Thr Asn Ile Ile Gly Gln Gly Gly Lys
 370 375 380
 Lys Leu Glu Ala Val Ala Arg Val Asp Tyr Lys Tyr Ser Pro Lys Leu
 385 390 395 400
 Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Val Asp Thr Asp Pro Glu
 405 410 415
 Ser Thr His His Asp Ala Val Arg Leu Gln Ala Leu Tyr Lys Phe
 420 425 430

<210> 41

<211> 431

<212> PRT

<213> Campylobacter jejuni

<400> 41

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Ser Ser Asn Pro Trp
 35 40 45

Ser Asn Ala Asn Phe Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys
 50 55 60

Tyr Arg Ala Gln Val Asn Phe Ser Gly Ala Ile Ser Asp Asn Phe Lys
 65 70 75 80

Ala Phe Val Gln Phe Asp Tyr Asn Ser Gln Asp Gly Gly Tyr Gly Thr
 85 90 95

Asp Ser Ile Ser Asn Thr Ser Asp Thr Leu Thr Val Arg Gln Leu Tyr
 100 105 110

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

Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Ile Asp Gly Leu Val
 130 135 140

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

Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Ala Ser Asp Thr Thr Val
 165 170 175

Thr Ile Thr Gln Asp Asn Asn Gln Lys Ile Thr Gly Val Gln Phe Asn
 180 185 190

Arg Gly Asn Pro Lys Gly Asp Ser Asp Val Ser Gly Ala Leu Asp Trp
 195 200 205

Ser Lys Asn Ile Tyr Gly Ala Ala Ala Ile Gly Ser Tyr Asp Ile Ala
 210 215 220

Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Met Ser Asp Asn
 225 230 235 240

Ala Phe Leu Tyr Ala Leu Asp Ala Ala Tyr Ser Thr Thr Ile Phe Asp
 245 250 255

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

Asn Lys Leu Lys Asp Arg Leu Asp Ala Ala Asn Gly Asn Phe Phe Ala
 275 280 285

Leu Arg Gly Thr Val Glu Val Asn Gly Trp Asp Ala Ser Leu Gly Gly
 290 295 300

Leu Tyr Tyr Gly Lys Lys Asp Lys Val Thr Leu Thr Thr Ile Glu Asp
 305 310 315 320

Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr
 325 330 335

Asn Gly Ser Asn Leu Asn Gly Asp Ile Gly Arg Asn Ile Phe Gly Tyr
 340 345 350

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

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

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

Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Val Asp Thr Asp Pro Glu
 405 410 415

Ser Thr His His Asp Ala Val Arg Leu Gln Ala Leu Tyr Lys Phe
 420 425 430

<210> 42

<211> 431

<212> PRT

<213> Campylobacter jejuni

<400> 42

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Ser Ser Asn Pro Trp
 35 40 45

Ser Asn Ala Asn Phe Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys
 50 55 60

Tyr Arg Ala Gln Val Asn Phe Ser Gly Ala Ile Ser Asp Asn Phe Lys
 65 70 75 80

Ala Phe Val Gln Phe Asp Tyr Asn Ser Gln Asp Gly Gly Tyr Gly Thr
 85 90 95

Asp Ser Ile Ser Asn Thr Ser Asp Thr Leu Thr Val Arg Gln Leu Tyr
 100 105 110

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

Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Ile Asp Gly Leu Val
 130 135 140

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

Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Ala Ser Asp Thr Thr Val
 165 170 175

Thr Ile Thr Gln Asp Asn Asn Gln Lys Ile Thr Gly Val Gln Phe Asn
 180 185 190

Arg Gly Asn Pro Lys Gly Asp Ser Asp Val Ser Gly Ala Leu Asp Trp
 195 200 205

Ser Lys Asn Ile Tyr Gly Ala Ala Ala Ile Gly Ser Tyr Asp Ile Ala
 210 215 220

Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Met Ser Asp Asn
 225 230 235 240

Ala Phe Leu Tyr Ala Leu Asp Ala Ala Tyr Ser Thr Thr Ile Phe Asp
 245 250 255

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

Asn Lys Leu Lys Asp Arg Leu Asp Ala Ala Asn Gly Asn Phe Phe Ala
 275 280 285

Leu Arg Gly Thr Val Glu Val Asn Gly Trp Asp Ala Ser Leu Gly Gly
 290 295 300

Leu Tyr Tyr Gly Lys Lys Asp Lys Val Thr Leu Thr Thr Ile Glu Asp
 305 310 315 320

Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr
 325 330 335

Asn Gly Ser Asn Leu Asn Gly Asp Ile Gly Arg Asn Ile Phe Gly Tyr
 340 345 350

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

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

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

Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Val Asp Thr Asp Pro Glu
 405 410 415

Ser Thr His His Asp Ala Val Arg Leu Gln Ala Leu Tyr Lys Phe
 420 425 430

<210> 43

<211> 431

<212> PRT

<213> Campylobacter jejuni

<400> 43

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Ser Ser Asn Pro Trp
 35 40 45

Ser Asn Ala Asn Phe Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys
 50 55 60

Tyr Arg Ala Gln Val Asn Phe Ser Gly Ala Ile Ser Asp Asn Phe Lys
 65 70 75 80

Ala Phe Val Gln Phe Asp Tyr Asn Ser Gln Asp Gly Gly Tyr Gly Thr
 85 90 95

Asp Ser Ile Ser Asn Thr Ser Asp Thr Leu Thr Val Arg Gln Leu Tyr
 100 105 110

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

Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu Val
 130 135 140

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

Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Ala Ser Asp Thr Thr Val
 165 170 175

Thr Ile Thr Gln Asp Asn Asn Gln Lys Ile Thr Gly Val Gln Phe Asn
 180 185 190

Arg Gly Asn Pro Lys Gly Asp Ser Asp Val Ser Gly Ala Leu Asp Trp
 195 200 205

Ser Lys Asn Ile Tyr Gly Ala Ala Ala Ile Gly Ser Tyr Asp Ile Ala
 210 215 220

Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Met Ser Asp Asn
 225 230 235 240

Ala Phe Leu Tyr Ala Leu Asp Ala Ala Tyr Ser Thr Thr Ile Phe Asn
245 250 255

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

Asn Lys Leu Lys Asp Arg Leu Asp Ala Ala Asn Gly Asn Phe Phe Ala
275 280 285

Leu Arg Gly Thr Val Glu Val Asn Gly Trp Asp Ala Ser Leu Gly Gly
290 295 300

Leu Tyr Tyr Gly Lys Lys Asp Lys Val Thr Leu Thr Thr Ile Glu Asp
305 310 315 320

Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr
325 330 335

Asn Gly Ser Asn Leu Asn Gly Asp Ile Gly Arg Asn Ile Phe Gly Tyr
340 345 350

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

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

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

Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Val Asp Thr Asp Pro Glu
405 410 415

Ser Thr His His Asp Ala Val Arg Leu Gln Ala Leu Tyr Lys Phe
420 425 430

<210> 44

<211> 431

<212> PRT

<213> Campylobacter jejuni

<400> 44

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

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

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Ser Ser Asn Pro Trp
35 40 45

Ser Asn Ala Asn Phe Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys
50 55 60

Tyr Arg Ala Gln Val Asn Phe Ser Gly Ala Ile Ser Asp Asn Phe Lys
65 70 75 80

Ala Phe Val Gln Phe Asp Tyr Asn Ser Gln Asp Gly Gly Tyr Gly Ala
 85 90 95

Asp Ser Ile Ser Asn Thr Ser Asp Thr Leu Thr Val Arg Gln Leu Tyr
 100 105 110

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

Gln Gln Leu Asn Phe Ile Trp Thr Asp Asn Ala Ile Asp Gly Leu Val
 130 135 140

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

Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Ala Ser Asp Thr Thr Val
 165 170 175

Thr Ile Thr Gln Asn Gly Ser Gln Lys Ile Thr Gly Val Gln Phe Asn
 180 185 190

Arg Gly Asn Pro Lys Gly Asp Gly Asp Ala Ser Gly Ala Leu Asp Trp
 195 200 205

Ser Lys Asn Ile Tyr Gly Ala Ala Ala Ile Gly Ser Tyr Asp Leu Ala
 210 215 220

Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Met Ser Asp Asn
 225 230 235 240

Ala Phe Leu Tyr Ala Leu Asp Ala Ala Tyr Ser Thr Thr Ile Phe Asp
 245 250 255

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

Asn Lys Leu Lys Asp Arg Leu Asn Val Ala Asn Gly Asn Phe Phe Ala
 275 280 285

Leu Arg Gly Thr Val Glu Val Asn Gly Trp Asp Ala Thr Leu Gly Gly
 290 295 300

Leu Tyr Tyr Gly Asp Lys Asp Asn Leu Thr Val Thr Thr Ile Glu Asp
 305 310 315 320

Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Glu Glu Ile Phe Tyr Thr
 325 330 335

Arg Gly Ser Asn Leu Asn Gly Asp Leu Gly Arg Asn Ile Phe Gly Tyr
 340 345 350

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

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

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

Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Val Asp Thr Asp Pro Glu
405 410 415

Ser Thr His His Asp Ala Val Arg Leu Gln Ala Leu Tyr Lys Phe
420 425 430

<210> 45

<211> 432

<212> PRT

<213> Campylobacter jejuni

<400> 45

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

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20 25 30

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Glu Ser Ser Asn Pro Trp
35 40 45

Ser Asn Gly Asn Tyr Gly Ser Gly Ile Ser Gly Lys Gln Asp His Lys
50 55 60

Tyr Arg Ala Gln Val Asn Phe Asn Thr Ala Ile Ala Asp Asn Phe Lys
65 70 75 80

Ala Phe Val Gln Phe Asp Tyr Asn Ser Lys Asp Gly Gly Tyr Gly Glu
85 90 95

Asn Ser Ile Ser Asn Thr Ser Asp Thr Leu Ser Val Arg Gln Leu Tyr
100 105 110

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

Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Gly Val Asp Gly Leu Val
130 135 140

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

Ala Ala Phe Ala Met Asp Ser Phe Asn Glu Ala Ser Asp Thr Thr Val
165 170 175

Ile Ile Thr Gln Asp Pro Ser Ser Asn Lys Ile Thr Gly Val Gln Phe
180 185 190

Asn Arg Gly Asn Pro Lys Gly Asp Gly Asp Val Ser Gly Ala Leu Asp
195 200 205

Trp Ser Lys Asn Ile Tyr Gly Ala Ala Ala Ile Gly Ser Tyr Asp Ile
210 215 220

Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp Leu Ala Tyr Met Ser Asp
225 230 235 240

Asn Ala Phe Leu Tyr Ala Leu Asp Ala Ala Tyr Asn Thr Thr Ile Phe
245 250 255

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

Asp Asn Lys Leu Lys Asp Arg Leu Asp Ala Ala Asn Gly Asn Phe Phe
275 280 285

Ala Leu Arg Gly Thr Val Glu Val Asn Gly Trp Asp Ala Ser Leu Gly
290 295 300

Gly Leu Tyr Tyr Gly Lys Lys Asp Lys Ala Thr Val Thr Thr Ile Glu
305 310 315 320

Asp Gln Gly Asn Leu Gly Ser Leu Leu Ala Gly Gln Glu Ile Phe Tyr
325 330 335

Thr Arg Gly Ser Asn Leu Asn Gly Asp Leu Gly Arg Asn Ile Phe Gly
340 345 350

Tyr Val Thr Ala Gly Tyr Thr Phe Asn Glu Ala Val Arg Val Gly Ala
355 360 365

Asp Phe Val Tyr Gly Gly Thr Lys Thr Gly Glu Ile Gly Asn Gly Gly
370 375 380

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

Leu Asn Phe Ser Ala Phe Tyr Ser Tyr Val Asn Val Asp Thr Asp Pro
405 410 415

Glu Ser Thr His His Asp Ala Val Arg Leu Gln Ala Leu Tyr Lys Phe
420 425 430

<210> 46

<211> 430

<212> PRT

<213> Campylobacter jejuni

<400> 46

Met Lys Leu Val Lys Leu Ser Leu Val Ala Ala Leu Ala Ala Gly Ala
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Phe Ser Ala Ala Asn Ala Thr Pro Leu Glu Glu Ala Ile Lys Asp Ile
20 25 30

Asp Val Ser Gly Val Leu Arg Tyr Arg Tyr Asp Thr Ser Asn Asp Trp
35 40 45

Asn Asn Ala Gly Phe Gly Ser Gly Ile Ser Gly Lys Gln Thr His Asn
50 55 60

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

Ala Phe Val Gln Phe Asp Tyr Ala Ala Val Asp Gly Gly Tyr Asn Val
85 90 95

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

Arg Gln Leu Tyr Leu Thr Tyr Thr Asn Glu Asp Val Ala Thr Ser Val
115 120 125

Ile Ala Gly Lys Gln Gln Leu Asn Thr Ile Trp Thr Asp Asn Asp Ile
130 135 140

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

Gly Leu Thr Leu Ala Ala Phe Ala Val Asp Ser Tyr Asn Thr Asp Glu
165 170 175

Gln Gly Tyr Lys Asp Asn Asn Gly Arg Pro Asp Leu Thr Tyr Thr Gly
180 185 190

Asp Ala Ser Gln Tyr Leu Thr Trp Gly Asn Ile Tyr Gly Ala Ala Ala
195 200 205

Val Gly Ser Tyr Asp Leu Ala Gly Gly Gln Phe Asn Pro Gln Leu Trp
210 215 220

Leu Ala Tyr Met Ser Asp Asn Ala Phe Leu Tyr Ala Leu Asp Leu Ala
225 230 235 240

Tyr Asn Thr Thr Ile Phe Asp Gly Ile Asn Trp Ser Ile Glu Gly Ala
245 250 255

Tyr Leu Gly Asn Ser Val Asp Asn Lys Leu Lys Asp Arg Phe His Ala
260 265 270

Ala Gly Asp Pro Glu Ser Ser Ala Ala Asn Gly Asn Phe Phe Ala Leu
275 280 285

Arg Gly Thr Val Glu Val Asn Gly Trp Asp Ala Ser Leu Gly Gly Leu
290 295 300

Tyr Tyr Gly Lys Lys Asp Lys Phe Thr Val Thr Thr Ile Glu Asp Gln
305 310 315 320

Gly	Asn	Leu	Gly	Ser	Leu	Leu	Ala	Gly	Glu	Ile	Phe	Tyr	Thr	His	
					325				330					335	
Gly	Ser	Arg	Leu	Asn	Gly	Asp	Ala	Gly	Arg	Asn	Ile	Phe	Gly	Tyr	Val
			340					345					350		
Thr	Gly	Gly	Tyr	Thr	Phe	Asn	Glu	Thr	Val	Arg	Val	Gly	Ala	Asp	Phe
		355					360					365			
Val	Tyr	Gly	Gly	Thr	Lys	Thr	Glu	Asn	Val	Gly	Glu	Gly	Gly	Lys	Lys
	370					375					380				
Leu	Glu	Ala	Val	Ala	Arg	Val	Asp	Tyr	Lys	Tyr	Ser	Pro	Lys	Leu	Asn
385					390					395					400
Phe	Ser	Ala	Phe	Tyr	Ser	Tyr	Val	Asn	Val	Asp	Arg	Asp	Pro	Glu	Ser
				405					410					415	
Thr	His	His	Asp	Ala	Val	Arg	Leu	Gln	Ala	Leu	Tyr	Lys	Phe		
			420					425					430		

REFERENCES CITED IN THE DESCRIPTION

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- **LEY RTURNBAUGH PKLEIN SGORDON J**Microbial ecology: human gut microbes

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Patentkrav**1.** Forbindelse til anvendelse i en fremgangsmåde valgt fra:

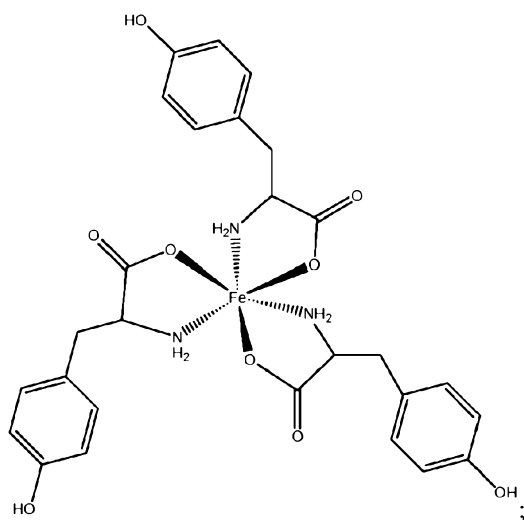
- 5 en fremgangsmåde til reducere af antallet af *Campylobacter* til stede i
gastrointestinalkanalen hos et dyr og derved desinficere dyret;
en fremgangsmåde til forebyggelse eller reducere af koloniseringen af
gastrointestinalkanalen hos et dyr med *Campylobacter*; eller
10 en fremgangsmåde til at forebygge *Campylobacter* i at danne en biofilm i
gastrointestinalkanalen hos et dyr, eller reducere mængden af biofilm
dannet af *Campylobacter* i gastrointestinalkanalen hos et dyr, og derved
desinficere dyret;

hvor forbindelsen til anvendelse eventuelt er i form af et dyrefoder,
dyredrikkevand, foderingrediens eller fodersupplement der omfatter forbindelsen,

15 og

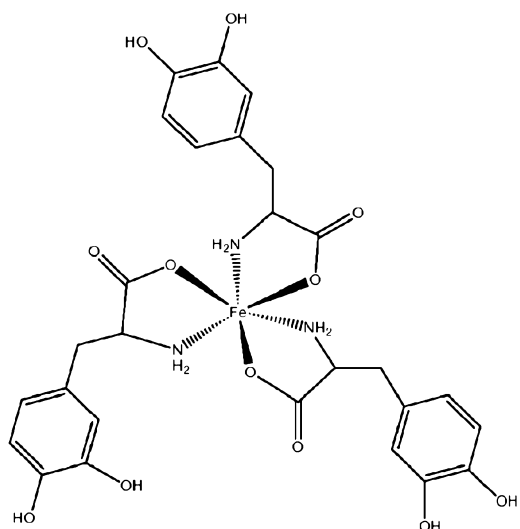
hvor forbindelsen er valgt fra gruppen bestående af:

- a) et kompleks af tyrosin med Fe III



- b) ferriquinat; og

c) et kompleks af 3,4 dihydroxyphenylalanin med Fe III



5 **2.** Anvendelse af en forbindelse ifølge krav 1,

hvor forbindelsen, i brug, eventuelt er i form af et dyrefoder, dyredrikkevand, foderingrediens eller fodersupplement der omfatter forbindelsen;

hvor anvendelsen er valgt fra en anvendelse:

- 10 til reducere af antallet af *Campylobacter* til stede i gastrointestinalkanalen hos et ikke-humant dyr og derved desinficere dyret, ved en fremgangsmåde omfattende at administrere mindst én forbindelse ifølge krav 1 i en effektiv mængde til dyret for at reducere antallet af *Campylobacter* til stede i gastrointestinalkanalen hos dyret, og så slagtning af dyret;
- 15 til forebyggelse eller reducere af koloniseringen af gastrointestinalkanalen hos et ikke-humant dyr af *Campylobacter*, ved en fremgangsmåde omfattende at administrere mindst én forbindelse ifølge krav 1 til dyret, og så slagtning af dyret; eller
- 20 til at forebygge *Campylobacter* i at danne en biofilm i gastrointestinalkanalen hos et ikke-humant dyr, eller reducere mængden af biofilm dannet af *Campylobacter* i gastrointestinalkanalen hos et ikke-humant dyr, og derved desinficere dyret, ved en fremgangsmåde omfattende at administrere mindst én forbindelse ifølge krav 1 i en effektiv mængde til dyret for at forhindre *Campylobacter* i at danne en biofilm i
- 25 dyrets gastrointestinalkanal eller til at reducere mængden af biofilm dannet

af *Campylobacter* i dyrets gastrointestinalkanal, og så slagtning af dyret.

3. Fremgangsmåde til reducere af antallet af *Campylobacter* til stede i gastrointestinalkanalen hos et ikke-humant dyr og derved desinficere dyret før

5 slagtning, hvilken fremgangsmåde omfatter:

- i) administrere mindst én forbindelse ifølge krav 1 i en effektiv mængde til dyret for at reducere antallet af *Campylobacter* til stede i gastrointestinalkanalen hos dyret, eventuelt hvor forbindelsen til anvendelse er i form af et dyrefoder, dyredrikkevand, foderingrediens eller fodersupplement der omfatter forbindelsen; og
- 10 ii) slagtning af dyret.

4. Fremgangsmåde til forebyggelse *Campylobacter* i at danne en biofilm i gastrointestinalkanalen hos et ikke-humant dyr, eller for at reducere mængden af

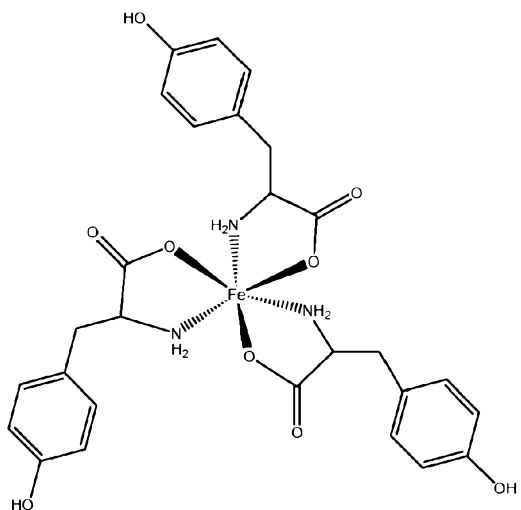
15 biofilm dannet af *Campylobacter* i dyrets gastrointestinalkanal, og derved desinficere dyret før slagtning, hvilken fremgangsmåde omfatter:

- i) administrere mindst én forbindelse ifølge krav 1 i en effektiv mængde til dyret for at forhindre *Campylobacter* i at danne en biofilm i dyrets gastrointestinalkanal eller til at reducere mængden af biofilm dannet af
- 20 *Campylobacter* i dyrets gastrointestinalkanal, eventuelt hvor forbindelsen til anvendelse er i form af et dyrefoder, dyredrikkevand, foderingrediens eller fodersupplement der omfatter forbindelsen; og
- ii) slagtning af dyret.

25 **5.** Forbindelse ifølge krav 1 til anvendelse i en fremgangsmåde til forebyggelse eller reducere af overførsel af *Campylobacter*-infektion fra et dyr til et andet, hvor forbindelsen til anvendelse eventuelt er i form af et dyrefoder, dyredrikkevand, foderbestanddel eller fodersupplement der omfatter forbindelsen; og

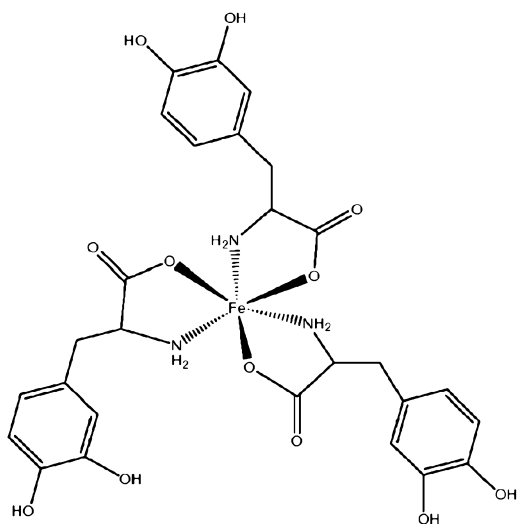
30 hvor fremgangsmåden omfatter at administrere forbindelsen til dyrene i en effektiv mængde for at forhindre *Campylobacter* i at danne en biofilm i dyrets gastrointestinalkanal eller til at reducere mængden af biofilm dannet af *Campylobacter* i dyrets gastrointestinalkanal.

- 6.** Anvendelse af en forbindelse ifølge krav 1 til forebyggelsen eller reduktion af overførsel af *Campylobacter*-infektion fra et ikke-humant dyr til et andet, hvor forbindelsen, i brug, eventuelt er i form af et dyrefoder, dyredrikkevand, foderingrediens eller fodersupplement der omfatter forbindelsen;
- 5 ved en fremgangsmåde omfattende administrationen af forbindelsen til dyrene i en effektiv mængde for at forhindre *Campylobacter* i at danne en biofilm i dyrets gastrointestinalkanal eller til at reducere mængden af biofilm dannet af *Campylobacter* i dyrets gastrointestinalkanal, og derefter slagtning af dyret.
- 10 **7.** Fremgangsmåde til forebyggelse eller reduktion af transmissionen af *Campylobacter*-infektion fra et ikke-humant dyr til et andet før slagtning, hvilken fremgangsmåde omfatter at:
- i) administrere mindst én forbindelse ifølge krav 1 til dyrene i en effektiv mængde for at forhindre *Campylobacter* i at danne en biofilm i dyrets
- 15 gastrointestinalkanal eller til at reducere mængden af biofilm dannet af *Campylobacter* i dyrets gastrointestinalkanal, eventuelt hvor forbindelsen til anvendelse er i form af et dyrefoder, dyredrikkevand, foderingrediens eller fodersupplement der omfatter forbindelsen; og
- ii) slagtning af dyret.
- 20 **8.** Forbindelse til anvendelse ifølge krav 5, anvendelsen ifølge krav 6, eller en fremgangsmåde ifølge krav 7, til forebyggelse eller reduktion af spredning af *Campylobacter*-infektion indenfor en flok eller besætning af dyr, fx til forebyggelse af spredning af *Campylobacter*-infektion indenfor en flok af kyllinger.
- 25 **9.** Forbindelsen til anvendelse ifølge krav 1, 5 eller 8, anvendelsen ifølge kravene 2, 6 eller 8, eller fremgangsmåden ifølge krav 3, 4, 7 eller 8 hvor *Campylobacteren* er *Campylobacter jejuni* eller *Campylobacter coli*.
- 30 **10.** Forbindelsen til anvendelse ifølge krav 1, 5, 8 eller 9, anvendelsen ifølge kravene 2, 6, 8 eller 9, eller fremgangsmåden ifølge krav 3, 4, 7, 8 eller 9, hvor forbindelsen er et kompleks af tyrosin med Fe III



11. Forbindelsen til anvendelse ifølge krav 1, 5, 8 eller 9, anvendelsen ifølge kravene 2, 6, 8 eller 9, eller fremgangsmåden ifølge krav 3, 4, 7, 8 eller 9, hvor forbindelsen er ferriquinat.

12. Forbindelsen til anvendelse ifølge krav 1, 5, 8 eller 9, anvendelsen ifølge kravene 2, 6, 8 eller 9, eller fremgangsmåden ifølge krav 3, 4, 7, 8 eller 9, hvor forbindelsen er et kompleks af 3,4 dihydroxyphenylalanin med Fe III



13. Forbindelsen til anvendelse ifølge krav 1, 5, 8 eller 9 til 12, anvendelsen ifølge kravene 2, 6, 8 eller 9 til 12, eller fremgangsmåden ifølge krav 3, 4, 7, 8 eller 9 til

12, hvor forbindelsen administreres oralt.

14. Forbindelsen til anvendelse ifølge krav 1, 5, 8 eller 9 til 13, anvendelsen ifølge kravene 2, 6, 8 eller 9 til 13, eller fremgangsmåden ifølge krav 3, 4, 7, 8 eller 9 til 5 13, hvor forbindelsen administreres til dyret i dyrets foder eller drikkevand.

15. Forbindelsen til anvendelse ifølge krav 1, 5, 8 eller 9 til 14, anvendelsen ifølge kravene 2, 6, 8 eller 9 til 14, eller fremgangsmåden ifølge krav 3, 4, 7, 8 eller 9 til 14, hvor dyret er et ikke-humant dyr og hvor forbindelsen administreres dagligt 10 mellem 1 og 10 dage, eller mellem 3 og 5 dage før slagtning af dyret.

16. Forbindelsen til anvendelse ifølge krav 1, 5, 8 eller 9 til 14, anvendelsen ifølge kravene 2, 6, 8 eller 9 til 14, eller fremgangsmåden ifølge krav 3, 4, 7, 8 eller 9 til 14, hvor forbindelsen administreres til en kylling mere end 10 dage før slagtning 15 for at forebygge overførsel af *Campylobacter* indenfor en kyllingebesætning.

17. Forbindelsen til anvendelse ifølge krav 1, 5, 8 eller 9 til 16, anvendelsen ifølge kravene 2, 6, 8 eller 9 til 16, eller fremgangsmåden ifølge krav 3, 4, 7, 8 eller 9 til 16, hvor forbindelsen administreres i en mængde på 0,3-32 mg/dag/kg 20 legemsvægt af dyret.

18. Anvendelse af en forbindelse ifølge et hvilket som helst af kravene 1, 10, 11 eller 12 for at reducere mængden af *Campylobacter* i kød ved en fremgangsmåde omfattende trinnene at:

25 (i) forsyne et ikke-humant dyr, eller en flok eller besætning af ikke-humane dyr, med en forbindelse ifølge et hvilket som helst af kravene 1, 10, 11 eller 12; og

(ii) fremstille et kødprodukt fra dyret; og

eventuelt, hvor forbindelsen, i brug, er i form af et dyrefoder, 30 dyredrikkevand, foderingrediens eller fodersupplement der omfatter forbindelsen.

19. Fremgangsmåde til reducere mængden af *Campylobacter* i kød omfattende trinnene at:

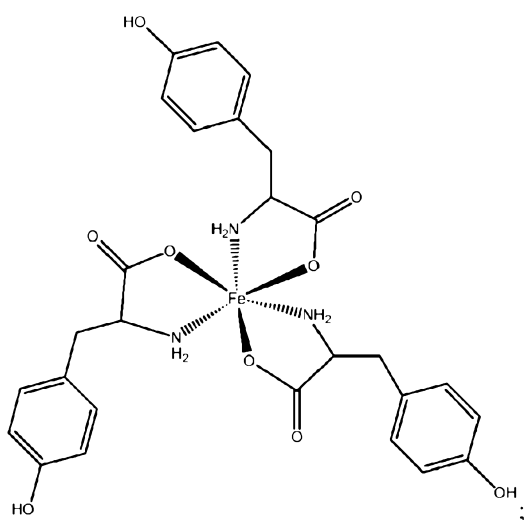
- (i) forsyne et ikke-humant dyr, eller en flok eller besætning af ikke-humane dyr, med en forbindelse ifølge et hvilket som helst af kravene 1, 10, 11 eller 12, eventuelt hvor forbindelsen til anvendelse er i form af et dyrefoder, dyredrikkevand, foderingrediens eller fodersupplement der omfatter forbindelsen; og
- (ii) fremstille et kødprodukt fra dyret.

20. Forbindelsen til anvendelse ifølge krav 1, 5, 8 eller 9 til 17, anvendelsen ifølge kravene 2, 6, 8 eller 9 til 17, eller fremgangsmåden ifølge krav 3, 4, 7, 8 eller 9 til 17, anvendelsen ifølge krav 18, eller fremgangsmåden ifølge krav 19, hvor dyret er valgt fra kvæg, får, grise, geder, hjorte, fisk, skaldyr og fjerkræ.

21. Forbindelsen til anvendelse, anvendelsen, eller fremgangsmåden, ifølge krav 20, hvor dyret er en fjerkræfugl, såsom en kylling, gås, kalkun eller and, og fortrinsvis en kylling.

22. Forbindelsen til anvendelse, anvendelsen, eller fremgangsmåden, ifølge krav 20 eller 21, hvor dyret er i en flok eller besætning.

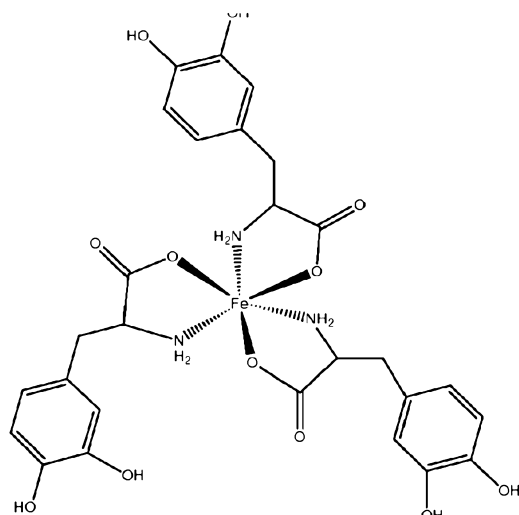
23. Dyrefoder, omfattende en forbindelse som en foderingrediens eller som en fodersupplement, hvor dyrefoderet er et foder tiltænkt til eller egnet til fortæring af dyr, og forbindelsen er:
et kompleks af tyrosin med Fe III



og hvor dyrefoderet omfatter forbindelsen i en mængde der er effektiv til at reducere

eller forebygge kolonisering af gastrointestinalkanalen hos et dyr med *Campylobacter*.

- 24.** Oral sammensætning, dyrefoder eller dyredrikkevand, omfattende en
5 forbindelse der er et kompleks af 3,4 dihydroxyphenylalanin med Fe III



hvor den orale sammensætning, dyrefoder, eller dyredrikkevand omfatter
forbindelsen i en mængde der er effektiv til at reducere eller forebygge
kolonisering af gastrointestinalkanalen hos et dyr med *Campylobacter*.

10

- 25.** Dyrefoder ifølge krav 23, eller en oral sammensætning, dyrefoder eller
dyredrikkevand ifølge krav 24, der er til et dyr valgt fra kvæg, får, grise, geder,
hjorte, fisk, skaldyr og fjerkræ.
- 26.** Dyrefoder ifølge krav 23, eller en oral sammensætning, dyrefoder eller
dyredrikkevand ifølge krav 24, der er til en fjerkræfugl, såsom en kylling, gås,
kalkun eller and, og fortrinsvis en kylling.
- 27.** Anvendelse af en forbindelse, ifølge krav 23 eller 24, som en fodersupplement
20 eller foderingsrediens i fremstillingen af et dyrefoder, eller som et additiv i
fremstillingen af dyredrikkevand.
- 28.** Fremgangsmåde til fremstilling af et dyrefoder eller dyredrikkevand, hvor
fremgangsmåden omfatter anvendelsen af en forbindelse, ifølge krav 23 eller krav
25 24, som en fodersupplement eller foderingsrediens i fremstillingen af dyrefoderet,

eller som et additiv i fremstillingen af dyredrikkevand.

29. Fremgangsmåde til desinficering af et levnedsmiddel omfattende administration af en forbindelse ifølge et hvilket som helst af kravene 1, 10, 11 eller 12 i en effektiv mængde til levnedsmidlet for at reducere mængden af *Campylobacter* i levnedsmidlet.

30. Anvendelse af en forbindelse ifølge et hvilket som helst af kravene 1, 10, 11 eller 12 til desinficering af et levnedsmiddel, ved at administrere i en effektiv mængde af forbindelsen til levnedsmidlet for at reducere mængden af *Campylobacter* i levnedsmidlet.

31. Fremgangsmåden ifølge krav 29, eller anvendelsen ifølge krav 30, hvor levnedsmidlet er en fødevare til human konsumtion.

15

32. Fremgangsmåden ifølge krav 29 eller 31, eller anvendelsen ifølge krav 30 eller 31, hvor levnedsmidlet er et kødprodukt, fx et friskt kødprodukt, et forarbejdet kødprodukt, et afkølet kødprodukt, et frosset kødprodukt eller et kogt kødprodukt.

20

33. Fremgangsmåden eller anvendelse ifølge krav 32, hvor kødproduktet er valgt fra okse-, lam-, gris-, and-, kylling-, gås-, kalkun-, kanin-, fisk- eller skaldyr-kødprodukt.

34. Forbindelse ifølge et hvilket som helst af kravene 1, 10, 11 eller 12 til anvendelse i profylaksen eller behandling af *Campylobacter*-infektion hos mennesker.

25

DRAWINGS

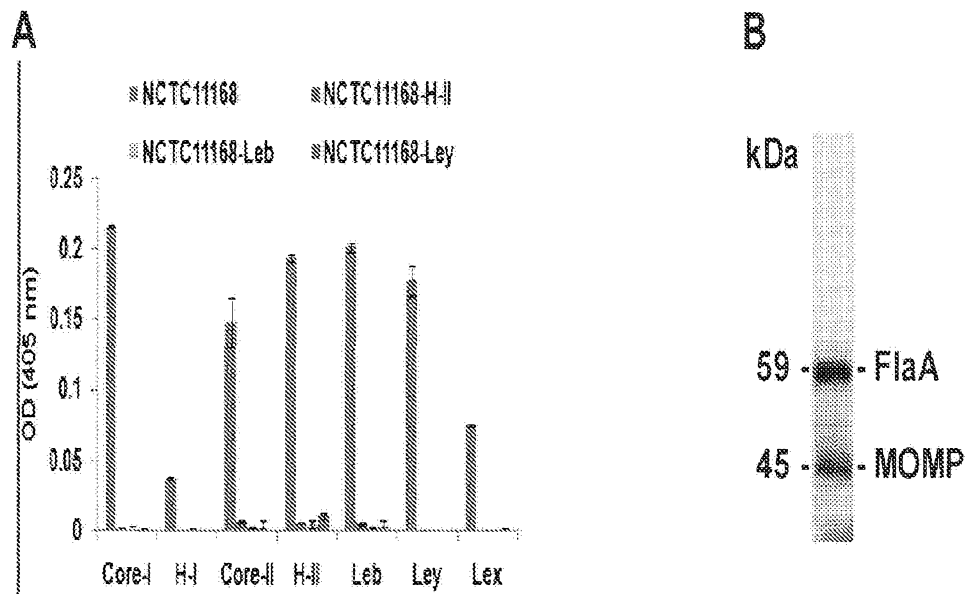


Fig. 1

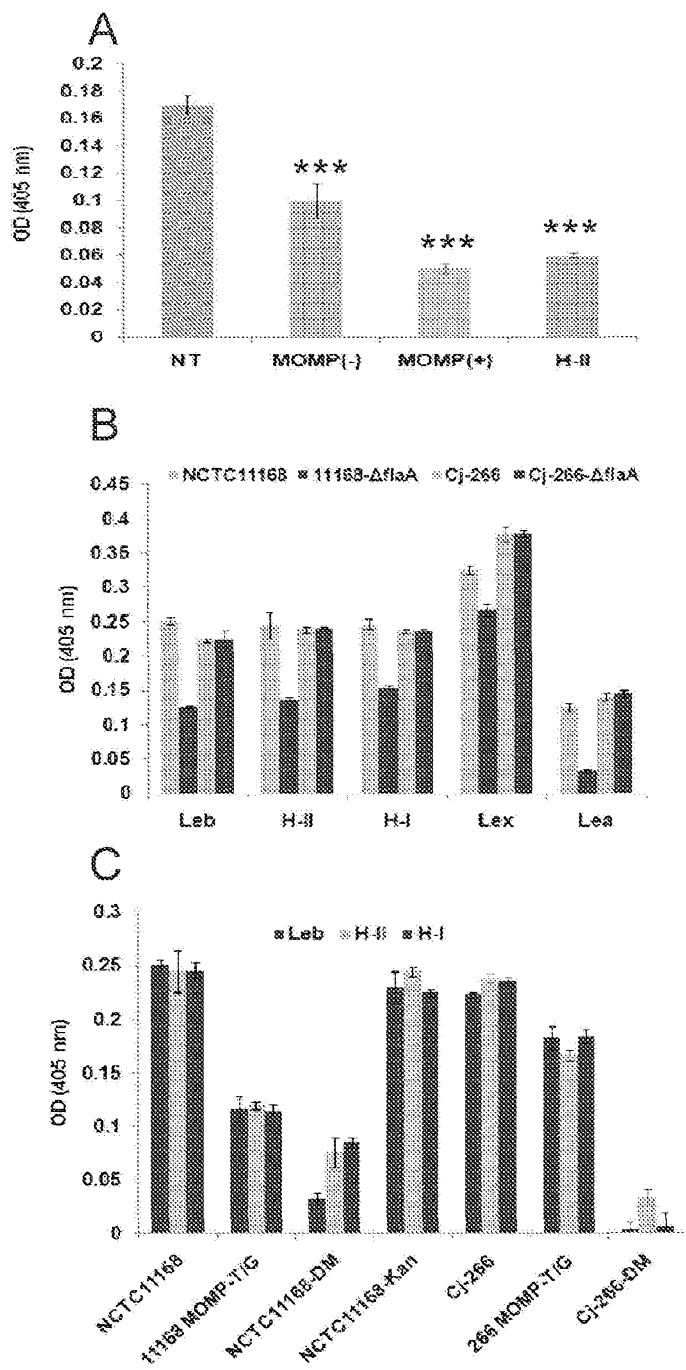


Fig. 2

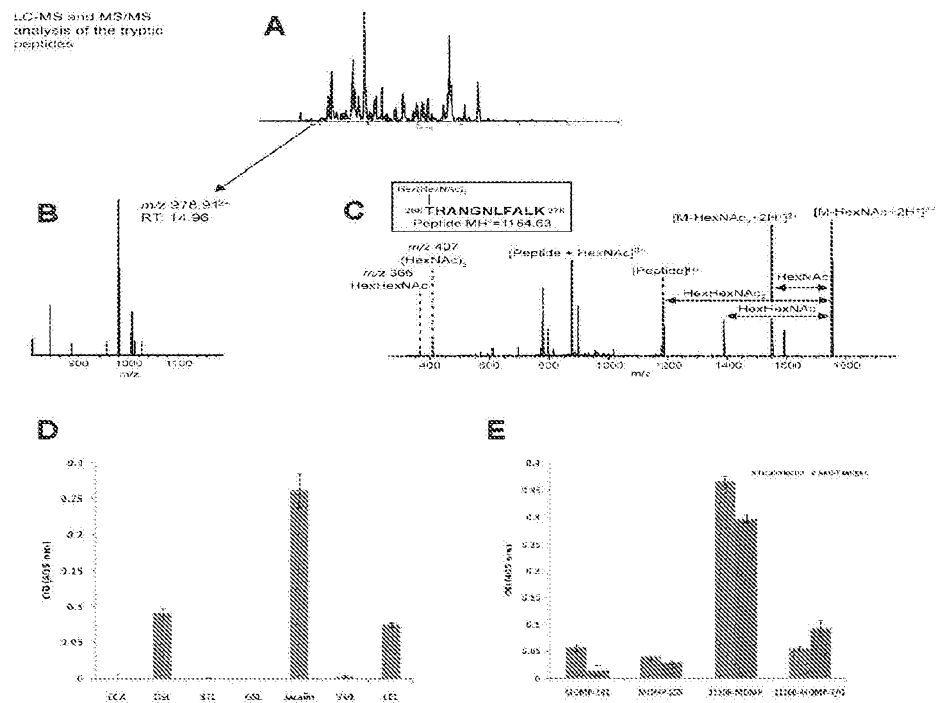
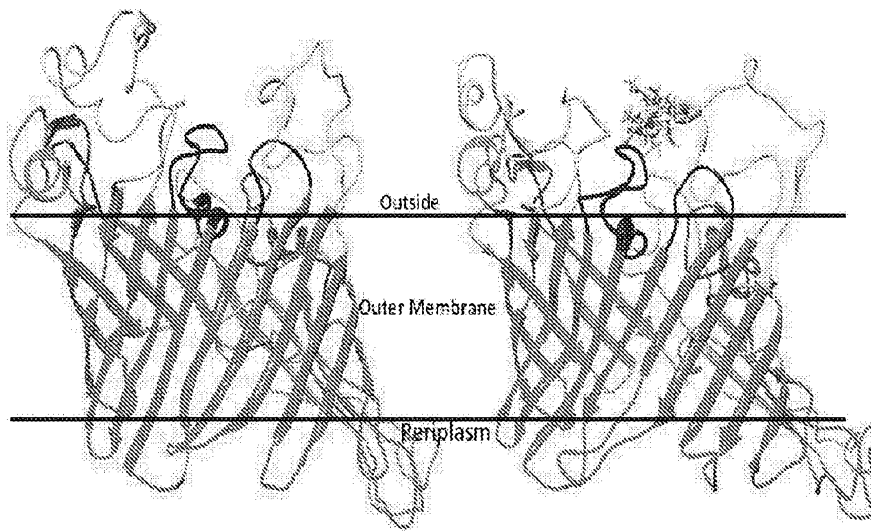
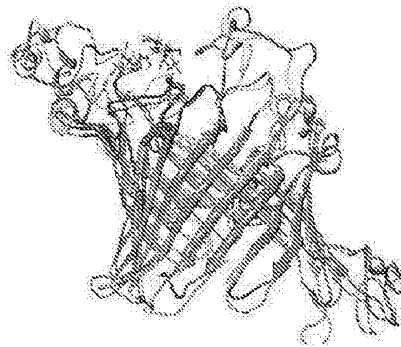


Fig. 3

A**B****Fig. 4**

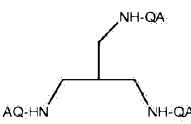
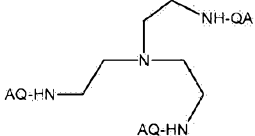
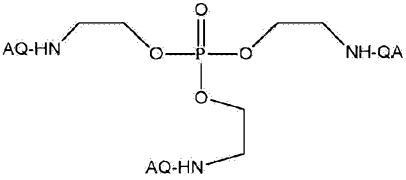
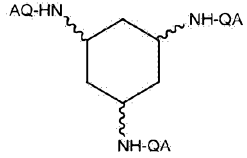
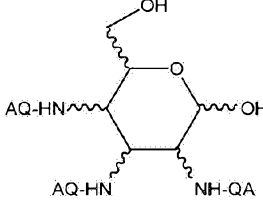
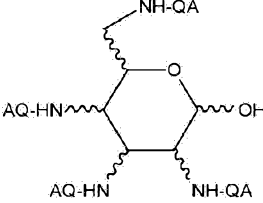
a		N-[3-quinylamino-2-(quinylamino-methyl)-propyl]-quinamide	GATRIQ
b		N-{2-[Bis-(2-quinylamino-ethyl)-amino]-ethyl}-quinamide	ETDAQ
c		Phosphoric acid tris-(2-quinylamino-ethyl) ester	PATQ
d		N-(3,5-Bis-quinylamino-cyclohexyl)-quinamide	CH135TQ
e		N-(4,5-Bis-quinylamino-2-hydroxy-6-hydroxymethyl-tetrahydro-pyran-3-yl)-quinamide	PY234TQ
f		N-(4,5-Bis-quinylamino-2-hydroxy-6-quinylaminomethyl-tetrahydro-pyran-3-yl)-quinamide	PY2346TE TQ

Fig. 6

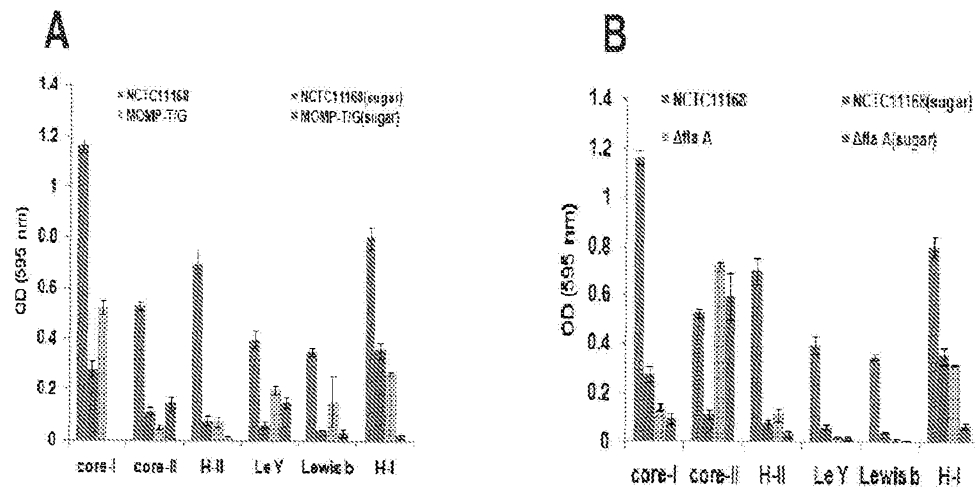


Fig. 7

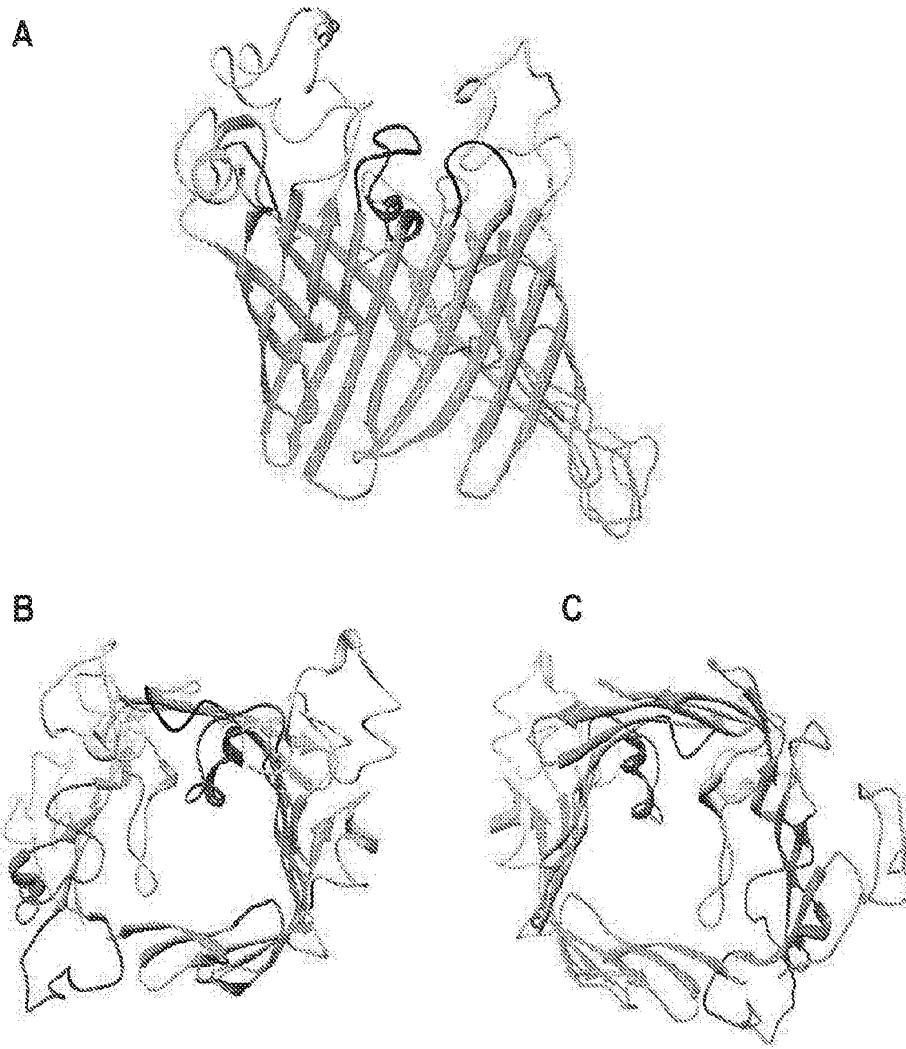
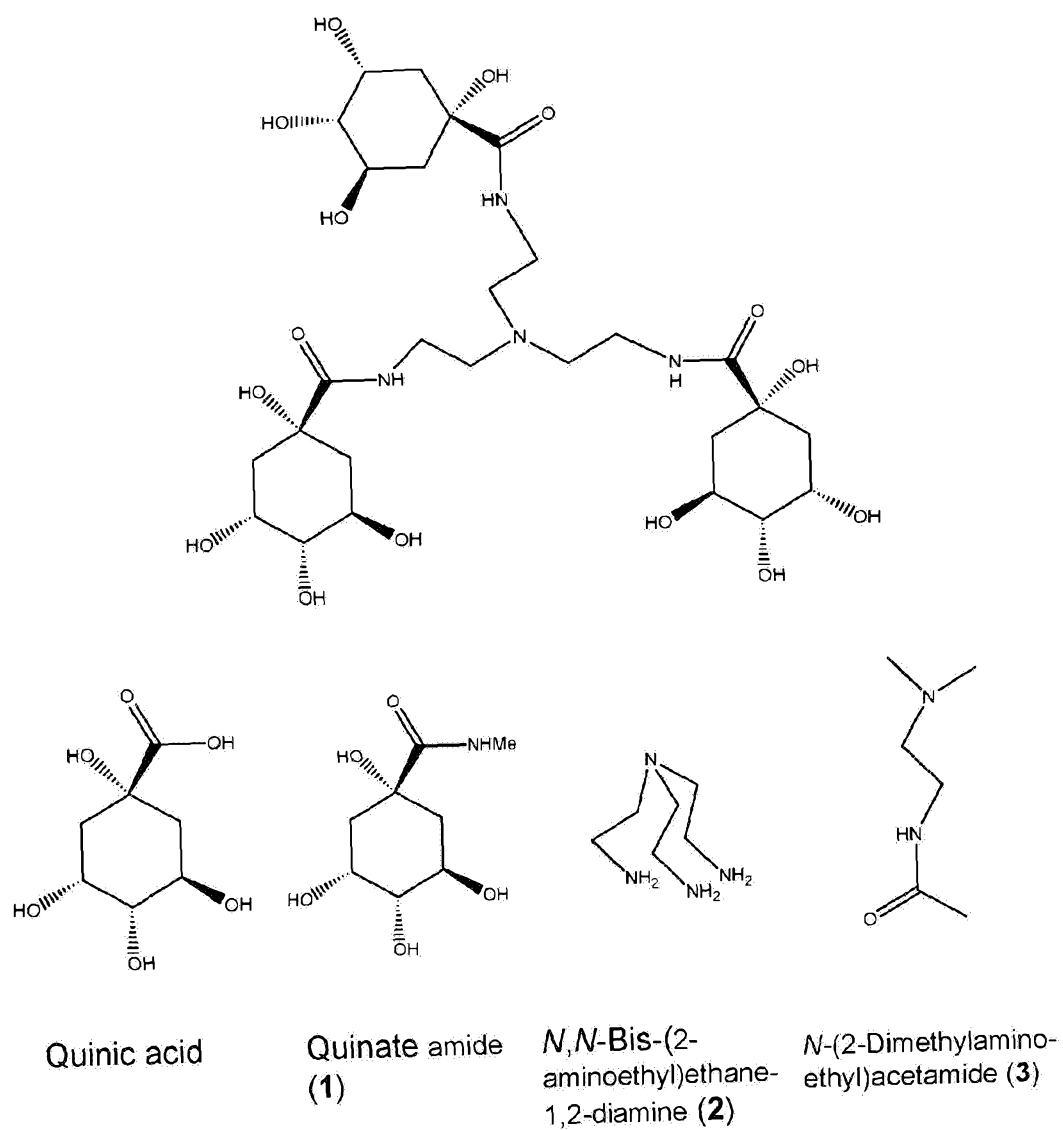
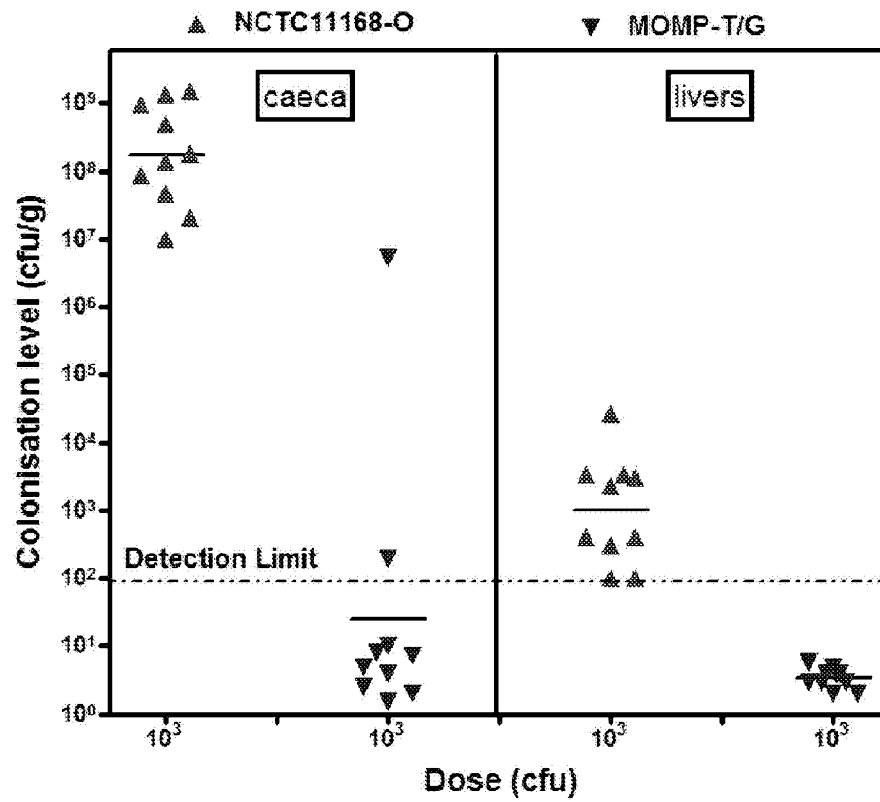
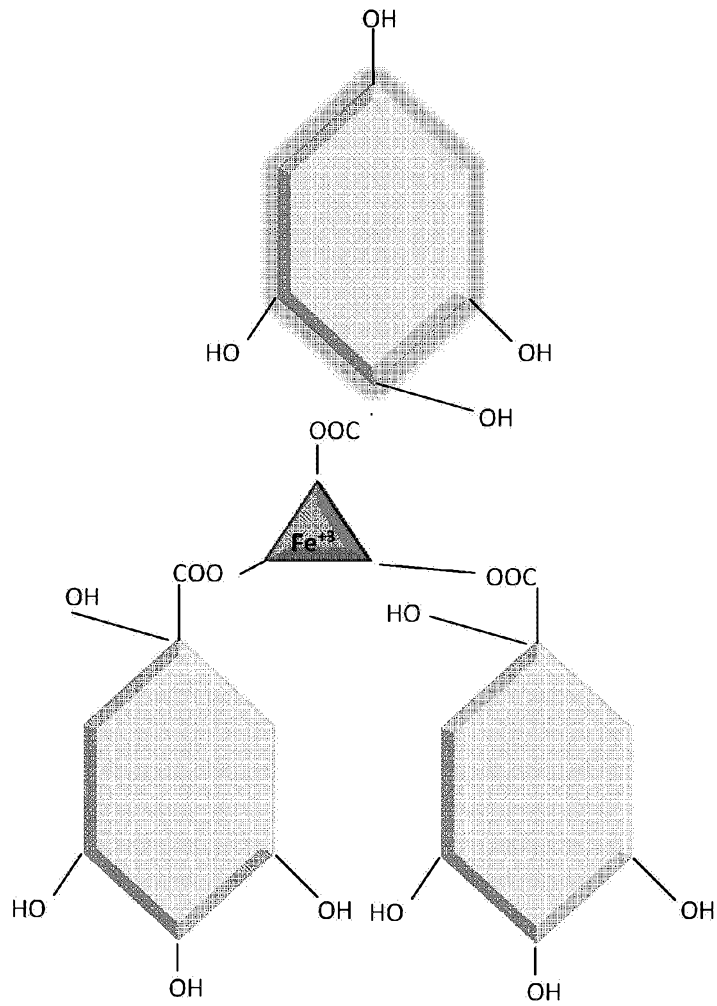


Fig. 8

**Fig. 9**

*Fig. 10*

**Fig. 11**

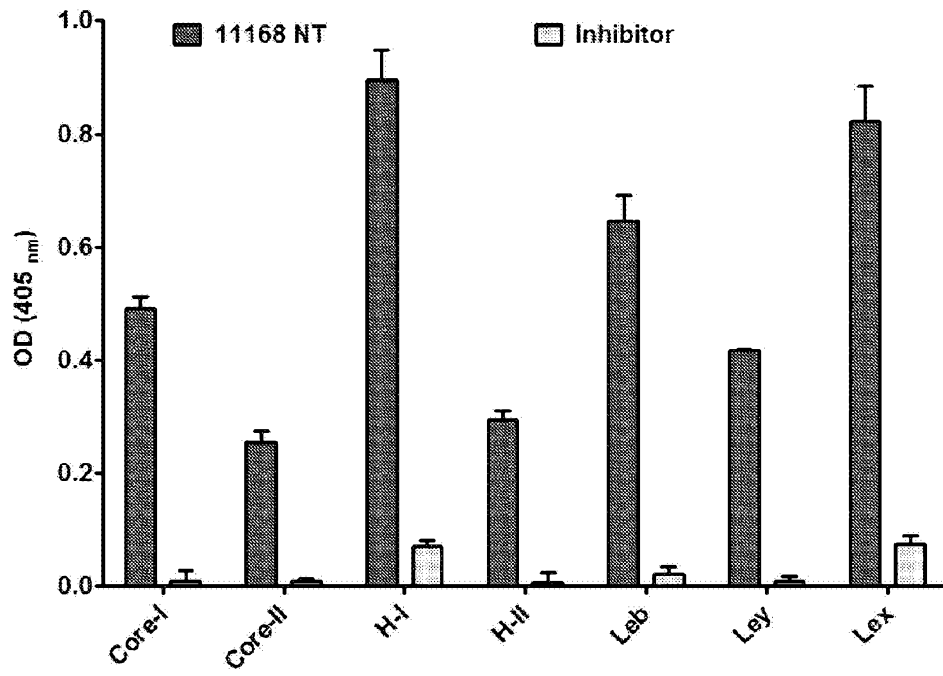
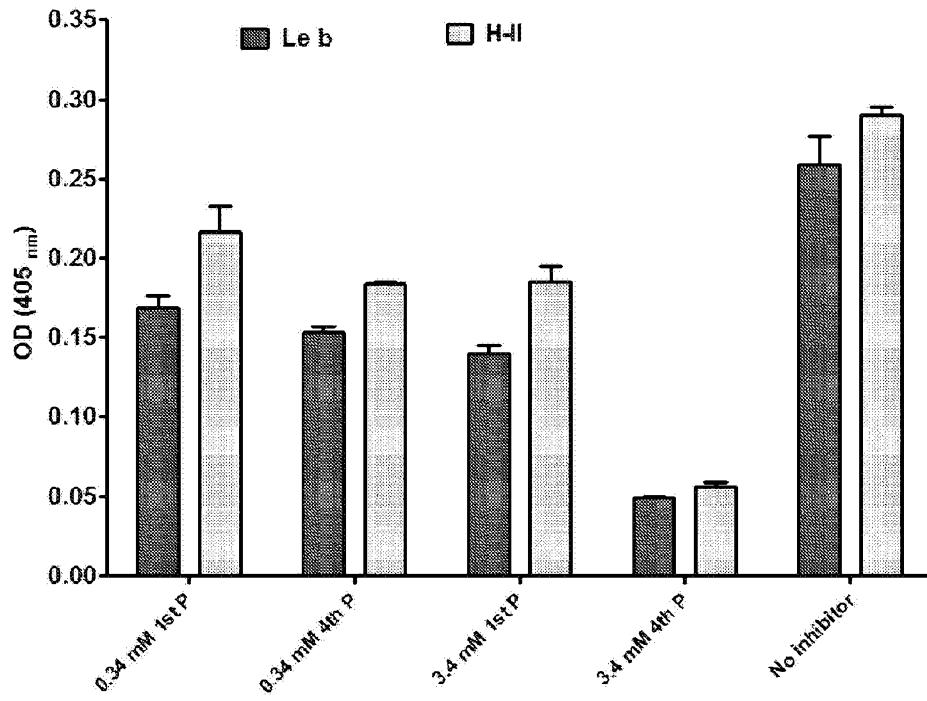
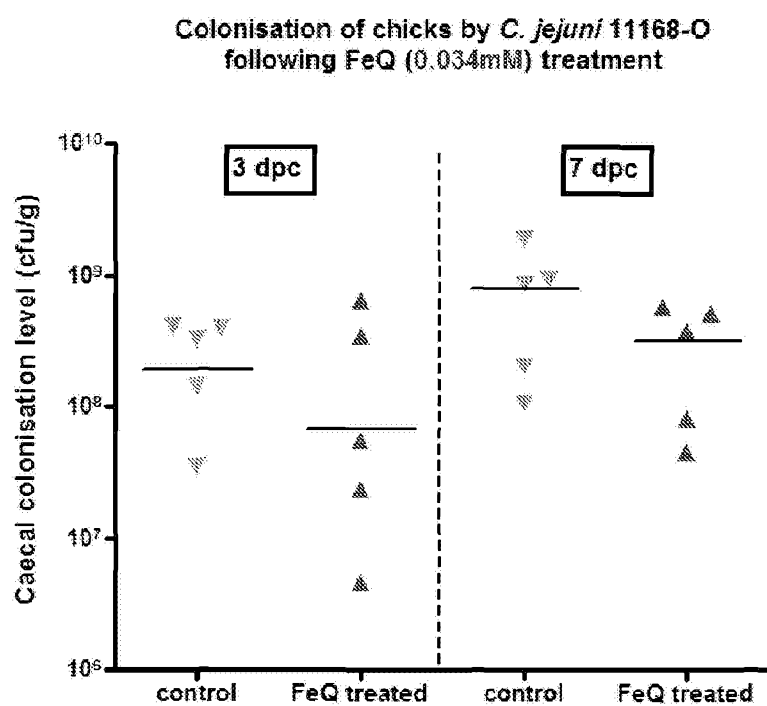
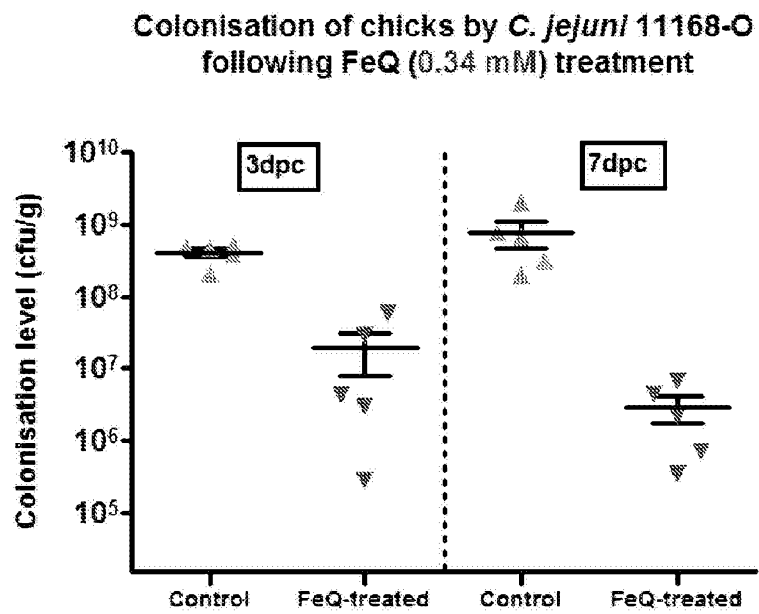


Fig. 12

*Fig. 13*

**Fig. 14**

**Fig. 15**

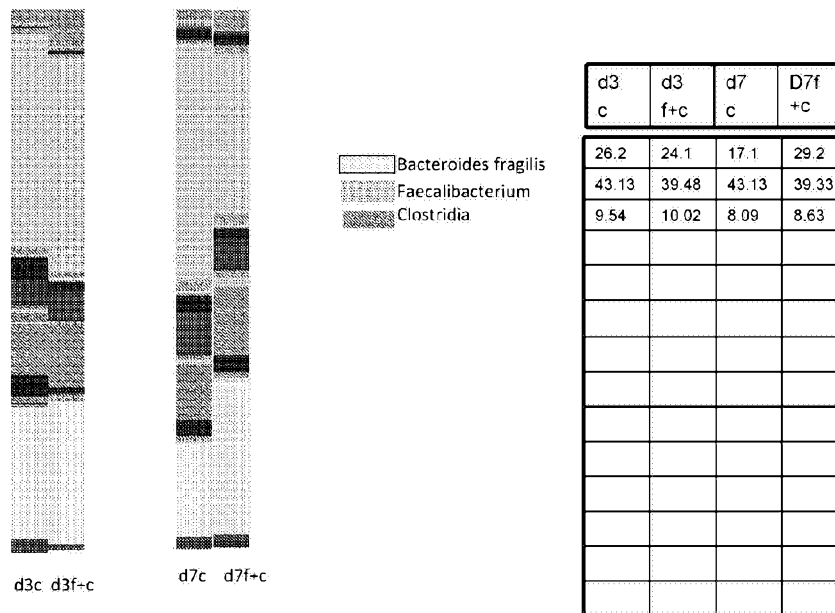
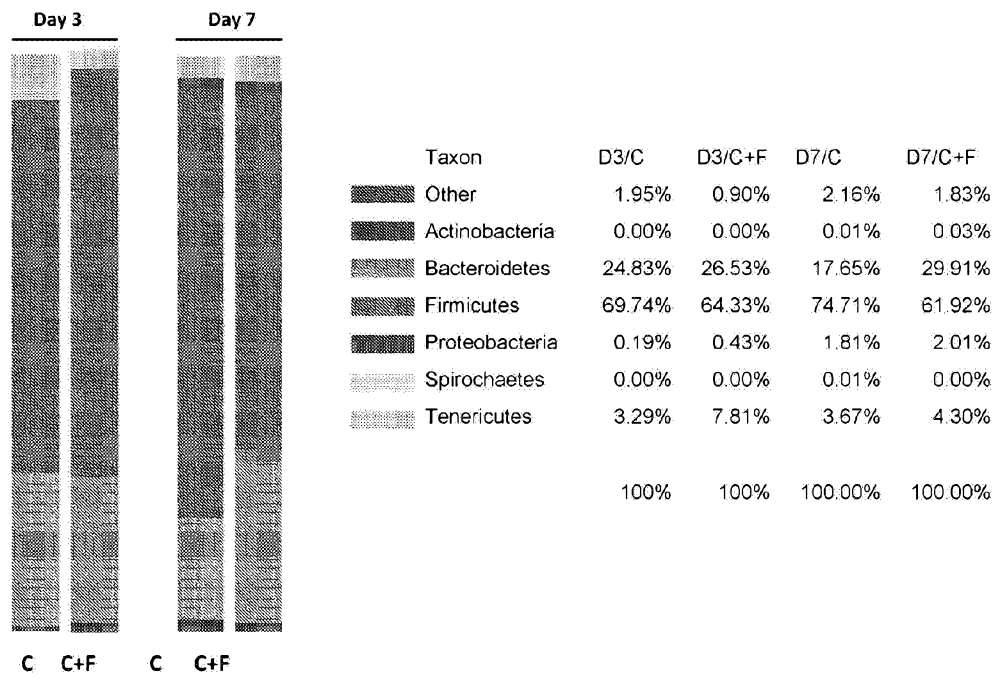


Fig. 16

**Fig. 17**